METHODS AND MATERIALS FOR ASSESSING AND TREATING CANCER

STATEMENT REGARDING FEDERAL FUNDING

[1] This invention was made with U.S. government support under Grant Nos. CA062924 and HG007804 from the National Institutes of Health. The U.S. government has certain rights in the invention.

SEQUENCE LISTING

[2] The instant application includes a Sequence Listing in electronic format submitted to the United States Patent and Trademark Office via the electronic filing system, and is hereby incorporated by reference in its entirety. Said sequence listing, created on August 6, 2018, is named 448070306WO1SL.txt and is 208,305 bytes in size.

ELECTRONICALLY-FILED TABLES

[3] The instant application includes tables in electronic format submitted to the United States Patent and Trademark Office via the electronic filing system. The ASCII text files, each of which is incorporated herein by reference in its entirety, include a text file named Table1.txt, created on August 7, 2018, having a size of 152,000 bytes; a text file named Table2.txt, created on August 7, 2018, having a size of 351,000 bytes; a text file named Table3.txt, created on August 7, 2018, having a size of 438,000 bytes; a text file named Table4.txt, created on August 7, 2018, having a size of 1,081,000 bytes; a text file named Table5.txt, created on August 7, 2018, having a size of 31,000 bytes; a text file named Table6.txt, created on August 7, 2018, having a size of 103,000 bytes; a text file named Table7.txt, created on August 7, 2018, having a size of 25,000 bytes; a text file named Table8.txt, created on August 7, 2018, having a size of 59,000 bytes; a text file named Table9.txt, created on August 7, 2018, having a size of 38,000 bytes; a text file named Table10.txt, created on August 7, 2018, having a size of 22,000 bytes; a text file named Table11.txt, created on August 7, 2018, having a size of 17,000 bytes; a text file named Table12.txt, created on August 7, 2018, having a size of 14,000 bytes; a text file named Table13.txt, created on August 7, 2018, having a size of 104,000 bytes; a text file named

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BACKGROUND

1. Technical Field

[4] Provided herein are methods and materials for detecting and/or treating subject (e.g., humans) having cancer. In some embodiments, methods and materials for identifying a subject as having cancer (e.g., a localized cancer) are provided in which the presence of two or more members of two or more classes of biomarkers are detected. In some embodiments, methods and materials for identifying a subject as having cancer (e.g., a localized cancer) are provided in which the presence of two or more members of at least one class of biomarkers and the presence of aneuploidy are detected. In some embodiments, methods described herein provide increased sensitivity and/or specificity of detecting cancer in a subject (e.g. a human).

2. Background Information

[5] Cancers will kill 592,000 Americans this year and according to the Center for Disease Control, cancers will soon be the leading cause of death in this country. How can this dire situation be averted? The vast majority of translational cancer research today is focused on prolonging survival in patients with advanced disease. Our research perspective is different: in the long term, prevention is always better than cure. Examples of the value of this perspective are abundant, ranging from infectious to cardiovascular diseases. Cardiovascular diseases are particularly relevant because the combination of primary and secondary prevention measures for this disease have reduced deaths by 75% in the last 60 years. In contrast, overall cancer deaths have barely changed over the same time period.

[6] Earlier detection through the application of blood tests for cancer can be viewed as a form of secondary prevention. The last three letters of the word "earlier" are particularly important. For all cancers that have been studied, the probability for cure is much higher with early, localized disease than for advanced disease. The earlier the stage, the more likely the tumor can be cured by surgery alone. Moreover, cancers do not have to be detected when they are at their initial stages to be cured. Theoretically, the responses to therapy are dictated by the total number of cancer cells prior to therapy and the rates of mutation in human cells. The more cancer cells, the more likely that at least one of them will contain or develop a mutation(s) that confers resistance to any form of therapy, be it conventional chemotherapy, radiotherapy, targeted therapy, or immunotherapy. Clinically, a large number of studies have shown that drugs can be curative in the adjuvant setting but not in patients with advanced disease. For example, nearly half of the patients with Stage III colorectal cancer who would die from their disease can be cured by adjuvant therapy, but virtually no patients with Stage IV colorectal cancers can be cured with the same regimens.

[7] There is a strong correlation between tumor stage and prognosis in many cancers (Ansari D, et al. (2017) Relationship between tumour size and outcome in pancreatic ductal adenocarcinoma. Br J Surg 104(5):600-607). Very few patients with cancers of the lung, colon, esophagus, or stomach who have distant metastasis at the time of diagnosis survive for more than five years (Howlader N, et al. (2016) SEER Cancer Statistics Review, 1975-2013,

National Cancer Institute. Bethesda, MD, http://seer.cancer.gov/csr/1975_2013/, based on November 2015 SEER data submission, posted to the SEER web site, April 2016). The size of cancers is also important in a general sense, in that smaller tumors have less often metastasized than larger tumors at the time of diagnosis, and are therefore are more likely to be curable by surgery alone. Even when cancers have metastasized to distant sites, a smaller burden of disease is much more easily managed than bulky lesions (Bozic I, et al. (2013) Evolutionary dynamics of cancer in response to targeted combination therapy. Elife 2:e00747). Thus, adjuvant chemotherapeutic agents administered to patients with micro-metastases stemming from a colorectal cancer can be curative in nearly 50% of cases (Semrad TJ, Fahrni AR, Gong IY, & Khatri VP (2015) Integrating Chemotherapy into the Management of Oligometastatic Colorectal Cancer: Evidence-Based Approach Using Clinical Trial Findings. Ann Surg Oncol 22 Suppl 3:S855-862; Moertel CG, et al. (1995) Fluorouracil plus levamisole as effective adjuvant therapy after resection of stage III colon carcinoma: a final report. Ann Intern Med 122(5):321-326; Andre T, et al. (2009) Improved overall survival with oxaliplatin, fluorouracil, and leucovorin as adjuvant treatment in stage II or III colon cancer in the MOSAIC trial. J Clin Oncol 27(19):3109-3116). The same chemotherapeutic agents delivered to patients with metastatic lesions that are radiologically visible produce virtually no cures (Dy GK, et al. (2009) Long-term survivors of metastatic colorectal cancer treated with systemic chemotherapy alone: a North Central Cancer Treatment Group review of 3811 patients, N0144. Clin Colorectal Cancer 8(2):88-93).

[8] It is therefore evident that the earlier detection of cancers is one key to reducing deaths from these diseases, including pancreatic cancer. In addition to offering the possibility of surgical resection, newly developed adjuvant chemotherapeutic and emerging immunotherapy regimens will undoubtedly prove more efficacious in patients with minimal disease beyond that which is curable surgically (Huang AC, et al. (2017) T-cell invigoration to tumour burden ratio associated with anti-PD-1 response. Nature 545(7652):60-65). Biomarkers in the circulation provide one of the best ways, in principle, to detect cancers at an earlier stage. Historically, the type of biomarkers used to monitor cancers were proteins (Liotta LA & Petricoin EF, 3rd (2003) The promise of proteomics. Clin Adv Hematol Oncol 1(8):460-462), and included carcinoembryonic antigen (CEA), carbohydrate antigen 19-9

(CA19-9), and cancer antigen 125 (CA125). These biomarkers have proven useful for following patients with known disease but none have been approved for screening purposes, in part because of their low sensitivity or specificity (Lennon AM & Goggins M (2010) Diagnostic and Therapeutic Response Markers. Pancreatic Cancer, (Springer New York, New York, NY), pp 675-701; Clarke-Pearson DL (2009) Clinical practice. Screening for ovarian cancer. N Engl J Med 361(2):170-177; Locker GY, et al. (2006) ASCO 2006 update of recommendations for the use of tumor markers in gastrointestinal cancer. J Clin Oncol 24(33):5313-5327). More recently, mutant DNA has been explored as a biomarker. The concept underlying this approach, often called "liquid biopsies" is that cancer cells, like normal self-renewing cells, turn over frequently. DNA released from the dying cells can escape into bodily fluids such as urine, stool, and plasma (Haber DA & Velculescu VE (2014) Blood-based analyses of cancer: circulating tumor cells and circulating tumor DNA. Cancer Discov 4(6):650-661; Dawson SJ, et al. (2013) Analysis of circulating tumor DNA to monitor metastatic breast cancer. N Engl J Med 368(13):1199-1209; Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224; Kinde I, et al. (2013) Evaluation of DNA from the Papanicolaou test to detect ovarian and endometrial cancers. Science translational medicine 5(167):167ra164; Wang Y, et al. (2015) Detection of somatic mutations and HPV in the saliva and plasma of patients with head and neck squamous cell carcinomas. Science translational medicine 7(293):293ra104; Wang Y, et al. (2015) Detection of tumor-derived DNA in cerebrospinal fluid of patients with primary tumors of the brain and spinal cord. Proc Natl Acad Sci U S A 112(31):9704-9709; Wang Y, et al. (2016) Diagnostic potential of tumor DNA from ovarian cyst fluid. Elife 5; Springer S, et al. (2015) A Combination of Molecular Markers and Clinical Features Improve the Classification of Pancreatic Cysts. Gastroenterology 149(6):1501-1510; Forshew T, et al. (2012) Noninvasive identification and monitoring of cancer mutations by targeted deep sequencing of plasma DNA. Science translational medicine 4(136):136ra168; Vogelstein B & Kinzler KW (1999) Digital PCR. Proc Natl Acad Sci U S A 96(16):9236-9241; Dressman D, Yan H, Traverso G, Kinzler KW, & Vogelstein B (2003) Transforming single DNA molecules into fluorescent magnetic particles for detection and enumeration of genetic variations. Proc Natl Acad Sci U S A

100(15):8817-8822). An advantage of using mutant DNA in the circulation as a biomarker is its exquisite specificity. Every cell within a cancer has a core set of somatic mutations in driver genes that are responsible for their clonal growth (Vogelstein B, et al. (2013) Cancer genome landscapes. Science 339(6127):1546-1558). In contrast, normal cells do not clonally expand during adulthood and the fraction of normal cells that have any specific somatic mutation is extremely low.

[9] Most studies of circulating tumor DNA (ctDNA) have focused on following patients with cancer rather than on evaluating their use in screening settings. Available data indicate that ctDNA is elevated in >85% of patients with advanced forms of many cancer types (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224; Wang Y, et al. (2015) Detection of somatic mutations and HPV in the saliva and plasma of patients with head and neck squamous cell carcinomas. Science translational medicine 7(293):293ra104). However, a considerably smaller fraction of patients with earlier stages of cancer have detectable levels of ctDNA in their plasma (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224; Wang Y, et al. (2015) Detection of somatic mutations and HPV in the saliva and plasma of patients with head and neck squamous cell carcinomas. Science translational medicine 7(293):293ra104).

[10] The majority of localized cancers can be cured by surgery alone, without any systemic therapy (Siegel *et al.*, 2017 *CA Cancer J Clin* 67:7-30). Once distant metastasis has occurred, however, surgical excision is rarely curative. One major goal in cancer research is therefore the detection of cancers before they metastasize to distant sites. Depending on the cancer type, 20 to 30 years appear to be required for typical cancers in adults to progress from incipient neoplastic lesions to late stage cancers (Vogelstein *et al.*, 2013 *Science* 339:1546-1558; Jones *et al.*, 2008 *Proc Natl Acad Sci U S A* 105:4283-4288; and Yachida *et al.*, 2012 *Clin Cancer Res* 18:6339-6347). Only in the last few years of this long process do neoplastic cells appear to successfully seed and give rise to metastatic lesions (Vogelstein *et al.*, 2013 *Science* 339:1546-1558; Jones *et al.*, 2008 *Proc Natl Acad Sci U S A* 105:4283-4288; Yachida *et al.*, 2012 *Clin Cancer Res* 18:6339-6347; and Vogelstein *et al.*, 2015 *N Engl*

J Med 373:1895-1898). Thus, there is a wide window of opportunity to detect cancers prior to the onset of metastasis. Once large, metastatic tumors are formed however, current therapies are not effective (Bozic *et al.*, 2013 *Elife* 2:e00747; Semrad et al., 2015 *Ann Surg Oncol* 22(Suppl 3):S855-862; Moertel *et al.*, 1995 *Ann Intern Med* 122: 321-326; Huang *et al.*, 2017 *Nature* 545:60-65).

[11] Pancreatic ductal adenocarcinoma (hereinafter "pancreatic cancer") is the third leading cause of cancer death and is predicted to become the second most common cause in the United States by 2030 (Rahib L, et al. (2014) Projecting cancer incidence and deaths to 2030: the unexpected burden of thyroid, liver, and pancreas cancers in the United States. Cancer Res 74(11):2913-2921). Pancreatic cancer is notoriously lethal, with fewer than 9% of patients surviving five years after diagnosis (Siegel RL, Miller KD, & Jemal A (2016) Cancer statistics, 2016. CA Cancer J Clin 66(1):7-30). The poor prognosis of patients with pancreatic cancer is in part due to the fact that 80% to 85% of patients are diagnosed at advanced stages, when either tumor invasion into the surrounding major vessels or distant metastases are evident upon radiologic studies (Ryan DP, Hong TS, & Bardeesy N (2014) Pancreatic adenocarcinoma. N Engl J Med 371(22):2140-2141). At this late point in the disease, pancreatic cancer is not amenable to surgical resection, and the 3-year survival rate is < 5%. In contrast, a five-year survival of almost 60% is reported for very small, localized tumors; among resectable cancers, the smaller the tumor, the better the prognosis (Ansari D, et al. (2017) Relationship between tumour size and outcome in pancreatic ductal adenocarcinoma. Br J Surg 104(5):600-607; Jung KW, et al. (2007) Clinicopathological aspects of 542 cases of pancreatic cancer: a special emphasis on small pancreatic cancer. J Korean Med Sci 22 Suppl:S79-85; Egawa S, et al. (2004) Clinicopathological aspects of small pancreatic cancer. Pancreas 28(3):235-240; Ishikawa O, et al. (1999) Minute carcinoma of the pancreas measuring 1 cm or less in diameter--collective review of Japanese case reports. Hepatogastroenterology 46(25):8-15; Tsuchiya R, et al. (1986) Collective review of small carcinomas of the pancreas. Ann Surg 203(1):77-81).

[12] Pancreatic cancer is not different from other cancers with respect to its strong correlation between tumor stage and prognosis (Ansari D, et al. (2017) Relationship between tumour size and outcome in pancreatic ductal adenocarcinoma. Br J Surg 104(5):600-607).

Very few patients with cancers of the lung, colon, esophagus, or stomach who have distant metastasis at the time of diagnosis survive for more than five years (Howlader N, et al. (2016) SEER Cancer Statistics Review, 1975-2013, National Cancer Institute. Bethesda, MD, http://seer.cancer.gov/csr/1975_2013/, based on November 2015 SEER data submission, posted to the SEER web site, April 2016). The size of cancers is also important in a general sense, in that smaller tumors have less often metastasized than larger tumors at the time of diagnosis, and are therefore are more likely to be curable by surgery alone. Even when cancers have metastasized to distant sites, a smaller burden of disease is much more easily managed than bulky lesions (Bozic I, et al. (2013) Evolutionary dynamics of cancer in response to targeted combination therapy. Elife 2:e00747). Thus, adjuvant chemotherapeutic agents administered to patients with micro-metastases stemming from a colorectal cancer can be curative in nearly 50% of cases (Semrad TJ, Fahrni AR, Gong IY, & Khatri VP (2015) Integrating Chemotherapy into the Management of Oligometastatic Colorectal Cancer: Evidence-Based Approach Using Clinical Trial Findings. Ann Surg Oncol 22 Suppl 3:S855-862; Moertel CG, et al. (1995) Fluorouracil plus levamisole as effective adjuvant therapy after resection of stage III colon carcinoma: a final report. Ann Intern Med 122(5):321-326; Andre T, et al. (2009) Improved overall survival with oxaliplatin, fluorouracil, and leucovorin as adjuvant treatment in stage II or III colon cancer in the MOSAIC trial. J Clin Oncol 27(19):3109-3116). The same chemotherapeutic agents delivered to patients with metastatic lesions that are radiologically visible produce virtually no cures (Dy GK, et al. (2009) Long-term survivors of metastatic colorectal cancer treated with systemic chemotherapy alone: a North Central Cancer Treatment Group review of 3811 patients, N0144. Clin Colorectal Cancer 8(2):88-93).

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Proc Natl Acad Sci U S A 96(16):9236-9241; Dressman D, Yan H, Traverso G, Kinzler KW, & Vogelstein B (2003) Transforming single DNA molecules into fluorescent magnetic particles for detection and enumeration of genetic variations. Proc Natl Acad Sci U S A 100(15):8817-882). An advantage of using mutant DNA in the circulation as a biomarker is its exquisite specificity. Every cell within a cancer has a core set of somatic mutations in driver genes that are responsible for their clonal growth (Vogelstein B, et al. (2013) Cancer genome landscapes. Science 339(6127):1546-1558). In contrast, normal cells do not clonally expand during adulthood and the fraction of normal cells that have any specific somatic mutation is extremely low.

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[15] There is a continuing need in the art to increase the sensitivity of detection of resectable or otherwise treatable cancers under conditions that preserve high specificity.

[16] The Papanicolaou (Pap) test has dramatically decreased the incidence and mortality of cervical cancer in the screened population. Unfortunately, the Pap test is generally unable to detect endometrial or ovarian cancers ((L. Geldenhuys, M. L. Murray, Sensitivity and specificity of the Pap smear for glandular lesions of the cervix and endometrium. Acta cytologica 51, 47-50 (2007); A. B. Ng, J. W. Reagan, S. Hawliczek, B. W. Wentz, Significance of endometrial cells in the detection of endometrial carcinoma and its

precursors. Acta cytologica 18, 356-361 (1974); P. F. Schnatz, M. Guile, D. M. O'Sullivan, J. I. Sorosky, Clinical significance of atypical glandular cells on cervical cytology. Obstetrics and gynecology 107, 701-708 (2006); C. Zhao, A. Florea, A. Onisko, R. M. Austin, Histologic follow-up results in 662 patients with Pap test findings of atypical glandular cells: results from a large academic womens hospital laboratory employing sensitive screening methods. Gynecologic oncology 114, 383-389 (2009)). In light of the success of the Pap test in detecting early-stage, curable cervical cancers, ovarian and endometrial cancers are currently the most lethal and most common gynecologic malignancies, respectively, in countries where Pap tests are routinely performed (N. Howladeret al., SEER Cancer Statistics Review, 1975-2014, National Cancer Institute. (2017)). Together, endometrial and ovarian cancers account for approximately 25,000 deaths each year and are the third leading cause of cancer-related mortality in women in the United States (N. Howlader et al., SEER Cancer Statistics Review, 1975-2014, National Cancer Institute. (2017)). Most of these deaths are caused by high-grade tumor subtypes, which tend to metastasize prior to the onset of symptoms (R. J. Kurman, M. Shih Ie, The origin and pathogenesis of epithelial ovarian cancer: a proposed unifying theory. The American journal of surgical pathology 34, 433-443 (2010); K. N. Moore, A. N. Fader, Uterine papillary serous carcinoma. Clin Obstet Gynecol 54, 278-291 (2011)).

[17] Endometrial cancer is the most common gynecologic malignancy, with 61,380 estimated new cases in 2017 in the United States (N. Howlader et al., SEER Cancer Statistics Review, 1975-2014, National Cancer Institute. (2017)). The incidence of endometrial cancer has been rising with increased obesity and increased life expectancy (M. Arnoldet al., Global burden of cancer attributable to high body-mass index in 2012: a population-based study. The Lancet. Oncology 16, 36-46 (2015)). At the same time, relative survival has not improved over the past decades (N. Howlader et al., SEER Cancer Statistics Review, 1975-2014, National Cancer Institute. (2017); L. Rahib et al., Projecting cancer incidence and deaths to 2030: the unexpected burden of thyroid, liver, and pancreas cancers in the United States. Cancer research 74, 2913-2921 (2014)). Much effort has been directed towards developing a screening test for this cancer type. The most common diagnostic test is transvaginal ultrasound (TVUS), which measures the thickness of the endometrium. The

potential of TVUS as a screening test is undermined by its inability to reliably distinguish between benign and malignant lesions, subjecting women without cancer to unnecessary invasive procedures and their associated complications. Its high false positive rate is demonstrated by the fact that as few as one in 50 women who tested positive by TVUS was proven to have endometrial cancer after undergoing additional diagnostic procedures (Jacobs et al., Sensitivity of transvaginal ultrasound screening for endometrial cancer in postmenopausal women: a case-control study within the UKCTOCS cohort. The Lancet. Oncology 12, 38-48 (2011)).

[18] Ovarian cancer is the second most common gynecologic malignancy in the U.S. and Europe. It is often diagnosed at a late stage, when the 5-year survival is less than 30% (N. Howlader et al., SEER Cancer Statistics Review, 1975-2014, National Cancer Institute. (2017)). The high mortality has made the development of an effective screening test a high priority. Large randomized trials have assessed the use of CA-125 and TVUS as potential screening tests for ovarian cancer (Buys et al., Effect of screening on ovarian cancer mortality: the Prostate, Lung, Colorectal and Ovarian (PLCO) Cancer Screening Randomized Controlled Trial. JAMA 305, 2295-2303 (2011); Kobayashi et al., A randomized study of screening for ovarian cancer: a multicenter study in Japan. Int J Gynecol Cancer 18, 414-420 (2008); Jacobs et al., Ovarian cancer screening and mortality in the UK Collaborative Trial of Ovarian Cancer Screening (UKCTOCS): a randomised controlled trial. Lancet 387, 945-956 (2016); Menon et al., Risk Algorithm Using Serial Biomarker Measurements Doubles the Number of Screen-Detected Cancers Compared With a Single-Threshold Rule in the United Kingdom Collaborative Trial of Ovarian Cancer Screening. J Clin Oncol 33, 2062-2071 (2015)). However, screening with current diagnostic approaches is not recommended for the general population, as it leads to "important harms, including major surgical interventions in women who do not have cancer" (V. A. Moyer, U. S. P. S. T. Force, Screening for ovarian cancer: U.S. Preventive Services Task Force reaffirmation recommendation statement. Annals of internal medicine 157, 900-904 (2012)). Thus, new diagnostic approaches are urgently needed.

[19] Among ovarian cancers, high-grade serous carcinomas (HGSC) account for 90% of all ovarian cancer deaths. Increasing evidence suggests that most HGSC arise in the fallopian tube and subsequently implant on the ovarian surface (*16-21*R. J. Kurman, M. Shih Ie, Molecular pathogenesis and extraovarian origin of epithelial ovarian cancer--shifting the paradigm. Human pathology 42, 918-931 (2011); Lee et al., A candidate precursor to serous carcinoma that originates in the distal fallopian tube. The Journal of pathology 211, 26-35 (2007) A candidate precursor to serous carcinoma that originates in the distal fallopian tube. The Journal of pathology 211, 26-35 (2007); Eckert et al., Genomics of Ovarian Cancer Progression Reveals Diverse Metastatic Trajectories Including Intraepithelial Metastasis to the Fallopian Tube. Cancer Discov 6, 1342-1351 (2016); A. M. Karst, K. Levanon, R. Drapkin, Modeling high-grade serous ovarian carcinogenesis from the fallopian tube. Proc Natl Acad Sci U S A 108, 7547-7552 (2011); Zhai et al., High-grade serous carcinomas arise in the mouse oviduct via defects linked to the human disease. The Journal of pathology 243, 16-25 (2017); R. J. Kurman, M. Shih Ie, The Dualistic Model of Ovarian Carcinogenesis: Revisited, Revised, and Expanded. Am J Pathol 186, 733-747 (2016)). A recent prospective study of symptomatic women reported that most early diagnosed HGSCs have extra-ovarian origins (Gilbert et al. Assessment of symptomatic women for early diagnosis of ovarian cancer: results from the prospective DOvE pilot project. The Lancet. Oncology 13, 285-291 (2012)). This might explain the low sensitivity of TVUS for early disease, when no ovarian abnormalities are detectable. Multimodal screening with serum CA-125 levels improves sensitivity, however CA-125 lacks specificity and is elevated in a variety of common benign conditions (H. Meden, A. Fattahi-Meibodi, CA 125 in benign gynecological conditions. Int J Biol Markers 13, 231-237 (1998)).

[20] Unlike markers associated with neoplasia, cancer driver gene mutations are causative agents of neoplasia and absent in non-neoplastic conditions. It has been shown that tumor DNA could be detected in the vaginal tract of women with ovarian cancer (Erickson et al., Detection of somatic TP53 mutations in tampons of patients with high-grade serous ovarian cancer. Obstetrics and gynecology 124, 881-885 (2014)). Furthermore, a recent proof-of-principle study showed that endometrial and ovarian cancers shed cells that collect at the cervix, allowing detectable levels of tumor DNA to be found in the fluids obtained during

routine Pap tests (Kinde et al., Evaluation of DNA from the Papanicolaou test to detect ovarian and endometrial cancers. Sci Transl Med 5, 167ra164 (2013)). These cells are sampled with a brush (a "Pap brush") that is inserted into the endocervical canal. The brush is then dipped into preservative fluid. For the detection of cervical cancers, cells from the fluid are applied to a slide for cytologic examination (the classic Pap smear). Additionally, DNA is often purified from the fluid to search for HPV sequences.

[21] Bladder cancer (BC) is the most common malignancy of the urinary tract. According to the American Cancer Society, 79,030 new cases of bladder cancer and 18,540 deaths are estimated to occur in the United States alone in 2017 [Siegel RL, Miller KD, Jemal A (2017) Cancer Statistics, 2017. CA Cancer J Clin 67:7-30]. Predominantly of urothelial histology, invasive BC arises from non-invasive papillary or flat precursors. Many BC patients suffer with multiple relapses prior to progression, providing ample lead-time for early detection and treatment prior to metastasis [Netto GJ (2013) Clinical applications of recent molecular advances in urologic malignancies: no longer chasing a "mirage"?. Adv Anat Pathol 20:175-203]. Urine cytology and cystoscopy with transurethral biopsy (TURB) are currently the gold standard for diagnosis and follow-up in bladder cancer. While urine cytology has value for the detection of high-grade neoplasms, it is unable to detect the vast majority of low-grade tumors [Netto GJ, Tafe LJ (2016) Emerging Bladder Cancer Biomarkers and Targets of Therapy. Urol Clin North Am 43:63-76; Lotan Y, Roehrborn CG (2003) Sensitivity and specificity of commonly available bladder tumor markers versus cytology: results of a comprehensive literature review and meta-analyses. Urology 61:109-18; discussion 118; Zhang ML, Rosenthal DL, VandenBussche CJ (2016) The cytomorphological features of low-grade urothelial neoplasms vary by specimen type. Cancer Cytopathol 124:552-564]. This fact, together with the high cost and invasive nature of repeated cystoscopy and TURB procedures, have led to many attempts to develop novel noninvasive strategies. These include urine or serum based genetic and protein assays for screening and surveillance [Kawauchi et al., (2009) 9p21 Index as Estimated by Dual-Color Fluorescence in Situ Hybridization is Useful to Predict Urothelial Carcinoma Recurrence in Bladder Washing Cytology. Hum Pathol 40:1783-1789; Kruger S, Mess F, Bohle A, Feller AC (2003) Numerical aberrations of chromosome 17 and the 9p21 locus are independent predictors of tumor recurrence in non-

invasive transitional cell carcinoma of the urinary bladder. Int J Oncol 23:41-48; Skacel et al., (2003) Multitarget fluorescence in situ hybridization assay detects transitional cell carcinoma in the majority of patients with bladder cancer and atypical or negative urine cytology. J Urol 169:2101-2105; Sarosdy et al., (2006) Use of a multitarget fluorescence in situ hybridization assay to diagnose bladder cancer in patients with hematuria. J Urol 176:44-47; Moonen et al., (2007) UroVysion compared with cytology and quantitative cytology in the surveillance of non-muscle-invasive bladder cancer. Eur Urol 51:1275-80; discussion 1280; Fradet Y, Lockhard C (1997) Performance characteristics of a new monoclonal antibody test for bladder cancer: ImmunoCyt trade mark. Can J Urol 4:400-405; Yafi et al., (2015) Prospective analysis of sensitivity and specificity of urinary cytology and other urinary biomarkers for bladder cancer. Urol Oncol 33:66.e25-66.e31; Serizawa et al., (2010) Integrated genetic and epigenetic analysis of bladder cancer reveals an additive diagnostic value of FGFR3 mutations and hypermethylation events. Int J Cancer; Kinde et al., (2013) TERT promoter mutations occur early in urothelial neoplasia and are biomarkers of early disease and disease recurrence in urine. Cancer Res 73:7162-7167; Hurst CD, Platt FM, Knowles MA (2014) Comprehensive mutation analysis of the TERT promoter in bladder cancer and detection of mutations in voided urine. Eur Urol 65:367-369; Wang et al., (2014) TERT promoter mutations are associated with distant metastases in upper tract urothelial carcinomas and serve as urinary biomarkers detected by a sensitive castPCR. Oncotarget 5:12428-12439; Ralla et al., (2014) Nucleic acid-based biomarkers in body fluids of patients with urologic malignancies. Crit Rev Clin Lab Sci 51:200-231; Ellinger J, Muller SC, Dietrich D (2015) Epigenetic biomarkers in the blood of patients with urological malignancies. Expert Rev Mol Diagn 15:505-516; Bansal N, Gupta A, Sankhwar SN, Mahdi AA (2014) Low- and high-grade bladder cancer appraisal via serum-based proteomics approach. Clin Chim Acta 436:97-103; Goodison S, Chang M, Dai Y, Urquidi V, Rosser CJ (2012) A multi-analyte assay for the non-invasive detection of bladder cancer. PLoS One 7:e47469; Allory et al., (2014) Telomerase reverse transcriptase promoter mutations in bladder cancer: high frequency across stages, detection in urine, and lack of association with outcome. Eur Urol 65:360-366]. Currently available U.S. Food and Drug Administration (FDA) approved assays include ImmunoCyt test (Scimedx Corp), nuclear matrix protein 22

(NMP22) immunoassay test (Matritech), and multitarget FISH (UroVysion) [Kawauchi et al., (2009) 9p21 Index as Estimated by Dual-Color Fluorescence in Situ Hybridization is Useful to Predict Urothelial Carcinoma Recurrence in Bladder Washing Cytology. Hum Pathol 40:1783-1789; Kruger S, Mess F, Bohle A, Feller AC (2003) Numerical aberrations of chromosome 17 and the 9p21 locus are independent predictors of tumor recurrence in non-invasive transitional cell carcinoma of the urinary bladder. Int J Oncol 23:41-48; Skacel et al., (2003) Multitarget fluorescence in situ hybridization assay detects transitional cell carcinoma in the majority of patients with bladder cancer and atypical or negative urine cytology. J Urol 169:2101-2105; Sarosdy et al., (2006) Use of a multitarget fluorescence in situ hybridization assay to diagnose bladder cancer in patients with hematuria. J Urol 176:44-47; Moonen et al., (2007) UroVysion compared with cytology and quantitative cytology in the surveillance of non-muscle-invasive bladder cancer. Eur Urol 51:1275-80; discussion 1280; Fradet Y, Lockhard C (1997) Performance characteristics of a new monoclonal antibody test for bladder cancer: ImmunoCyt trade mark. Can J Urol 4:400-405; Yafi et al., (2015) Prospective analysis of sensitivity and specificity of urinary cytology and other urinary biomarkers for bladder cancer. Urol Oncol 33:66.e25-66.e31]. Sensitivities between 62% and 69% and specificities between 79% and 89% have been reported for some of these tests. However, due to assay performance inconsistencies, cost or required technical expertise, integration of such assays into routine clinical practice has not yet occurred.

[22] Bladder cancer typically falls into three types that begin in cells in the lining of the bladder. In some embodiments, bladder cancers are named for the type of cells that become malignant (cancerous) including transitional cell carcinoma, squamous cell carcinoma, and adenocarcinoma. Transitional cell carcinomas begin in cells in the innermost tissue layer of the bladder. Transitional cell carcinomas can be low-grade or high-grade. Low-grade transitional cell carcinomas can recur after treatment, but rarely spread into the muscle layer of the bladder or to other parts of the body. High-grade transitional cell carcinomas can recur after treatment and often spreads into the muscle layer of the bladder, to other parts of the body, and to lymph nodes. Almost all deaths from bladder cancer are due to high-grade disease. Squamous cell carcinomas begin in squamous cells, which are thin, flat cells that may form in the bladder after long-term infection or irritation. Adenocarcinomas begin in

glandular (secretory) cells that are found in the lining of the bladder, and are a very rare type of bladder cancer.

[23] High rates of activating mutations in the upstream promoter of the TERT gene are found in the majority of BC as well as in other cancer types [Huang FW, Hodis E, Xu MJ, Kryukov GV, Chin L, Garraway LA (2013) Highly recurrent TERT promoter mutations in human melanoma. Science 339:957-959; Killela et al., (2013) TERT promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal. Proc Natl Acad Sci U S A 110:6021-6026; Scott GA, Laughlin TS, Rothberg PG (2014) Mutations of the TERT promoter are common in basal cell carcinoma and squamous cell carcinoma. Mod Pathol 27:516-523]. TERT promoter mutations predominantly affect two hot spots, g.1295228 C>T and g.1295250 C>T. They lead to the generation of CCGGAA/T or GGAA/T motifs altering binding site for ETS transcription factors and subsequently increased TERT promoter activity [Huang FW, Hodis E, Xu MJ, Kryukov GV, Chin L, Garraway LA (2013) Highly recurrent TERT promoter mutations in human melanoma. Science 339:957-959; Horn et al., (2013) TERT promoter mutations in familial and sporadic melanoma. Science 339:959-961]. TERT promoter mutations occur in up to 80% of invasive urothelial carcinomas of the bladder and upper urinary tract as well as in several of its histologic variants [Kinde et al., (2013) TERT promoter mutations occur early in urothelial neoplasia and are biomarkers of early disease and disease recurrence in urine. Cancer Res 73:7162-7167; Killela et al., (2013) TERT promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal. Proc Natl Acad Sci U S A 110:6021-6026; Allory et al., (2014) Telomerase reverse transcriptase promoter mutations in bladder cancer: high frequency across stages, detection in urine, and lack of association with outcome. Eur Urol 65:360-366; Cowan et al., (2016) Detection of TERT promoter mutations in primary adenocarcinoma of the urinary bladder. Hum Pathol 53:8-13; Nguyen et al., (2016) High prevalence of TERT promoter mutations in micropapillary urothelial carcinoma. Virchows Arch 469:427-434]. Moreover, TERT promoter mutations occur in 60-80% of BC precursors, including Papillary Urothelial Neoplasms of Low Malignant Potential [Rodriguez et al., (2017) Spectrum of genetic mutations in de novo PUNLMP of the urinary bladder. Virchows Arch], non-invasive Low

Grade Papillary Urothelial Carcinoma, non-invasive High Grade Papillary Urothelial Carcinoma and "flat" Carcinoma in Situ (CIS), as well as in urinary cells from a subset of these patients [Kinde et al., (2013) TERT promoter mutations occur early in urothelial neoplasia and are biomarkers of early disease and disease recurrence in urine. Cancer Res 73:7162-7167]. TERT promoter mutations have thus been established as the most common genetic alteration in BC [Kinde et al., (2013) TERT promoter mutations occur early in urothelial neoplasia and are biomarkers of early disease and disease recurrence in urine. Cancer Res 73:7162-7167; Cheng L, Montironi R, Lopez-Beltran A (2017) TERT Promoter Mutations Occur Frequently in Urothelial Papilloma and Papillary Urothelial Neoplasm of Low Malignant Potential. Eur Urol 71:497-498]. Other oncogene-activating mutations include those in FGFR3, RAS and PIK3CA, which have been shown to occur in a high fraction of non- muscle invasive bladder cancers [International Agency for Research on Cancer. (2016) WHO Classification of Tumours of the Urinary System and Male Genital Organs. World Health Organization; 4 edition; Netto GJ (2011) Molecular biomarkers in urothelial carcinoma of the bladder: are we there yet?. Nat Rev Urol 9:41-51]. In muscle-invasive bladder cancers, mutations in TP53, CDKN2A, MLL and ERBB2 are also frequently found [Netto GJ (2011) Molecular biomarkers in urothelial carcinoma of the bladder: are we there yet?. Nat Rev Urol 9:41-51; Mo et al., (2007) Hyperactivation of Ha-ras oncogene, but not Ink4a/Arf deficiency, triggers bladder tumorigenesis. J Clin Invest 117:314-325; Sarkis et al., (1993) Nuclear overexpression of p53 protein in transitional cell bladder carcinoma: a marker for disease progression. J Natl Cancer Inst 85:53-59; Lin et al., (2010) Increase sensitivity in detecting superficial, low grade bladder cancer by combination analysis of hypermethylation of E-cadherin, p16, p14, RASSF1A genes in urine. Urol Oncol 28:597-602; Sarkis et al., (1994) Association of P53 nuclear overexpression and tumor progression in carcinoma in situ of the bladder. J Urol 152:388-392; Wu XR (2005) Urothelial tumorigenesis: a tale of divergent pathways. Nat Rev Cancer 5:713-725; Cancer Genome Atlas Research Network (2014) Comprehensive molecular characterization of urothelial bladder carcinoma. Nature 507:315-322].

[24] Because urine cytology is relatively insensitive for the detection of recurrence, cystoscopies are performed as often as every three months in such patients in the U.S. In

fact, the cost of managing these patients is in aggregate higher than the cost of managing any other type of cancer, and amounts to 3 billion dollars annually [Netto GJ, Epstein JI (2010) Theranostic and prognostic biomarkers: genomic applications in urological malignancies. Pathology 42:384-394]. A non-invasive test that could predict which of these patients were most likely to develop recurrent BC could thereby be both medically and economically important.

[25] More than 400,000 new cases of urologic transitional cell carcinoma are diagnosed worldwide each year (Antoni, S., Ferlay, J., Soerjomataram, I., Znaor, A., Jemal, A., & Bray, F. (2017). Bladder Cancer Incidence and Mortality: A Global Overview and Recent Trends. Eur Urol, 71(1), 96-108. doi: 10.1016/j.eururo.2016.06.010). Although most of these urothelial carcinomas arise in the bladder in the lower urinary tract, 5-10% originate in the upper urinary tract in the renal pelvis and/or ureter (Roupret, M., Babjuk, M., Comperat, E., Zigeuner, R., Sylvester, R. J., Burger, M., Cowan, N. C., Bohle, A., Van Rhijn, B. W., Kaasinen, E., Palou, J., & Shariat, S. F. (2015). European Association of Urology Guidelines on Upper Urinary Tract Urothelial Cell Carcinoma: 2015 Update. Eur Urol, 68(5), 868-879. doi: 10.1016/j.eururo.2015.06.044; Soria, F., Shariat, S. F., Lerner, S. P., Fritsche, H. M., Rink, M., Kassouf, W., Spiess, P. E., Lotan, Y., Ye, D., Fernandez, M. I., Kikuchi, E., Chade, D. C., Babjuk, M., Grollman, A. P., & Thalmann, G. N. (2017). Epidemiology, diagnosis, preoperative evaluation and prognostic assessment of upper-tract urothelial carcinoma (UTUC). World J Urol, 35(3), 379-387. doi: 10.1007/s00345-016-1928-x). The annual incidence of these upper tract urothelial carcinomas (UTUCs) in Western countries is 1-2 cases per 100,000, but occurs at a much higher rate in populations exposed to aristolochic acid (AA) (Chen, C. H., Dickman, K. G., Moriya, M., Zavadil, J., Sidorenko, V. S., Edwards, K. L., Gnatenko, D. V., Wu, L., Turesky, R. J., Wu, X. R., Pu, Y. S., & Grollman, A. P. (2012). Aristolochic acid-associated urothelial cancer in Taiwan. Proc Natl Acad Sci U S A, 109(21), 8241-8246. doi: 10.1073/pnas.1119920109; Grollman, A. P. (2013). Aristolochic acid nephropathy: Harbinger of a global iatrogenic disease. Environ Mol Mutagen, 54(1), 1-7. doi: 10.1002/em.21756; Lai, M. N., Wang, S. M., Chen, P. C., Chen, Y. Y., & Wang, J. D. (2010). Population-based case-control study of Chinese herbal products containing aristolochic acid and urinary tract cancer risk. J Natl Cancer Inst, 102(3), 179-186. doi:

10.1093/jnci/djp467; Taiwan Cancer Registry. (2017). Bureau of Health Promotion, Dept. of Health, Taiwan. The incidence of renal pelvic and ureteral tumor in Taiwan. Taiwan cancer registry. Retrieved August 14, 2017, from URL cris.bhp.doh.gov.tw/pagepub/Home.aspx?itemNo=cr.q.10). AA is a carcinogenic and nephrotoxic nitrophenanthrene carboxylic acid produced by Aristolochia plants (Hsieh, S. C., Lin, I. H., Tseng, W. L., Lee, C. H., & Wang, J. D. (2008). Prescription profile of potentially aristolochic acid containing Chinese herbal products: an analysis of National Health Insurance data in Taiwan between 1997 and 2003, Chin Med, 3, 13. doi: 10.1186/1749-8546-3-13; National Toxicology Program. (2011). Aristolochic acids. Rep Carcinog, 12, 45-49). An etiological link between AA exposure and UTUC has been established in two distinct populations. The first resides in Balkan countries where Aristolochia plants grow naturally in wheat fields (Jelakovic, B., Karanovic, S., Vukovic-Lela, I., Miller, F., Edwards, K. L., Nikolic, J., Tomic, K., Slade, N., Brdar, B., Turesky, R. J., Stipancic, Z., Dittrich, D., Grollman, A. P., & Dickman, K. G. (2012). Aristolactam-DNA adducts are a biomarker of environmental exposure to aristolochic acid. Kidney Int, 81(6), 559-567. doi: 10.1038/ki.2011.371). The second population is in Asia, where Aristolochia herbs are widely used in the practice of Traditional Chinese Medicine (Grollman, 2013; National Toxicology Program, 2011). The public health threat posed by the medicinal use of Aristolochia herbs is exemplified by Taiwan, which has the highest incidence of UTUC in the world (Chen, C. H., Dickman, K. G., Moriya, M., Zavadil, J., Sidorenko, V. S., Edwards, K. L., Gnatenko, D. V., Wu, L., Turesky, R. J., Wu, X. R., Pu, Y. S., & Grollman, A. P. (2012). Aristolochic acid-associated urothelial cancer in Taiwan. Proc Natl Acad Sci U S A, 109(21), 8241-8246. doi: 10.1073/pnas.1119920109; Yang, M. H., Chen, K. K., Yen, C. C., Wang, W. S., Chang, Y. H., Huang, W. J., Fan, F. S., Chiou, T. J., Liu, J. H., & Chen, P. M. (2002). Unusually high incidence of upper urinary tract urothelial carcinoma in Taiwan. Urology, 59(5), 681-687). More than one-third of the adult population in Taiwan has been prescribed herbal remedies containing AA (Hsieh, S. C., Lin, I. H., Tseng, W. L., Lee, C. H., & Wang, J. D. (2008). Prescription profile of potentially aristolochic acid containing Chinese herbal products: an analysis of National Health Insurance data in Taiwan between 1997 and 2003. Chin Med, 3, 13. doi: 10.1186/1749-8546-3-13), resulting in an unusually high (37%) proportion of UTUC

cases relative to all urothelial cancers (Taiwan Cancer Registry. (2017). Bureau of Health Promotion, Dept. of Health, Taiwan. The incidence of renal pelvic and ureteral tumor in Taiwan. Taiwan cancer registry. Retrieved August 14, 2017, from URL cris.bhp.doh.gov.tw/pagepub/Home.aspx?itemNo=cr.q.10).

[26] Nephroureterectomy can be curative for patients with UTUC when it is detected at an early stage (Li, C. C., Chang, T. H., Wu, W. J., Ke, H. L., Huang, S. P., Tsai, P. C., Chang, S. J., Shen, J. T., Chou, Y. H., & Huang, C. H. (2008). Significant predictive factors for prognosis of primary upper urinary tract cancer after radical nephroureterectomy in Taiwanese patients. Eur Urol, 54(5), 1127-1134. doi: 10.1016/j.eururo.2008.01.054). However, these cancers are largely silent until the onset of overt clinical symptoms, typically hematuria, and as a result, most patients are diagnosed only at an advanced stage (Roupret, M., Babjuk, M., Comperat, E., Zigeuner, R., Sylvester, R. J., Burger, M., Cowan, N. C., Bohle, A., Van Rhijn, B. W., Kaasinen, E., Palou, J., & Shariat, S. F. (2015). European Association of Urology Guidelines on Upper Urinary Tract Urothelial Cell Carcinoma: 2015 Update. Eur Urol, 68(5), 868-879. doi: 10.1016/j.eururo.2015.06.044). Diagnostic tests for the detection of early-stage UTUC are not currently available. There is thus a need for clinical tools that can be used to identify early UTUCs in populations at risk for developing this type of malignancy. Relapse following surgery is also a concern, as UTUC can recur in the contralateral upper urinary tract and/or in the bladder (Roupret, M., Babjuk, M., Comperat, E., Zigeuner, R., Sylvester, R. J., Burger, M., Cowan, N. C., Bohle, A., Van Rhijn, B. W., Kaasinen, E., Palou, J., & Shariat, S. F. (2015). European Association of Urology Guidelines on Upper Urinary Tract Urothelial Cell Carcinoma: 2015 Update. Eur Urol, 68(5), 868-879. doi: 10.1016/j.eururo.2015.06.044; Soria, F., Shariat, S. F., Lerner, S. P., Fritsche, H. M., Rink, M., Kassouf, W., Spiess, P. E., Lotan, Y., Ye, D., Fernandez, M. I., Kikuchi, E., Chade, D. C., Babjuk, M., Grollman, A. P., & Thalmann, G. N. (2017). Epidemiology, diagnosis, preoperative evaluation and prognostic assessment of upper-tract urothelial carcinoma (UTUC). World J Urol, 35(3), 379-387. doi: 10.1007/s00345-016-1928-x). Vigilant surveillance for signs of malignancy is therefore an essential part of follow-up care in UTUC patients, and non-invasive tests for recurrent disease could substantially improve post-surgical management, particularly as urine cytology cannot detect the majority of

UTUCs (Baard, J., de Bruin, D. M., Zondervan, P. J., Kamphuis, G., de la Rosette, J., & Laguna, M. P. (2017). Diagnostic dilemmas in patients with upper tract urothelial carcinoma. Nat Rev Urol, 14(3), 181-191. doi: 10.1038/nrurol.2016.252).

SUMMARY

[27] In general, methods and materials for identifying the presence of cancer in a subject with increased sensitivity and specificity as compared to conventional methods of identifying the presence of cancer in a subject are provided herein. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with increased sensitivity and specificity are performed on a liquid sample obtained from the subject (e.g., blood, plasma, or serum), whereas conventional methods of identifying the presence of cancer in a subject do not achieve the level of sensitivity, the level of specificity, or both when performed on a liquid sample obtained from the subject. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with increased sensitivity and specificity are performed prior to having determined that the subject already suffers from cancer, prior to having determined that the subject harbors a cancer cell, and/or prior to the subject exhibiting symptoms associated with cancer. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with increased sensitivity and specificity are used as a first line detection method, and not simply as a confirmation (e.g., an "overcall") of another detection method that the subject has cancer.

[28] In some embodiments, provided herein are methods for identifying the presence of pancreatic cancer in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following genes: KRAS, TP53, CDKN2A, or SMAD4; detecting a level of one or more of the following protein biomarkers in a second biological sample obtained from the subject: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), or osteopontin (OPN); comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of pancreatic cancer in the subject when the presence of one or more genetic biomarkers is detected, the detected levels of the one or more protein biomarkers are higher

than the reference levels of the one or more protein biomarkers, or both. In some of methods for identifying the presence of pancreatic cancer in a subject, the first biological sample, the second biological sample, or both includes plasma. In some of methods for identifying the presence of pancreatic cancer in a subject, the first and second biological samples are the same. In some of methods for identifying the presence of pancreatic cancer in a subject, the presence of one or more genetic biomarkers in each of: KRAS, TP53, CDKN2A, and SMAD4 is detected. In some of methods for identifying the presence of pancreatic cancer in a subject, the level of each of carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), and osteopontin (OPN) is detected. In some of methods for identifying the presence of pancreatic cancer in a subject, the presence of one or more genetic biomarkers in one or more of KRAS, TP53, CDKN2A, or SMAD4 is detected using a multiplex PCR-based sequencing assay that includes a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some of methods for identifying the presence of pancreatic cancer in a subject, detecting the presence of one or more genetic biomarkers, detecting the level of one or more protein biomarkers, or both is performed when the subject is not known to harbor a cancer cell. In some of methods for identifying the presence of pancreatic cancer in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[29] In some embodiments, provided herein are methods for identifying the presence of cancer in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS; detecting a level of one or more of the following protein biomarkers in a second biological sample obtained from the subject: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, or MPO; comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of cancer in the subject when the presence of one or

more genetic biomarkers is detected, the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers, or both. In some embodiments of methods for identifying the presence of cancer in a subject, the first biological sample, the second biological sample, or both includes plasma. In some embodiments of methods for identifying the presence of cancer in a subject, the first and second biological samples are the same. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in each of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the level of each of CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and MPO is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS is detected using a multiplex PCR-based sequencing assay that includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of methods for identifying the presence of cancer in a subject, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers, detecting the level of one or more protein biomarkers, or both is performed when the subject is not known to harbor a cancer cell. In some embodiments of methods for identifying the presence of cancer in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[30] In some embodiments, provided herein are methods for identifying the presence of cancer in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following

genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS; detecting a level of one or more of the following protein biomarkers in a second biological sample obtained from the subject: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, or CA15-3; comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of cancer in the subject when the presence of one or more genetic biomarkers is detected, the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers, or both. In some embodiments of methods for identifying the presence of cancer in a subject, the first biological sample, the second biological sample, or both includes plasma. In some embodiments of methods for identifying the presence of cancer in a subject, the first and second biological samples are the same. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in each of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the level of each of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3 is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS is detected using a multiplex PCR-based sequencing assay that includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of methods for identifying the presence of cancer in a subject, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers, detecting the level of one or more protein biomarkers, or both is performed when the subject is not known to harbor a cancer cell. In some embodiments of

methods for identifying the presence of cancer in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[31] In some embodiments, provided herein are methods for identifying the presence of cancer in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS; detecting a level of one or more of the following protein biomarkers in a second biological sample obtained from the subject: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, or CA15-3; comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of cancer in the subject when the presence of one or more genetic biomarkers is detected, the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers, or both. In some embodiments of methods for identifying the presence of cancer in a subject, the first biological sample, the second biological sample, or both includes plasma. In some embodiments of methods for identifying the presence of cancer in a subject, the first and second biological samples are the same. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in each of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the level of each of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3 is detected. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers in one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS is detected using a multiplex PCR-based sequencing assay that includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c.

redundantly sequencing the amplification products. In some embodiments of methods for identifying the presence of cancer in a subject, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of methods for identifying the presence of cancer in a subject, the presence of one or more genetic biomarkers, detecting the level of one or more protein biomarkers, or both is performed when the subject is not known to harbor a cancer cell. In some embodiments of methods for identifying the presence of cancer in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[32] In some embodiments, provided herein are methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL; detecting the presence of at least one mutation in a TERT promoter in a second biological sample obtained from the subject; and detecting the presence of aneuploidy in a third biological sample obtained from the subject; and identifying the presence of bladder cancer or an upper tract urothelial carcinoma in the subject when the presence of one or more genetic biomarkers is detected, the presence of the at least one mutation in the TERT promoter, the presence of aneuploidy is detected, or combinations thereof. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the first biological sample and the second biological sample are the same; the first biological sample and the third biological sample are the same; the second biological sample and the third biological sample are the same; or the first biological sample, the second biological sample, and the third biological sample are the same. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the first biological sample, the second biological sample, or the third biological sample is a urine sample. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the presence of aneuploidy is detected on one

or more of chromosome arms 5q, 8q, or 9p. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the presence of one or more genetic biomarkers in each of: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL is detected. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the presence of one or more genetic biomarkers in one or more of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL is detected using a multiplex PCR-based sequencing assay that comprises: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, detecting the presence of one or more genetic biomarkers, detecting the presence of the at least one mutation in the TERT promoter, or detecting the presence of aneuploidy is performed when the subject is not known to harbor a cancer cell. In some embodiments of methods for identifying the presence of bladder cancer or an upper tract urothelial carcinoma in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[33] In some embodiments, provided herein are methods for identifying the presence of ovarian or endometrial cancer in a subject that include: detecting in a first biological sample obtained from the subject the presence of one or more genetic biomarkers in one or more of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A; detecting the presence of aneuploidy in a second biological sample obtained from the subject; and identifying the presence of ovarian or endometrial cancer in the subject when the presence of one or more genetic biomarkers is detected, the presence of aneuploidy is detected, or both. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the first biological sample and the second biological sample are the same. In some embodiments of methods for identifying the presence of

ovarian or endometrial cancer in a subject, the first biological sample or the second biological sample is a cervical sample or an endometrial sample. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the presence of aneuploidy is detected on one or more of chromosome arms 4p, 7q, 8q, or 9q. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the presence of one or more genetic biomarkers in each of: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A is detected. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the presence of one or more genetic biomarkers in one or more of: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A is detected using a multiplex PCR-based sequencing assay that comprises: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the methods further include detecting in a circulating tumor DNA (ctDNA) sample obtained from the subject the presence of at least one genetic biomarker in one or more of the following genes: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, or TP53. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the presence of one or more genetic biomarkers or detecting the presence of aneuploidy is performed when the subject is not known to harbor a cancer cell. In some embodiments of methods for identifying the presence of ovarian or endometrial cancer in a subject, the subject is administered one or more therapeutic interventions (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, and/or an immune checkpoint inhibitor).

[34] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present invention; other,

suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. Headers used in various sections herein are not to be construed as limiting the disclosure of that section to the topic of the header, nor as limiting the disclosure of other sections to topics other than that of the header. Such headers are exemplary, and are simply included for ease of reading. Such headers are further not intended to restrict the applicability or generality of that section to other parts of this disclosure.

[35] Other features and advantages of the invention will be apparent from the following detailed description and figures, and from the claims.

DESCRIPTION OF THE DRAWINGS

[36] Figure 1 contains a schematic overview showing a CancerSEEK test for the detection and localization of cancers.

[37] Figure 2 contains graphs showing the development of a PCR-based assay to identify tumor-specific mutations in plasma samples. Colored curves indicate the proportion of cancers of the eight types evaluated in this study that can be detected with an increasing number of short (< 40 bp) amplicons. The sensitivity of detection increases with the number of amplicons but plateaus at ~ 60 amplicons. Colored dots indicate the fraction of cancers detected using the 61-amplicon panel used in 805 cancers evaluated in our study, which averaged 82% (see main text). Publicly available sequencing data was obtained from the Catalog of Somatic Mutations in Cancer (COSMIC) repository.

[38] Figure 3 contains a graph showing the distribution of the number of detectable mutations within the 805 primary tumors evaluated.

[39] Figure 4 contains graphs showing the performance of CancerSEEK. (A) A receiver operator characteristic (ROC) curve for CancerSEEK. The red point on the curve indicate the test's average performance (61%) at > 99% specificity. Error bars represent 95% confidence intervals for sensitivity and specificity at this particular point. The median performance

among the 8 cancer types assessed was 70%, as noted in the main text. (B) Sensitivity of CancerSEEK by stage. Error bars represent standard errors of the median. (C) Sensitivity of CancerSEEK by tumor type. Error bars represent 95% confidence intervals.

[40] Figure 5 contains waterfall plots of the ctDNA and eight protein features used in CancerSEEK illustrate the separation between healthy donors and healthy patients. Values are sorted from high (left) to low (right). Each column represents an individual patient sample (red, cancer patient; blue, healthy control).

[41] Figure 6 contains a graph showing the principle component analysis of the ctDNA and eight protein features used in CancerSEEK. Each dot represents an individual patient sample (red, cancer patient; blue, healthy control).

[42] Figure 7 contains graphs showing the effect of individual CancerSEEK features on sensitivity. (A) Sensitivity of CancerSEEK by tumor type as in Fig. 4C. (B-J) Each panel displays the sensitivity achieved when a particular CancerSEEK feature is excluded from the logistic regression. The difference in sensitivity relative to that achieved by CancerSEEK reflects the relative contribution of each biomarker to the performance of the CancerSEEK test.

[43] Figure 8 contains a graph showing identification of cancer type by supervised machine learning for patients classified by CancerSEEK as positive. Percentages correspond to the proportion of patients correctly classified by one of the two most likely types (sum of light and dark blue bars) or the most likely type (light blue bar). Predictions for all patients for all cancer types are provided in Table 6. Error bars represent 95% confidence intervals.

[44] Figure 9 contains graphs combining ctDNA *KRAS* mutations with protein biomarkers increases sensitivity for early detection of PDAC. (A) Sensitivities of ctDNA *KRAS* mutations alone, ctDNA *KRAS* mutations plus CA19-9, and ctDNA *KRAS* mutations with CA19-9 and other proteins (combination assay) with respect to AJCC stage. (B) Sensitivities of ctDNA *KRAS* mutations alone, ctDNA *KRAS* mutations plus CA19-9, and ctDNA *KRAS* mutations with CA19-9 and other proteins (combination assay) with respect to tumor size. Error bars represent 95% confidence intervals.

[45] Figure 10 contains a diagram showing that combining ctDNA and protein markers increases sensitivity because a large proportion of patients are detected by only one marker.

Number of patients detected by ctDNA *KRAS* mutations (red circle), CA19-9 (green circle), and the three other protein biomarkers (blue circle), and combinations thereof (overlapping regions). Eighty patients (36% of the total) were not detectable by any of the three makers.

[46] Figure 11 contains a graph showing that mutant allele frequencies (MAFs) of *KRAS* and *TP53* mutations are strongly correlated (Pearson's r = 0.885) in the plasma of the 12 patients whose plasma contained detectable amounts of both mutations, providing validation of the reliability of the ctDNA assay and its quantitative nature. Shaded region represents the 95% confidence interval.

[47] Figure 12 contains a Kaplan–Meier survival plot of the 221 PDAC patients included in this study stratified by AJCC stage (stage IA or IB: blue curve, stage IIA or IIB: red curve).

[48] Figure 13 contains graphs showing correlations between triplex assay markers and tumor size. (A) KRAS mutations were found more frequently in larger tumors than smaller tumors, but the mutant allele frequency did not correlate with tumor size (Pearson's r = 0.039). (B) In patients with elevated CA19-9, CA19-9 plasma concentration weakly correlates with tumor size (Pearson's r = 0.287). (C-E) Plasma levels of CEA, HGF, and OPN were less dependent on tumor size than KRAS mutations or CA19-9 (CEA Pearson's r = 0.153; HGF Pearson's r = 0.037; OPN Pearson's r = 0.018). Shaded regions represent 95% confidence intervals.

[49] Figure 14 contains graphs showing that levels of prolactin (G) and midkine (E) were significantly elevated in samples that were collected after the administration of anesthesia but before surgical excision. In contrast, no difference was observed in the proportion of samples with mutant KRAS ctDNA (A), CA19-9 plasma concentration (B), CEA plasma concentration (C), HGF plasma concentration (D), and OPN plasma concentration between samples that were collected before or after the administration of anesthesia. N.S. not significant, $P > 0.05$ (Exact permutation t-test).

[50] Figure 15 contains a graph showing fold change in protein biomarker levels from 29 pairs plasma samples collected before and immediately after the administration of anesthesia. Of the six markers evaluated, only prolactin and midkine were found to be elevated by

anesthesia, in perfect according with the correlation between collection site and protein levels.

[51] Figure 16 contains Kaplan–Meier survival plots stratified by independent predictors of overall survival identified by multivariate analysis: (A) combination assay status (HR = 1.76, 95% CI, 1.10–2.84, p = 0.018); (B) grade of differentiation (poorly differentiated, HR = 1.72, 95% CI 1.11–2.66, p = 0.015); (C) lymphovascular invasion (present, HR = 1.81, 95% CI 1.06 – 3.09, p = 0.028); (D) nodal disease (present, HR = 2.35, 95% CI 1.20 – 4.61, p = 0.013); (E) margin status (HR = 1.59, 95% CI 1.01 – 2.55, p = 0.050)

[52] Figure 17 contains receiver operator characteristic (ROC) curves for (A) KRAS mutations, (B) CA19-9, (C) CEA, (D) HGF, (E) OPN, and (F) Combination assay. (A-E) ROC curves demonstrate the performance of each combination assay biomarker individually. The red points on the curves indicate the marker performance at the thresholds used in the combination assay. Error bars represent 95% confidence intervals for sensitivity and specificity at the particular threshold (red font). (D) ROC curves demonstrating the performance of the combination assay when the KRAS threshold was varied and CA19-9, CEA, HGF, and OPN thresholds were fixed at the levels used in the combination assay (black curve), the CA19-9 threshold was varied and KRAS, CEA, HGF, and OPN thresholds were fixed at the levels used in the combination assay (red curve), the CEA threshold was varied and KRAS, CA19-9, HGF, and OPN thresholds were fixed at the levels used in the combination assay (blue curve), the HGF threshold was varied and KRAS, CA19-9, CEA, and OPN thresholds were fixed at the levels used in the combination assay (green curve), and the OPN threshold was varied and KRAS, CA19-9, CEA, and HGF thresholds were fixed at the levels used in the combination assay (orange curve). The intersection of these three curves designates the overall performance of the triplex assay (64% sensitivity, 99.5% sensitivity).

[53] Figure 18 shows performance of marker panel for identifying cancer in 8 cancer types. (A) Numerical data. (B) Graphical data.

[54] Figure 19 contains a schematic of an exemplary PapSEEK test for the detection of tumor DNA in the Pap brush, Tao brush, and plasma samples of patients with endometrial or ovarian cancers. Tumor cells shed from ovarian or endometrial cancers are carried into the

uterine cavity, where they can be collected by the Tao brush. The tumor cells that pass down into the endocervical canal can be captured by the Pap brush used in the routine Pap test. These brushes are dipped into a liquid fixative, from which DNA is isolated and sequenced. The sequences are analyzed for somatic mutations and aneuploidy. Additionally, tumor DNA shed into the bloodstream can be detected by ctDNA analysis.

[55] Figure 20 contains graphs showing detection of aneuploidy and somatic mutations (PapSEEK) in Pap brush (A) and Tao brush samples (B) from healthy controls and patients with endometrial and ovarian cancers. Error bars represent 95% confidence intervals.

[56] Figure 21 contains Venn diagrams showing that combined testing for somatic mutations and aneuploidy increased sensitivity for both ovarian and endometrial cancers, in the Pap (A) as well as the Tao brush (B) samples. For ovarian cancer, combined testing of Pap brush and plasma samples also increased sensitivity compared to testing either sample type alone (C).

[57] Figure 22 contains graphs showing detection of endometrial (A) or ovarian cancers (B) in Pap or Tao brush samples with PapSEEK, by stage. Error bars represent 95% confidence intervals.

[58] Figure 23 contains a graph showing detection of ovarian cancer in Pap and plasma samples. Error bars represent 95% confidence intervals.

[59] Figure 24 contains a graph showing detection of endometrial and ovarian cancers with PapSEEK in the Pap brush, Tao brush, and plasma samples. Error bars represent 95% confidence intervals.

[60] Figure 25 contains a schematic drawing of an exemplary approach used to evaluate urinary cells in this study.

[61] Figure 26 contains a flow diagram indicating the number of patients in the Early Detection Cohort and the Surveillance Cohort with summaries of the data. Cytology was performed on a subset of the patients.

[62] Figure 27 contains graphs showing the fraction of mutations found in the ten-gene panel in 231 urinary cell samples assessed in the Early Detection Cohort (A) and 132 urinary cell samples assessed in the Surveillance Cohort (B).

[63] Figure 28 contains Venn Diagrams of the distribution of samples that were positive by each of the three assays for the Early Detection Cohort (A) and the Surveillance Cohort (B). URO = Ten gene panel, *TERT* = *TERT* promoter region, ANEU = Aneuploidy test.

[64] Figure 29 contains bar graphs of the lead time between a positive UroSEEK test and the detection of disease at the clinical level in the Early Detection Cohort (A) and the Surveillance Cohort (B).

[65] Figure 30 contains bar graphs showing the performance of cytology compared to UroSEEK in diagnosis of low and high grade urothelial neoplasms in the Early Detection Cohort and the Surveillance Cohort.

[66] Figure 31 contains a schematic diagram of an exemplary non-invasive detection of upper tract urothelial cancer (UTUC) through genetic analysis of urinary cell DNA. Upper urinary tract tumors arise in the renal pelvis and/or ureter and are in direct contact with urine. Urine contains a mixture of normal cells that are constitutively shed from various sites along the urinary system, along with malignant cells when present (blue). The UroSEEK assay relies on mutational analyses of genes frequently mutated in urinary cancers along with a determination of chromosome losses and gains.

[67] Figure 32 contains a Venn diagram showing the distribution of positive results for each of the three UroSEEK assays.

[68] Figure 33 contains a graph showing a comparison of copy number variations in matched tumor and urinary cell DNA samples from the UTUC cohort. Primary tumor is shown in the top of each section and urinary cell DNA on the bottom. Chromosome gains are in blue while losses are in red. Significance levels for gains and losses were set at Z scores >3 and <-3, respectively. X axis is Chromosome Arm. Y axis is Z score.

[69] Figure 34 contains a graph showing the fraction of total mutations for each gene in the 10-gene panel used to analyze urinary cell DNA from UTUC patients.

[70] Figure 35 contains graphs showing comparisons of copy number variations in matched tumor and urinary cell DNA samples from four individual UTUC patients (Figs. 35A-D). Z-scores >3 or <-3 were considered as significant for chromosome gains or losses, respectively. N.S. indicates not significant. Data for all 56 patients are provided in Table 28.

[71] Figure 36 contains a schematic showing an overview of an exemplary WALDO approach. (A) A single primer pair amplifies ~38,000 long interspersed nucleotide elements (LINEs). (B) A test sample is matched to seven euploid samples with genomic DNA of similar size. (C) The genome is divided into 4361 intervals, each of 500-kb in size. (D) The reads within these 500-kb genomic intervals in the euploid samples are grouped into 4361 clusters. All the 500-kb genomic intervals in the clusters have similar read depths. (E) The reads from each of the 500-kb genomic intervals in the test sample are placed into the pre-defined clusters. (F) Statistical tests, including a Support Vector Machine (SVM)-based algorithm, are used to determine whether the total reads from all the 500-kb genomic intervals on each chromosome arm are distributed as expected if the sample was euploid. The statistical tests are based on the observed distribution of reads within the clusters of the test sample, not by comparison to the reads in euploid samples. (G) Germline sequence variants at sites of known common polymorphisms within the LINEs provide information about arm-level allelic imbalance that can also be used to assess aneuploidy of individual chromosome arms. These same polymorphisms can be used to determine whether any two samples are derived from the same individual. (H) When there is a matched normal sample from the same individual available, WALDO can detect the number and nature of single base substitutions and insertions and deletions within the LINEs.

[72] Figure 37 contains a graph showing individual chromosome arm gains and losses that were identified in nine cancer types. The average fraction of tumors with a gain or loss in each chromosome arm are depicted in the figure. The same nine tumor types were analyzed in both cohorts, but there was no overlap between the samples assessed by WALDO (red) or GISTIC (blue). WALDO employed the data from LINE sequencing of tumors reported here while GISTIC employed the data from Affymetrix SNP6.0 arrays provided by the TCGA.

[73] Figure 38 shows aneuploidy detected in plasma samples from cancer patients. Receiver operating characteristics (ROC) and area under the curve (AUC) are shown for three ranges of neoplastic cell fractions. True positives were defined as those samples from cancer patients scoring positive while false positives were defined as those from normal individuals scoring positive. The neoplastic cell fraction of each plasma samples was estimated from driver gene sequencing data as described in the text. (A) Samples with

neoplastic cell fractions <0.5%. (B) Samples with neoplastic cell fractions ranging from 0.5-1%. (C) Samples with neoplastic cell fractions > 1%.

[74] Figure 39 contains graphs showing aneuploidy correlation comparisons of cancers detected using FAST-SeqS and WALDO compared to The Cancer Genome Atlas (TCGA) using Affymetrix SNP6.0 and GISTIC across 9 different cancer types. (A) Correlation of the fraction of chromosome arm gains. (B) Correlation of the fraction of chromosome arm losses.

[75] Figure 40 contains graphs showing aneuploidy comparisons of individual cancer types that were detected using the WALDO framework compared to The Cancer Genome Atlas (TCGA). For each cancer type, the fraction of each chromosome arms gained and lost were compared. The correlation of these gains and losses in WALDO to TCGA was compared. Each sub-figure represents a different cancer type. (A) Breast invasive carcinoma (BRCA). (B) Colon adenocarcinoma and rectum adenocarcinoma (COAD; COADREAD). (C) Esophageal carcinoma (ESCA). (D) Head and neck squamous cell carcinoma (HNSC). (E) Liver hepatocellular carcinoma (LIHC). (F) Pancreatic adenocarcinoma (PAAD). (G) Ovarian serous cystadenocarcinoma (OV). (H) stomach adenocarcinoma (STAD). (I) Uterine corpus endometrial carcinoma (UCEC).

[76] Figure 41 contains graphs showing Trisomy 21 performance as a function of read depth. DNA samples from individuals with trisomies were physically mixed at a ratio of 2 ng of normal DNA and ~0.2 ng of Trisomy 21 DNA and normal peripheral white blood cell (WBC) samples. The mixtures were created to replicate typical fetal fractions in noninvasive prenatal testing (approximately 10%). Using polymorphisms in the LINE-amplicons, the trisomy admixture of the samples was estimated to range from 7.7% to 10.4%). Using a z threshold of 2.5, sensitivities (A) and specificities (B) were calculated for a range of read depths.

[77] Figure 42 contains a graph showing a comparison of the total number of somatic single base substitutions (SBS) that were detected in Exome Sequence vs WALDO.

[78] Figure 43 contains a graph showing a comparison of the percentages of single base substitution mutations that are A:T>T:A Mutations that were detected via Exome sequencing vs WALDO.

[79] Figure 44 contains graphs showing the spectrums of single base substitution (SBS) mutations. (A) SBS identified by WALDO. (B) SBS identified by exome sequencing.

[80] Figure 45 contains a graph showing a distribution of the number of genomic intervals included in a cluster for a representative normal WBC sample.

[81] Figure 46 contains graphs showing distributions of scaled reads. (A) Distribution of scaled reads illustrating that reads in FAST-SeqS amplicon sequencing were not randomly distributed. (B) Representative cluster for a normal WBC sample illustrating the normality of the scaled reads in a cluster. (C) Representative cluster for an aneuploid primary tumor sample illustrating the normality of the scaled reads in a cluster.

[82] Figure 47 contains graphs showing an example of the statistical procedure to identify a chromosome arm gain or loss.

[83] Figure 48 contains a graph showing an empirical estimation of the variance of the B-allele frequency for heterozygous SNPs as a function of read depth. Increasing UID depth improved the estimation of the B-allele frequency for heterozygous SNPs.

[84] Figure 49 shows an exemplary pseudocode to generate synthetics with one arm alteration.

[85] Figure 50 shows an exemplary pseudocode to generate synthetics with multiple arm alterations.

[86] Figure 51 contains a graph showing a distribution of genome wide aneuploidy scores (SVM Scores) as a function of read depth. Lower read depth was more likely to produce higher scores, and failing to correct for UID depth, can produce false positives.

[87] Figure 52 contains a schematic showing an exemplary overview of a bottleneck sequencing methodology. Each color at the top of the figure represents double-stranded DNA from a genome of one cell within a population. Random, nonclonal point mutations (red) are private to individual cells. In contrast, clonal reference changes (A in black) are present in all genomes within the cell population. (step 1) Random shearing generates variably sized DNA molecules. (step 2) Noncomplementary single-stranded regions of the Illumina Y-adapters (P5 in gray and P7 in black) are represented as forked structures ligated to both ends of each DNA molecule. (step 3) Dilution decreases the number of DNA molecules (five are shown) from the original population in a random manner. Ends of the DNA molecules align uniquely

to the reference genome. Mapping coordinates are used as unique molecule "barcodes" during data processing. (step 4) PCR primer (black arrowhead) anneals and primer extends (hashed lines) the Watson and Crick template of the original DNA molecule independently. The red asterisk represents an error generated during PCR of the library. (step 5) Watson and Crick templates generate two families of PCR duplicates. Orientation of P5 (gray) and P7 (black) containing adapters to the DNA molecule (insert) distinguishes the two families. P5 and P7 sequences dictate which end will be sequenced in read 1 vs. read 2, respectively, on the Illumina flow cell. Red asterisks represent the PCR error propagated in the Watson but not the Crick family members. In contrast to artifacts, real mutations (C:G mutation in red) will be present in both the Watson and Crick family members. (step 6) The BotSeqS pipeline identifies and quantifies the number of unique DNA molecules and point mutations (C:G in red) in the sequencing data by eliminating artifacts and clonal changes (A:T in black).

[88] Figure 53 contains graphs showing nuclear point mutations increase in normal tissues from individuals with defects in DNA repair or with exposure to environmental carcinogens compared with controls. (A) Comparison of point mutation prevalences in nuclear (*Left*) and mitochondrial (*Right*) genome in age-matched normal colon epithelium (filled circle) with different DNA mismatch repair genotypes ($PMS2^{+/+}$ or $PMS2^{-/-}$) or in age-matched normal kidney cortex (filled square) without (none) or with (aristolochic acid or smoking) carcinogen exposure. Red lines represent average. $*P < 0.05$, *t* test; $**P < 0.001$ and $***P < 0.0001$, one-way ANOVA with Bonferroni multiple comparison posttest; ns, not significant, indicates $P > 0.05$. (B) Stacked columns representing the substitution frequencies (*y* axis) of each substitution out of the six possible types (see legend). Cohort labels are indicated in *A* directly above each column. Number of substitutions (N) generating each mutational spectrum is indicated on the *x* axis. n.d., not determined due to an insufficient number of mutations ($N = 7$) for mutational spectrum analysis. $*P = 0.04$, Fisher's exact test; $**P = 2.6 \times 10^{-8}$ and $***P = 1.5 \times 10^{-16}$, Fisher's exact test with Bonferroni multiple comparison correction; ns, not significant, indicates $P > 0.05$. All statistical tests in this figure were two-tailed.

[89] Figure 54 contains graphs showing normal human tissues accumulate point mutations over a lifetime with genome-specific and tissue-specific mutational patterns. Point mutation

prevalences in nuclear (Top) and mitochondrial (Bottom) genome measured in four normal tissue types (brain frontal cortex of 9 individuals, kidney cortex of 5 individuals, colon epithelium of 11 individuals, and duodenum of 1 individual). Twenty-six total individuals were assessed, with each individual contributing to one normal tissue type. Pie chart *Insets* show the prevalences of each substitution out of the six possible substitution types (see pie chart legend, right side). Each pie chart was compiled from the individuals represented in their respective scatter plots, with the exception that duodenum was omitted. The number of substitutions generating the pie charts for the nuclear genome was $n = 31$ for brain, $n = 73$ for kidney, and $n = 94$ for colon, and for the mitochondrial genome was $n = 181$ for brain, $n = 299$ for kidney, and $n = 116$ for colon.

[90] Figure 55 contains an assessment of duplicate counts with MiSeq™ prerun. Histograms showing the distribution of family members (PCR duplicates from individual template molecules, shown on the x-axis). Either two or three serial dilutions (103, 104, 105, or 106) were evaluated on the MiSeq™ for six samples (COL373, SA_117, KID038, BRA01, BRA04, BRA07) to generate ~5 M properly paired reads per library. Family member counts were determined here using Picard's Estimate Library Complexity program. Libraries generated from the 105 dilution (blue) were subsequently used for the final HiSeq™ run reported in this study. Note that the HiSeq™ distribution is expected to shift to the right compared to the MiSeq™ distribution due to the increase of clusters sequenced per library (~5 M clusters scaled to ~70 M clusters). For example, the BotSeqS libraries from the 106 dilution (red) were not used because the members per family would be too high on a HiSeq™ run, limiting the number of different families that could be evaluated with a given amount of sequencing.

[91] Figure 56 contains a graph showing family member counts of 44 BotSeqS libraries reported in this study. Horizontal box and whisker plots for 44 BotSeqS libraries (y-axis) and number of members per family (duplicate count, x-axis). White boxes represent the first to third quartile range with the hash mark indicating the median. Whiskers represent 1.5*IQR (interquartile range) and data points outside the whiskers are shown as outliers. An average of 3.97 M (range 0.38 to 10.91 M) unfiltered families per library were assessed. Families were identified through the BotSeqS pipeline using the genomic mapping coordinates as

unique molecule identifiers. Names in blue indicate technical replicate samples. Note that Bot01-Bot06 and Bot23-28 were performed on the same samples with a 100-fold difference in dilution (see Table 43).

[92] Figure 57 contains graphs showing Consideration of both Watson and Crick family members decreases artifacts, specifically G>T transversions. (A) Nuclear point mutation frequencies (y-axis) considering mutations observed in "Watson AND/OR Crick" (black circle) or "Watson AND Crick" families (black square) in normal tissues derived from brain frontal cortex (left side), kidney cortex (middle, shaded), or colon epithelium (right side). Specifically, "OR" mutations represent ≥ 90% mutation fraction in Watson family with a minimum of two Watson reads *or* ≥ 90% mutation fraction Crick family with a minimum of two Crick reads. Note that the "OR" mutations have only the Watson or Crick families represented in the data but not both. "AND" mutations represent ≥ 90% mutation fraction in Watson family with a minimum of two Watson reads *and* ≥ 90% mutation fraction Crick family with a minimum of two Crick reads. "AND" mutations are an internal subset of the "AND/OR" dataset, which is a modified version of the BotSeqS pipeline. Twenty-five individuals are organized by increasing age within each tissue. (B) Pie charts of the frequencies of each nuclear substitution out of the six possible substitution types (see legend) from (a) considering Watson AND/OR Crick (top pies) or Watson AND Crick (bottom pies) in each normal tissue type. The number of nuclear mutations generating mutational spectra for Watson AND/OR Crick was n=616 for brain, n=1,257 for kidney, n=2,542 for colon and for Watson AND Crick was n=33 for brain, n=74 for kidney, n=99 for colon.

[93] Figure 58 contains graphs showing rare point mutations accumulate in normal tissues of the colon more than in brain. Point mutation frequency (y-axis) in nuclear (top graph) and mitochondrial (bottom graph) genome in normal brain frontal cortex (left side) and normal colon epithelium (right side) grouped by age (young infant/child in green, young adult in purple, old adult in blue). Averages of each age cohort are shown with error bars representing the standard deviations. Two-way ANOVA with Bonferroni multiple comparison post-test was performed using GraphPad Prism™ 5.0f software with *P* values reported above bars. n.s. (not significant) indicates $P > 0.05$. For brain, the number of individuals and average age of group are as follows- infant/child: n=3, 3.5 years old (y/o) (BRA01, BRA02, BRA03); young

adult: n=3 individuals, 22 y/o (BRA04, BRA05, BRA06); and old adult: n=3, 93 y/o (BRA07, BRA08, BRA09). For colon, infant/child: n=2, 5.5 y/o (COL229, COL231); young adult: n=6, 28 (COL235, COL236, COL237, COL373, COL374, COL375); old adult: n=3, 96 y/o (COL232, COL233, COL234).

[94] Figure 59 contains a graph showing Mitochondrial and nuclear point mutation frequencies in normal tissues from the same individual. Data points represent the ratio between mitochondrial to nuclear point mutation frequencies (y-axis) within the normal tissue of the same individual. Individuals were grouped into four cohorts (x-axis) with n=24 individuals for Control (see Table 51), n=2 individuals (COL238, COL239) for DNA repair defect *PMS2-/-*, n=3 individuals (AA_105, AA_124, AA_126) for aristolochic acid exposure, and n=3 individuals (SA_117, SA_118, SA_119) for smoking exposure. One ratio from the control cohort (COL229) was zero and omitted from this analysis. Average (red line) ratio for each cohort is 24.5 for Control, 0.5 for DNA repair defect *PMS2-/-*, 1.1 for aristolochic acid exposure, and 2.0 for smoking exposure. $*P < 0.05$, $**P < 0.01$, one-way ANOVA with Bonferroni multiple comparison post-test.

[95] Figure 60 contains graphs showing Normal tissues and tumors derived from the same tissue type have similar mutation spectra. (A) Pie charts of nuclear and mitochondrial frequencies of each substitution out of the six possible substitution types (see legend) comparing normal (left side) and tumors (right side) derived from colon (top) and kidney (bottom). "Normal" represents the rare mutational spectra data derived from normal tissues shown in Figure 54. "Nuclear tumor mutations" represent clonal mutation data from colorectal carcinomas (COAD/READ) or clear cell renal carcinoma (KIRC) from the TCGA dataset #!Synapse:syn1729383 found at the website of synapse.org. "mtDNA tumor mutations" from colon and kidney were acquired from “colorectal” and “renal” tumor types in supplementary file 2 of Ju *et al.* (2014 eLife 3). For normal tissues, the number of substitutions assessed was as follows: colon nuclear n=94 from 13 individuals, colon mtDNA n=116 from 12 individuals, kidney nuclear n=73 from 7 individuals, and kidney mtDNA n=299 from five individuals. For tumor tissue, the number of substitutions assessed was as follows: colorectal carcinoma nuclear n=18,538 from 193 individuals, colorectal carcinoma mtDNA n=64 from 76 individuals, clear cell renal cell carcinoma nuclear n=24,559 from 417

individuals, and renal carcinoma mtDNA n=16 from 23 individuals. (B) Principal component analysis (PCA) of mutational spectra from the cohorts indicated in (A). PCA performed and graphed using R software.

[96] Figure 61 contains a schematic showing elements of Safe-SeqS. In the first step, each fragment to be analyzed is assigned a unique identification (UID) sequence (metal hatch or stippled bars). In the second step, the uniquely tagged fragments are amplified, producing UID-families, each member of which has the same UID. A super-mutant is defined as a UID-family in which ≥95% of family members have the same mutation.

[97] Figure 62 contains a schematic showing an exemplary Safe-SeqS with endogenous UIDs plus capture. The sequences of the ends of each fragment produced by random shearing (variously shaded bars) serve as the unique identifiers (UIDs). These fragments are ligated to adapters (earth hatched and cross hatched bars) so they can subsequently be amplified by PCR. One uniquely identifiable fragment is produced from each strand of the double-stranded template; only one strand is shown. Fragments of interest are captured on a solid phase containing oligonucleotides complementary to the sequences of interest. Following PCR amplification to produce UID-families with primers containing 5' "grafting" sequences (adhesive filled and light stippled bars), sequencing is performed and super-mutants are defined as in Fig. 61.

[98] Figure 63 contains a schematic showing an exemplary Safe-SeqS with exogenous UIDs. DNA (sheared or unsheared) is amplified with a set of gene-specific primers. One of the primers has a random DNA sequence (e.g., a set of 14 N's) that forms the unique identifier (UID; variously shaded bars), located 5' to its gene-specific sequence, and both have sequences that permit universal amplification in the next step (earth hatched and cross hatched bars). Two UID assignment cycles produce two fragments - each with a different UID - from each double-stranded template molecule, as shown. Subsequent PCR with universal primers, which also contain "grafting" sequences (adhesive filled and light stippled bars), produces UID-families which are directly sequenced. Super-mutants are defined as in the legend to Fig. 61.

[99] Figure 64 contains graphs showing single base substitutions identified by conventional and Safe-SeqS analysis. The exogenous UID strategy depicted in Fig. 63 was

used to produce PCR fragments from the CTNNB1 gene of three normal, unrelated individuals. Each position represents one of 87 possible single base substitutions (3 possible substitutions/base x 29 bases analyzed). These fragments were sequenced on an Illumina GA IIx instrument and analyzed in the conventional manner (A) or with Safe-SeqS (B). Safe-SeqS results are displayed on the same scale as conventional analysis for direct comparison; the inset is a magnified view. Note that most of the variants identified by conventional analysis are likely to represent sequencing errors, as indicated by their high frequency relative to Safe-SeqS and their consistency among unrelated samples.

[100] Figure 65 contains a schematic showing an exemplary Safe-SeqS with endogenous UIDs plus inverse PCR. The sequence of the ends of each fragment produced by random shearing serve as unique identifiers (UIDs; variously shaded bars). These fragments are ligated to adapters (earth hatched and cross hatched bars) as in a standard Illumina library preparation. One uniquely tagged fragment is produced from each strand of the double-stranded template; only one strand is shown. Following circularization with a ligase, inverse PCR is performed with gene-specific primers that also contain 5' "grafting" sequences (adhesive filled and lightly stippled bars). This PCR produces UID-families which are directly sequenced. Super-mutants are defined as in Fig. 61.

[101] Figure 66 contains graphs showing single base substitutions position vs. error frequency in oligonucleotides synthesized with phosphoramidites and Phusion. A representative portion of the same 31-base DNA fragment synthesized with phosphoramidites (A) or Phusion polymerase (B) was analyzed by Safe-SeqS. The means and standard deviations for seven independent experiments of each type are plotted. There was an average of 1,721 ± 383 and 196 ± 143 SBS super-mutants identified in the phosphoramidite-synthesized and Phusion-generated fragments, respectively. The y-axis indicates the fraction of the total errors at the indicated position. Note that the errors in the phosphoramidite-synthesized DNA fragment were consistent among the seven replicates, as would be expected if the errors were systematically introduced during the synthesis itself. In contrast, the errors in the Phusion-generated fragments appeared to be heterogeneous among samples, as expected from a stochastic process (Luria and Delbruck, 1943 *Genetics* 28:491-511).

[102] Figure 67 contains a graph showing UID-family member distribution. The exogenous UID strategy depicted in Fig. 63 was used to produce PCR fragments from a region of CTNNB1 from three normal, unrelated individuals (Table 53); a representative example of the UID-families with ≤ 300 members (99% of total UID-families) generated from one individual is shown. The y-axis indicates the number of different UID-families that contained the number of family members shown on the x-axis.

[103] Figure 68 contains an exemplary Random Forest model tree for classification of tumor location. (A) shows the complete tree, and (B) – (K) contain magnified images of sections of the complete tree as indicated in (A).

[104] Figure 69 contains exemplary rules for tissue recognition extracted from the random forest model. The randomForest function from the randomForest package (v4.6-14) was applied to protein data from the CancerSEEK project. The protein data have 33 proteins and the 626 tumor samples that were predicted correctly as cancer by CancerSEEK. The values of each protein were set to zero if they were less than the 25th quantile of values in the normal samples. To get the specific decision rules (Table 58), the inTrees package (v1.2) was applied to extract all rules of length less than or equal to 6 from all 500 trees created by randomForest. From this set of rules, using the functions (selectRuleRRF, buildLearner, applyLearner) from the inTrees package, relevant and non-redundant rules were selected, a classifier was created and applied to the data, and the final list of rules was extracted. This final list of rules performs similarly to the full random forest and it represents a good approximation of the full forest.

DETAILED DESCRIPTION

Definitions

[105] As used herein, the word "a" before a noun represents one or more of the particular noun. For example, the phrase "a genetic alteration" encompasses "one or more genetic alterations."

[106] As used herein, the term "about" means approximately, in the region of, roughly, or around. When used in conjunction with a numerical range, the term "about" modifies that range by extending the boundaries above and below the numerical values set forth. In

general, the term "about" is used herein to modify a numerical value above and below the stated value by a variance of 10%.

[107] As used herein, the term "aneuploidy" refers to the condition of having less than or more than the natural diploid number of chromosomes, or any deviation from euploidy.

[108] As used herein in the context of circulating tumor DNA or cell-free DNA, the phrase "derived from a gene" means that the circulating tumor DNA is shed from tumor cells (e.g., tumor cells that have lysed or otherwise died). For example, circulating tumor DNA "derived from a KRAS gene" means that the circulating tumor DNA was originally present in a tumor cell. When detecting a mutation that is present in circulating tumor DNA derived from a gene, it is not necessary to have first identified the mutation in the tumor cell itself.

[109] As used herein, the phrases "genetic biomarker" and "genetic marker" refer to a nucleic acid that is characteristic, alone in combination with other genetic or other biomarkers, of cancer in a subject. A genetic biomarker can include a modification (e.g., a mutation) in a gene. Examples of modifications include, without limitation, single base substitutions, insertions, deletions, indels, translocations, and copy number variations. In some embodiments, a genetic biomarker includes a modification (e.g., an inactivating modification) in a tumor suppressor gene. In some embodiments, a genetic biomarker includes a modification (e.g., an activating modification) in an oncogene. Various genetic biomarkers and genetic biomarker panels are described in more detail herein.

[110] As used herein, the terms "mutation", "genetic modification", and "genetic alteration" are used interchangeably to indicate a change in a wild type nucleic acid sequence. For example, in some embodiments, methods of detecting a mutation in cell-free DNA (e.g., ctDNA) are described herein. It is to be understood that such methods can be interchangeably described as detecting mutations, genetic modifications, or genetic alterations.

[111] As used herein, the phrases "protein biomarker", "protein marker", "peptide biomarker", and "peptide marker" refer to a protein that is characteristic, alone in combination with other protein or other biomarkers, of cancer in a subject. In some embodiments, a protein biomarker includes an elevated level of the protein in a subject (e.g., a subject having cancer regardless of whether the subject is known to have cancer) as

compared to a reference subject that does not have cancer. In some embodiments, a protein biomarker includes a decreased level of the protein in a subject (e.g., a subject having cancer regardless of whether the subject is known to have cancer) as compared to a reference subject that does not have cancer. As used herein, the phrase "detecting a protein biomarker" can refer to detecting a level (e.g., an increased level or a decreased level) of the protein biomarker. Various protein biomarkers and protein biomarker panels are described in more detail herein. In some embodiments, peptides that are distinct from a protein biomarker are used in methods provided herein.

[112] As used herein with reference to protein biomarkers, the phrase "elevated level" refers to a level of the protein biomarker that is greater than a reference level of the protein biomarker typically observed in a sample (e.g., a reference sample) from a healthy subject (e.g., a subject that does not exhibit a particular disease or condition). In some embodiments, a reference sample can be a sample obtained from a subject (e.g., a different or reference subject) that does not have a cancer. For example, for a protein biomarker associated with colorectal cancer, a reference sample can be a sample obtained from a different or reference subject that does not have colorectal cancer. In some embodiments, a reference sample can be a sample obtained from the same subject in which the elevated level of a protein biomarker is observed, where the reference sample was obtained prior to onset of the cancer. In some embodiments, such a reference sample obtained from the same subject is frozen or otherwise preserved for future use as a reference sample. In some embodiments, when reference samples have undetectable levels of a protein biomarker, an elevated level can be any detectable level of the protein biomarker. It will be appreciated that levels from comparable samples can be used when determining whether or not a particular level is an elevated level.

[113] As used herein with reference to protein biomarkers, the phrase "reference level" refers to the level of the protein biomarker that is typically present in a healthy subject (e.g., a subject that does not exhibit a particular disease or condition). A reference level of a protein biomarker can be a level that is present in a reference subject that does not exhibit a disease or condition (e.g., cancer). For example, for a protein biomarker associated with colorectal cancer, a reference sample can be a sample obtained from a subject that does not have

colorectal cancer. As another example, a reference level of a protein biomarker can be a level that is present in a subject prior to the onset of the disease or condition (e.g., cancer) in that subject. In some embodiments, a disease or condition can be identified in a subject when the measured or detected level of one or more protein biomarkers is higher than reference level(s) of the one or more protein biomarkers.

[114] As used herein, the term "sensitivity" refers to the ability of a method to correctly identify or diagnose the presence of a disease in a subject (e.g., the sensitivity of a method can be described as the ability of the method to identify the true positive rate or probability of detecting a condition in a subject). For example, when used in reference to any of the variety of methods described herein that can detect the presence of cancer in a subject, a high sensitivity means that the method correctly identifies the presence of cancer in the subject a large percentage of the time. For example, a method described herein that correctly detects the presence of cancer in a subject 95% of the time the method is performed is said to have a sensitivity of 95%. In some embodiments, a method described herein that can detect the presence of cancer in a subject provides a sensitivity of at least 80% (e.g., at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or higher). In some embodiments, methods provided herein that include detecting the presence of one or more members of two or more classes of biomarkers (e.g., genetic biomarkers and/or protein biomarkers) provide a higher sensitivity than methods that include detecting the presence of one or more members of only one class of biomarkers.

[115] As used herein, the term "specificity" refers to the ability of a method to correctly reject the presence of a disease in a subject (e.g., the specificity of a method can be described as the ability of the method to identify the true negative rate or probability of correctly determining that a condition does not exist in a subject. For example, when used in reference to any of the variety of methods described herein that can detect the presence of cancer in a subject, a high specificity means that the method correctly identifies the absence of cancer in the subject a large percentage of the time (e.g., the method does not incorrectly identify the presence of cancer in the subject a large percentage of the time). For example, a method described herein that correctly detects the absence of cancer in a subject 95% of the time the

method is performed is said to have a specificity of 95%. In some embodiments, a method described herein that can detect the absence of cancer in a subject provides a specificity of at least 80% (e.g., at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or higher). In some embodiments, methods provided herein that include detecting the presence of one or more members of two or more classes of biomarkers (e.g., genetic biomarkers and/or protein biomarkers) provide a higher specificity than methods that include detecting the presence of one or more members of only one class of biomarkers.

[116] As used herein, the term "subject" is used interchangeably with the term "patient" and means a vertebrate, including any member of the class mammalia, including humans, domestic and farm animals, and zoo, sports or pet animals, such as mouse, rabbit, pig, sheep, goat, cattle, horse (e.g., race horse), and higher primates. In some embodiments, the subject is a human. In some embodiments, the subject has a disease. In some embodiments, the subject has cancer. In some embodiments, the subject is a human harboring a cancer cell. In some embodiments, the subject is a human harboring a cancer cell, but is not known to harbor the cancer cell. In some embodiments, the subject has a viral disease. In some embodiments, the subject has a bacterial disease. In some embodiments, the subject has a fungal disease. In some embodiments, the subject has a parasitic disease. In some embodiments, the subject has asthma. In some embodiments, the subject has an autoimmune disease. In some embodiments, the subject has graft vs. host disease.

[117] As used herein, the term "treatment" is used interchangeably with the phrase "therapeutic intervention."

[118] Methods of testing DNA isolated or obtained from white blood cells (e.g., white blood cell clones arising during age-associated clonal hematopoiesis (e.g., clonal hematopoietic expansion, also known as clonal hematopoiesis of indeterminate potential or CHIP) or myelodysplasia) for the presence or absence of a genetic mutation that is associated with cancer in order to determine whether that genetic alteration originates from a cancer cell in the subject are generically described herein as "verifying a genetic alteration against white blood cells", "verifying a genetic alteration against DNA from white blood cells", "white blood cell verification", and similar phrases.

Overview

[119] In general, methods and materials for detecting or identifying the presence of cancer in a subject with high sensitivity and specificity as compared to conventional methods of identifying the presence of cancer in a subject are provided herein. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with high sensitivity and specificity are performed on a liquid sample(s) obtained from the subject (e.g., blood, plasma, or serum), whereas conventional methods of identifying the presence of cancer in a subject do not achieve the level of sensitivity, the level of specificity, or both when performed on a liquid sample obtained from the subject. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with high sensitivity and specificity are performed prior to having determined that the subject already suffers from cancer, prior to having determined that the subject harbors a cancer cell, and/or prior to the subject exhibiting symptoms associated with cancer. Thus, in some embodiments, methods provided herein for identifying the presence of cancer in a subject with high sensitivity and specificity are used as a first-line detection method, and not simply as a confirmation (e.g., an "overcall") of another detection method that the subject has cancer.

[120] In some embodiments, methods and materials provided herein provide high sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer). In some embodiments, methods and materials provided herein provide a sensitivity of at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. In some embodiments, methods and materials provided herein provide high sensitivity in detecting a single type of cancer. In some embodiments, methods and materials provided herein provide high sensitivity in detecting two or more types of cancers.

Any of a variety of cancer types can be detected using methods and materials provided herein (see, e.g., the section entitled "Cancers"). In some embodiments, cancers that can be detected using methods and materials provided herein include pancreatic cancer. In some embodiments, cancers that can be detected using methods and materials provided herein include liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. In some embodiments, cancers that can be detected using methods and materials provided herein include cancers of the female reproductive tract (e.g., cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer). In some embodiments, cancers that can be detected using methods and materials provided herein include bladder cancer or upper-tract urothelial carcinomas.

[121] In some embodiments, methods and materials provided herein provide high specificity in the detection or diagnosis of cancer (e.g., a low frequency or incidence of incorrectly identifying a subject as having cancer when that subject does not have cancer). In some embodiments, methods and materials provided herein provide a specificity of at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. As will be understood by those of ordinary skill in the art, a specificity of 99% means that only 1% of subjects that do not have cancer are incorrectly identified as having cancer. In some embodiments, methods and materials provided herein provide high specificity in detecting a single cancer (e.g., there is a low probability of incorrectly identifying that subject as having that single cancer type). In some embodiments, methods and materials provided herein provide high specificity in detecting two or more cancers (e.g., there is a low probability of incorrectly identifying that subject as having those two or more cancer types).

[122] As will be appreciated by those of ordinary skill in the art, an appropriate sensitivity or specificity in the detection or diagnosis of cancer can be chosen based on a variety of factor. As one non-limiting example, a method designed to provide a lower specificity in the

detection or diagnosis of cancer can be designed to have an increased sensitivity. As another non-limiting example, a method designed to provide an increased specificity in the detection or diagnosis of cancer can be designed to have a lower sensitivity. In some embodiments, even a low sensitivity can be advantageous (e.g., in screening a population that is not normally screened). In some embodiments, in populations where cancer (e.g., a particular type of cancer) is prevalent, a method to detect or diagnose the presence of cancer can be designed to have a relatively high sensitivity, even at the cost of decreased specificity. In some embodiments, the sensitivity and specificity of various detection methods provided herein is determined based on the prevalence of the disease in a specific patient population. In example, screening tests for a general patient population not known to have cancer can be chosen to have high specificity (so as to eliminate false positive diagnoses and unnecessary further diagnostic testing and/or monitoring). As another example, screening tests for high risk populations (e.g., populations in which the risk of having or developing cancer is higher than the general population overall, e.g., due to the population engaging or having engaged in in risky behaviors, having risky family histories, experiencing or having experienced risky environments, and the like) cancer can be chosen to have high sensitivity (in order to increase the provide greater certainty of detecting a cancer that is present, even at the expense of additional further diagnostic testing and/or monitoring that may not be appropriate for the general population). As one non-limiting example, a test with 90% sensitivity and 95% specificity will have positive predictive value (PPV) of 15% and a negative predictive value (NPV) of > 99% in a population with prevalence of 0.01%, while both predictive values can be greater than 99% if the prevalence was 40% (high risk population). PPV can be calculated as follows: # true positives (TP)/(#true positives + # false positives). PPV can also be calculated as follows: (sensitivity X prevalence)/(sensitivity X prevalence) + ((1-specificity) x (1-prevalnce)). NPV can be calculated as follows: # true negatives / # of negative calls. PPV can also be calculated as follows: specificity X (1-prevalence)/ ((1-sensitivity) x prevalence) + (specificity X (1-prevalence). See, e.g., Lalkhen and McCluskey, Clinical tests: sensitivity and specificity, Continuing Education in Anaesthesia, Critical Care & Pain, Volume 8, 2008, incorporated herein by reference in its entirety.

Methods of Detecting

[123] Provided herein are methods and materials for detecting the presence of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of both simultaneous and sequential testing for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[124] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include detecting the presence of one or more members

of a class of genetic biomarkers in a sample obtained from a subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from a subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from a subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[125] In some embodiments, methods provided herein include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[126] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy. Alternatively, two or more samples can be obtained from a subject,

and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy. As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy. As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample).

[127] In some embodiments, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy (e.g., detected by any of the variety of methods disclosed herein) in a sample obtained from a subject is associated with a disease and indicates the subject suffers from that disease. In some embodiments, a subject is diagnosed with a disease when the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy (which biomarkers and/or aneuploidy are associated with a disease) in a sample obtained from a subject is detected. In some embodiments, the disease is cancer (e.g., any of the variety of cancers described herein). In some embodiments, a subject is not known to have a disease (e.g., cancer) prior to detecting the presence of one or more members of one or more classes of biomarkers and/or the

presence of aneuploidy. In some embodiments, a subject is not known to harbor a cancer cell prior to detecting the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy. In some embodiments, a subject does not exhibit symptoms associated with cancer prior to detecting the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy.

Methods of Diagnosis

[128] Also provided herein are methods and materials for diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[129] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more

classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[130] In some embodiments, methods provided herein include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments,

methods provided herein include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of aneuploidy in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein include diagnosing the presence cancer in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[131] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or

more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed as having cancer (e.g., is identified as having cancer) when the presence of the one

or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[132] In some embodiments of diagnosing or identifying the presence of a disease (e.g., cancer) in a subject (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate for further diagnostic testing. In some embodiments of diagnosing or identifying the presence of a disease (e.g., cancer) in a subject (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate for increased monitoring. In some embodiments of diagnosing or identifying the presence of a disease (e.g., cancer) in a subject (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate that will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein). In some embodiments of diagnosing or identifying the presence of a disease (e.g., cancer) in a subject (e.g., using any of the variety of methods described herein), the subject is also administered a treatment (e.g., any of the variety of therapeutic interventions described herein).

Methods of Identifying a Subject as Being at Risk of Having or Developing a Disease

[133] Provided herein are methods and materials for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as being at risk (e.g., increased

risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[134] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include identifying a subject as being at risk

(e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[135] In some embodiments, methods provided herein for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of aneuploidy in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from the subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples

obtained from the subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[136] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample

obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[137] In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate for further diagnostic testing. In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate for increased monitoring. In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., using any of the variety of methods described herein), the subject is also identified as a

candidate that will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein including, without limitation, a chemopreventive). In some embodiments of identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., using any of the variety of methods described herein), the subject is also administered a treatment (e.g., any of the variety of therapeutic interventions described herein including, without limitation, a chemopreventive).

Methods of Treatment

[138] Also provided herein are methods and materials for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be

performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[139] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include treating a subject who has been diagnosed or identified

as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[140] In some embodiments, methods provided herein for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of

biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[141] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be treated when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be treated when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be treated when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or

developing a disease (e.g., cancer) and/or the subject is treated when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is treated when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is treated when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[142] In some embodiments of treating a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or

developing a disease by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject, the treatment is any of the variety of therapeutic interventions disclosed herein including without limitation, chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors), targeted therapy such as administration of kinase inhibitors (e.g., kinase inhibitors that target a particular genetic lesion, such as a translocation or mutation), (e.g. a kinase inhibitor, an antibody, a bispecific antibody), signal transduction inhibitors, bispecific antibodies or antibody fragments (e.g., BiTEs), monoclonal antibodies, immune checkpoint inhibitors, surgery (e.g., surgical resection), or any combination of the above. In some embodiments in which the disease is cancer, a therapeutic intervention reduces the severity of the cancer, reduces a symptom of the cancer, and/or reduces the number of cancer cells present within the subject.

[143] In some embodiments of treating a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a subject who will or is likely to respond to that treatment. In some embodiments of treating a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a candidate for further diagnostic testing (e.g., prior to administration of the treatment and/or after administration of the treatment to determine the effect of that treatment and/or whether the subject is a candidate for additional administrations of the same or a different treatment). In some embodiments of treating a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a candidate for increased monitoring (e.g., prior to administration of the treatment and/or after administration of the treatment to determine the effect of that treatment

and/or whether the subject is a candidate for additional administrations of the same or a different treatment).

Method of Identifying a Treatment

[144] Also provided herein are methods and materials for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer), the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[145] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of

having or developing a disease (e.g., cancer) by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[146] In some embodiments, methods provided herein for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) include detecting the presence of one or more members of two or more classes of biomarkers in one or more

samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[147] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment for the subject can be identified when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment for the subject can be identified when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment for the subject is identified when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment

for the subject is identified when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment for the subject is identified when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or a treatment for the subject is identified when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[148] In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased

risk) of having or developing a disease by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject, the identified treatment is any of the variety of therapeutic interventions disclosed herein including without limitation, chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors), targeted therapy such as administration of kinase inhibitors (e.g., kinase inhibitors that target a particular genetic lesion, such as a translocation or mutation), (e.g. a kinase inhibitor, an antibody, a bispecific antibody), signal transduction inhibitors, bispecific antibodies or antibody fragments (e.g., BiTEs), monoclonal antibodies, immune checkpoint inhibitors, surgery (e.g., surgical resection), or any combination of the above. In some embodiments in which the disease is cancer, an identified therapeutic intervention reduces the severity of the cancer, reduces a symptom of the cancer, and/or reduces the number of cancer cells present within the subject.

[149] In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a subject who will or is likely to respond to that treatment. In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a candidate for further diagnostic testing. In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is also identified as a candidate for increased monitoring. In some embodiments of identifying a treatment for a subject who has been diagnosed or identified as having a disease or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., by any of the variety of methods described herein), the subject is

also administered a treatment (e.g., any of the variety of therapeutic interventions described herein).

Identifying a Subject Who Will or is Likely to Respond to a Treatment

[150] Also provided herein are methods and materials for identifying a subject who will or is likely to respond to a treatment by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of identifying a subject who will or is likely to respond to a treatment, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject who will or is likely to respond to a treatment, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject who will or is likely to respond to a treatment that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[151] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some

embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include identifying a subject who will or is likely to respond to a treatment by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[152] In some embodiments, methods provided herein for identifying a subject who will or is likely to respond to a treatment include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a subject who will or is likely to respond to a treatment include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a subject who will or is likely to respond to a treatment include detecting the presence of one or more members of a single class of biomarkers in one or more samples

obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for identifying a subject who will or is likely to respond to a treatment include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for identifying a subject who will or is likely to respond to a treatment include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[153] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who will or is likely to respond to a treatment when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who will or is likely to respond to a treatment when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who will or

is likely to respond to a treatment when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who will or is likely to respond to a treatment when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who will or is likely to respond to a treatment when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of

biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who will or is likely to respond to a treatment when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[154] In some embodiments of identifying a subject who will or is likely to respond to a treatment by detecting of one or more members (e.g., increased risk) of having or developing a disease by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject, the subject is identified as a subject who will or is likely to respond to a treatment that is any of the variety of therapeutic interventions disclosed herein including without limitation, chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors), targeted therapy such as administration of kinase inhibitors (e.g., kinase inhibitors that target a particular genetic lesion, such as a translocation or mutation), (e.g. a kinase inhibitor, an antibody, a bispecific antibody), signal transduction inhibitors, bispecific antibodies or antibody fragments (e.g., BiTEs), monoclonal antibodies, immune checkpoint inhibitors, surgery (e.g., surgical resection), or any combination of the above. In some embodiments in which the disease is cancer, a subject that is identified as a subject who will or is likely to respond to an identified therapeutic intervention is identified as a subject in whom the therapeutic intervention will or is likely to reduce the severity of the cancer, reduce a symptom of the cancer, and/or reduce the number of cancer cells present within the subject.

[155] In some embodiments, a subject identified as a subject who will or is likely to respond to a treatment (e.g., using any of the variety of methods described herein) is also

identified for further diagnostic testing. In some embodiments, a subject identified as a subject who will or is likely to respond to a treatment (e.g., using any of the variety of methods described herein) is also identified for increased monitoring. Additionally or alternatively, a subject identified as a subject who will or is likely to respond to a treatment (e.g., using any of the variety of methods described herein) is also administered a treatment (e.g., any of the variety of therapeutic interventions described herein).

Methods of Identifying a Subject as a Candidate for Further Diagnostic Testing

[156] Also provided herein are methods and materials for identifying a subject as a candidate for further diagnostic testing by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of identifying a subject as a candidate for further diagnostic testing, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as a candidate for further diagnostic testing, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as a candidate for further diagnostic testing that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[157] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of

Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include identifying a subject as a candidate for further diagnostic testing by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[158] In some embodiments, methods provided herein for identifying a subject as a candidate for further diagnostic testing include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided

herein for identifying a subject as a candidate for further diagnostic testing include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for i identifying a subject as a candidate for further diagnostic testing include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for identifying a subject as a candidate for further diagnostic testing include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for identifying a subject as a candidate for further diagnostic testing include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[159] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more

members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of

biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for further diagnostic testing when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[160] In some embodiments of identifying a subject identifying a subject as a candidate for further diagnostic testing by detecting of one or more members (e.g., increased risk) of having or developing a disease by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject, the subject is for any of the variety of types of further diagnostic testing disclosed herein including, without limitation, a scan (e.g., a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, a positron emission tomography and computed tomography (PET-CT) scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, or a DEXA scan) or a physical examination (e.g., an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, or a pelvic exam).

[161] In some embodiments, a subject identified as a candidate for further diagnostic testing (e.g., using any of the variety of methods described herein) is also identified as a candidate for increased monitoring. Additionally or alternatively, a subject identified as a candidate for further diagnostic testing (e.g., using any of the variety of methods described herein) is also identified as a subject who will or is likely to respond to a treatment. Additionally or alternatively, a subject identified as a candidate for further diagnostic testing (e.g., using any of the variety of methods described herein) is also administered a treatment (e.g., any of the variety of therapeutic interventions described herein).

Methods of Identifying a Subject as a Candidate for Increased Monitoring

[162] Also provided herein are methods and materials for identifying a subject as a candidate for increased monitoring by detecting of one or more members (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more members) of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from the subject. In some embodiments of identifying a subject as a candidate for increased monitoring, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested simultaneously (e.g., in one testing procedure, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as a candidate for increased monitoring, the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy are tested sequentially (e.g., in two or more different testing procedures conducted at two or more different time points, including embodiments in which the testing procedure itself may include multiple discrete test methods of systems). In some embodiments of identifying a subject as a candidate for increased monitoring that include either simultaneous or sequential testing (or both) for the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy, the testing may be performed on a single sample or may be performed on two or more different samples (e.g., two or more different samples obtained from the same subject).

[163] Any of the variety of detection methods described herein (see, e.g., sections entitled "Detection of Genetic Biomarkers", "Detection of Protein Biomarkers", and "Detection of Aneuploidy") can be used to detect the presence of one or more members of one or more classes of biomarkers and/or the presence of aneuploidy in a sample obtained from a subject. In some embodiments, the one or more members of the one or more classes of biomarkers and/or the one or more classes of biomarkers are associated with a disease in a subject. In some embodiments, aneuploidy is associated with a disease in a subject. In some embodiments, the disease is cancer (e.g., any of the variety of types of cancer described herein). In some embodiments, the one or more members are members of a class of genetic biomarkers. In some embodiments, the one or more members are members of a class of protein biomarkers. In some embodiments, methods that include identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of one or more classes of biomarkers in a sample obtained from the subject further include detecting the presence of aneuploidy in a sample obtained from the subject. For example, methods that include identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a class of genetic biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). As another example, methods that include identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two different samples from the subject). In some embodiments, methods that include identifying a subject as a candidate for increased monitoring by detecting both the presence of one or more members of a class of genetic biomarkers and detecting the presence of one or more members of a class of protein biomarkers in a sample obtained from the subject can further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample or two or more different samples from the subject).

[164] In some embodiments, methods provided herein for identifying a subject as a candidate for increased monitoring include detecting the presence of one or more members of

a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for identifying a subject as a candidate for increased monitoring include detecting the presence of aneuploidy in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers). In some embodiments, methods provided herein for i identifying a subject as a candidate for increased monitoring include detecting the presence of one or more members of a single class of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers or protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject. In some embodiments, methods provided herein for identifying a subject as a candidate for increased monitoring include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers). In some embodiments, methods provided herein for identifying a subject as a candidate for increased monitoring include detecting the presence of one or more members of two or more classes of biomarkers in one or more samples obtained from a subject (e.g., genetic biomarkers and protein biomarkers) and detecting the presence of aneuploidy in one or more samples obtained from the subject.

[165] In some embodiments, a single sample obtained from a subject can be tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the one or more classes of biomarkers and/or the presence of aneuploidy is detected. Alternatively, two or more samples can be obtained from a subject, and each of the two or more samples can be individually tested to detect the presence of one or more members of one or more classes of biomarkers and/or for the presence of aneuploidy, and the subject can be diagnosed or identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject can be identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the one or more classes of

biomarkers and/or the presence of aneuploidy is detected. As one non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers), and a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the first class of biomarkers is detected and/or the presence of the one or more members of the second class of biomarkers is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence of the one or more members of the second class of biomarkers are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a class of biomarkers (e.g., genetic biomarkers or protein biomarkers), and a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the class of biomarkers is detected and/or the presence aneuploidy is detected (e.g., when the presence of the one or more members of the class of biomarkers is detected and the presence aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic biomarkers) and to detect the presence of one or more members of a second class of biomarkers (e.g., protein biomarkers), while a second sample obtained from the subject can be tested to detect the presence of aneuploidy, wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of

aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected). As another non-limiting example, a first sample obtained from a subject can be tested to detect the presence of one or more members of a first class of biomarkers (e.g., genetic or protein biomarkers) and to detect the presence of aneuploidy, while a second sample obtained from the subject can be tested to detect the presence of one or more members of a second class of biomarkers (e.g., a class of biomarkers that is different from the first class that is tested for in the first sample), wherein the subject is diagnosed or identified as having a disease (e.g., cancer) or as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) and/or the subject is identified as a subject who is a candidate for increased monitoring when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and/or the presence of aneuploidy is detected (e.g., when the presence of the one or more members of the first class of biomarkers is detected, the presence of the one or more members of the second class of biomarkers is detected, and the presence of aneuploidy are detected).

[166] In some embodiments, a subject identified as a candidate for increased monitoring (e.g., using any of the variety of methods described herein) is also identified as a candidate for further diagnostic testing. Additionally or alternatively, a subject identified as a candidate for increased monitoring (e.g., using any of the variety of methods described herein) is also identified as a subject who will or is likely to respond to a treatment. Additionally or alternatively, a subject identified as a candidate for increased monitoring (e.g., using any of the variety of methods described herein) is also administered a treatment (e.g., any of the variety of therapeutic interventions described herein).

Genetic Biomarkers in Combination with Protein Biomarkers

[167] In one aspect, provided herein are methods and materials for detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject.

In another aspect, provided herein are methods and materials for diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a panel of genetic

biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from the subject.

[168] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide a sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the sensitivity provided by separately detecting the presence of one or more members of a panel of genetic biomarkers or the presence of one or more members of a panel of protein biomarkers. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide a sensitivity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high sensitivity in detecting a single type of cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high sensitivity in detecting two or more types of cancers. Any of a variety of cancer types can be detected using methods and materials provided herein (see, e.g., the section entitled "Cancers"). In some embodiments, cancers that can be detected using methods and materials

that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include pancreatic cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include cancers of the female reproductive tract (e.g., cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include bladder cancer or upper-tract urothelial carcinomas.

[169] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high specificity in the detection or diagnosis of cancer (e.g., a low frequency or incidence of incorrectly identifying a subject as having cancer when that subject does not have cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide a specificity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the specificity provided by separately detecting the presence of one or more members of a panel of genetic biomarkers or the presence of one or more members of a panel of protein biomarkers. In some embodiments, methods and materials provided herein that include that

include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide a specificity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. As will be understood by those of ordinary skill in the art, a specificity of 99% means that only 1% of subjects that do not have cancer are incorrectly identified as having cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high specificity in detecting a single cancer (e.g., there is a low probability of incorrectly identifying that subject as having that single cancer type). In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject provide high specificity in detecting two or more cancers (e.g., there is a low probability of incorrectly identifying that subject as having those two or more cancer types).

[170] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers

in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types

of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[171] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the

following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[172] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more

(e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[173] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61),

TP53, CDKN2A, and/or SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, a subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing pancreatic cancer.

[174] A sample obtained from a subject can be any of the variety of samples described herein that contains cell-free DNA (e.g., ctDNA) and/or proteins. In some embodiments, cell-free DNA (e.g., ctDNA) and/or proteins in a sample obtained from the subject are derived from a tumor cell. In some embodiments, cell-free DNA (e.g., ctDNA) in a sample obtained from the subject includes one or more genetic biomarkers. In some embodiments, proteins in a sample obtained from the subject includes one or more protein biomarkers. Non-limiting examples of samples in which genetic biomarkers and/or protein biomarkers can be detected include blood, plasma, and serum. In some embodiments, the presence of one or more genetic biomarkers and the presence of one or more protein biomarkers is detected in a single sample obtained from the subject. In some embodiments, the presence of one or more genetic biomarkers is detected in a first sample obtained from a subject, and the presence of one or more protein biomarkers is detected in a second sample obtained from the subject.

[175] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers (e.g., each member of a panel of genetic biomarkers) and the presence of one or more members of a panel of protein biomarkers (e.g., each member of a panel of protein biomarkers) in one or more samples obtained from a subject, an elevated level of one or more members of the panel of protein biomarkers can be detected. For example, an elevated level of a protein biomarker can be a level that is higher that a reference level. A reference level can be any level of the protein biomarker that is not associated with the presence of cancer. For example, a reference level of a protein biomarker can be a level that is present in a reference subject that does not have cancer or does not harbor a cancer cell. A reference level of a protein biomarker can be the average level that is present in a plurality of reference subjects that do not have cancer or do not harbor a cancer cell. A reference level of a protein biomarker in a subject determined to have cancer can be the level that was presence in the subject prior to the onset of cancer. In

some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, or each of): CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, or each of): CA19-9, CEA, HGF, and/or OPN.

[176] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers (e.g., each member of a panel of genetic biomarkers) and the presence of one or more members of a panel of protein biomarkers (e.g., each member of a panel of protein biomarkers) in one or more samples obtained from a subject, a decreased level of one or more members of the panel of protein biomarkers can be detected. For example, a decreased level of a protein biomarker can be a level that is lower that a reference level. A reference level can be any level of the protein biomarker that is not associated with the presence of cancer. For example, a reference level of a protein biomarker can be a level that is present in a reference subject that does not have cancer or does not harbor a cancer cell. A reference level of a protein biomarker can be the average level that is present in a plurality of reference subjects that do not have cancer or do not harbor a cancer cell. A reference level of a protein biomarker in a subject determined to have cancer can be the level that was presence in the subject prior to the onset of cancer. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, or each of): CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,

or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, or each of): CA19-9, CEA, HGF, and/or OPN.

[177] In some embodiments, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer (e.g., by detecting: 1) the presence of one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) the presence of one or more protein biomarkers in any of the panels described herein as being useful in conjunction with this genetic biomarker panel), the subject is selected as a candidate for (e.g., is selected for) further diagnostic testing (e.g., any of the variety of further diagnostic testing methods described herein), the subject is selected as a candidate for (e.g. is selected for) increased monitoring (e.g., any of the variety of increasing monitoring methods described herein), the subject is identified as a subject who will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein), the subject is selected as a candidate for (e.g., is selected for) a treatment, a treatment (e.g., any of the variety of therapeutic interventions described herein) is selected for the subject, and/or a treatment (e.g., any of the variety of therapeutic interventions described herein) is administered to the subject. For example, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer, the subject can undergo further diagnostic testing, which further diagnostic testing can confirm the presence of cancer in the subject. Additionally or alternatively, the subject can be monitored at in increased frequency. In some embodiments of a subject determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer in which the subject undergoes further

diagnostic testing and/or increased monitoring, the subject can additionally be administered a therapeutic intervention. In some embodiments, after a subject is administered a therapeutic intervention, the subject undergoes additional further diagnostic testing (e.g., the same type of further diagnostic testing as was performed previously and/or a different type of further diagnostic testing) and/or continued increased monitoring (e.g., increased monitoring at the same or at a different frequency as was previously done). In embodiments, after a subject is administered a therapeutic intervention and the subject undergoes additional further diagnostic testing and/or additional increased monitoring, the subject is administered another therapeutic intervention (e.g., the same therapeutic intervention as was previously administered and/or a different therapeutic intervention). In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for the presence of one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) the presence of one or more protein biomarkers in any of the panels described herein as being useful in conjunction with this genetic biomarker panel.

[178] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). The presence of aneuploidy in any chromosome or portion thereof (e.g., an arm of a chromosome) can be detected. In some embodiments of methods that include detecting the presence of genetic biomarkers, protein biomarkers, and aneuploidy, the presence of aneuploidy on one or more of chromosome arms 5q, 8q, and 9p is detected. In some embodiments of methods that include detecting the presence of genetic biomarkers, protein biomarkers, and aneuploidy, the presence of aneuploidy on one or more of chromosome arms 4p, 7q, 8q, and 9q is detected.

[179] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO), the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples

obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), and 3) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[180] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that

include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that

detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, and 3) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[181] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments or methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting

in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, 2) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, and 3) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[182] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in

one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a different sample). In some embodiments or methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4, and 2) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN, the methods further include detecting the presence of aneuploidy in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers, or a

different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4, and 2) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, a subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing pancreatic cancer.

[183] In some embodiments, any of the variety of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject further include detecting the presence of one or more members of one or more additional classes of biomarkers. Non-limiting examples of such additional classes of biomarkers includes: copy number changes, DNA methylation changes, other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements), peptides, and/or metabolites.

[184] In some embodiments, the one or more additional classes of biomarkers include a metabolite biomarker. In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more metabolites indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more metabolites indicative of cancer. Non-limiting examples of metabolites indicative of cancer include: 5-methylthioadenosine (MTA), Glutathione reduced (GSH), N-acetylglutamate, Lactose, N-acetylneuraminate, UDP-acetylglucosamine, UDP-Acetylgalactosamine, UDP-glucuronate, Pantothenate, Arachidonate (20:4n6), Choline, Cytidine 5′-diphosphocholine, Dihomo-linolenate (20:3n3), Docosapentaenoate (DPA 22:5n3), Eicosapentaenoate (EPA 20:5n3), Glycerophosphorylcholine (GPC), Docosahexaenoate (DHA 22:6n3), Linoleate (18:2n6), Cytidine 5′-monophosphate (5′-CMP), Gamma-glutamylglutamate, X – 14577, X – 11583, Isovalerylcarnitine, Phosphocreatine, 2-Aminoadipic acid, Gluconic acid, O-Acetylcarnitine, aspartic acid, Deamido-NAD+, glutamic acid, Isobutyrylcarnitine, Carnitine, Pyridoxal, Citric acid, Adenosine, ATP, valine, XC0061, Isoleucine, γ-Butyrobetaine, Lactic acid,

alanine, phenylalanine, Gluconolactone, leucine, Glutathione (GSSG)_divalent, tyrosine, NAD+, XC0016, UTP, creatine, Theobromine, CTP, GTP, 3-Methylhistidine, Succinic acid, Glycerol 3-phosphate, glutamine, 5-Oxoproline, Thiamine, Butyrylcarnitine, 4-Acetamidobutanoic acid, UDP-Glucose, UDP-Galactose, threonine, N-Acetylglycine, proline, ADP, Choline, Malic acid, S-Adenosylmethionine, Pantothenic acid, Cysteinesulfinic acid, 6-Aminohexanoic acid, Homocysteic acid, Hydroxyproline, Methionine sulfoxide, 3-Guanidinopropionic acid, Glucose 6-phosphate, Phenaceturic acid, Threonic acid, tryptophan, Pyridoxine, N-Acetylaspartic acid, 4-Guanidinobutyric acid, serine, Citrulline, Betaine, N-Acetylasparagine, 2-Hydroxyglutaric acid, arginine, Glutathione (GSH), creatinine, Dihydroxyacetone phosphate, histidine, glycine, Glucose 1-phosphate, N-Formylglycine, Ketoprofen, lysine, beta-alanine, N-Acetylglutamic acid, 2-Amino-2-(hydroxymethyl)-1,3-propanediol, Ornithine, Phosphorylcholine, Glycerophosphocholine, Terephthalic acid, Glyceraldehyde 3-phosphate, Gly-Asp, Taurine, Fructose 1,6-diphosphate, 3-Aminoisobutyric acid, Spermidine, GABA, Triethanolamine, Glycerol, N-Acetylserine, N-Acetylornithine, Diethanolamine, AMP, Cysteine glutathione disulfide, Streptomycin sulfate +H2O divalent, trans-Glutaconic acid, Nicotinic acid, Isobutylamine, Betaine aldehyde +H2O, Urocanic acid, 1-Aminocyclopropane-1-carboxylic acid Homoserinelactone, 5-Aminovaleric acid, 3-Hydroxybutyric acid, Ethanolamine, Isovaleric acid, N-Methylglutamic acid, Cystathionine, Spermine, Carnosine, 1-Methylnicotinamide, N-Acetylneuraminic acid, Sarcosine, GDP, N-Methylalanine, palmitic acid, 1,2-dioleoyl-sn-glycero-3-phospho-rac-glycerolcholesterol 5α,6α epoxidelanosterol, lignoceric acid, 1oleoyl_rac_GL, cholesterol_epoxide, erucic acid, T-LCA, oleoyl-L-carnitine, oleanolic acid, 3-phosphoglycerate, 5-hydroxynorvaline, 5-methoxytryptamine, adenosine-5-monophosphate, alpha-ketoglutarate, asparagine, benzoic acid, hypoxanthine, maltose, maltotriose, methionine sulfoxide, nornicotine, phenol, Phosphoethanolamine, pyrophosphate, pyruvic acid, quinic acid, taurine, uric acid, inosine, lactamide, 5-hydroxynorvaline NIST, cholesterol, deoxypentitol, 2-hydroxyestrone, 2-hydroxyestradiol, 2-metholyestrone, 2-metholxyestradiol, 2-hydroxyestrone-3-methyl ether, 4-hydroxyestrone, 4-metholxyestrone, 4-methoxyestradiol, 16alpha-hydroxyestrone, 17-epiestriol, estriol, 16-Ketoestradiol, 16-epiestriol, acylcarnitine C18:1, amino acids citrulline and trans-4-hydroxyproline,

glycerophospholipids PC aa C28:1, PC ae C30:0 and PC ae C30:2, and sphingolipid SM (OH) C14:1. See e.g., Halama et al., Nesting of colon and ovarian cancer cells in the endothelial niche is associated with alterations in glycan and lipid metabolism, Scientific Reports volume 7, Article number: 39999 (2017); Hur et al., Systems approach to characterize the metabolism of liver cancer stem cells expressing CD133, Sci Rep., 7: 45557, doi: 10.1038/srep45557, (2017); Eliassen et al., Urinary Estrogens and Estrogen Metabolites and Subsequent Risk of Breast Cancer among Premenopausal Women, Cancer Res; 72(3); 696–706 (2011); Gangi et al., Metabolomic profile in pancreatic cancer patients: a consensus-based approach to identify highly discriminating metabolites, Oncotarget,Feb 2; 7(5): 5815–5829 (2016); Kumar et al., Serum and Plasma Metabolomic Biomarkers for Lung Cancer, Bioinformation, 13(6): 202–208, doi: 10.6026/97320630013202 (2017); Schmidt et al., Pre-diagnostic metabolite concentrations and prostate cancer risk in 1077 cases and 1077 matched controls in the European Prospective Investigation into Cancer and Nutrition, BMC Med.,15: 122, doi: 10.1186/s12916-017-0885-6 (2017); each of which is incorporated herein by reference in its entirety.

[185] In some embodiments, the one or more additional classes of biomarkers include a peptide (e.g., a peptide that is distinct from the various protein biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a peptide is derived from a protein (e.g., the peptide includes an amino acid sequence present in a protein biomarker or a different protein). Non-limiting examples of peptides indicative of cancer include the following peptides and peptides derived from the following proteins: CEACAM, CYFRA21-1, CA125, PKLK, ProGRP, NSE, TPA 6, TPA 7, TPA 8, NRG, NRG 100, CNDP, APOB100, SCC, VEGF, EGFR, PIK3CA, HER2, BRAF, ROS, RET, NRAS, MET, MEK1, HER2, C4.4A, PSF3, FAM83B, ECD, CTNNB, VIM, S100A4, S100A7, COX2, MUC1, KLKB1, SAA, HP-β chain, C9, Pgrmc1, Ciz1, Transferrin, α-1 antitrypsin, apolipo protein 1, complement c3a, Caveolin-1, Kallikrein 6, Glucose regulated protein- 8, α defensing -1,-2,-3, Serum C-peptide, Alpha -2- HS glycol

protein, Tryptic KRT 8 peptide, Plasma glycol protein, Catenin, Defensin α 6, MMPs, Cyclin D, S100 P, Lamin A/C filament protein, Heat shock protein, aldehyde dehydrogenase, Txl-2, (thioredoxin like protein-2), P53, nm23, u-PA, VEGF, Eph B4, CRABP2, WT-1, Rab-3D, Mesothelin, ERα, ANXA4, PSAT1, SPB5, CEA5, CEA6, A1AT, SLPI, APOA4, VDBP, HE4, IL-1, -6, -7, -8, -10, -11, -12, -16, -18, -21, -23, -28A, -33, LIF, TNFR1–2, HVEM (TNFRSF14), IL1R-a, IL1R-b, IL-2R, M-CSF, MIP-1a, TNF-α, CD40, RANTES, CD40L, MIF, IFN-β, MCP-4 (CCL13), MIG (CXCL9), MIP-1δ (CCL15), MIP3a (CCL20), MIP-4 (CCL18), MPIF-1, SDF-1a + b (CXCL12), CD137/4–1BB, lymphotactin (XCL1), eotaxin-1 (CCL11), eotaxin-2 (CCL24), 6Ckine/CCL21), BLC (CXCL13), CTACK (CCL27), BCA-1 (CXCL13), HCC4 (CCL16), CTAP-3 (CXCL7), IGF1, VEGF, VEGFR3, EGFR, ErbB2, CTGF, PDGF AA, BB, PDGFRb, bFGF, TGFbRIII, β-cellulin, IGFBP1–4, 6, BDNF, PEDF, angiopoietin-2, renin, lysophosphatidic acid, β2-microglobulin, sialyl TN, ACE, CA 19–9, CEA, CA 15–3, CA-50, CA 72–4, OVX1, mesothelin, sialyl TN, MMP-2, -3, -7, -9, VAP-1, TIMP1–2, tenascin C, VCAM-1, osteopontin, KIM-1, NCAM, tetranectin, nidogen-2, cathepsin L, prostasin, matriptase, kallikreins 2, 6, 10, cystatin C, claudin, spondin2, SLPI, bHCG, urinary gonadotropin peptide, inhibin, leptin, adiponectin, GH, TSH, ACTH, PRL, FSH, LH, cortisol, TTR, osteocalcin, insulin, ghrelin, GIP, GLP-1, amylin, glucagon, peptide YY, follistatin, hepcidin, CRP, Apo A1, CIII, H, transthyretin, SAA, SAP, complement C3,4, complement factor H, albumin, ceruloplasmin, haptoglobin, β-hemoglobin, transferrin, ferritin, fibrinogen, thrombin, von Willebrand factor, myoglobin, immunosuppressive acidic protein, lipid- associated sialic acid, S100A12 (EN-RAGE), fetuin A, clusterin, α1-antitrypsin, a2- macroglobulin, serpin1 (human plasminogen activator inhibitor-1), Cox-1, Hsp27, Hsp60, Hsp80, Hsp90, lectin-type oxidized LDL receptor 1, CD14, lipocalin 2, ITIH4, sFasL, Cyfra21–1, TPA, perforin, DcR3, AGRP, creatine kinase-MB, human milk fat globule 1–2, NT-Pro-BNP, neuron-specific enolase, CASA, NB/70K, AFP, afamin, collagen, prohibitin, keratin-6, PARC, B7-H4, YK-L40, AFP-L3, DCP, GPC3, OPN, GP73, CK19, MDK, A2, 5-HIAA, CA15-3, CA19-9, CA27.29, CA72-4, calcitonin, CGA, BRAF V600E, BAP, BCT-ABL fusion protein, KIT, KRAS, PSA, Lactate dehydrogenase, NMP22, PAI-1, uPA, fibrin D-dimer, S100, TPA, thyroglobulin, CD20, CD24, CD44, RS/DJ-1, p53, alpha-2-HS-glycoprotein, lipophilin B, beta-globin, hemopexin, UBE2N, PSMB6, PPP1CB, CPT2,

COPA, MSK1/2, Pro-NPY, Secernin-1, Vinculin, NAAA, PTK7, TFG, MCCC2, TRAP1, IMPDH2, PTEN, POSTN, EPLIN, eIF4A3, DDAH1, ARG2, PRDX3&4, P4HB, YWHAG, Enoyl CoA-hydrase, PHB, TUBB, KRT2, DES, HSP71, ATP5B, CKB, HSPD1, LMNA, EZH2, AMACR, FABP5, PPA2, EZR, SLP2, SM22, Bax, Smac/Diablo phosphorylated Bcl2, STAT3 and Smac/Diablo expression, PHB, PAP, AMACR, PSMA, FKBP4, PRDX4, KRT7/8/18, GSTP1, NDPK1, MTX2, GDF15, PCa-24, Caveolin-2, Prothrombin, Antithrombin-III, Haptoglobin, Serum amyloid A-1 protein, ZAG, ORM2, APOC3, CALML5, IGFBP2, MUC5AC, PNLIP, PZP, TIMP1, AMBP, inter-alpha-trypsin inhibitor heavy chain H1, inter-alpha-trypsin inhibitor heavy chain H2, inter-alpha-trypsin inhibitor heavy chain H3, V-type proton ATPase subunit B, kidney isoform, Hepatocyte growth factor-like protein, Serum amyloid P-component, Acylglycerol kinase, Leucine-rich repeat-containing protein 9, Beta-2-glycoprotein 1, Plasma protease C1 inhibitor, Lipoxygenase homology domain-containing protein 1, Protocadherin alpha-13. See, e.g., Kuppusamy et al., Volume 24, Issue 6, September 2017, Pages 1212-1221; Elzek and Rodland, Cancer Metastasis Rev. 2015 Mar; 34(1): 83–96; Noel and Lokshin, Future Oncol. 2012 Jan; 8(1): 55–71; Tsuchiya et al., World J Gastroenterol. 2015 Oct 7; 21(37): 10573–10583; Lou et al., Biomark Cancer. 2017; 9: 1–9; Park et al., Oncotarget. 2017 Jun 27; 8(26): 42761–42771; Saraswat et al., Cancer Med. 2017 Jul; 6(7): 1738–1751; Zamay et al., Cancers (Basel). 2017 Nov; 9(11): 155; Tanase et al., Oncotarget. 2017 Mar 14; 8(11): 18497–18512, each of which is incorporated herein by reference in its entirety.

[186] In some embodiments, the one or more additional classes of biomarkers include nucleic acid lesions or variations (e.g., a nucleic acid lesion or variation that is distinct from the various genetic biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. Non-limiting examples of nucleic acid lesions or variations include copy number changes, DNA methylation changes, and/or other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements).

Translocations and genomic rearrangements have been correlated with various cancers (e.g., prostate, glioma, lung cancer, non-small cell lung cancer, melanoma, and thyroid cancer) and used as biomarkers for years (e.g., Demeure et al., 2014, World J Surg., 38:1296-305; Hogenbirk et al., 2016, PNAS USA, 113:E3649-56; Gasi et al., 2011, PLoS One, 6:e16332; Ogiwara et al., 2008, Oncogene, 27:4788-97; US Patent No. 9,745,632; and US Patent No. 6,576,420). In addition, changes in copy number have been used as biomarkers for various cancers including, without limitation, head and neck squamous cell carcinoma, lymphoma (e.g., non-Hodgkin's lymphoma) and colorectal cancer (Kumar et al., 2017, Tumour Biol, 39:1010428317740296; Kumar et al., 2017, Tumour Biol., 39:1010428317736643; Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22; and US Patent No. 9,816,139). DNA methylation and changes in DNA methylation (e.g., hypomethylation, hypermethylation) also are used as biomarkers in cancer. For example, hypomethylation has been associated with hepatocellular carcinoma (see, for example, Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22), esophageal carcinogenesis (see, for example, Alvarez et al., 2011, PLoS Genet., 7:e1001356) and gastric and liver cancer (see, for example, US Patent No. 8,728,732), and hypermethylation has been associated with colorectal cancer (see, for example, US Patent No. 9,957,570;). In addition to genome-wide changes in methylation, specific methylation changes within particular genes can be indicative of specific cancers (see, for example, US Patent No. 8,150,626). Li et al. (2012, J. Epidemiol., 22:384-94) provides a review of the association between numerous cancers (e.g., breast, bladder, gastric, lung, prostate, head and neck squamous cell, and nasopharyngeal) and aberrant methylation. Additionally or alternatively, additional types of nucleic acids or features of nucleic acids have been associated with various cancers. Non-limiting examples of such nucleic acids or features of nucleic acids include the presence or absence of various microRNAs (miRNAs) have been used in the diagnosis of colon, prostate, colorectal, and ovarian cancers (see, for example, D'Souza et al., 2018, PLos One, 13:e0194268; Fukagawa et al., 2017, Cancer Sci., 108:886-96; Giraldez et al., 2018, Methods Mol. Biol., 1768:459-74; US Patent Nos. 8,343,718; 9,410,956; and 9,074,206). For a review on the specific association of miR-22 with cancer, see Wang et al. (2017, Int. J. Oncol., 50:345-55); the abnormal expression of long non-coding RNAs (lncRNAs) also have been used as a biomarker in cancers such as prostate

cancer, colorectal cancer, cervical cancer, melanoma, non-small cell lung cancer, gastric cancer, endometrial carcinoma, and hepatocellular carcinoma (see, for example, Wang et al., 2017, Oncotarget, 8:58577086; Wang et al., 2018, Mol. Cancer, 17:110; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4812-9; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:993-1002; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4820-7; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:2304-9; Xie et al., 2018, EBioMedicine, 33:57-67; and US Patent No. 9,410,206); the presence or absence of circular RNA (circRNA) has been used as a biomarker in lung cancer, breast cancer, gastric cancer, colorectal cancer, and liver cancer (e.g., Geng et al., 2018, J. Hematol. Oncol., 11:98) and melanoma (e.g., Zhang et al., 2018, Oncol. Lett., 16:1219-25); changes in telomeric DNA (e.g., in length or in heterozygosity) or centromeric DNA (e.g., changes in expression of centromeric genes) also have been associated with cancers (e.g., prostate, breast, lung, lymphoma, and Ewing's sarcoma) (see, for example, Baretton et al., 1994, Cancer Res., 54:4472-80; Liscia et al., 1999, Br. J. Cancer, 80:821-6; Proctor et al., 2009, Biochim. Biophys. Acta, 1792:260-74; and Sun et al., 2016, Int. J. Cancer, 139:899-907); various mutations (e.g., deletions), rearrangements and/or copy number changes in mitochondrial DNA (mtDNA) have been used prognostically and diagnostically for various cancers (e.g., prostate cancer, melanoma, breast cancer, lung cancer, and colorectal cancer). See, for example, Maragh et al., 2015, Cancer Biomark., 15:763-73; Shen et al., 2010, Mitochondrion, 10:62-68; Hosgood et al., 2010, Carcinogen., 31:847-9; Thyagarajan et al., 2012, Cancer Epid. Biomarkers & Prev., 21:1574-81; and US Patent No. 9,745,632; and the abnormal presence, absence or amount of messenger RNAs (mRNAs) also have been correlated with various cancers including, without limitation, breast cancer, Wilms' tumors, and cervical cancer (see, for example, Guetschow et al., 2012, Anal. Bioanaly. Chem., 404:399-406; Schwienbacher et al., 2000, Cancer Res., 60:1521-5; and Ngan et al., 1997, Genitourin Med., 73:54-8). Each of these citations is incorporated herein by reference in its entirety.

[187] This document provides methods and materials for assessing and/or treating mammals (e.g., humans) having, or suspected of having, cancer. In some embodiments, this document provides methods and materials for identifying a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to

determine if the mammal has cancer based, at least in part, on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) in the sample. A biomarker panel (e.g., a set of one or more biomarkers) described herein can include the presence of two or more (e.g., three, five, nine, 10, 25, 100, 250, 500, 1000, 1500, 2000, 2500, or more) biomarkers (e.g., biomarkers associated with cancer). In some embodiments, a biomarker panel can include about 2,011 biomarkers (e.g., about 2,001 genomic biomarkers and about 10 peptide biomarkers). In some embodiments, methods and materials described herein also can include identifying the location (e.g., the anatomic site) of a cancer in a mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine the location of the cancer in the mammal based, at least in part, on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers). In some embodiments, methods and materials described herein also can include treating a mammal having cancer (e.g., administering one or more cancer treatments to treat the mammal). For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers), and administering one or more cancer treatments to treat the mammal (e.g., to reduce the severity of the cancer, to reduce a symptom of the cancer, and/or to reduce the number of cancer cells present within the mammal).

[188] The term "elevated level" as used herein with respect to a level of a peptide biomarker refers to any level that is greater than the reference level of the peptide typically observed in a sample (e.g., a reference sample) from one or more healthy mammals. In some embodiments, a reference sample can be a sample obtained from a mammal that does not have a cancer. For example, for a peptide biomarker associated with colorectal cancer, a reference sample can be a sample obtained from a subject that does not have colorectal cancer. In some embodiments, a reference sample can be a sample obtained from the same mammal in which the elevated level of a peptide biomarker is observed, where the reference sample was obtained prior to onset of the cancer. In some embodiments, such a reference

sample obtained from the same mammal is frozen or otherwise preserved for future use as a reference sample. In some embodiments, when reference samples have undetectable levels of a peptide biomarker, an elevated level can be any detectable level of the peptide biomarker. It will be appreciated that levels from comparable samples are used when determining whether or not a particular level is an elevated level.

[189] Any appropriate mammal can be assessed and/or treated as described herein. A mammal can be a mammal having cancer. A mammal can be a mammal suspected of having cancer. In some embodiments, humans or other primates such as monkeys can be assessed for the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) as described herein. In some embodiments, dogs, cats, horses, cows, pigs, sheep, mice, and rats can be assessed for the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) as described herein. For example, a human can be assessed for the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) as described herein and, optionally, can be treated with one or more cancer treatments as described herein.

[190] Any appropriate sample from a mammal can be assessed as described herein (e.g., assessed for the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers)). In some embodiments, a sample can include DNA (e.g., genomic DNA). In some embodiments, a sample can include cell-free DNA (e.g., circulating tumor DNA (ctDNA)). In some embodiments, a sample can include peptides. For example, a sample can include circulating peptides (e.g., cancer related peptides). As used herein a "circulating peptide" is a peptide that can be detected in any closed system (e.g., the circulatory system) within the body of a mammal. In some embodiments, a sample can be fluid sample (e.g., a liquid biopsy). Examples of samples that can contain DNA and/or peptides include, without limitation, blood (e.g., whole blood, serum, or plasma), amnion, tissue, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites,

pap smears, breast milk, and exhaled breath condensate. For example, a plasma sample can be assessed for the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) as described herein.

[191] In some embodiments, a sample can be processed (e.g., to isolate and/or purify DNA and/or peptides from the sample). For example, DNA isolation and/or purification can include cell lysis (e.g., using detergents and/or surfactants), protein removal (e.g., using a protease), and/or RNA removal (e.g., using an RNase). As another example, peptide isolation and/or purification can include cell lysis (e.g., using detergents and/or surfactants), DNA removal (e.g., using a DNase), and/or RNA removal (e.g., using an RNase).

[192] Any appropriate biomarkers can be used as described herein (e.g., to determine if a mammal has cancer based, at least in part, on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) in the sample). Examples of biomarkers include, without limitation, genetic biomarkers, peptide biomarkers, metabolites, mRNA transcripts, miRNAs, methylation patterns (e.g., DNA methylation patterns), proteins (e.g., antibodies), and chromatin patterns. In some embodiments, the presence of one or more genetic biomarkers can be used to identify a mammal as having cancer. In some embodiments, an elevated level one or more peptide biomarkers can be used to identify a mammal as having cancer. In some embodiments, the presence of one or more genetic biomarkers and an elevated level of one or more peptide biomarkers in combination can be used to identify a mammal as having cancer. In some embodiments, detecting the presence of one or more genetic biomarkers and an elevated level of one or more peptide biomarkers in combination can increase the specificity and/or sensitivity of detection as compared to detecting either genetic biomarkers or peptide biomarkers alone.

[193] A genetic biomarker can be any appropriate genetic biomarker. For example, a genetic biomarker can be a genetic biomarker associated with cancer. A genetic biomarker can include a modification in a gene. Examples of modifications include, without limitation, single base substitutions, insertions, deletions, indels, translocations, and copy number

variations. A genetic biomarker can be in any appropriate gene. In some embodiments, a genetic biomarker can include a modification (e.g., an inactivating modification) in a tumor suppressor gene. In some embodiments, a genetic biomarker can include a modification (e.g., an activating modification) in an oncogene. Examples of genes that can include a genetic biomarker include, without limitation, NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, GNAS, JUN, ABCA7, ACVR1B, ACVR2A, AJUBA, AKT1, ALB, ALDOB, ALK, AMBRA1, AMER1, AMOT, ANKRD46, APC, AR, ARHGAP35, ARID1A, ARID1B, ARID2, ARID4B, ARL15, ARMCX1, ASXL1, ASXL2, ATAD2, ATG14, ATG5, ATM, ATRX, ATXN2, AXIN1, B2M, BAP1, BCL9, BCLAF1, BCOR, BIRC6, BIRC8, BLVRA, BRAF, BRCA1, BRCA2, BRD7, BRE, BRWD3, BTBD7, BTRC, C11orf70, C12orf57, C2CD5, C3orf62, C8orf34, CAMKV, CAPG, CASP8, CBFB, CBX4, CCAR1, CCDC117, CCDC88A, CCM2, CCNC, CCND1, CCR3, CD1D, CD79B, CDC73, CDCP1, CDH1, CDK12, CDK4, CDKN1A, CDKN1B, CDKN2A, CEBPA, CELF1, CENPB, CEP128, CHD2, CHD4, CHD8, CHEK2, CHRDL1, CHUK, CIC, CLEC4C, CMTR2, CNN2, CNOT1, CNOT4, COL11A1, COPS4, COX7B2, CREBBP, CSDE1, CSMD3, CTCF, CTDNEP1, CTNNB1, CUL1, CUL2, CYB5B, DACH1, DCHS1, DCUN1D1, DDX3X, DDX5, DHX15, DHX16, DICER1, DIRC2, DIS3, DIXDC1, DKK2, DNAJB5, DNER, DNM1L, DNMT3A, EED, EGFR, EIF1AX, EIF2AK3, EIF2S2, EIF4A1, EIF4A2, ELF3, EMG1, EMR3, EP300, EPB41L4A, EPHA2, EPS8, ERBB2, ERBB3, ERRFI1, EXO5, EZH2, F5, FANCM, FAT1, FBN2, FBXW7, FCER1G, FGFR1, FGFR2, FGFR3, FLT3, FN1, FOXA1, FUBP1, FUS, GALNTL5, GATA3, GGCT, GIGYF2, GK2, GLIPR2, GNPTAB, GNRHR, GOLM1, GOT2, GPS2, GPX7, GRK1, GSE1, GZMA, HDAC1, HERC1, HERC4, HGF, HIST1H2BO, HLA-A, HLA-B, HMCN1, HNRNPA1, HRAS, HSP90AB1, ID3, IDH1, IDH2, IFNGR2, IFT88, IKZF2, INO80C, INPP4A, INPPL1, IWS1, JAK1, JAK2, KANSL1, KAT8, KATNAL1, KBTBD7, KCNMB4, KDM5C, KDM6A, KEAP1, KIAA1467, KLF4, KMT2A, KMT2B, KMT2C, KMT2D, KMT2E, KRAS, KRT15, LAMTOR1, LARP4B, LPAR2, LYN, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAP4K3, MAPK1, MAX, MB21D2, MBD1, MBD6, MBNL1, MBNL3, MED12, MED23, MEN1, MGA, MKLN1, MLLT4, MOAP1, MORC4, MS4A1, MSI1, MTOR, MYC, MYCN, MYD88, MYL6, MYO1B, MYO6,

NAA15, NAA25, NAP1L2, NAP1L4, NCOA2, NCOR1, NEK9, NF1, NF2, NFE2L2, NFE2L3, NIPBL, NIT1, NKX3-1, NME4, NOTCH1, NOTCH2, NPM1, NRAS, NSD1, PBRM1, PCBP1, PCOLCE2, PHF6, PIK3CA, PIK3CB, PIK3R1, POLA2, POT1, PPARD, PPM1D, PPP2R1A, PPP6C, PRKACA, PRKCI, PRPF40A, PSIP1, PTEN, PTH2, PTMS, PTN, PTPN11, RAB18, RAC1, RAF1, RANBP3L, RAPGEF6, RASA1, RB1, RBBP6, RBM10, RBM26, RC3H2, REL, RERE, RFC4, RHEB, RHOA, RIMS2, RIT1, RNF111, RNF43, RPL11, RPL5, RQCD1, RRAS2, RUNX1, RXRA, SARM1, SCAF11, SEC22A, SENP3, SENP8, SETD1B, SETD2, SF3A3, SF3B1, SFPQ, SIN3A, SKAP2, SMAD2, SMAD3, SMAD4, SMARCA4, SMARCB1, SMARCC2, SNCB, SOS1, SOX4, SOX9, SP3, SPEN, SPOP, SPSB2, STAG2, STK11, STK31, SUFU, TAF1A, TARDBP, TAS2R30, TBL1XR1, TBX3, TCF12, TCF7L2, TET2, TEX11, TFDP2, TGFBR2, THRAP3, TM9SF1, TMCO2, TMED10, TMEM107, TMEM30A, TMPO, TNFRSF9, TNRC6B, TP53, TP53BP1, TRAF3, TRIM8, TRIP12, TSC1, TTK, TTR, TUBA3C, U2AF1, UBE2D3, UBR5, UNC13C, UNKL, UPP1, USO1, USP28, USP9X, VHL, VN1R2, VPS33B, WAC, WDR33, WDR47, WT1, WWP1, XPO1, YOD1, ZC3H13, ZDHHC4, ZFHX3, ZFP36L1, ZFP36L2, ZGRF1, ZMYM3, ZMYM4, ZNF234, ZNF268, ZNF292, ZNF318, ZNF345, ZNF600, ZNF750, and ZNF800. For example, a genetic biomarker can be in one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS. In some embodiments, methods and materials described herein can include detecting one or more genetic biomarkers (e.g., one or more modifications in one or more genes). For example, methods and materials described herein can include detecting mutations in one or more genes encoding any of the proteins set forth in Example 1, or in one or more of the genes set forth in Table 3 or Table 5. In some embodiments, methods and materials described herein can include detecting one or more of the modifications set forth in Table 3 or Table 5. In some embodiments, methods and materials described herein can include detecting the presence or absence of about 2,001 modifications in about 16 genes. For example, methods and materials described herein can include detecting the presence or absence about 2,001 genetic biomarkers in one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS. In some embodiments, genetic biomarkers can

be as described elsewhere (see, e.g., Bettegowda *et al.*, 2014 *Science translational medicine* 6:224ra224; Haber et al., 2014 *Cancer Discov* 4: 650-661; Dawson *et al.*, 2013 *N Engl J Med* 368:1199-1209; Wang *et al.*, 2015 *Science translational medicine* 7:293ra104; Forshew *et al.*, 2012 *Science translational medicine* 4:136ra168; Abbosh *et al.*, 2017 *Nature* 545:446-451; Beddowes et al., 2017 *Breast* 34(Suppl 1):S31-S35; and Phallen *et al.*, 2017 *Science translational medicine* 9).

[194] Any appropriate method can be used to detect the presence or absence of one or more biomarkers (e.g., genetic biomarkers) as described herein. In some embodiments, one or more genetic biomarkers can be detected independently (e.g., via singleplex peptide tools). In some embodiments, one or more genetic biomarkers can be detected simultaneously (e.g., via multiplex DNA tools such as "chips" or microarrays). Examples of methods for detecting genetic biomarkers include, without limitation, sequencing (e.g., PCR-based sequencing such as multiplex PCR-based sequencing), DNA hybridization methods (e.g., Southern blotting), restriction enzyme digestion methods, PCR-based multiplex methods, digital PCR methods, droplet digital PCR (ddPCR) methods, PCR-based singleplex PCR methods, Sanger sequencing methods, next-generation sequencing methods (e.g., single-molecule real-time sequencing, nanopore sequencing, and Polony sequencing), quantitative PCR methods, ligation methods, and microarray methods. In some embodiments, methods and materials described herein can include multiplex PCR-based sequencing. For example, methods and materials described herein can include multiplex PCR-based sequencing as set forth in Example 1. In some embodiments of methods provided herein, the presence of one or more mutations present in a sample obtained from a subject is detected using a method is performed that can increase the sensitivity of massively parallel sequencing instruments with an error reduction technique. For example, such techniques can permit the detection of rare mutant alleles in a range of 1 mutant template among 5,000 to 1,000,000 wild-type templates. In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected by amplifying DNA (e.g., DNA obtained from cells in a sample or cell-free DNA) to form families of amplicons in which each member of a family is derived from a single template molecule in the cell-free DNA, wherein each member of a family is marked by a common oligonucleotide barcode, and wherein each family is marked by a

distinct oligonucleotide barcode. For example, the presence of one or more mutations present in a sample obtained from a subject can be detected by assigning a unique identifier (UID) to each template molecule, amplifying each uniquely tagged template molecule to create UID-families, and redundantly sequencing the amplification products. In some embodiments, the oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers that collectively contain a plurality of oligonucleotide barcodes. In some embodiments, the oligonucleotide barcode is endogenous to the template molecule, and an adapter comprising a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the oligonucleotide barcode. See, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535.

[195] In some embodiments of methods provided herein, the presence of one or more mutations present in a sample obtained from a subject is detected using sequencing technology (e.g., a next-generation sequencing technology). A variety of sequencing technologies are known in the art. For example, methods for detection and characterization of circulating tumor DNA in cell-free DNA can be described elsewhere (see, e.g., Haber and Velculescu, 2014 *Cancer Discov.*, 4:650-61). Non-limiting examples of such techniques include SafeSeqs (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci USA*;108:9530-5), OnTarget (see, e.g., Forshew et al., 2012 *Sci Transl Med*; 4:136ra68,), and TamSeq (see, e.g., Thompson et al., 2012 *PLoS ONE*, 7:e31597). In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected using droplet digital PCR (ddPCR), a method that is known to be highly sensitive for mutation detection. In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected using other sequencing technologies, including but not limited to, chain-termination techniques, shotgun techniques, sequencing-by-synthesis methods, methods that utilize microfluidics, other capture technologies, or any of the other sequencing techniques known in the art that are useful for detection of small amounts of DNA in a sample (e.g., ctDNA in a cell-free DNA sample).

[196] In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected using array-based methods. For example, the step of

detecting a genetic alteration (e.g., one or more genetic alterations) in cell-free DNA is performed using a DNA microarray. In some embodiments, a DNA microarray can detect one more of a plurality of cancer cell mutations. In some embodiments, cell-free DNA is amplified prior to detecting the genetic alteration. Non-limiting examples of array-based methods that can be used in any of the methods described herein, include: a complementary DNA (cDNA) microarray (see, e.g., Kumar et al. 2012 J. Pharm. Bioallied Sci. 4(1):21-26; Laere et al. 2009 Methods Mol. Biol. 512:71-98; Mackay et al. 2003 Oncogene 22:2680-2688; Alizadeh et al. 1996 Nat. Genet. 14:457-460), an oligonucleotide microarray (see, e.g., Kim et al. 2006 Carcinogenesis 27(3):392-404; Lodes et al. 2009 PLoS One 4(7):e6229), a bacterial artificial chromosome (BAC) clone chip (see, e.g., Chung et al. 2004 Genome Res. 14(1):188-196; Thomas et al. 2005 Genome Res. 15(12):1831-1837), a single-nucleotide polymorphism (SNP) microarray (see, e.g., Mao et al. 2007 Curr. Genomics 8(4):219-228; Jasmine et al. 2012 PLoS One 7(2):e31968), a microarray-based comparative genomic hybridization array (array-CGH) (see, e.g., Beers and Nederlof, 2006 *Breast Cancer Res.* 8(3):210; Pinkel et al. 2005 *Nat. Genetics* 37:S11-S17; Michels et al. 2007 *Genet. Med.* 9:574-584), a molecular inversion probe (MIP) assay (see, e.g., Wang et al. 2012 *Cancer Genet* 205(7-8):341-55; Lin et al. 2010 *BMC Genomics* 11:712). In some embodiments, the cDNA microarray is an Affymetrix microarray (see, e.g., Irizarry 2003 *Nucleic Acids Res* 31:e15; Dalma-Weiszhausz et al. 2006 *Methods Enzymol.* 410:3-28), a NimbleGen microarray (see, e.g., Wei et al. 2008 *Nucleic Acids Res* 36(9):2926-2938; Albert et al. 2007 *Nat. Methods* 4:903-905), an Agilent microarray (see, e.g., Hughes et al. 2001 *Nat. Biotechnol.* 19(4):342-347), or a BeadArray array (see, e.g., Liu et al. 2017 *Biosens Bioelectron* 92:596-601). In some embodiments, the oligonucleotide microarray is a DNA tiling array (see, e.g., Mockler and Ecker, 2005 *Genomics* 85(1):1-15; Bertone et al. 2006 *Genome Res* 16(2):271-281). Other suitable array-based methods are known in the art.

[197] In some embodiments, multiplex PCR-based sequencing can include a number of amplicons that provides improved sensitivity of detection of one or more genetic biomarkers. For example, multiplex PCR-based sequencing can include about 60 amplicons (e.g., 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, or 70 amplicons). In some embodiments, multiplex PCR-based sequencing can include 61 amplicons. Amplicons

produced using multiplex PCR-based sequencing can include nucleic acids having a length from about 15 bp to about 1000 bp (e.g., from about 25 bp to about 1000 bp, from about 35 bp to about 1000 bp, from about 50 bp to about 1000 bp, from about 100 bp to about 1000 bp, from about 250 bp to about 1000 bp, from about 500 bp to about 1000 bp, from about 750 bp to about 1000 bp, from about 15 bp to about 750 bp, from about 15 bp to about 500 bp, from about 15 bp to about 300 bp, from about 15 bp to about 200 bp, from about 15 bp to about 100 bp, from about 15 bp to about 80 bp, from about 15 bp to about 75 bp, from about 15 bp to about 50 bp, from about 15 bp to about 40 bp, from about 15 bp to about 30 bp, from about 15 bp to about 20 bp, from about 20 bp to about 100 bp, from about 25 bp to about 50 bp, or from about 30 bp to about 40 bp). For example, amplicons produced using multiplex PCR-based sequencing can include nucleic acids having a length of about 33 bp.

[198] A peptide biomarker can be any appropriate peptide biomarker. In some embodiments, a peptide biomarker can be a peptide biomarker associated with cancer. For example, a peptide biomarker can be a peptide having elevated levels in a cancer (e.g., as compared to a reference level of the peptide). Examples of peptide biomarkers include, without limitation, AFP, Angiopoietin-2, AXL, CA125, CA 15-3, CA19-9, CD44, CEA, CYFRA 21-1, DKK1, Endoglin, FGF2, Follistatin, Galectin-3, G-CSF, GDF15, HE4, HGF, IL-6, IL-8, Kallikrein-6, Leptin, LRG-1, Mesothelin, Midkine, Myeloperoxidase, NSE, OPG, OPN, PAR, Prolactin, sEGFR, sFas, SHBG, sHER2/sEGFR2/sErbB2, sPECAM-1, TGFa, Thrombospondin-2, TIMP-1, TIMP-2, and Vitronectin. For example, a peptide biomarker can include one or more of OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine and/or TIMP-1. In some embodiments, methods and materials described herein can include one or more peptide biomarkers (e.g., one or more peptides have elevated levels in a cancer). For example, methods and materials described herein can include one or more of the peptide biomarkers set forth in Example 1. For example, methods and materials described herein can include elevated levels one or more of the peptide biomarkers set forth in Table 4. In some embodiments, methods and materials described herein can include detecting the levels of about 10 peptides. For example, methods and materials described herein can include detecting the level of OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and/or TIMP-1. In some embodiments, peptide biomarkers can be as

described elsewhere (see, e.g., Liotta et al., 2003 *Clin Adv Hematol Oncol* 1:460-462; Wang *et al.*, 2016 *Expert Rev Proteomics* 13: 99-114; and Patz, Jr. *et al.*, 2007 *J Clin Oncol* 25:5578-5583).

[199] Any appropriate method can be used to detect the level (e.g., an elevated level) of one or more biomarkers (e.g., peptide biomarkers) as described herein. In some embodiments, the levels of one or more peptide biomarkers can be detected independently (e.g., via singleplex peptide tools). In some embodiments, the levels of one or more peptide biomarkers can be detected simultaneously (e.g., via multiplex peptide tools such as "chips" or microarrays). Examples of methods for detecting peptide levels include, without limitation, spectrometry methods (e.g., high-performance liquid chromatography (HPLC) and liquid chromatography–mass spectrometry (LC/MS)), antibody dependent methods (e.g., enzyme-linked immunosorbent assay (ELISA), protein immunoprecipitation, immunoelectrophoresis, western blotting, and protein immunostaining), and aptamer dependent methods. In some embodiments, the level of one or more peptide biomarkers can be detected as described in the Examples. For example, the level of one or more peptide biomarkers can be detected by multiplex immunoassay.

[200] Any appropriate cancer can be identified and/or treated as described herein. In some embodiments, a cancer can be a common cancer. In some embodiments, a cancer can be a cancer where no blood-based test is available. In some embodiments, a cancer can be a cancer where no test for early detection is available. In some embodiments, a cancer can be a Stage I cancer. In some embodiments, a cancer can be a Stage II cancer. In some embodiments, a cancer can be a Stage III cancer. In some embodiments, a cancer can be a Stage IV cancer. In some embodiments, a cancer can be a surgically resectable cancer. Examples of cancers that be identified as described herein (e.g., based at least in part on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers)) include, without limitation, liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, and prostate cancer.

[201] Methods and materials provided herein also can identify the location of cancer (e.g., can determine the cancer site and/or type) in a mammal. The location of any cancer (e.g., the cancer site and/or type) that has mutations in one or more genetic biomarkers and/or one or more peptide biomarkers as described herein can be determined. In some embodiments, materials and methods provided herein can identify the presence of a colorectal cancer. For example, the presence of one or more genetic biomarkers in one or more of APC, KRAS, and/or TP53 gene mutations and an elevated level of CEA in a sample obtained from a mammal can be used to identify the presence of a colorectal cancer in the mammal. In some embodiments, materials and methods provided herein can identify the presence of a liver cancer. For example, the presence of one or more genetic biomarkers in one or more of TP53, CTNNB1, and/or TERT and an elevated level of AFP in a sample obtained from a mammal can be used to identify the presence of a liver cancer in the mammal. In some embodiments, materials and methods provided herein can identify the presence of an ovarian cancer. For example, the presence of one or more genetic biomarkers in TP53 and an elevated level CA125 in a sample obtained from a mammal can be used to identify the presence of an ovarian cancer in the mammal. In some embodiments, materials and methods provided herein can identify the presence of a pancreatic cancer. For example, the presence of one or more genetic biomarkers in KRAS (e.g., KRAS codon 12) and an elevated level of CA19-9 in a sample obtained from a mammal can be used to identify the presence of a pancreatic cancer in the mammal.

[202] In some embodiments, a mammal identified as having cancer as described herein (e.g., based at least in part on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers)) can have the cancer diagnosis confirmed using any appropriate method. Examples of methods that can be used to diagnose or confirm diagnosis of a cancer include, without limitation, physical examinations (e.g., pelvic examination), imaging tests (e.g., ultrasound or CT scans), cytology, and tissue tests (e.g., biopsy).

[203] In some embodiments, any of the variety of methods disclosed herein can be performed on subjects who have previously undergone treatments for cancer. In some

embodiments, methods provided herein can be used to determine the efficacy of the treatment. For example, a subject having cancer can be administered a treatment (also referred to herein as a "therapeutic intervention"), after which the continued presence of cancer or the amount of cancer (or lack thereof) is determined by detecting the presence of one or more mutations in one or more genes (e.g., NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS) and/or elevated levels of one or more peptide biomarkers (e.g., OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and/or TIMP-1).

[204] In some embodiments, once a subject has been determined to have a cancer, the subject may be additionally monitored or selected for increased monitoring. In some embodiments, methods provided herein can be used to select a subject for increased monitoring at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for increased monitoring can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for increased monitoring can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for increased monitoring can be administered a one or more additional diagnostic tests compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered two diagnostic tests, whereas a subject that has not been selected for increased monitoring is administered only a single diagnostic test (or no diagnostic tests). In some embodiments, a subject that has been selected for increased monitoring can also be selected for further diagnostic testing. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the subject and/or to assess the

development of additional cancer cell mutations), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell). In some embodiments, a therapeutic intervention is administered to the subject that is selected for increased monitoring after a cancer cell mutation is detected. Any of the therapeutic interventions disclosed herein or known in the art can be administered. For example, a subject that has been selected for increased monitoring can be further monitored, and a therapeutic intervention can be administered if the presence of the cancer cell is maintained throughout the increased monitoring period. Additionally or alternatively, a subject that has been selected for increased monitoring can be administered a therapeutic intervention, and further monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for increased monitoring has been administered a therapeutic intervention, the increased monitoring will reveal one or more additional cancer cell mutations. In some embodiments, such one or more additional cancer cell mutations will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

[205] In some embodiments, once a subject has been determined to have a cancer, the subject may be administered further tests or selected for further diagnostic testing. In some embodiments, methods provided herein can be used to select a subject for further diagnostic testing at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for further diagnostic testing can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for further diagnostic testing can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for further diagnostic testing can be administered a one or more additional

diagnostic tests compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered two diagnostic tests, whereas a subject that has not been selected for further diagnostic testing is administered only a single diagnostic test (or no diagnostic tests). In some embodiments, the diagnostic testing method can determine the presence of the same type of cancer as the cancer that was original detected. Additionally or alternatively, the diagnostic testing method can determine the presence of a different type of cancer as the cancer that was original detected. In some embodiments, the diagnostic testing method is a scan. In some embodiments, the scan is a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, a DEXA scan. In some embodiments, the diagnostic testing method is a physical examination, such as an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, a pelvic exam, a positron emission tomography and computed tomography (PET-CT) scan. In some embodiments, a subject that has been selected for further diagnostic testing can also be selected for increased monitoring. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the subject and/or to assess the development of additional cancer cell mutations), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell). In some embodiments, a therapeutic intervention is administered to the subject that is selected for further diagnostic testing after a cancer cell mutation is detected. Any of the therapeutic interventions disclosed herein or known in the art can be administered. For example, a subject that has been selected for further diagnostic testing can be administered a further diagnostic test, and a therapeutic intervention can be administered if the presence of the cancer cell is confirmed. Additionally or alternatively, a subject that has been selected for further diagnostic testing can be administered a therapeutic intervention, and can be further

monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for further diagnostic testing has been administered a therapeutic intervention, the additional testing will reveal one or more additional cancer cell mutations. In some embodiments, such one or more additional cancer cell mutations will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

[206] Once identified as having a cancer as described herein (e.g., based at least in part on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers) and/or the presence of aneuploidy), a mammal can be treated with one or more cancer treatments (also referred to herein as "therapeutic interventions").

[207] In certain aspects, provided herein are state-of-the-art tests that can detect mutations in cancer cells that are released into the blood stream. In some embodiments, one or more cancer types can be detected. Assays as described herein can be used as a cancer screening test with improved sensitivity while retaining specificity. For example, such assays can combine detection of genetic biomarkers (e.g., mutations in circulating tumor DNA (ctDNA)) with detection of thresholded protein markers in plasma. In some embodiments, a genetic biomarker (e.g., a mutation in circulating tumor DNA (ctDNA)) is tested alone. In some embodiments, protein biomarkers are tested alone. In some embodiments, the combination of the genetic biomarker (e.g., a mutation in circulating tumor DNA (ctDNA)) and protein markers can be superior to any single marker. In an exemplary pilot study of 1,703 patients (1,240 cancer and 463 healthy controls), the ctDNA and protein biomarkers panel had a sensitivity of 64% and a specificity of 99.35%.

[208] In some embodiments, assays as described herein may be applied to apparently healthy individuals. For example, assays as described herein may reduce deaths and suffering from cancer by detecting pre-symptomatic cancers through a blood test taken during routine office visits to physicians. Additionally, assays as described herein may be applied to patients with localized cancers, particularly those that have been or can be treated

or resected. Assays as described herein may improve management and prognosis though the earlier detection of recurrence.

[209] In some embodiments, genetic biomarkers (e.g., mutations in cell-free DNA (e.g., ctDNA)) may be tested from any of a variety of biological samples obtained from a subject (e.g., a human subject) including, but not limited to blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof.

[210] In some embodiments, genetic biomarkers (e.g., mutations in ctDNA) in 10 exemplary genes (AKT1, APC, BRAF, CDKN2A, CTNNB1, FBXW7, FGF2, GNAS, HRAS, KRAS) and elevation of 11 exemplary protein markers in serum beyond a threshold (CA19-9 (>92 U/ml), CEA (>7,507 pg/ml), CA125 (>577 U/ml), AFP (>21,321 pg/ml), Prolactin (>145,345 pg/ml), HGF (>899 pg/ml), OPN (>157,772 pg/ml), TIMP-1 (>176,989 pg/ml), Follistatin (>1,970 pg/ml), G-CSF (>800 pg/ml), and CA15-3 (>98 U/ml)) may be tested in the assay. In some embodiments, genetic biomarkers (e.g., mutations in ctDNA)in 16 exemplary genes (KT1, APC, BRAF, CDKN2, CTNNB1, FBXW7, FGFR2, GNAS, HRAS, KRAS, PPP2R1A, TP53, PTEN, PIK3CA, EGFR and NRAS) and elevation of 11 exemplary protein biomarkers in serum beyond a threshold (CA19-9 (>92 U/ml), CEA (>7,507 pg/ml), CA125 (>577 U/ml), AFP (>21,321 pg/ml), Prolactin (>145,345 pg/ml), HGF (>899 pg/ml), OPN (>157,772 pg/ml), TIMP-1 (>176,989 pg/ml), Follistatin (>1,970 pg/ml), G-CSF (>800 pg/ml), and CA15-3 (>98 U/ml)) may be tested in the assay. In some embodiments, the presence of a genetic biomarker (e.g., a mutation) or an elevation beyond threshold of any one of the protein biomarkers constitutes a positive result (e.g., identification of cancer in a subject). In some embodiments, the presence of genetic biomarkers (e.g., mutations) or elevations in two or more protein biomarkers constitute a positive result. For example, the presence of genetic biomarkers (e.g., mutations) in two, three, four, five, six, seven, eight, nine, or ten exemplary genes and/or elevations in two, three, four, five, six, seven, eight, nine, ten, or eleven protein biomarkers constitute a positive result.

[211] In some embodiments, proteins (e.g., protein biomarkers) may be tested from any of a variety of biological samples obtained from a subject (e.g., a human subject) including, but not limited to blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. Proteins (e.g., protein biomarkers) that are found in high amounts in cancers can be tested for amounts of the proteins that do not occur in healthy human subjects. Examples of proteins (e.g., protein biomarkers), any one, two, three, four, five, six, seven, eight, nine, ten, or eleven of which may be tested, include, without limitation, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3. Any protein biomarker known in the art may be used when a threshold value is obtained above which normal, healthy human subjects do not fall, but human subjects with cancer do fall.

[212] In some embodiments, a threshold level of CA19-9 can be at least about 92 U/mL (e.g., about 92 U/mL). In some embodiments, a threshold level of CA19-9 can be 92 U/mL. In some embodiments, a threshold level of CEA can be at least about 7,507 pg/ml (e.g., about 7,507 pg/ml). In some embodiments, a threshold level of CEA can be 7.5 ng/mL. In some embodiments, a threshold level of HGF can be at least about 899 pg/ml (e.g., about 899 pg/ml). In some embodiments, a threshold level of HGF can be 0.92 ng/mL. In some embodiments, a threshold level of OPN can be at least about 157,772 pg/ml (e.g., about 157,772 pg/ml). In some embodiments, a threshold level of OPN can be 158 ng/mL. In some embodiments, a threshold level of CA125 can be at least about 577 U/ml (e.g., about 577 U/ml). In some embodiments, a threshold level of CA125 can be 577 U/mL. In some embodiments, a threshold level of AFP can be at least about 21,321 pg/ml (e.g., about 21,321 pg/ml). In some embodiments, a threshold level of AFP can be 21,321 pg/ml. In some embodiments, a threshold level of prolactin can be at least about 145,345 pg/ml (e.g., about 145,345 pg/ml). In some embodiments, a threshold level of prolactin can be 145,345 pg/ml. In some embodiments, a threshold level of TIMP-1 can be at least about 176,989 pg/ml (e.g., about 176,989 pg/ml). In some embodiments, a threshold level of TIMP-1 can be 176,989 pg/ml. In some embodiments, a threshold level of follistatin can be at least about 1,970 pg/ml (e.g., about 1,970 pg/ml). In some embodiments, a threshold level of follistatin can be

1,970 pg/ml. In some embodiments, a threshold level of G-CSF can be at least about 800 pg/ml (e.g., about 800 pg/ml). In some embodiments, a threshold level of G-CSF can be 800 pg/ml. In some embodiments, a threshold level of CA15-3 can be at least about 98 U/ml (e.g., about 98 U/ml). In some embodiments, a threshold level of CA15-3 can be 98 U/ml. In some embodiments, a threshold level of CA19-9, CEA, and/or OPN can be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100% or more greater than the threshold levels listed above (e.g., greater than a threshold level of 92 U/mL for CA-19-9, 7,507 pg/ml for CEA, 899 pg/ml for HGF, 157,772 pg/ml for OPN, 577 U/ml for CA125, 21,321 pg/ml for AFP, 145,345 pg/ml for prolactin, 176,989 pg/ml for TIMP-1, 1,970 pg/ml for follistatin, 800 pg/ml for G-CSF, and/or 98 U/ml for CA15-3).

[213] In some embodiments, a threshold level of protein biomarker can be greater than the levels that are typically tested for diagnostic or clinical purposes. For example, the threshold level of CA19-9 can be greater than about 37 U/ml (e.g., greater than about 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or more U/mL). Additionally or alternatively, the threshold level of CEA can be greater than about 2.5 ug/L (e.g., greater than about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5 or more ug/L). Additionally or alternatively, the threshold level of CA125 can be greater than about 35 U/mL (e.g., greater than about 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550 or more U/mL). Additionally or alternatively, the threshold level of AFP can be greater than about 21 ng/mL (e.g., greater than about 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400 or more ng/L). Additionally or alternatively, the threshold level of TIMP-1 can be greater than about 2300 ng/mL (e.g., greater than about 2,500, 3,000, 4,000, 5,000 , 6,000, 7,000, 8,000, 9,000, 10,000, 15,000, 20,000, 25,000, 30,000, 35,000, 40,000 or more ng/L). Additionally or alternatively, the threshold level of follistatin can be greater than about 2 ug/mL (e.g., greater than about 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5 or more ug/L). Additionally or alternatively, the threshold level of CA15-3 can be greater than about 30 U/mL (e.g., greater than about 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or more U/mL). In some embodiments, detecting one or more protein biomarkers at threshold levels

that are higher than are typically tested for during traditional diagnostic or clinical assays can improve the sensitivity of cancer detection.

[214] In some embodiments, an assay includes detection of thresholded protein biomarkers in a biological sample (e.g., any biological sample disclosed herein such as plasma) without detection of genetic biomarkers (e.g., mutations in circulating tumor DNA (ctDNA)). For example, an assay may include detection of one or more of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3 in a biological sample. In some embodiments, an assay may include detection of one or more of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3 in a biological sample at any of the threshold levels disclosed herein. In some embodiments, once an assay that includes detection of thresholded protein biomarkers in a biological sample is performed, subsequent testing or monitoring is performed (e.g., any of the variety of further diagnostic testing or increased monitoring techniques disclosed herein). In some embodiments, once an assay that includes detection of thresholded protein markers in a biological sample is performed, a second assay that includes detecting a genetic biomarker (e.g., a genetic biomarker present in cell-free DNA (e.g., ctDNA)) can be performed (e.g., detecting any of the variety of genetic alterations in genetic biomarkers that are present in cell-free DNA or ctDNA as described herein).

[215] In some embodiments, an assay includes detection of a genetic biomarker in circulating tumor DNA (ctDNA) in a biological sample (e.g., any biological sample disclosed herein such as plasma) without detection of thresholded protein biomarkers. For example, an assay may include detection of genetic biomarkers (e.g., genetic alterations) in one or more of any of the genes disclosed herein including, without limitation, CDKN2A, FGF2, GNAS, ABL1, EVI1, MYC, APC, IL2, TNFAIP3, ABL2, EWSR1, MYCL1, ARHGEF12, JAK2, TP53, AKT1, FEV, MYCN, ATM, MAP2K4, TSC1, AKT2, FGFR1, NCOA4, BCL11B, MDM4, TSC2, ATF1, FGFR1OP, NFKB2, BLM, MEN1, VHL, BCL11A, FGFR2, NRAS, BMPR1A, MLH1, WRN, BCL2, FUS, NTRK1, BRCA1, MSH2, WT1, BCL3, GOLGA5, NUP214, BRCA2, NF1, BCL6, GOPC, PAX8, CARS, NF2, BCR, HMGA1, PDGFB, CBFA2T3, NOTCH1, BRAF, HMGA2, PIK3CA, CDH1, NPM1,

CARD11, HRAS, PIM1, CDH11, NR4A3, CBLB, IRF4, PLAG1, CDK6, NUP98, CBLC, JUN, PPARG, SMAD4, PALB2, CCND1, KIT, PTPN11, CEBPA, PML, CCND2, KRAS, RAF1, CHEK2, PTEN, CCND3, LCK, REL, CREB1, RB1, CDX2, LMO2, RET, CREBBP, RUNX1, CTNNB1, MAF, ROS1, CYLD, SDHB, DDB2, MAFB, SMO, DDX5, SDHD, DDIT3, MAML2, SS18, EXT1, SMARCA4, DDX6, MDM2, TCL1A, EXT2, SMARCB1, DEK, MET, TET2, FBXW7, SOCS1, EGFR, MITF, TFG, FH, STK11, ELK4, MLL, TLX1, FLT3, SUFU, ERBB2, MPL, TPR, FOXP1, SUZ12, ETV4, MYB, USP6, GPC3, SYK, ETV6, IDH1, and/or TCF3. In some embodiments, an assay may include detection of genetic biomarkers (e.g., genetic alterations) in one or more of AKT1, APC, BRAF, CDKN2A, CTNNB1, FBXW7, FGF2, GNAS, HRAS, KRAS. In some embodiments, an assay may include detection of genetic biomarkers (e.g., genetic alterations) in one or more of KT1, APC, BRAF, CDKN2, CTNNB1, FBXW7, FGFR2, GNAS, HRAS, KRAS, PPP2R1A, TP53, PTEN, PIK3CA, EGFR and NRAS. In some embodiments, once an assay that includes detection of a genetic biomarker present in ctDNA in a biological sample is performed, subsequent testing or monitoring is performed (e.g., any of the variety of further diagnostic testing or increased monitoring techniques disclosed herein). In some embodiments, once an assay that includes detection of a genetic biomarker present in ctDNA in a biological sample is performed, a second assay that includes detecting protein biomarkers at high thresholds can be performed (e.g., detecting any of the variety of protein biomarkers described herein including, but not limited to, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3 and combinations thereof).

[216] In some embodiments, at least two codons or at least two amplicons of a tumor suppressor gene or an oncogene can be tested. In some embodiments, at least three, at least four, or at least five or more codons or amplicons of an individual tumor suppressor gene or oncogene can be assayed. In some embodiments, the more distributed the mutations are in a gene, the more codons or amplicons one may desirably test.

[217] Exemplary codons of tumor suppressor genes and oncogenes which may be tested include, without limitation, one or more of the following codons and their surrounding splice

sites: codons 16-18 of AKT1; codons 1304-1311, 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58, 76-88 of CDKN2A; codons 31-39, 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, 143-148 of KRAS; codons 3-15, 54-63 of NRAS; codons 80-90, 343-348, 541-551, 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; codons 90-98, 125-132, 133-146, 145-154 of PTEN; and codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, 374-386 of TP53. All or some of these regions may be tested. In some embodiments, the mutation can be in KRAS, e.g., in codon 12 or 61. In other embodiments, the mutation may be in other codons of KRAS. In some embodiments, the mutation can be in CDKN2A (e.g., any of the CDKN2A mutations identified in Example 2), In some embodiments, the mutation may be in tumor suppressors or oncogenes, including but not limited to ABL1; EVI1; MYC; APC; IL2; TNFAIP3; ABL2; EWSR1; MYCL1; ARHGEF12; JAK2; TP53; AKT1; FEV; MYCN; ATM; MAP2K4; TSC1; AKT2; FGFR1; NCOA4; BCL11B; MDM4; TSC2; ATF1; FGFR1OP; NFKB2; BLM; MEN1; VHL; BCL11A; FGFR2; NRAS; BMPR1A; MLH1; WRN; BCL2; FUS; NTRK1; BRCA1; MSH2; WT1; BCL3; GOLGA5; NUP214; BRCA2; NF1; BCL6; GOPC; PAX8; CARS; NF2; BCR; HMGA1; PDGFB; CBFA2T3; NOTCH1; BRAF; HMGA2; PIK3CA; CDH1; NPM1; CARD11; HRAS; PIM1; CDH11; NR4A3; CBLB; IRF4; PLAG1; CDK6; NUP98; CBLC; JUN; PPARG; SMAD4; PALB2; CCND1; KIT; PTPN11; CEBPA; PML; CCND2; KRAS; RAF1; CHEK2; PTEN; CCND3; LCK; REL; CREB1; RB1; CDX2; LMO2; RET; CREBBP; RUNX1; CTNNB1; MAF; ROS1; CYLD; SDHB; DDB2; MAFB; SMO; DDX5; SDHD; DDIT3; MAML2; SS18; EXT1; SMARCA4; DDX6; MDM2; TCL1A; EXT2; SMARCB1; DEK; MET; TET2; FBXW7; SOCS1; EGFR; MITF; TFG; FH; STK11; ELK4; MLL; TLX1; FLT3; SUFU; ERBB2; MPL; TPR; FOXP1; SUZ12; ETV4; MYB; USP6; GPC3; SYK; ETV6; IDH1; and TCF3. Testing may include amplification and/or sequencing.

[218] In some embodiments, sequence determination to a high degree of accuracy can be advantageous when analytes are present in low quantities and/or fractions. High accuracy

sequence determination may employ oligonucleotide barcodes, whether endogenous or exogenous. These may be introduced into a template analyte by amplification, for example, in the case of an exogenous barcode. Alternatively, an endogenous oligonucleotide barcode may be used by attaching to it, for example, by means of ligation, an oligonucleotide adapter molecule. The adapter molecule may contain a priming site for DNA synthesis, and/or for hybridization to a solid surface. The adapter can be immediately adjacent to the endogenous barcode or a fixed number of nucleotides from the endogenous barcode.

[219] In some embodiments, oligonucleotide barcodes permit the labeling of individual template molecules in the sample prior to processing, in particular amplification. For example, by demanding that all or a high proportion or a threshold proportion of family members (having the same oligonucleotide barcode) display a mutation, it is possible to filter out or minimize false positive mutations that arise during amplification and/or other DNA synthesis or processing. See, e.g., Kinde I, Wu J, Papadopoulos N, Kinzler KW, & Vogelstein B (2011) Detection and quantification of rare mutations with massively parallel sequencing. Proc Natl Acad Sci U S A 108(23):9530-9535, the content of which is explicitly incorporated by reference. Additionally or alternatively, a threshold for mutation calling that a mutation occurs in two different families. Multiple filters of this nature may be applied.

[220] In some embodiments, methods provided herein can be used to detect a genetic biomarker (e.g., a genetic alteration (e.g., one or more genetic alterations)) in circulating tumor DNA present in cell-free DNA, where the cell-free DNA is present in an amount less than about 1500 ng, e.g., less than about 1400 ng, less than about 1300 ng, less than about 1200 ng, less than about 1100 ng, less than about 1000 ng, less than about 900 ng, less than about 800 ng, less than about 700 ng, less than about 600 ng, less than about 500 ng, less than about 400 ng, less than about 300 ng, less than about 200 ng, less than about 150 ng, less than about 100 ng, less than about 95 ng, less than about 90 ng, less than about 85 ng, less than about 80 ng, less than about 75 ng, less than about 70 ng, less than about 65 ng, less than about 60 ng, less than about 55 ng, less than about 50 ng, less than about 45 ng, less than about 40 ng, less than about 35 ng, less than about 30 ng, less than about 25 ng, less than about 20 ng, less than about 15 ng, less than about 10 ng, or less than about 5 ng. In some

embodiments, methods provided herein can be used to detect a genetic biomarker (e.g., a genetic alteration (e.g., one or more genetic alterations)) in circulating tumor DNA present in cell-free DNA, where the circulating tumor DNA represents 100% of the cell-free DNA. In some embodiments, methods provided herein can be used to detect a genetic biomarker (e.g., a genetic alteration (e.g., one or more genetic alterations)) in circulating tumor DNA present in cell-free DNA, where the circulating tumor DNA represents less than 100% of the cell-free DNA, e.g. about 95%, about 90%, about 85%, about 80%, about 75%, about 70%, about 65%, about 60%, about 55%, about 50%, about 45%, about 40%, about 35%, about 30%, about 25%, about 20%, about 15%, about 10%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.95%, about 0.90%, about 0.85%, about 0.80%, about 0.75%, about 0.70%, about 0.65%, about 0.60%, about 0.55%, about 0.50%, about 0.45%, about 0.40%, about 0.35%, about 0.30%, about 0.25%, about 0.20%, about 0.15%, about 0.10%, about 0.09%, about 0.08%, about 0.07%, about 0.06%, about 0.05% of the cell-free DNA, or less.

[221] In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and/or one or more protein biomarkers can be tested from any of a variety of biological samples isolated or obtained from a subject (e.g., a human subject) including, but not limited to the blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from the same sample. For example, a single sample can be isolated or obtained from a subject, which single sample can be tested for one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA), one or more protein biomarkers, or both. One or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from the sample at the same time or at different times. For example, the sample can be tested for one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA)) at a first time, and for one or more protein biomarkers at a second time, or vice versa. In some embodiments, the sample can be refrigerated, frozen, or otherwise stored for future testing. In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from different samples. For example, a first sample can be isolated

or obtained from a subject and tested for one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA), and a second sample can be isolated or obtained from the subject and tested for one or more protein biomarkers. The first and second samples can be of the same type (e.g., plasma or serum), or of different types. The first and/or second samples can be refrigerated, frozen, or otherwise stored for future testing.

[222] In some embodiments, any of the variety of assays disclosed herein can be repeated to increase the accuracy of mutation detection. Assays may be done in duplicate or triplicate, for example. In some embodiments, positive assays can be repeated on the same initial sample from a patient. Additionally or alternatively, a second sample may be obtained from a patient at a later time, for example, when a positive results is found. Any of the variety of assays described herein, including ctDNA, and/or protein biomarkers, may be repeated or run in parallel replicates.

[223] In some embodiments, a radiologic, sonographic, or other technique may be applied to any subject (e.g., a human subject) in which a mutation is detected. The technique may be applied to the whole body, to a single organ, or to a region of the body. The technique may be used, for example, to ascertain a particular type of cancer is present, to confirm a cancer is present, or to identify location of a cancer in the body. In some embodiments, the technique is a scan. In some embodiments, the scan is a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, a DEXA scan, or a positron emission tomography and computed tomography (PET-CT) scan. In some embodiments, the technique is a physical examination, such as an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, or a pelvic exam, In some embodiments, the technique is a biopsy (e.g., a bone marrow aspiration, a tissue biopsy). In some embodiments, the biopsy is performed by fine needle aspiration or by surgical excision. In some embodiments, the technique further includes obtaining a biological sample (e.g., a

tissue sample, a urine sample, a blood sample, a check swab, a saliva sample, a mucosal sample (e.g., sputum, bronchial secretion), a nipple aspirate, a secretion or an excretion). In some embodiments, the technique includes determining exosomal proteins (e.g., an exosomal surface protein (e.g., CD24, CD147, PCA-3)) (Soung et al. (2017) Cancers 9(1):pii:E8). In some embodiments, the diagnostic testing method is an oncotype DX® test (Baehner (2016) Ecancermedicalscience 10:675).

[224] In some embodiments, various methods described herein can be used to detect cancers selected from the group consisting of: pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, and breast cancer, and combinations thereof.

[225] In some embodiments, methods provided herein (e.g., methods in which genetic biomarkers present in cell-free DNA (e.g., ctDNA) and high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a treatment for a subject. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, or breast cancer) by any of the variety of methods disclosed herein, an appropriate treatment can be selected (e.g., any of the variety of therapeutic interventions described herein). In some embodiments, methods provided herein (e.g., methods in which genetic biomarkers present in cell-free DNA (e.g., ctDNA) and high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for treatment. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, or breast cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive a treatment (e.g., any of the variety of therapeutic interventions described herein). In some embodiments, methods provided herein (e.g., methods in which genetic biomarkers present in cell-free DNA (e.g., ctDNA) and high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for increased monitoring. For example, once a subject has been determined to have cancer (e.g.,

pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, or breast cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive increased monitoring (e.g., any of the variety of monitoring techniques described herein). In some embodiments, methods provided herein (e.g., methods in which genetic biomarkers present in cell-free DNA (e.g., ctDNA) and high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for further diagnostic testing. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, or breast cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive further diagnostic testing (e.g., any of the variety of diagnostic techniques described herein).

[226] In some embodiments, methods provided herein can be used to detect the presence of cancer (e.g., pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, or breast cancer) at a time period prior to diagnosis of the subject with an early-stage cancer and/or at a time prior to the subject exhibiting symptoms associated with cancer. For example, methods provided herein can be used when a subject has not been diagnosed with cancer and/or when a subject is not known to harbor a cancer cell.

[227] In some embodiments, certain protein biomarkers can be detected at high threshold levels to detect specific types of cancers. For example, high threshold levels of CA19-9 can be detected to indicate the presence of pancreatic cancer. Additionally or alternatively, high threshold levels of CEA can be detected to indicate the presence of, for example, colon, gastric, pancreatic, lung, and/or breast cancer. Additionally or alternatively, high threshold levels of CA-125 can be detected to indicate the presence of, for example, ovarian cancer. Additionally or alternatively, high threshold levels of AFP can be detected to indicate the presence of liver cancer. Additionally or alternatively, high threshold levels of prolactin can be detected to indicate the presence of, for example, ovarian, breast, and/or lung cancer. Additionally or alternatively, high threshold levels of HFG can be detected to indicate the

presence of, for example, esophageal, gastric, and/or liver cancer. Additionally or alternatively, high threshold levels of OPN can be detected to indicate the presence of, for example, ovarian, breast, and/or lung cancer. Additionally or alternatively, high threshold levels of TIMP-1 can be detected to indicate the presence of, for example, colon and/or pancreatic cancer. Additionally or alternatively, high threshold levels of follistatin can be detected to indicate the presence of, for example, ovarian and/or lung cancer. Additionally or alternatively, high threshold levels of G-CSF can be detected to indicate the presence of, for example, ovarian cancer. Additionally or alternatively, high threshold levels of CA15-3 can be detected to indicate the presence of, for example, breast cancer. Exemplary protein biomarkers detected in various cancer types are shown in Example 2.

[228] In some embodiments, assays for genetic biomarkers (e.g., genetic alterations) can be combined with assays for elevated protein biomarkers to increase the sensitivity of a blood test for low stage pancreatic cancers. In some embodiments, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of such cancers can be detected through this combination test, including some patients with a favorable prognosis. In some embodiments, 64% of such cancers can be detected through this combination test, including some patients with a favorable prognosis. One of the design features of certain studies presented herein was that only patients with resectable pancreatic cancers were included, and patients with advanced disease (i.e., Stage III or IV) were excluded. Though this exclusion reduced the sensitivity that could be otherwise be achieved by evaluating all pancreatic cancer patients, regardless of stage, the resectable cases are represent a promising group with advantageous clinical relevance with respect to evaluating a screening technology. In some embodiments, methods provided herein can be used to detect all pancreatic cancers in subjects (e.g., human subjects).

[229] Whether combining genetic biomarkers present in ctDNA and protein markers could increase sensitivity over either alone was not known prior to the present disclosure. In fact, it was conceivable that the same patients with detectable circulating protein markers would largely overlap those releasing DNA into the circulation. This was of particular concern for early stage cancer patients, because both ctDNA and protein-based markers are known to be

considerably higher in patients with advanced cancers compared to those with earlier stage cancers (Lennon AM & Goggins M (2010) Diagnostic and Therapeutic Response Markers. Pancreatic Cancer, (Springer New York, New York, NY), pp 675-701, Locker GY, et al. (2006) ASCO 2006 update of recommendations for the use of tumor markers in gastrointestinal cancer. J Clin Oncol 24(33):5313-5327, Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224).

[230] In some embodiments of the methods provided herein, very high specificity (e.g., 99.5%: 95% CI 97-100%) can be achieved. For example, only one false positive among 182 healthy individuals of average age 64 was observed in the studies presented herein. Given the relative infrequency of cancer in the general population, the specificity of any potentially useful blood-based screening test for pancreatic cancer is preferably high, e.g., preferably >99%. Otherwise, the number of false positives would greatly exceed the number of true positives (i.e., have suboptimal positive predictive value) (Lennon AM, et al. (2014) The Early Detection of Pancreatic Cancer: What Will It Take to Diagnose and Treat Curable Pancreatic Neoplasia? Cancer Res 74(13):3381-3389). Such stringency for screening tests is not typically required for tests to monitor disease in patients with known cancer. For monitoring, specificity can be relaxed somewhat in the interest of obtaining higher sensitivity. High specificity was achieved with various methods disclosed herein in at least two ways. First, ctDNA was used as one of the components of the test. KRAS mutations are exquisitely specific for neoplasia and their specificity has traditionally been limited by technical rather than biological factors. The incorporation of molecular barcoding into various assays described herein (e.g., using a Safe-SeqS technique) can minimize the false positive results from sequencing that have traditionally been major technical issues confronting any ctDNA-based assays. KRAS mutations are particularly suitable for early detection strategies because they are rarely found in clones arising during age-associated clonal hematopoiesis. Such clones, which may represent early forms of myelodysplasia, are a potential source of false positive ctDNA assays. The vast majority of such mutations occur within nine genes (DNMT3A, TET2, JAK2, ASXL1, TP53, GNAS, PPM1D, BCORL1 and SF3B1) (48-50), posing challenges for the use of these genes as biomarkers in ctDNA-based

assays. Second, high thresholds were used for scoring the protein markers as positive. These thresholds were based on prior studies in the literature or on an independent set of controls, permitting avoidance of positive scores in the vast majority of healthy patients (Kim JE, et al. (2004) Clinical usefulness of carbohydrate antigen 19-9 as a screening test for pancreatic cancer in an asymptomatic population. J Gastroenterol Hepatol 19(2):182-186). In some embodiments, such high thresholds can be used without an overall reduction in sensitivity because the ctDNA assay added sensitivity on its own and the ctDNA-positive cases only partially overlapped the protein-biomarker-positive cases (See, e.g., Fig. 9, Fig. 10, and Example 2).

[231] Protein biomarkers have been combined with each other in the past to achieve higher sensitivity (Dong T, Liu CC, Petricoin EF, & Tang LL (2014) Combining markers with and without the limit of detection. Stat Med 33(8):1307-132). For example, it was shown that combining CA19-9 and TIMP-1 was more sensitive for the detection of PDAC than either biomarker alone (Zhou W, et al. (1998) Identifying markers for pancreatic cancer by gene expression analysis. Cancer Epidemiol Biomarkers Prev 7(2):109-112). More recently, it was shown that the combination of CA19-9, TIMP-1, and LRG-1 was more sensitive for the detection of early PDAC than CA19-9 alone (Dong T, Liu CC, Petricoin EF, & Tang LL (2014) Combining markers with and without the limit of detection. Stat Med 33(8):1307-1320). The combination of protein biomarkers with ultrasensitive ctDNA, as disclosed herein, is different. A recent study evaluated a combination of ctDNA and CA19-9 for pancreatic cancer but found no benefit to combining the biomarkers over CA19-9 alone. Without being bound by theory, it is possible this conclusion was reached due to inadequate sensitivity of the test used in detecting KRAS mutations (Le Calvez-Kelm F, et al. (2016) KRAS mutations in blood circulating cell-free DNA: a pancreatic cancer case-control. Oncotarget 7(48):78827-78840). Furthermore, the specificity for ctDNA achieved in that study was relatively low, reducing its suitability for screening.

[232] In some embodiments, methods provided herein can be used to detect resectable cancers through a non-invasive blood test in a majority of patients.

[233] In some embodiments, results obtained using any of the variety of methods disclosed herein can underestimate the survival benefits of early detection. The majority of the patients that were studied herein, even though they had resectable cancers, were symptomatic and their cancers were discovered only by virtue of their symptoms. Accordingly, 77% of patients in the cohort described herein were Stage IIB and the median size of tumors in these patients was 3 cm. In some embodiments, in a screening study of asymptomatic individuals, a greater proportion of earlier stage patients, with smaller tumors, can be discovered using any of the variety of methods disclosed herein. In some embodiments, any of the variety of methods disclosed herein can be more sensitive for the detection of patients with larger tumors and with a poorer prognosis than for patients with smaller tumors, even though all tumors can be surgically resectable (See, e.g., Fig. 9B, and Example 2). In some embodiments, KRAS mutations can be found in the circulation of patients with cancer types other than those of the pancreas, primarily those of the lung (Herbst RS, Heymach JV, & Lippman SM (2008) Lung cancer. N Engl J Med 359(13):1367-1380), and CA19-9, CEA, HGF, and OPN expression can be elevated in several other cancer types (Kim JE, et al. (2004) Clinical usefulness of carbohydrate antigen 19-9 as a screening test for pancreatic cancer in an asymptomatic population. J Gastroenterol Hepatol 19(2):182-186; Thomas DS, et al. (2015) Evaluation of serum CEA, CYFRA21-1 and CA125 for the early detection of colorectal cancer using longitudinal preclinical samples. Br J Cancer 113(2):268-274; Di Renzo MF, et al. (1995) Overexpression and amplification of the met/HGF receptor gene during the progression of colorectal cancer. Clin Cancer Res 1(2):147-154; El-Tanani MK, et al. (2006) The regulation and role of osteopontin in malignant transformation and cancer. Cytokine Growth Factor Rev 17(6):463-474). Thus, in some embodiments, patients testing positive using any of the variety of methods disclosed herein can undergo additional appropriate imaging studies to identify tumor localization.

[234] In some embodiments, methods provided herein lay a foundation for evaluation of patients at high risk for PDAC, and for implementation of early detection strategies (Kalinich M, et al. (2017) An RNA-based signature enables high specificity detection of circulating tumor cells in hepatocellular carcinoma. Proc Natl Acad Sci U S A 114(5):1123-1128). As an example, new-onset diabetes is known to be associated with an increased risk for

pancreatic cancer. Approximately 1% of diabetic patients aged 50 and older are diagnosed with pancreatic cancer within 3 years of first meeting criteria for diabetes (Chari ST, et al. (2005) Probability of pancreatic cancer following diabetes: a population-based study. Gastroenterology 129(2):504-511). With an incidence of 1%, the PPV/NPV of certain combination assays disclosed herein is expected to be 54% and 99.6%, respectively, in this population, which is well within the range of currently approved screening tests for cancers.

[235] Available evidence indicates that many cancers have detectable genetic biomarkers present in ctDNA in their earliest stages, often more commonly than observed in pancreatic cancer (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224). Similarly, a large number of protein biomarkers have already been described for the detection of numerous cancer types (Liotta LA & Petricoin EF, 3rd (2003) The promise of proteomics. Clin Adv Hematol Oncol 1(8):460-462). These protein biomarkers can be thresholded according to any of the variety of methods described herein, permitting the use ctDNA-protein combinations to detect a variety of cancer types (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224).

[236] In certain aspects, provided herein are assays that can be used as a cancer screening test with improved sensitivity while retaining specificity. In some embodiments, the assays combine detection of mutations in genetic biomarkers present in circulating tumor DNA (ctDNA) with detection of thresholded protein biomarkers in plasma. In some embodiments, ctDNA is tested for the presence of genetic biomarkers alone. In some embodiments, protein biomarkers are tested alone. In some embodiments, the combination of the genetic biomarkers present in ctDNA and protein markers can be superior to any single marker. For example, in some embodiments the combination can detect nearly two-thirds of pancreatic cancers that have no evidence of distant metastasis at the time of surgical resection. In some embodiments, sequence determination to a high degree of accuracy can be advantageous when analytes are present in low quantities and/or fractions. High accuracy sequence determination may employ oligonucleotide barcodes, whether endogenous or exogenous.

These may be introduced into a template analyte by amplification, for example, in the case of an exogenous barcode. Alternatively, an endogenous oligonucleotide barcode may be used by attaching to it, for example, by means of ligation, an oligonucleotide adapter molecule. The adapter molecule may contain a priming site for DNA synthesis, and/or for hybridization to a solid surface. The adapter can be immediately adjacent to the endogenous barcode or a fixed number of nucleotides from the endogenous barcode.

[237] In some embodiments, oligonucleotide barcodes permit the labeling of individual template molecules in the sample prior to processing, in particular amplification. For example, by demanding that all or a high proportion or a threshold proportion of family members (having the same oligonucleotide barcode) display a mutation, it is possible to filter out or minimize false positive mutations that arise during amplification and/or other DNA synthesis or processing. See, e.g., Kinde I, Wu J, Papadopoulos N, Kinzler KW, & Vogelstein B (2011) Detection and quantification of rare mutations with massively parallel sequencing. Proc Natl Acad Sci U S A 108(23):9530-9535, the content of which is explicitly incorporated by reference. Additionally or alternatively, a threshold for mutation calling that a mutation occurs in two different families. Multiple filters of this nature may be applied.

[238] In some embodiments, methods provided herein can be used to detect a genetic alteration (e.g., one or more genetic alterations) in circulating tumor DNA present in cell-free DNA, where the cell-free DNA is present in an amount less than about 1500 ng, e.g., less than about 1400 ng, less than about 1300 ng, less than about 1200 ng, less than about 1100 ng, less than about 1000 ng, less than about 900 ng, less than about 800 ng, less than about 700 ng, less than about 600 ng, less than about 500 ng, less than about 400 ng, less than about 300 ng, less than about 200 ng, less than about 150 ng, less than about 100 ng, less than about 95 ng, less than about 90 ng, less than about 85 ng, less than about 80 ng, less than about 75 ng, less than about 70 ng, less than about 65 ng, less than about 60 ng, less than about 55 ng, less than about 50 ng, less than about 45 ng, less than about 40 ng, less than about 35 ng, less than about 30 ng, less than about 25 ng, less than about 20 ng, less than about 15 ng, less than about 10 ng, or less than about 5 ng. In some embodiments, methods provided herein can be used to detect a genetic alteration (e.g., one or more genetic

alterations) in circulating tumor DNA present in cell-free DNA, where the circulating tumor DNA represents 100% of the cell-free DNA. In some embodiments, methods provided herein can be used to detect a genetic alteration (e.g., one or more genetic alterations) in circulating tumor DNA present in cell-free DNA, where the circulating tumor DNA represents less than 100% of the cell-free DNA, e.g. about 95%, about 90%, about 85%, about 80%, about 75%, about 70%, about 65%, about 60%, about 55%, about 50%, about 45%, about 40%, about 35%, about 30%, about 25%, about 20%, about 15%, about 10%, about 5%, about 4%, about 3%, about 2%, about 1%, about 0.95%, about 0.90%, about 0.85%, about 0.80%, about 0.75%, about 0.70%, about 0.65%, about 0.60%, about 0.55%, about 0.50%, about 0.45%, about 0.40%, about 0.35%, about 0.30%, about 0.25%, about 0.20%, about 0.15%, about 0.10%, about 0.09%, about 0.08%, about 0.07%, about 0.06%, about 0.05% of the cell-free DNA, or less.

[239] In some embodiments, the presence of genetic biomarkers (e.g., mutations in cell-free DNA (e.g., ctDNA)) may be tested from any of a variety of biological samples isolated or obtained from a subject (e.g., a human subject) including, but not limited to blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from the same sample. For example, a single sample can be isolated or obtained from a subject, which single sample can be tested for genetic biomarkers present in cell-free DNA (e.g., ctDNA), one or more protein biomarkers, or both. The presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more protein biomarkers can be tested from the sample at the same time or at different times. For example, the sample can be tested for the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) at a first time, and for the presence of one or more protein biomarkers at a second time, or vice versa. In some embodiments, the sample can be refrigerated, frozen, or otherwise stored for future testing. In some embodiments, the presence of genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more protein biomarkers can be tested from different samples. For example, a first sample can be isolated or obtained from a subject and tested for the presence

of genetic biomarkers in cell-free DNA (e.g., ctDNA), and a second sample can be isolated or obtained from the subject and tested for the presence of one or more protein biomarkers. The first and second samples can be of the same type (e.g., plasma or serum), or of different types. The first and/or second samples can be refrigerated, frozen, or otherwise stored for future testing.

[240] In some embodiments, any of the variety of assays disclosed herein can be repeated to increase the accuracy of mutation detection. Assays may be done in duplicate or triplicate, for example. In some embodiments, positive assays can be repeated on the same initial sample from a patient. Additionally or alternatively, a second sample may be obtained from a patient at a later time, for example, when a positive results is found. Any of the variety of assays described herein, including ctDNA and/or protein biomarkers, may be repeated or run in parallel replicates.

[241] In some embodiments, a genetic biomarker (e.g., a mutation in cell-free DNA) may be in a tumor suppressor gene or an oncogene. For example, the genetic biomarkers (e.g., mutations) may be in hot spots for mutations, *e.g.,* sites that are frequently muted in tumors or other cancers. In some embodiments, the mutation can be in *KRAS*, e.g., in codon 12 or 61. In other embodiments, the genetic biomarker (e.g., mutation) may be in other codons of *KRAS*. In some embodiments, the genetic biomarker (e.g., mutation) can be in CDKN2A (e.g., any of the CDKN2A mutations identified in Example 2), In some embodiments, the genetic biomarker (e.g., mutation) may be in tumor suppressor genes or oncogenes, including but not limited to ABL1; EVI1; MYC; APC; IL2; TNFAIP3; ABL2; EWSR1; MYCL1; ARHGEF12; JAK2; TP53; AKT1; FEV; MYCN; ATM; MAP2K4; TSC1; AKT2; FGFR1; NCOA4; BCL11B; MDM4; TSC2; ATF1; FGFR1OP; NFKB2; BLM; MEN1; VHL; BCL11A; FGFR2; NRAS; BMPR1A; MLH1; WRN; BCL2; FUS; NTRK1; BRCA1; MSH2; WT1; BCL3; GOLGA5; NUP214; BRCA2; NF1; BCL6; GOPC; PAX8; CARS; NF2; BCR; HMGA1; PDGFB; CBFA2T3; NOTCH1; BRAF; HMGA2; PIK3CA; CDH1; NPM1; CARD11; HRAS; PIM1; CDH11; NR4A3; CBLB; IRF4; PLAG1; CDK6; NUP98; CBLC; JUN; PPARG; SMAD4; PALB2; CCND1; KIT; PTPN11; CEBPA; PML; CCND2; KRAS; RAF1; CHEK2; PTEN; CCND3; LCK; REL; CREB1; RB1; CDX2; LMO2; RET; CREBBP;

RUNX1; CTNNB1; MAF; ROS1; CYLD; SDHB; DDB2; MAFB; SMO; DDX5; SDHD; DDIT3; MAML2; SS18; EXT1; SMARCA4; DDX6; MDM2; TCL1A; EXT2; SMARCB1; DEK; MET; TET2; FBXW7; SOCS1; EGFR; MITF; TFG; FH; STK11; ELK4; MLL; TLX1; FLT3; SUFU; ERBB2; MPL; TPR; FOXP1; SUZ12; ETV4; MYB; USP6; GPC3; SYK; ETV6; IDH1; and TCF3. In some embodiments, protein biomarkers may be tested from any of a variety of biological samples isolated or obtained from a subject (e.g., a human subject) including, but not limited to blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. Protein biomarkers that are found in high amounts in cancers can be tested for amounts of the protein biomarkers that do not occur in healthy human subjects. Examples of protein biomarkers, any one, two, three, or four of which may be tested, include, without limitation, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), and osteopontin (OPN). In some embodiments, a threshold level of CA19-9 can be at least about 100 U/mL (e.g., about 100 U/mL). In some embodiments, a threshold level of CA19-9 can be 100 U/mL. In some embodiments, a threshold level of CEA can be at least about 7.5 ng/mL (e.g., about 7.5 ng/mL). In some embodiments, a threshold level of CEA can be 7.5 ng/mL. In some embodiments, a threshold level of HGF can be at least about 0.92 ng/mL (e.g., about 0.92 ng/mL). In some embodiments, a threshold level of HGF can be 0.92 ng/mL. In some embodiments, a threshold level of OPN can be at least about 158 ng/mL (e.g., about 158 ng/mL). In some embodiments, a threshold level of OPN can be 158 ng/mL. In some embodiments, a threshold level of CA19-9, CEA, and/or OPN can be 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100% or more greater than the threshold levels listed above (e.g., greater than a threshold level of 100 U/mL for CA-19-9, 7.5 ng/mL for CEA, 0.92 ng/mL for HGF, and/or 158 ng/mL for OPN).

[242] Any protein biomarker known in the art may be used when a threshold value is obtained above which normal, healthy human subjects do not fall, but human subjects with cancer do fall. Non-limiting examples of such protein biomarkers include Translation elongation factor (EEF1A1); Glyceraldehyde-3-phosphate dehydrogenase (GAPDH); Actin gamma (ACTG1); Ferritin, heavy polypeptide 1 (FTH1); Eukaryotic translation elongation

factor 1 gamma (EEF1G); Ribosomal protein, large subunit, P0 (RPLP0); Heat shock protein 90 kDa alpha (cytosolic), class B member 1 (HSP90AB1); Pyruvate kinase, muscle (PKM2); Ferritin, light polypeptide (FTL); and Ribosomal protein L3 (RPL3). Protein biomarkers known to be overexpressed in serum include but are not limited to Transferrin, α-1 antitrypsin, apolipo protein 1, complement c3a, Caveolin-1, Kallikrein 6, Glucose regulated protein- 8, α defensing -1,-2,-3, Serum C-peptide, Alpha -2- HS glycol protein, Catenin, Defensin α 6, MMPs, Cyclin D, S100 P, Lamin A/C filament protein, and Txl-2, (thioredoxin like protein-2).

[243] In some embodiments, an assay includes detection of thresholded protein biomarkers in a biological sample (e.g., any biological sample disclosed herein such as plasma) without detection of genetic biomarkers (e.g., mutations in circulating tumor DNA (ctDNA)). For example, an assay may include detection of one or more of CA19-9, CEA, HGF, and/or OPN in a biological sample. In some embodiments, an assay may include detection of one or more of CA19-9, CEA, HGF, and/or OPN in a biological sample at any of the threshold levels disclosed herein. In some embodiments, once an assay that includes detection of thresholded protein biomarkers in a biological sample is performed, subsequent testing or monitoring is performed (e.g., any of the variety of further diagnostic testing or increased monitoring techniques disclosed herein). In some embodiments, once an assay that includes detection of thresholded protein biomarkers in a biological sample is performed, a second assay that includes detecting one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) can be performed (e.g., detecting any of the variety of genetic alterations that are present in cell-free DNA or ctDNA as described herein).

[244] In some embodiments, an assay includes detection of one or more genetic biomarkers present in circulating tumor DNA (ctDNA) in a biological sample (e.g., any biological sample disclosed herein such as plasma) without detection of thresholded protein biomarkers. For example, an assay may include detection of genetic biomarkers (e.g., genetic alterations) in one or more of any of the genes disclosed herein including, without limitation, CDKN2A, FGF2, GNAS, ABL1, EVI1, MYC, APC, IL2, TNFAIP3, ABL2, EWSR1, MYCL1, ARHGEF12, JAK2, TP53, AKT1, FEV, MYCN, ATM, MAP2K4, TSC1, AKT2, FGFR1,

NCOA4, BCL11B, MDM4, TSC2, ATF1, FGFR1OP, NFKB2, BLM, MEN1, VHL, BCL11A, FGFR2, NRAS, BMPR1A, MLH1, WRN, BCL2, FUS, NTRK1, BRCA1, MSH2, WT1, BCL3, GOLGA5, NUP214, BRCA2, NF1, BCL6, GOPC, PAX8, CARS, NF2, BCR, HMGA1, PDGFB, CBFA2T3, NOTCH1, BRAF, HMGA2, PIK3CA, CDH1, NPM1, CARD11, HRAS, PIM1, CDH11, NR4A3, CBLB, IRF4, PLAG1, CDK6, NUP98, CBLC, JUN, PPARG, SMAD4, PALB2, CCND1, KIT, PTPN11, CEBPA, PML, CCND2, KRAS, RAF1, CHEK2, PTEN, CCND3, LCK, REL, CREB1, RB1, CDX2, LMO2, RET, CREBBP, RUNX1, CTNNB1, MAF, ROS1, CYLD, SDHB, DDB2, MAFB, SMO, DDX5, SDHD, DDIT3, MAML2, SS18, EXT1, SMARCA4, DDX6, MDM2, TCL1A, EXT2, SMARCB1, DEK, MET, TET2, FBXW7, SOCS1, EGFR, MITF, TFG, FH, STK11, ELK4, MLL, TLX1, FLT3, SUFU, ERBB2, MPL, TPR, FOXP1, SUZ12, ETV4, MYB, USP6, GPC3, SYK, ETV6, IDH1, and/or TCF3. In some embodiments, an assay may include detection of genetic alterations in KRAS (e.g., in codons 12 and/or 61 of KRAS). In some embodiments, once an assay that includes detection of one or more genetic biomarkers present in ctDNA in a biological sample is performed, subsequent testing or monitoring is performed (e.g., any of the variety of further diagnostic testing or increased monitoring techniques disclosed herein). In some embodiments, once an assay that includes detection of one or more genetic biomarkers present in ctDNA in a biological sample is performed, a second assay that includes detecting one or more protein biomarkers at high thresholds can be performed (e.g., detecting any of the variety of protein biomarkers described herein including, but not limited to, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), and combinations thereof).

[245] In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and/or one or more protein biomarkers can be tested from any of a variety of biological samples isolated or obtained from a subject (e.g., a human subject) including, but not limited to the blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from the same sample. For example, a single sample can be isolated or obtained from a subject, which single sample can be tested

for the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA), the presence of one or more protein biomarkers, or both. Genetic biomarkers present in cell-free DNA (e.g., ctDNA) and one or more protein biomarkers can be tested from the sample at the same time or at different times. For example, the sample can be tested for the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) at a first time, and for one or more protein biomarkers at a second time, or vice versa. In some embodiments, the sample can be refrigerated, frozen, or otherwise stored for future testing. In some embodiments, the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more protein biomarkers can be tested from different samples. For example, a first sample can be isolated or obtained from a subject and tested for the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA), and a second sample can be isolated or obtained from the subject and tested for the presence of one or more protein biomarkers. The first and second samples can be of the same type (e.g., plasma or serum), or of different types. The first and/or second samples can be refrigerated, frozen, or otherwise stored for future testing.

[246] In some embodiments, multiple codons or gene regions in a tumor suppressor gene or oncogene may be tested to identify a genetic biomarker (e.g., a mutation). For example, at least two, at least three, at least four, at least five or more codons or gene regions may be tested in a gene. Additionally or alternatively, multiple genes may be tested for mutations to increase the scope of an assay for more types of cancers or more cancers within a single type.

[247] In some embodiments, a radiologic, sonographic, or other technique may be applied to any subject (e.g., a human subject) in which genetic biomarker (e.g., a mutation) is detected. The technique may be applied to the whole body, to a single organ, or to a region of the body. The technique may be used, for example, to ascertain a particular type of cancer is present, to confirm a cancer is present, or to identify location of a cancer in the body. In some embodiments, the technique is a scan. In some embodiments, the scan is a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, a DEXA scan, or a positron

emission tomography and computed tomography (PET-CT) scan. In some embodiments, the technique is a physical examination, such as an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, or a pelvic exam, In some embodiments, the technique is a biopsy (e.g., a bone marrow aspiration, a tissue biopsy). In some embodiments, the biopsy is performed by fine needle aspiration or by surgical excision. In some embodiments, the technique further includes obtaining a biological sample (e.g., a tissue sample, a urine sample, a blood sample, a check swab, a saliva sample, a mucosal sample (e.g., sputum, bronchial secretion), a nipple aspirate, a secretion or an excretion). In some embodiments, the technique includes determining exosomal proteins (e.g., an exosomal surface protein (e.g., CD24, CD147, PCA-3)) (Soung et al. (2017) Cancers 9(1):pii:E8). In some embodiments, the diagnostic testing method is an oncotype DX® test (Baehner (2016) Ecancermedicalscience 10:675).

[248] In some embodiments, cancers of organs other than pancreatic cancer may be detected according to any of the variety of methods described herein.

[249] In some embodiments, methods provided herein (e.g., methods in which the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a treatment for a subject. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer) by any of the variety of methods disclosed herein, an appropriate treatment can be selected (e.g., any of the variety of therapeutic interventions described herein). In some embodiments, methods provided herein (e.g., methods in which the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for treatment. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive a treatment (e.g., any of the variety of therapeutic interventions

described herein). In some embodiments, methods provided herein (e.g., methods in which the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for increased monitoring. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive increased monitoring (e.g., any of the variety of monitoring techniques described herein). In some embodiments, methods provided herein (e.g., methods in which the presence of one or more genetic biomarkers in cell-free DNA (e.g., ctDNA) and the presence of one or more high threshold protein biomarkers are detected in a biological sample isolated from the subject) can be used for selecting a subject for further diagnostic testing. For example, once a subject has been determined to have cancer (e.g., pancreatic cancer) by any of the variety of methods disclosed herein, that subject can be identified as an appropriate subject to receive further diagnostic testing (e.g., any of the variety of diagnostic techniques described herein).

[250] In some embodiments, methods provided herein can be used to detect the presence of cancer (e.g., pancreatic cancer) at a time period prior to diagnosis of the subject with an early-stage cancer and/or at a time prior to the subject exhibiting symptoms associated with cancer. For example, methods provided herein can be used when a subject has not been diagnosed with cancer and/or when a subject is not known to harbor a cancer cell.

[251] In some embodiments of any of the methods described herein, the subject can be administered a single or multiple doses (e.g., two, three, four, five, six, seven, eight, nine, or ten doses) of any of the therapeutic interventions described herein.

[252] In some embodiments, assays for genetic biomarkers (e.g., genetic alterations) can be combined with assays for elevated protein biomarkers to increase the sensitivity of a blood test for low stage pancreatic cancers. In some embodiments, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of such cancers can be detected through this combination test, including some patients with a favorable prognosis. In some embodiments, 64% of such cancers can be detected through this combination test, including some patients

with a favorable prognosis. One of the design features of certain studies presented herein was that only patients with resectable pancreatic cancers were included, and patients with advanced disease (*i.e.,* Stage III or IV) were excluded. Though this exclusion reduced the sensitivity that could be otherwise be achieved by evaluating all pancreatic cancer patients, regardless of stage, the resectable cases are represent a promising group with advantageous clinical relevance with respect to evaluating a screening technology. In some embodiments, methods provided herein can be used to detect all pancreatic cancers in subjects (e.g., human subjects).

[253] Whether combining genetic biomarkers present in ctDNA and protein marker biomarkers could increase sensitivity over either alone was not known prior to the present disclosure. In fact, it was conceivable that the same patients with detectable circulating protein biomarkers would largely overlap those releasing DNA into the circulation. This was of particular concern for early stage cancer patients, because both ctDNA and protein-based biomarkers are known to be considerably higher in patients with advanced cancers compared to those with earlier stage cancers (Lennon AM & Goggins M (2010) Diagnostic and Therapeutic Response Markers. Pancreatic Cancer, (Springer New York, New York, NY), pp 675-701; Locker GY, et al. (2006) ASCO 2006 update of recommendations for the use of tumor markers in gastrointestinal cancer. J Clin Oncol 24(33):5313-5327; Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224).

[254] In some embodiments of the methods provided herein, very high specificity (e.g., 99.5%: 95% CI 97—100%) can be achieved For example, only one false positive among 182 healthy individuals of average age 64 was observed in the studies presented herein. Given the relative infrequency of cancer in the general population, the specificity of any potentially useful blood-based screening test for pancreatic cancer is preferably high, e.g., preferably >99%. Otherwise, the number of false positives would greatly exceed the number of true positives (*i.e.,* have suboptimal positive predictive value) (Lennon AM, et al. (2014) The Early Detection of Pancreatic Cancer: What Will It Take to Diagnose and Treat Curable Pancreatic Neoplasia? Cancer Res 74(13):3381-3389). Such stringency for screening tests is

not typically required for tests to monitor disease in patients with known cancer. For monitoring, specificity can be relaxed somewhat in the interest of obtaining higher sensitivity. High specificity was achieved with methods disclosed herein in at least two ways. First, ctDNA was used as one of the components of the test. *KRAS* mutations are exquisitely specific for neoplasia and their specificity has traditionally been limited by technical rather than biological factors. The incorporation of molecular barcoding into various assays described herein (e.g., using a Safe-SeqS technique) can minimize the false positive results from sequencing that have traditionally been major technical issues confronting any ctDNA-based assays. *KRAS* mutations are particularly suitable for early detection strategies because they are rarely found in clones arising during age-associated clonal hematopoiesis. Such clones, which may represent early forms of myelodysplasia, are a potential source of false positive ctDNA assays. The vast majority of such mutations occur within nine genes (*DNMT3A, TET2, JAK2, ASXL1, TP53, GNAS, PPM1D, BCORL1* and *SF3B1*) (48-50), posing challenges for the use of these genes as biomarkers in ctDNA-based assays. Second, high thresholds were used for scoring the protein biomarkers as positive. These thresholds were based on prior studies in the literature or on an independent set of controls, permitting avoidance of positive scores in the vast majority of healthy patients (Kim JE, et al. (2004) Clinical usefulness of carbohydrate antigen 19-9 as a screening test for pancreatic cancer in an asymptomatic population. J Gastroenterol Hepatol 19(2):182-186). In some embodiments, such high thresholds can be used without an overall reduction in sensitivity because the ctDNA assay added sensitivity on its own and the ctDNA-positive cases only partially overlapped the protein-biomarker-positive cases (See, e.g., Fig. 9, Fig. 10, and Example 2).

[255] Protein biomarkers have been combined with each other in the past to achieve higher sensitivity (Dong T, Liu CC, Petricoin EF, & Tang LL (2014) Combining markers with and without the limit of detection. Stat Med 33(8):1307-1320). For example, it was shown that combining CA19-9 and TIMP-1 was more sensitive for the detection of PDAC than either biomarker alone (Zhou W, et al. (1998) Identifying markers for pancreatic cancer by gene expression analysis. Cancer Epidemiol Biomarkers Prev 7(2):109-112). More recently, it was shown that the combination of CA19-9, TIMP-1, and LRG-1 was more sensitive for the

detection of early PDAC than CA19-9 alone (Capello M, et al. (2017) Sequential Validation of Blood-Based Protein Biomarker Candidates for Early-Stage Pancreatic Cancer. J Natl Cancer Inst 109(4)). The combination of protein biomarkers with ultrasensitive ctDNA, as disclosed herein, is different. A recent study evaluated a combination of ctDNA and CA19-9 for pancreatic cancer but found no benefit to combining the biomarkers over CA19-9 alone. Without being bound by theory, it is possible this conclusion was reached due to inadequate sensitivity of the test used in detecting *KRAS* mutations (Le Calvez-Kelm F, et al. (2016) KRAS mutations in blood circulating cell-free DNA: a pancreatic cancer case-control. Oncotarget 7(48):78827-78840). Furthermore, the specificity for ctDNA achieved in that study was relatively low, reducing its suitability for screening.

[256] In some embodiments, methods provided herein can be used to detect resectable pancreatic cancers through a non-invasive blood test in a majority of patients.

[257] In some embodiments, results obtained using any of the variety of methods disclosed herein can underestimate the survival benefits of early detection. The majority of the patients that were studied herein, even though they had resectable cancers, were symptomatic and their cancers were discovered only by virtue of their symptoms. Accordingly, 77% of patients in the cohort described herein were Stage IIB and the median size of tumors in these patients was 3 cm. In some embodiments, in a screening study of asymptomatic individuals, a greater proportion of earlier stage patients, with smaller tumors, can be discovered using any of the variety of methods disclosed herein. In some embodiments, any of the variety of methods disclosed herein can be more sensitive for the detection of patients with larger tumors and with a poorer prognosis than for patients with smaller tumors, even though all tumors can be surgically resectable (See, e.g., Fig. 9B and Example 2). In some embodiments, *KRAS* mutations can be found in the circulation of patients with cancer types other than those of the pancreas, primarily those of the lung (Herbst RS, Heymach JV, & Lippman SM (2008) Lung cancer. N Engl J Med 359(13):1367-1380), and CA19-9, CEA, HGF, and OPN expression can be elevated in several other cancer types (Kim JE, et al. (2004) Clinical usefulness of carbohydrate antigen 19-9 as a screening test for pancreatic cancer in an asymptomatic population. J Gastroenterol Hepatol 19(2):182-186; Thomas DS,

et al. (2015) Evaluation of serum CEA, CYFRA21-1 and CA125 for the early detection of colorectal cancer using longitudinal preclinical samples. Br J Cancer 113(2):268-274; Di Renzo MF, et al. (1995) Overexpression and amplification of the met/HGF receptor gene during the progression of colorectal cancer. Clin Cancer Res 1(2):147-154; El-Tanani MK, et al. (2006) The regulation and role of osteopontin in malignant transformation and cancer. Cytokine Growth Factor Rev 17(6):463-474). Thus, in some embodiments, patients testing positive using any of the variety of methods disclosed herein can undergo additional appropriate imaging studies to identify tumor localization.

[258] In some embodiments, methods provided herein lay a foundation for evaluation of patients at high risk for PDAC, and for implementation of early detection strategies (Kalinich M, et al. (2017) An RNA-based signature enables high specificity detection of circulating tumor cells in hepatocellular carcinoma. Proc Natl Acad Sci U S A 114(5):1123-1128). As an example, new-onset diabetes is known to be associated with an increased risk for pancreatic cancer. Approximately 1% of diabetic patients aged 50 and older are diagnosed with pancreatic cancer within 3 years of first meeting criteria for diabetes (Chari ST, et al. (2005) Probability of pancreatic cancer following diabetes: a population-based study. Gastroenterology 129(2):504-511). With an incidence of 1%, the PPV/NPV of certain combination assays disclosed herein is expected to be 54% and 99.6%, respectively, in this population, which is well within the range of currently approved screening tests for cancers.

[259] Available evidence indicates that many cancers have detectable ctDNA in their earliest stages, often more commonly than observed in pancreatic cancer (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224). Similarly, a large number of protein biomarkers have already been described for the detection of numerous cancer types (Liotta LA & Petricoin EF, 3rd (2003) The promise of proteomics. Clin Adv Hematol Oncol 1(8):460-462). These protein biomarkers can be thresholded according to any of the variety of methods described herein, permitting the use ctDNA-protein combinations to detect a variety of cancer types (Bettegowda C, et al. (2014) Detection of circulating tumor DNA in early- and late-stage human malignancies. Science translational medicine 6(224):224ra224).

Genetic Biomarkers in Combination with Aneuploidy

[260] In one aspect, provided herein are methods and materials for detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a

panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from the subject.

[261] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the sensitivity provided by separately detecting the presence of one or more members of a panel of genetic biomarkers or the presence of aneuploidy. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a sensitivity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting a single type of cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting two or more types of cancers. Any of a variety of cancer types can be detected using methods and materials provided herein (see, e.g., the section entitled "Cancers"). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include pancreatic cancer. In some embodiments, cancers that can be detected

using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include cancers of the female reproductive tract (e.g., cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include bladder cancer or upper-tract urothelial carcinomas.

[262] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in the detection or diagnosis of cancer (e.g., a low frequency or incidence of incorrectly identifying a subject as having cancer when that subject does not have cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a specificity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the specificity provided by separately detecting the presence of one or more members of a panel of genetic biomarkers or the presence of aneuploidy. In some embodiments, methods and materials provided herein that include that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a specificity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. As will be understood by those of ordinary skill in the art, a specificity of 99% means that only 1% of subjects that do

not have cancer are incorrectly identified as having cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting a single cancer (e.g., there is a low probability of incorrectly identifying that subject as having that single cancer type). In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting two or more cancers (e.g., there is a low probability of incorrectly identifying that subject as having those two or more cancer types).

[263] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, and 2) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A, and 2) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, and 2) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g.

diagnosed as being) at elevated risk of having or developing one of the following types of cancer: cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer.

[264] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more genetic biomarkers in each of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: bladder cancer or an upper-tract urothelial carcinoma.

[265] A sample obtained from a subject can be any of the variety of samples described herein that contains DNA (e.g., ctDNA in the blood, or DNA present in bladder, cervical, endometrial, or uterine samples) and/or proteins. In some embodiments, DNA (e.g., cell-free DNA (e.g., ctDNA) or DNA present in bladder, cervical, endometrial, or uterine samples) and/or proteins in a sample obtained from the subject are derived from a tumor cell. In some

embodiments, DNA (e.g., cell-free DNA (e.g., ctDNA) in a sample obtained from the subject includes one or more genetic biomarkers and or aneuploid DNA. In some embodiments, proteins in a sample obtained from the subject includes one or more protein biomarkers. Non-limiting examples of samples in which genetic biomarkers and/or protein biomarkers and/or aneuploidy can be detected include a blood sample, a plasma sample, a serum sample, a urine sample, an endometrial sample, a cervical sample, and a uterine sample. In some embodiments, the presence of one or more genetic biomarkers and the presence of aneuploidy in a single sample obtained from the subject. In some embodiments, the presence of one or more genetic biomarkers is detected in a first sample obtained from a subject, and the presence of aneuploidy is detected in a second sample obtained from the subject.

[266] In some embodiments, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer (e.g., by detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, and 2) the presence of aneuploidy), the subject is selected as a candidate for (e.g., is selected for) further diagnostic testing (e.g., any of the variety of further diagnostic testing methods described herein), the subject is selected as a candidate for (e.g. is selected for) increased monitoring (e.g., any of the variety of increasing monitoring methods described herein), the subject is identified as a subject who will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein), the subject is selected as a candidate for (e.g., is selected for) a treatment, a treatment (e.g., any of the variety of therapeutic interventions described herein) is selected for the subject, and/or a treatment (e.g., any of the variety of therapeutic interventions described herein) is administered to the subject. In some embodiments, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer (e.g., by detecting the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation

(e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy), the subject is selected as a candidate for (e.g., is selected for) further diagnostic testing (e.g., any of the variety of further diagnostic testing methods described herein), the subject is selected as a candidate for (e.g. is selected for) increased monitoring (e.g., any of the variety of increasing monitoring methods described herein), the subject is identified as a subject who will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein), the subject is selected as a candidate for (e.g., is selected for) a treatment, a treatment (e.g., any of the variety of therapeutic interventions described herein) is selected for the subject, and/or a treatment (e.g., any of the variety of therapeutic interventions described herein) is administered to the subject. For example, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer, the subject can undergo further diagnostic testing, which further diagnostic testing can confirm the presence of cancer in the subject. Additionally or alternatively, the subject can be monitored at in increased frequency. In some embodiments of a subject determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer in which the subject undergoes further diagnostic testing and/or increased monitoring, the subject can additionally be administered a therapeutic intervention. In some embodiments, after a subject is administered a therapeutic intervention, the subject undergoes additional further diagnostic testing (e.g., the same type of further diagnostic testing as was performed previously and/or a different type of further diagnostic testing) and/or continued increased monitoring (e.g., increased monitoring at the same or at a different frequency as was previously done). In embodiments, after a subject is administered a therapeutic intervention and the subject undergoes additional further diagnostic testing and/or additional increased monitoring, the subject is administered another therapeutic intervention (e.g., the same therapeutic intervention as was previously administered and/or a different therapeutic intervention). In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1,

CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, and 2) the presence of aneuploidy. In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy.

[267] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy further include detecting the presence one or more members of a panel of protein biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, or a different sample). Any of a variety of protein biomarkers can be detected (e.g., any of the variety of protein biomarkers and/or protein biomarker panels described herein).

[268] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, and 2) the presence of aneuploidy, the methods further include detecting the presence of one or more members of a panel of protein biomarkers in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A, and 2) the presence of aneuploidy, the methods further include detecting the presence of one or

more members of a panel of protein biomarkers in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, 2) the presence of aneuploidy, and 3) the presence of one or more members of a panel of protein biomarkers, the presence of one or more members of , the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer.

[269] In some embodiments or methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy, the methods further include detecting the presence of one or more members of a panel of protein biomarkers in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in each of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), and 3) the presence of aneuploidy, the methods further include detecting the presence of one or more members of a panel of protein biomarkers in a sample obtained from the subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, or a different sample). In some

embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, 2) the presence of a TERT promoter mutation (e.g., a genetic biomarker in a TERT promoter), 3) the presence of aneuploidy, and 4) the presence of one or more members of a panel of protein biomarkers, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: bladder cancer or an upper-tract urothelial carcinoma.

[270] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, each of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO).

[271] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, each of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3.

[272] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers can further

be detected: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, each of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3.

[273] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, and/or OPN. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, each of the following protein biomarkers can further be detected: CA19-9, CEA, HGF, and OPN.

[274] In some embodiments, any of the variety of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy in one or more samples obtained from a subject further include detecting the presence of one or more members of one or more additional classes of biomarkers. Non-limiting examples of such additional classes of biomarkers includes: copy number changes, DNA methylation changes, other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements), peptides, and/or metabolites.

[275] In some embodiments, the one or more additional classes of biomarkers include a metabolite biomarker. In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more metabolites indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more metabolites indicative of cancer. Non-limiting examples of metabolites indicative of cancer include: 5-methylthioadenosine (MTA), Glutathione reduced (GSH), N-acetylglutamate, Lactose, N-acetylneuraminate, UDP-acetylglucosamine, UDP-Acetylgalactosamine, UDP-glucuronate, Pantothenate, Arachidonate (20:4n6), Choline, Cytidine 5′-diphosphocholine, Dihomo-linolenate (20:3n3),

Docosapentaenoate (DPA 22:5n3), Eicosapentaenoate (EPA 20:5n3), Glycerophosphorylcholine (GPC), Docosahexaenoate (DHA 22:6n3), Linoleate (18:2n6), Cytidine 5′-monophosphate (5′-CMP), Gamma-glutamylglutamate, X – 14577, X – 11583, Isovalerylcarnitine, Phosphocreatine, 2-Aminoadipic acid, Gluconic acid, O-Acetylcarnitine, aspartic acid, Deamido-NAD+, glutamic acid, Isobutyrylcarnitine, Carnitine, Pyridoxal, Citric acid, Adenosine, ATP, valine, XC0061, Isoleucine, γ-Butyrobetaine, Lactic acid, alanine, phenylalanine, Gluconolactone, leucine, Glutathione (GSSG)_divalent, tyrosine, NAD+, XC0016, UTP, creatine, Theobromine, CTP, GTP, 3-Methylhistidine, Succinic acid, Glycerol 3-phosphate, glutamine, 5-Oxoproline, Thiamine, Butyrylcarnitine, 4-Acetamidobutanoic acid, UDP-Glucose, UDP-Galactose, threonine, N-Acetylglycine, proline, ADP, Choline, Malic acid, S-Adenosylmethionine, Pantothenic acid, Cysteinesulfinic acid, 6-Aminohexanoic acid, Homocysteic acid, Hydroxyproline, Methionine sulfoxide, 3-Guanidinopropionic acid, Glucose 6-phosphate, Phenaceturic acid, Threonic acid, tryptophan, Pyridoxine, N-Acetylaspartic acid, 4-Guanidinobutyric acid, serine, Citrulline, Betaine, N-Acetylasparagine, 2-Hydroxyglutaric acid, arginine, Glutathione (GSH), creatinine, Dihydroxyacetone phosphate, histidine, glycine, Glucose 1-phosphate, N-Formylglycine, Ketoprofen, lysine, beta-alanine, N-Acetylglutamic acid, 2-Amino-2-(hydroxymethyl)-1,3-propanediol, Ornithine, Phosphorylcholine, Glycerophosphocholine, Terephthalic acid, Glyceraldehyde 3-phosphate, Gly-Asp, Taurine, Fructose 1,6-diphosphate, 3-Aminoisobutyric acid, Spermidine, GABA, Triethanolamine, Glycerol, N-Acetylserine, N-Acetylornithine, Diethanolamine, AMP, Cysteine glutathione disulfide, Streptomycin sulfate +H2O divalent, trans-Glutaconic acid, Nicotinic acid, Isobutylamine, Betaine aldehyde +H2O, Urocanic acid, 1-Aminocyclopropane-1-carboxylic acid Homoserinelactone, 5-Aminovaleric acid, 3-Hydroxybutyric acid, Ethanolamine, Isovaleric acid, N-Methylglutamic acid, Cystathionine, Spermine, Carnosine, 1-Methylnicotinamide, N-Acetylneuraminic acid, Sarcosine, GDP, N-Methylalanine, palmitic acid, 1,2-dioleoyl-sn-glycero-3-phospho-rac-glycerolcholesterol 5α,6α epoxidelanosterol, lignoceric acid, 1oleoyl_rac_GL, cholesterol_epoxide, erucic acid, T-LCA, oleoyl-L-carnitine, oleanolic acid, 3-phosphoglycerate, 5-hydroxynorvaline, 5-methoxytryptamine, adenosine-5-monophosphate, alpha-ketoglutarate, asparagine, benzoic acid, hypoxanthine, maltose, maltotriose,

methionine sulfoxide, nornicotine, phenol, Phosphoethanolamine, pyrophosphate, pyruvic acid, quinic acid, taurine, uric acid, inosine, lactamide, 5-hydroxynorvaline NIST, cholesterol, deoxypentitol, 2-hydroxyestrone, 2-hydroxyestradiol, 2-metholyestrone, 2-metholxyestradiol, 2-hydroxyestrone-3-methyl ether, 4-hydroxyestrone, 4-metholxyestrone, 4-methoxyestradiol, 16alpha-hydroxyestrone, 17-epiestriol, estriol, 16-Ketoestradiol, 16-epiestriol, acylcarnitine C18:1, amino acids citrulline and trans-4-hydroxyproline, glycerophospholipids PC aa C28:1, PC ae C30:0 and PC ae C30:2, and sphingolipid SM (OH) C14:1. See e.g., Halama et al., Nesting of colon and ovarian cancer cells in the endothelial niche is associated with alterations in glycan and lipid metabolism, Scientific Reports volume 7, Article number: 39999 (2017); Hur et al., Systems approach to characterize the metabolism of liver cancer stem cells expressing CD133, Sci Rep., 7: 45557, doi: 10.1038/srep45557, (2017); Eliassen et al., Urinary Estrogens and Estrogen Metabolites and Subsequent Risk of Breast Cancer among Premenopausal Women, Cancer Res; 72(3); 696–706 (2011); Gangi et al., Metabolomic profile in pancreatic cancer patients: a consensus-based approach to identify highly discriminating metabolites, Oncotarget,Feb 2; 7(5): 5815–5829 (2016); Kumar et al., Serum and Plasma Metabolomic Biomarkers for Lung Cancer, Bioinformation, 13(6): 202–208, doi: 10.6026/97320630013202 (2017); Schmidt et al., Pre-diagnostic metabolite concentrations and prostate cancer risk in 1077 cases and 1077 matched controls in the European Prospective Investigation into Cancer and Nutrition, BMC Med.,15: 122, doi: 10.1186/s12916-017-0885-6 (2017); each of which is incorporated herein by reference in its entirety.

[276] In some embodiments, the one or more additional classes of biomarkers include a peptide (e.g., a peptide that is distinct from the various protein biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a peptide is derived from a protein (e.g., the peptide includes an amino acid sequence present in a protein biomarker or a different protein). Non-limiting examples of peptides indicative of cancer include the following peptides and peptides derived from the

following proteins: CEACAM, CYFRA21-1, CA125, PKLK, ProGRP, NSE, TPA 6, TPA 7, TPA 8, NRG, NRG 100, CNDP, APOB100, SCC, VEGF, EGFR, PIK3CA, HER2, BRAF, ROS, RET, NRAS, MET, MEK1, HER2, C4.4A, PSF3, FAM83B, ECD, CTNNB, VIM, S100A4, S100A7, COX2, MUC1, KLKB1, SAA, HP-β chain, C9, Pgrmc1, Ciz1, Transferrin, α-1 antitrypsin, apolipo protein 1, complement c3a, Caveolin-1, Kallikrein 6, Glucose regulated protein- 8, α defensing -1,-2,-3, Serum C-peptide, Alpha -2- HS glycol protein, Tryptic KRT 8 peptide, Plasma glycol protein, Catenin, Defensin α 6, MMPs, Cyclin D, S100 P, Lamin A/C filament protein, Heat shock protein, aldehyde dehydrogenase, Txl-2, (thioredoxin like protein-2), P53, nm23, u-PA, VEGF, Eph B4, CRABP2, WT-1, Rab-3D, Mesothelin, ERα, ANXA4, PSAT1, SPB5, CEA5, CEA6, A1AT, SLPI, APOA4, VDBP, HE4, IL-1, -6, -7, -8, -10, -11, -12, -16, -18, -21, -23, -28A, -33, LIF, TNFR1–2, HVEM (TNFRSF14), IL1R-a, IL1R-b, IL-2R, M-CSF, MIP-1a, TNF-α, CD40, RANTES, CD40L, MIF, IFN-β, MCP-4 (CCL13), MIG (CXCL9), MIP-1δ (CCL15), MIP3a (CCL20), MIP-4 (CCL18), MPIF-1, SDF-1a + b (CXCL12), CD137/4–1BB, lymphotactin (XCL1), eotaxin-1 (CCL11), eotaxin-2 (CCL24), 6Ckine/CCL21), BLC (CXCL13), CTACK (CCL27), BCA-1 (CXCL13), HCC4 (CCL16), CTAP-3 (CXCL7), IGF1, VEGF, VEGFR3, EGFR, ErbB2, CTGF, PDGF AA, BB, PDGFRb, bFGF, TGFbRIII, β-cellulin, IGFBP1–4, 6, BDNF, PEDF, angiopoietin-2, renin, lysophosphatidic acid, β2-microglobulin, sialyl TN, ACE, CA 19–9, CEA, CA 15–3, CA-50, CA 72–4, OVX1, mesothelin, sialyl TN, MMP-2, -3, -7, -9, VAP-1, TIMP1–2, tenascin C, VCAM-1, osteopontin, KIM-1, NCAM, tetranectin, nidogen-2, cathepsin L, prostasin, matriptase, kallikreins 2, 6, 10, cystatin C, claudin, spondin2, SLPI, bHCG, urinary gonadotropin peptide, inhibin, leptin, adiponectin, GH, TSH, ACTH, PRL, FSH, LH, cortisol, TTR, osteocalcin, insulin, ghrelin, GIP, GLP-1, amylin, glucagon, peptide YY, follistatin, hepcidin, CRP, Apo A1, CIII, H, transthyretin, SAA, SAP, complement C3,4, complement factor H, albumin, ceruloplasmin, haptoglobin, β-hemoglobin, transferrin, ferritin, fibrinogen, thrombin, von Willebrand factor, myoglobin, immunosuppressive acidic protein, lipid- associated sialic acid, S100A12 (EN-RAGE), fetuin A, clusterin, α1-antitrypsin, a2- macroglobulin, serpin1 (human plasminogen activator inhibitor-1), Cox-1, Hsp27, Hsp60, Hsp80, Hsp90, lectin-type oxidized LDL receptor 1, CD14, lipocalin 2, ITIH4, sFasL, Cyfra21–1, TPA, perforin, DcR3, AGRP, creatine kinase-MB, human milk fat

globule 1–2, NT-Pro-BNP, neuron-specific enolase, CASA, NB/70K, AFP, afamin, collagen, prohibitin, keratin-6, PARC, B7-H4, YK-L40, AFP-L3, DCP, GPC3, OPN, GP73, CK19, MDK, A2, 5-HIAA, CA15-3, CA19-9, CA27.29, CA72-4, calcitonin, CGA, BRAF V600E, BAP, BCT-ABL fusion protein, KIT, KRAS, PSA, Lactate dehydrogenase, NMP22, PAI-1, uPA, fibrin D-dimer, S100, TPA, thyroglobulin, CD20, CD24, CD44, RS/DJ-1, p53, alpha-2-HS-glycoprotein, lipophilin B, beta-globin, hemopexin, UBE2N, PSMB6, PPP1CB, CPT2, COPA, MSK1/2, Pro-NPY, Secernin-1, Vinculin, NAAA, PTK7, TFG, MCCC2, TRAP1, IMPDH2, PTEN, POSTN, EPLIN, eIF4A3, DDAH1, ARG2, PRDX3&4, P4HB, YWHAG, Enoyl CoA-hydrase, PHB, TUBB, KRT2, DES, HSP71, ATP5B, CKB, HSPD1, LMNA, EZH2, AMACR, FABP5, PPA2, EZR, SLP2, SM22, Bax, Smac/Diablo phosphorylated Bcl2, STAT3 and Smac/Diablo expression, PHB, PAP, AMACR, PSMA, FKBP4, PRDX4, KRT7/8/18, GSTP1, NDPK1, MTX2, GDF15, PCa-24, Caveolin-2, Prothrombin, Antithrombin-III, Haptoglobin, Serum amyloid A-1 protein, ZAG, ORM2, APOC3, CALML5, IGFBP2, MUC5AC, PNLIP, PZP, TIMP1, AMBP, inter-alpha-trypsin inhibitor heavy chain H1, inter-alpha-trypsin inhibitor heavy chain H2, inter-alpha-trypsin inhibitor heavy chain H3, V-type proton ATPase subunit B, kidney isoform, Hepatocyte growth factor-like protein, Serum amyloid P-component, Acylglycerol kinase, Leucine-rich repeat-containing protein 9, Beta-2-glycoprotein 1, Plasma protease C1 inhibitor, Lipoxygenase homology domain-containing protein 1, Protocadherin alpha-13. See, e.g., Kuppusamy et al., Volume 24, Issue 6, September 2017, Pages 1212-1221; Elzek and Rodland, Cancer Metastasis Rev. 2015 Mar; 34(1): 83–96; Noel and Lokshin, Future Oncol. 2012 Jan; 8(1): 55–71; Tsuchiya et al., World J Gastroenterol. 2015 Oct 7; 21(37): 10573–10583; Lou et al., Biomark Cancer. 2017; 9: 1–9; Park et al., Oncotarget. 2017 Jun 27; 8(26): 42761–42771; Saraswat et al., Cancer Med. 2017 Jul; 6(7): 1738–1751; Zamay et al., Cancers (Basel). 2017 Nov; 9(11): 155; Tanase et al., Oncotarget. 2017 Mar 14; 8(11): 18497–18512, each of which is incorporated herein by reference in its entirety.

[277] In some embodiments, the one or more additional classes of biomarkers include nucleic acid lesions or variations (e.g., a nucleic acid lesion or variation that is distinct from the various genetic biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing

cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. Non-limiting examples of nucleic acid lesions or variations include copy number changes, DNA methylation changes, and/or other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements). Translocations and genomic rearrangements have been correlated with various cancers (e.g., prostate, glioma, lung cancer, non-small cell lung cancer, melanoma, and thyroid cancer) and used as biomarkers for years (e.g., Demeure et al., 2014, World J Surg., 38:1296-305; Hogenbirk et al., 2016, PNAS USA, 113:E3649-56; Gasi et al., 2011, PLoS One, 6:e16332; Ogiwara et al., 2008, Oncogene, 27:4788-97; US Patent No. 9,745,632; and US Patent No. 6,576,420). In addition, changes in copy number have been used as biomarkers for various cancers including, without limitation, head and neck squamous cell carcinoma, lymphoma (e.g., non-Hodgkin's lymphoma) and colorectal cancer (Kumar et al., 2017, Tumour Biol, 39:1010428317740296; Kumar et al., 2017, Tumour Biol., 39:1010428317736643; Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22; and US Patent No. 9,816,139). DNA methylation and changes in DNA methylation (e.g., hypomethylation, hypermethylation) also are used as biomarkers in cancer. For example, hypomethylation has been associated with hepatocellular carcinoma (see, for example, Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22), esophageal carcinogenesis (see, for example, Alvarez et al., 2011, PLoS Genet., 7:e1001356) and gastric and liver cancer (see, for example, US Patent No. 8,728,732), and hypermethylation has been associated with colorectal cancer (see, for example, US Patent No. 9,957,570;). In addition to genome-wide changes in methylation, specific methylation changes within particular genes can be indicative of specific cancers (see, for example, US Patent No. 8,150,626). Li et al. (2012, J. Epidemiol., 22:384-94) provides a review of the association between numerous cancers (e.g., breast, bladder, gastric, lung, prostate, head and neck squamous cell, and nasopharyngeal) and aberrant methylation. Additionally or alternatively, additional types of nucleic acids or features of nucleic acids have been associated with various cancers. Non-limiting examples of such nucleic acids or features of nucleic acids include the presence or absence of various microRNAs (miRNAs) have been

used in the diagnosis of colon, prostate, colorectal, and ovarian cancers (see, for example, D'Souza et al., 2018, PLos One, 13:e0194268; Fukagawa et al., 2017, Cancer Sci., 108:886-96; Giraldez et al., 2018, Methods Mol. Biol., 1768:459-74; US Patent Nos. 8,343,718; 9,410,956; and 9,074,206). For a review on the specific association of miR-22 with cancer, see Wang et al. (2017, Int. J. Oncol., 50:345-55); the abnormal expression of long non-coding RNAs (lncRNAs) also have been used as a biomarker in cancers such as prostate cancer, colorectal cancer, cervical cancer, melanoma, non-small cell lung cancer, gastric cancer, endometrial carcinoma, and hepatocellular carcinoma (see, for example, Wang et al., 2017, Oncotarget, 8:58577086; Wang et al., 2018, Mol. Cancer, 17:110; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4812-9; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:993-1002; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4820-7; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:2304-9; Xie et al., 2018, EBioMedicine, 33:57-67; and US Patent No. 9,410,206); the presence or absence of circular RNA (circRNA) has been used as a biomarker in lung cancer, breast cancer, gastric cancer, colorectal cancer, and liver cancer (e.g., Geng et al., 2018, J. Hematol. Oncol., 11:98) and melanoma (e.g., Zhang et al., 2018, Oncol. Lett., 16:1219-25); changes in telomeric DNA (e.g., in length or in heterozygosity) or centromeric DNA (e.g., changes in expression of centromeric genes) also have been associated with cancers (e.g., prostate, breast, lung, lymphoma, and Ewing's sarcoma) (see, for example, Baretton et al., 1994, Cancer Res., 54:4472-80; Liscia et al., 1999, Br. J. Cancer, 80:821-6; Proctor et al., 2009, Biochim. Biophys. Acta, 1792:260-74; and Sun et al., 2016, Int. J. Cancer, 139:899-907); various mutations (e.g., deletions), rearrangements and/or copy number changes in mitochondrial DNA (mtDNA) have been used prognostically and diagnostically for various cancers (e.g., prostate cancer, melanoma, breast cancer, lung cancer, and colorectal cancer). See, for example, Maragh et al., 2015, Cancer Biomark., 15:763-73; Shen et al., 2010, Mitochondrion, 10:62-68; Hosgood et al., 2010, Carcinogen., 31:847-9; Thyagarajan et al., 2012, Cancer Epid. Biomarkers & Prev., 21:1574-81; and US Patent No. 9,745,632; and the abnormal presence, absence or amount of messenger RNAs (mRNAs) also have been correlated with various cancers including, without limitation, breast cancer, Wilms' tumors, and cervical cancer (see, for example, Guetschow et al., 2012, Anal. Bioanaly. Chem., 404:399-406; Schwienbacher et al., 2000,

Cancer Res., 60:1521-5; and Ngan et al., 1997, Genitourin Med., 73:54-8). Each of these citations is incorporated herein by reference in its entirety.

[278] In certain aspects, provided herein are methods of detecting diseases in a subject (e.g., a human). Various methods disclosed herein provide a broadly applicable approach for non-invasive detection of cancer in subjects (e.g., a cancer such as, without limitation, endometrial or ovarian cancer). Various methods disclosed herein provide a broadly applicable approach treatment of a subject having or suspected of having cancer after non-invasive detection of cancer in subjects (e.g., a cancer such as, without limitation, endometrial or ovarian cancer).

[279] In some embodiments, methods provided herein include detecting genetic biomarkers (e.g., mutations) in one or more genes from cells present in a sample (e.g., a cervical or endometrial sample) obtained from a subject. For example, methods provided herein can be used to detect the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes selected from the group consisting of: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A, wherein the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes is indicative of the presence of ovarian or endometrial cancer in the subject. In some embodiments, the methods provided herein include detecting in a sample obtained from a subject the presence of aneuploidy (e.g., monosomy or trisomy), wherein the presence aneuploidy is indicative of the presence of ovarian or endometrial cancer in the subject. In some embodiments, methods provided herein include detecting in a sample obtained from a subject each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and the presence of aneuploidy (e.g., monosomy or trisomy). In some embodiments, methods which include detecting in a sample obtained from a subject each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and the presence of aneuploidy (e.g., monosomy or trisomy) provide a better indication that the

subject has a cancer (e.g., a endometrial or ovarian cancer) than methods in which either aspect is tested individually.

[280] In some embodiments, a sample for detecting the presence of a cancer (e.g. an ovarian or endometrial cancer) can be collected using a Pap brush. In some embodiments of any of the variety of methods provided herein, a sample for detecting the presence of a cancer (e.g. an ovarian or endometrial cancer) can be collected using a Tao brush.

[281] In some embodiments, methods provided herein further include testing a sample obtained from a subject (e.g., a plasma sample) for genetic biomarkers in nucleic acids that are present as circulating tumor DNA (ctDNA). For example, a sample (e.g., a plasma sample) can be tested to detect genetic biomarkers in nucleic acids that harbor one or more mutations in one or more of the following genes: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and/or TP53.

[282] In various embodiments of methods provided herein in which one or more genetic biomarkers (e.g., mutations) in genes in cells present in a sample (e.g., a cervical or endometrial sample) obtained from a subject are detected, genetic biomarkers (e.g., mutations) in one or more of NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A can be detected. In some embodiments, one or more genetic biomarkers (e.g., mutations) in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 of these genes can be detected. In some embodiments, one or more genetic biomarkers (e.g., mutations) in all 18 of these genes can be detected. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation shown in Table 15. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation shown in Table 16. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation shown in Table 17. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation in a gene shown in Table 15. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation in a gene shown in Table 16. In some embodiments, the one

or more genetic biomarkers (e.g., mutations) in these genes can be a mutation in a gene shown in Table 17. In some embodiments, methods provided herein to detect the presence of an ovarian or endometrial cancer by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPPF2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A can be combined with the detection of aneuploidy, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both. In some embodiments, combining with the detection of aneuploidy, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both can increase the specificity and/or sensitivity of detecting ovarian or endometrial cancer. In some embodiments, the sample is collected using a Pap brush. In some embodiments, the sample is collected using a Tao brush.

[283] In some embodiments, methods provided herein can be used to detect the presence of an endometrial cancer. For example, methods provided herein can be used to detect the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A, wherein the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes is indicative of the presence of endometrial cancer in the subject. In some embodiments, one or more genetic biomarkers (e.g., mutations) in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 of these genes can be detected. In some embodiments, one or more genetic biomarkers (e.g., mutations) in all 12 of these genes can be detected. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be any mutation described herein (e.g., a mutation as shown in any one of Tables 15, 16, or 17). In some embodiments, methods provided herein to detect the presence of an endometrial cancer by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A can be combined with the detection of aneuploidy, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both. In some embodiments, combining with the detection of aneuploidy, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both can increase the specificity and/or

sensitivity of detecting endometrial cancer. In some embodiments, the sample is collected using a Pap brush. In some embodiments, the sample is collected using a Tao brush.

[284] In some embodiments, methods provided herein can be used to detect the presence of an ovarian cancer. For example, methods provided herein can be used to detect the presence of one or more genetic biomarkers (e.g., mutations) in TP53, wherein the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes is indicative of the presence of ovarian cancer in the subject. In some embodiments, an ovarian cancer detected by detecting the presence of a genetic biomarker (e.g., mutation) in TP53 can be a high-grade ovarian cancer. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in TP53 can be any TP53 mutation described herein (e.g., a TP53 mutation as shown in any one of Tables 15, 16, or 17). In some embodiments, methods provided herein to detect the presence of an endometrial cancer by detecting the presence of one or more genetic biomarkers (e.g., mutations) in TP53 can be combined with the detection of aneuploidy, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both. In some embodiments, combining with the detection of aneuploidy, the detection of mutations present in ctDNA, or both can increase the specificity and/or sensitivity of detecting ovarian cancer. In some embodiments, the sample is collected using a Pap brush. In some embodiments, the sample is collected using a Tao brush.

[285] Genetic biomarkers (e.g., mutations) in one or more of the genes described herein can be detected by any of the exemplary techniques for detecting mutations described herein. Moreover, those of ordinary skill in the art will be aware of other suitable methods for detecting genetic biomarkers (e.g., mutations) in these genes.

[286] In some embodiments, methods provided herein (e.g., method including the detection of one or more genetic biomarkers (e.g., mutations) in any of the genes described herein, the detection of aneuploidy, or both) further include testing a sample obtained from a subject (e.g., a plasma sample) for genetic biomarkers in nucleic acids that are present as circulating tumor DNA (ctDNA). In some embodiments, the sample includes nucleic acids that harbor one or more of genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1,

PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) which nucleic acids can be assayed according to any of the variety of methods disclosed herein. In some embodiments, the plasma sample includes nucleic acids that harbor one or more of genetic biomarkers (e.g., mutations) in one or more genes (e.g., AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and/or TP53) which nucleic acids can be assayed according to any of the variety of methods disclosed herein. In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) in a gene listed in Table 15 can be detected in a sample (e.g., a plasma sample). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) listed in Table 15 can be detected in a sample (e.g., a plasma sample). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) in a gene listed in Table 16 can be detected in a sample (e.g., a plasma sample). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) listed in Table 16 can be detected in a sample (e.g., a plasma sample). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) in a gene listed in Table 17 can be detected in a sample (e.g., a plasma sample). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) listed in Table 17 can be detected in a sample (e.g., a plasma sample). As will be appreciated by those of ordinary skill in the art, such ctDNA can represent nucleic acids that are shed from cancer cells (e.g., cervical cancer, endometrial cancer cells, ovarian cancer cells, and/or fallopian tubal cancer cells) and as such, can be assayed using any of the variety of methods provided herein to determine the presence of a cancer in the subject. In some embodiments, the sample for detecting the presence of one or more mutations in ctDNA is, or can include, blood (e.g., whole blood, serum, or plasma), amnion, tissue, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid (e.g., ovarian cyst fluid), stool, ascites, pap smears, peritoneal fluid, peritoneal lavage, uterine lavage, and combinations thereof. Mutations in ctDNA can be detected by any of the exemplary techniques for detecting mutations described herein. Moreover, those of ordinary skill in the art will be aware of other suitable methods for detecting mutations in ctDNA.

[287] In some embodiments, methods provided herein include detecting in a sample (e.g., a cervical or endometrial sample) obtained from a subject the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or aneuploidy (e.g., monosomy or trisomy). In some embodiments, the sample is a cervical sample. In some embodiments, the sample is an endometrial sample. In some embodiment, the sample comprises tissue or cells from each of the cervix and the endometrium. In some embodiments, a sample is obtained with a Pap brush. In some embodiments, a sample is obtained with a Tao brush. In some embodiments, methods include isolating cells from the rest of the sample. For example, cells can be completely isolated from other components of the sample, or can be isolated to a degree such that the isolated cells include only small amounts of other material from the sample. In some embodiments, nucleic acids present in cells isolated from a sample can be assayed using any of the variety of methods provided herein. For example, nucleic acids present in cells from the sample can be isolated and assayed.

[288] In some embodiments, methods provided herein include detecting in a sample (e.g., a cervical or endometrial sample) obtained from a subject the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, wherein at least one of the genetic biomarker (e.g., at least one of the mutations) is present at a low frequency in the sample. For example, methods provided herein can detect a genetic biomarker (e.g., a mutation) when the genetic biomarker (e.g., the mutation) is present in 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1% or fewer of the cells in the sample. In some embodiments, methods provided herein can detect a genetic biomarker (e.g., a mutation) when the genetic biomarker (e.g., the mutation) is present in less than 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, or 1% of the total nucleic acid present in the sample.

[289] In some embodiments of any of the variety of methods disclosed herein in which the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g.,

NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or the presence of aneuploidy (e.g., monosomy or trisomy), cytology may be performed in combination with or independently of the method. For example, cytology can be performed in combination with any of the variety of methods disclosed herein to improve the detection of a cancer (e.g., an ovarian or endometrial cancer) in the subject. In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or the presence of aneuploidy (e.g., monosomy or trisomy) increases the sensitivity of the assay (e.g., by at least 10%, 20%, 30%, 40%, 50%, 60% or more). In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or the presence of aneuploidy (e.g., monosomy or trisomy) increases the specificity of the assay (e.g., by at least 10%, 20%, 30%, 40%, 50%, 60% or more). In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or the presence of aneuploidy (e.g., monosomy or trisomy) permits the detection of cancers that would otherwise be undetectable or only rarely detectable with cytology alone (e.g., low-grade tumors). As another example, cytology can be performed independently to confirm the presence of a cancer (e.g., an ovarian or endometrial cancer) once its presence is determined by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or aneuploidy (e.g., monosomy or trisomy). In some embodiments, methods provided herein include detecting each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more

genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and the presence of aneuploidy (e.g., monosomy or trisomy), and performing cytology.

[290] In some embodiments, any of the variety of methods disclosed herein can be performed on subjects who have previously undergone treatments for cancer (e.g., an ovarian or endometrial cancer). In some embodiments, methods provided herein can be used to determine the efficacy of the treatment. For example, a subject having an ovarian or endometrial cancer can be administered a treatment (also referred to herein as a "therapeutic intervention"), after which the continued presence of cancer or the amount of cancer (or lack thereof) is determined by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A) and/or the presence of aneuploidy (e.g., monosomy or trisomy).

[291] In certain aspects, provided herein are methods of detecting diseases in a subject (e.g., a human). Various methods disclosed herein provide a broadly applicable approach for non-invasive detection of cancer (e.g., an early-stage cancer such as, without limitation, bladder cancer or upper tract urothelial carcinomas (UTUC)). In some embodiments, the disease detected is cancer. In some embodiments, the cancer detected is malignant. In some embodiments, the disease detected is related to urinary tract. In some embodiments, the disease detected is a cancer affecting the urinary tract. In some embodiments, the disease detected is bladder cancer. In some embodiments, the disease detected is related to renal pelvis. In some embodiments, the disease detected is a cancer affecting renal pelvis. In some embodiments, the disease detected is an UTUC.

[292] In some embodiments, methods provided herein include detecting mutations in one or more genes in a sample (e.g., a urine sample) obtained from a subject. For example, methods provided herein can be used to detect the presence of one or more genetic biomarkers (e.g., one or more mutations) in one or more of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL. In some embodiments, methods provided herein include detecting the presence of at least one genetic biomarker (e.g., mutation) in a *TERT* promoter in a sample obtained from a subject. In some

embodiments, the methods provided herein include detecting the presence of aneuploidy (e.g., monosomy or trisomy) in a sample obtained from a subject. In some embodiments, methods provided herein include detecting in a sample obtained from a subject two or more of: genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and the presence of at least one genetic biomarker (e.g., mutation) in a *TERT* promoter. In some embodiments, methods provided herein include detecting in a sample obtained from a subject each of the presence of one or more genetic biomarkers (e.g., one or more mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and the presence of at least one genetic biomarker (e.g., mutation) in a *TERT* promoter. In some embodiments, methods which include detecting in a sample obtained from a subject each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and the presence of at least one genetic biomarker (e.g., mutation) in a *TERT* promoter provide a better indication that the subject has a cancer (e.g., a bladder cancer or an UTUC) than methods in which fewer than all of these three parameters are tested. In some embodiments, methods which include detecting in a sample obtained from a subject each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and the presence of at least one genetic biomarker (e.g., mutation) in a *TERT* promoter can increase the specificity and/or sensitivity of detecting ovarian or endometrial cancer (e.g., a bladder cancer or an UTUC).

[293] In various embodiments of methods provided herein in which one or more genetic biomarkers (e.g., one or more mutations) in genes in a sample (e.g., a urine sample) obtained from a subject are detected, genetic biomarkers (e.g., mutations) in one or more of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL can be detected. In some embodiments, genetic biomarkers (e.g., mutations) in 1, 2, 3, 4, 5, 6, 7, 8, or 9 of these genes can be detected. In some embodiments, genetic biomarkers (e.g.,

mutations) in all 10 of these genes can be detected. In some embodiments, the one or more genetic biomarkers (e.g., mutations) in these genes can be any mutation disclosed herein. For example, the one or more genetic biomarkers (e.g., mutations) in these genes can be a mutation shown in Table 19 or Table 29. In some embodiments, at least one genetic biomarkers (e.g., mutations) in one of TR53 or FGFR3 are detected. In some embodiments, at least one genetic biomarker (e.g., at least one mutation) in each of TR53 or FGFR3 are detected.

[294] In some embodiments, methods provided herein include detecting the presence of at least one genetic biomarker (e.g., mutation) in a TERT promoter in a sample (e.g., a urine sample) obtained from a subject. Any genetic biomarker (e.g., mutation) in a TERT promoter disclosed herein can be detected. For example, any of the variety of TERT promoter genetic biomarkers (e.g., mutations) shown in Table 26 or Table 30 can be detected using methods provided herein. In some embodiments, TERT promoter genetic biomarkers (e.g., mutations) that can be detected according to various methods provided herein include the g.1295228 C>T and/or g.1295250 C>T mutations. In some embodiments, TERT promoter genetic biomarkers (e.g., mutations) that can be detected according to various methods provided herein include mutations at positions hg1295228 and/or hg 1295250, which are 66 and 88 bp upstream of the transcription start site, respectively. In some embodiments, a genetic biomarker (e.g., a mutation) in a TERT promoter is identified using a singleplex PCR assay. In some embodiments, a genetic biomarker (e.g., a mutation) in a TERT promoter is identified using a multiplex PCR assay. In some embodiments, single amplification primer can be used to amplify a segment containing the region of the TERT promoter known to harbor genetic biomarkers (e.g., mutations) in cancer (e.g., bladder cancer or UTUC).

[295] As used herein, the term "TERT" refers to the gene and/or the protein encoded by the gene, which is telomerase reverse transcriptase, a catalytic subunit of the enzyme telomerase, which, together with the telomerase RNA component (TERC), comprises the most important unit of the telomerase complex. High rates of activating mutations in the upstream promoter of the TERT gene are found in the majority of BC as well as in other cancer types. TERT promoter mutations commonly affect two hot spots: g.1295228 C>T and g.1295250 C>T.

These mutations lead to the generation of CCGGAA/T or GGAA/T motifs altering binding site for ETS transcription factors and subsequently increased TERT promoter activity. TERT promoter mutations occur in up to 80% of invasive urothelial carcinomas of the bladder and upper urinary tract as well as in several of its histologic variants. Moreover, TERT promoter mutations occur in 60-80% of BC precursors, including Papillary Urothelial Neoplasms of Low Malignant Potential, non-invasive Low Grade Papillary Urothelial Carcinoma, non-invasive High Grade Papillary Urothelial Carcinoma and "flat" Carcinoma in Situ (CIS), as well as in urinary cells from a subset of these patients. TERT promoter mutations have thus been established as a common genetic alteration in BC. Human TERT promoter sequences are known in the art.

[296] Genetic biomarkers (e.g., mutations) in one or more of the genes described herein can be detected by any of the exemplary techniques for detecting mutations described herein. Moreover, those of ordinary skill in the art will be aware of other suitable methods for detecting genetic biomarkers (e.g., mutations) in these genes.

[297] In some embodiments, methods provided herein include detecting in a sample (e.g., a urine sample) obtained from a subject the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, the presence of at least one genetic biomarker (e.g., at least one mutation) in a TERT promoter, or both. In some embodiments, the sample is a urine sample. In some embodiments provided herein, methods include isolating such cells from the rest of the sample. For example, cells can be completely isolated from other components of the sample, or can be isolated to a degree such that the isolated cells include only small amounts of other material(s) from the sample. In some embodiments, the presence of genetic biomarkers in nucleic acids present in cells isolated from a sample and/or the presence of aneuploidy in cells isolated from a sample can be assayed using any of the variety of methods provided herein. For example, nucleic acids present in cells from the sample can be isolated and assayed for the presence of one or more genetic biomarkers and/or the presence of aneuploidy. In some embodiments, cells are not isolated from the sample prior to isolating their nucleic acids for analysis. In some embodiments, the sample includes nucleic acids that harbor one or more genetic biomarkers (e.g., mutations) in one or

more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), at least one genetic biomarker (e.g., a mutation) in a TERT promoter, and/or aneuploidy (e.g., monosomy or trisomy), which nucleic acids are assayed according to any of the variety of methods disclosed herein. As will be appreciated by those of ordinary skill in the art, such nucleic acids can represent nucleic acids that are shed from cancer cells (e.g., bladder cancer cells or cells from UTUCs) and as such, can be assayed using any of the variety of methods provided herein to determine the presence of a cancer in the subject.

[298] In some embodiments, methods provided herein include detecting in a sample (e.g., a urine sample) obtained from a subject the presence of one or more genetic biomarkers (e.g., mutations) in one or more of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL, the presence of at least one genetic biomarker (e.g., a mutation) in a TERT promoter, or both, wherein at least one of the genetic biomarkers (e.g., at least one of the mutations) is present at a low frequency in the sample. For example, methods provided herein can detect a genetic biomarker (e.g., a mutation) when the genetic biomarker (e.g., the mutation) is present in 0.01%, 0.02%, 0.03%, 0.04%, 0.05%, 0.06%, 0.07%, 0.08%, 0.09%, 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1% or fewer of the cells in the sample. In some embodiments, methods provided herein can detect a genetic biomarker (e.g., a mutation) when the genetic biomarker (e.g., the mutation) is present in 0.03% or fewer of the cells in the sample. In some embodiments, methods provided herein can detect a genetic biomarker (e.g., a mutation) when the genetic biomarker (e.g., the mutation) is present in less than 0.01%, 0.02%, 0.03%, 0.04%, 0.05%, 0.06%, 0.07%, 0.08%, 0.09%, 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, or 1% of the total nucleic acid present in the sample.

[299] In some embodiments of any of the variety of methods disclosed herein in which the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one genetic biomarker (e.g., a mutation) in a *TERT* promoter is detected, cytology may be performed in combination with or independently of the method. For example, cytology can be performed in combination with any of the variety of methods disclosed herein to improve

the detection of a cancer (e.g., a bladder cancer or an UTUC) in the subject. In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one genetic biomarker (e.g., a mutation) in a *TERT* promoter increases the sensitivity of the assay as compared to cytology alone (e.g., by at least 10%, 20%, 30%, 40%, 50%, 60% or more). In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one mutation in a TERT promoter (e.g., a genetic biomarker in a TERT promoter) increases the specificity of the assay as compared to cytology alone (e.g., by at least 10%, 20%, 30%, 40%, 50%, 60% or more). In some embodiments, performing cytology in combination with detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one genetic biomarker (e.g., a mutation) in a *TERT* promoter permits the detection of cancers that would otherwise be undetectable or only rarely detectable with cytology alone (e.g., low-grade tumors). As another example, cytology can be performed independently to confirm the presence of a cancer (e.g., a bladder cancer or an UTUC) once its presence is determined by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one genetic biomarker (e.g., a mutation) in a *TERT* promoter. In some embodiments, methods provided herein include detecting each of the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), the presence of at least one genetic biomarker (e.g., a mutation) in a *TERT* promoter, and performing cytology.

[300] In some embodiments, any of the variety of methods disclosed herein can be performed on subjects who have previously undergone treatments for cancer (e.g., bladder cancer or UTUC). In some embodiments, methods provided herein can be used to determine the efficacy of the treatment. For example, a subject having bladder cancer or UTUC can be administered a treatment (also referred to herein as a "therapeutic intervention"), after which the continued presence of cancer or the amount of cancer (or lack thereof) is determined by detecting the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes (e.g., TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL), the presence of aneuploidy (e.g., monosomy or trisomy), and/or the presence of at least one genetic biomarker (e.g., a mutation) in a TERT promoter.

[301] Some embodiments of methods provided herein include testing cytological specimens for cancer. In some embodiments, one or more cytological tests are used for diagnosis or screening. In some embodiments, the one or more cytological tests are used for diagnosing cancer. In some embodiments, the one or more cytological tests are used for screening cancer. In some embodiments, one or more cytological tests are used for classifying a disease or condition. In some embodiments, one or more cytological tests are used for classifying a cancer.

[302] Various methods may be used to collect a sample including, but not limited to, aspiration cytology (e.g. fine needle aspiration), exfolative cytology (e.g. impression smears and tissue scrapings), cystoscopy.

[303] In some embodiments, the cytological test includes a gross examination. In some embodiments, the cytological test includes a histological examination. In some embodiments, the cytological test includes a frozen section exam. In some embodiments, the cytological test is administered in conjunction with another method or test. In some embodiments, the other method or test includes a histochemical stain. In some embodiments, the other method or test includes an immunohistochemical stain. In some embodiments, the other method or test includes electron microscopy. In some embodiments, the other method or test includes flow cytometry. In some embodiments, the other method or test includes image cytometry. In some embodiments, the other method or test includes genetic tests. For

example, the genetic test may include, but is not limited to, a cytogenetic test, a fluorescent in situ hybridization (FISH) test, and/or a molecular genetic test.

[304] In some embodiments, a molecular genetic test is used on a cytological sample (e.g., a sample on which cytology is also performed) to detect the presence of one or more genetic biomarkers (e.g., mutations) in PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A. In some embodiments, a molecular genetic test is used on a cytological sample (e.g., a sample on which cytology is also performed) to detect the presence of one or more genetic biomarkers (e.g., mutations) in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL. In some embodiments, a molecular genetic test is used on a cytological sample (e.g., a sample on which cytology is also performed) to detect the presence of one or more genetic biomarkers (e.g., mutations) in NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A. In some embodiments, a molecular genetic test is used on a cytological sample (e.g., a sample on which cytology is also performed) to detect the presence of one or more genetic biomarkers (e.g., mutations) in TP53.

Protein Biomarkers in Combination with Aneuploidy

[305] In one aspect, provided herein are methods and materials for detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g.,

increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from the subject.

[306] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the sensitivity provided by separately detecting the presence of one or more members of a panel of protein biomarkers or the presence of aneuploidy. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the

presence of aneuploidy in one or more samples obtained from a subject provide a sensitivity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting a single type of cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting two or more types of cancers. Any of a variety of cancer types can be detected using methods and materials provided herein (see, e.g., the section entitled "Cancers"). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include pancreatic cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include cancers of the female reproductive tract (e.g., cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include bladder cancer or upper-tract urothelial carcinomas.

[307] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one

or more samples obtained from a subject provide high specificity in the detection or diagnosis of cancer (e.g., a low frequency or incidence of incorrectly identifying a subject as having cancer when that subject does not have cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a specificity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer) that is higher than the specificity provided by separately detecting the presence of one or more members of a panel of protein biomarkers or the presence of aneuploidy. In some embodiments, methods and materials provided herein that include that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide a specificity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. As will be understood by those of ordinary skill in the art, a specificity of 99% means that only 1% of subjects that do not have cancer are incorrectly identified as having cancer. In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting a single cancer (e.g., there is a low probability of incorrectly identifying that subject as having that single cancer type). In some embodiments, methods and materials provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting two or more cancers (e.g., there is a low probability of incorrectly identifying that subject as having those two or more cancer types).

[308] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN,

CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), and 2) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO), and the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), and 2) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[309] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, and 2) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3, and 2) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, and 2) the

presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[310] In some embodiments, methods provided herein that include the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, and 2) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of one or more members of a panel of protein biomarkers in one or more samples obtained from a subject include detecting the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3, and 2) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, and 2) the presence of aneuploidy, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[311] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of: 1) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, and 2) the presence of aneuploidy. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting

the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN, and 2) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy in one or more samples obtained from a subject include detecting the presence of1) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, and 2) the presence of aneuploidy, a subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing pancreatic cancer.

[312] A sample obtained from a subject can be any of the variety of samples described herein that contains DNA (e.g., ctDNA in the blood, or DNA present in bladder, cervical, endometrial, or uterine samples) and/or proteins. In some embodiments, DNA (e.g., cell-free DNA (e.g., ctDNA) or DNA present in bladder, cervical, endometrial, or uterine samples) and/or proteins in a sample obtained from the subject are derived from a tumor cell. In some embodiments, DNA (e.g., cell-free DNA (e.g., ctDNA) in a sample obtained from the subject includes one or more genetic biomarkers and or aneuploid DNA. In some embodiments, proteins in a sample obtained from the subject includes one or more protein biomarkers. Non-limiting examples of samples in which genetic biomarkers and/or protein biomarkers and/or aneuploidy can be detected include a blood sample, a plasma sample, a serum sample, a urine sample, an endometrial sample, a cervical sample, and a uterine sample. In some embodiments, the presence of one or more protein biomarkers and the presence aneuploidy is detected in a single sample obtained from the subject. In some embodiments, the presence of one or more protein biomarkers is detected in a first sample obtained from a subject, and the presence of aneuploidy is detected in a second sample obtained from the subject.

[313] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers (e.g., each member of a panel of protein biomarkers) and the presence of aneuploidy in one or more samples obtained from a subject, an elevated level of one or more members of the panel of protein biomarkers can be detected. For example, an elevated level of a protein biomarker can be a level that is higher that a reference level. A reference level can be any level of the protein biomarker that is not associated with the presence of cancer. For example, a reference level of a protein biomarker

can be a level that is present in a reference subject that does not have cancer or does not harbor a cancer cell. A reference level of a protein biomarker can be the average level that is present in a plurality of reference subjects that do not have cancer or do not harbor a cancer cell. A reference level of a protein biomarker in a subject determined to have cancer can be the level that was presence in the subject prior to the onset of cancer. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, or each of): CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at an elevated level includes one or more of (e.g., 1, 2, 3, or each of): CA19-9, CEA, HGF, and/or OPN.

[314] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers (e.g., each member of a panel of protein biomarkers) and the presence of aneuploidy in one or more samples obtained from a subject, a decreased level of one or more members of the panel of protein biomarkers can be detected. For example, a decreased level of a protein biomarker can be a level that is lower that a reference level. A reference level can be any level of the protein biomarker that is not associated with the presence of cancer. For example, a reference level of a protein biomarker can be a level that is present in a reference subject that does not have cancer or does not harbor a cancer cell. A reference level of a protein biomarker can be the average level that is present in a plurality of reference subjects that do not have cancer or do not harbor a cancer cell. A reference level of a protein biomarker in a subject determined to have cancer can be the level that was presence in the subject prior to the onset of cancer. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a

decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, or each of): CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or each of): CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, a panel of protein biomarkers in which one or more members of the panel is present at a decreased level includes one or more of (e.g., 1, 2, 3, or each of): CA19-9, CEA, HGF, and/or OPN.

[315] In some embodiments, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer (e.g., by detecting: 1) the presence of aneuploidy, and 2) the presence of one or more protein biomarkers in any of the panels described herein as being useful in conjunction with the presence of aneuploidy), the subject is selected as a candidate for (e.g., is selected for) further diagnostic testing (e.g., any of the variety of further diagnostic testing methods described herein), the subject is selected as a candidate for (e.g. is selected for) increased monitoring (e.g., any of the variety of increasing monitoring methods described herein), the subject is identified as a subject who will or is likely to respond to a treatment (e.g., any of the variety of therapeutic interventions described herein), the subject is selected as a candidate for (e.g., is selected for) a treatment, a treatment (e.g., any of the variety of therapeutic interventions described herein) is selected for the subject, and/or a treatment (e.g., any of the variety of therapeutic interventions described herein) is administered to the subject. For example, when a subject is determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer, the subject can undergo further diagnostic testing, which further diagnostic testing can confirm the presence of cancer in the subject. Additionally or alternatively, the subject can be monitored at in increased frequency. In some embodiments of a subject determined as having (e.g., diagnosed to have) cancer or determined to be (e.g. diagnosed as being) at

elevated risk of having or developing cancer in which the subject undergoes further diagnostic testing and/or increased monitoring, the subject can additionally be administered a therapeutic intervention. In some embodiments, after a subject is administered a therapeutic intervention, the subject undergoes additional further diagnostic testing (e.g., the same type of further diagnostic testing as was performed previously and/or a different type of further diagnostic testing) and/or continued increased monitoring (e.g., increased monitoring at the same or at a different frequency as was previously done). In embodiments, after a subject is administered a therapeutic intervention and the subject undergoes additional further diagnostic testing and/or additional increased monitoring, the subject is administered another therapeutic intervention (e.g., the same therapeutic intervention as was previously administered and/or a different therapeutic intervention). In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for 1) the presence of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), and 2) the presence of aneuploidy. In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for 1) the presence of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, and 2) the presence of aneuploidy. In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for 1) the presence of one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, and 2) the presence of aneuploidy. In some embodiments, after a subject is administered a therapeutic intervention, the subject is tested for 1) the presence of one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, and 2) the presence of aneuploidy.

[316] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein

biomarkers and the presence of aneuploidy, or a different sample). Any of a variety of genetic biomarkers can be detected (e.g., any of the variety of genetic biomarkers and/or genetic biomarker panels described herein).

[317] In some embodiments, methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), and 2) the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments, methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO), and the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), 2) the presence of aneuploidy, and 3) the presence of one or more members of a panel of genetic biomarkers, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[318] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, and 2) the presence of aneuploidy, the

methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3, and 2) the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, 2) the presence of aneuploidy, and 3) the presence of one or more members of a panel of genetic biomarkers, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing cancer one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[319] In some embodiments of methods provided herein that detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, and 2) the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments or methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-

1, and CA15-3, and 2) the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, 2) the presence of aneuploidy, and 3) the presence of one or more members of a panel of genetic biomarkers, the subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing one of the following types of cancer: liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and/or breast cancer.

[320] In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, and 2) the presence of aneuploidy, the methods further include detecting the presence one or more members of a panel of genetic biomarkers in one or more samples obtained from a subject (e.g., the same sample use to detect either or both of the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, or a different sample). In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of: 1) each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN, and 2) the presence of aneuploidy. In some embodiments of methods provided herein that include detecting in one or more samples obtained from a subject the presence of1) one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN, 2) the presence of aneuploidy, and 3) the presence of one or more members of a panel of genetic biomarkers, a subject is determined as having (e.g., diagnosed to have) or is determined to be (e.g. diagnosed as being) at elevated risk of having or developing pancreatic cancer.

[321] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes can further be detected: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in each of the following genes can further be detected: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS.

[322] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes can further be detected: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in each of the following genes can further be detected: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4.

[323] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes can further be detected: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in each of the following genes can further be detected: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL.

[324] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy,

one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes can further be detected: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in each of the following genes can further be detected: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A.

[325] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes can further be detected: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in each of the following genes can further be detected: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A.

[326] In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the presence of aneuploidy, one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes can further be detected: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and/or TP53. In some embodiments of methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers and the presence of aneuploidy, one or more protein biomarkers in each of the following genes can further be detected: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and TP53.

[327] In some embodiments, any of the variety of methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers and the

presence of aneuploidy in one or more samples obtained from a subject further include detecting the presence of one or more members of one or more additional classes of biomarkers. Non-limiting examples of such additional classes of biomarkers includes: copy number changes, DNA methylation changes, other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements), peptides, and/or metabolites.

[328] In some embodiments, the one or more additional classes of biomarkers include a metabolite biomarker. In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more metabolites indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more metabolites indicative of cancer. Non-limiting examples of metabolites indicative of cancer include: 5-methylthioadenosine (MTA), Glutathione reduced (GSH), N-acetylglutamate, Lactose, N-acetylneuraminate, UDP-acetylglucosamine, UDP-Acetylgalactosamine, UDP-glucuronate, Pantothenate, Arachidonate (20:4n6), Choline, Cytidine 5′-diphosphocholine, Dihomo-linolenate (20:3n3), Docosapentaenoate (DPA 22:5n3), Eicosapentaenoate (EPA 20:5n3), Glycerophosphorylcholine (GPC), Docosahexaenoate (DHA 22:6n3), Linoleate (18:2n6), Cytidine 5′-monophosphate (5′-CMP), Gamma-glutamylglutamate, X – 14577, X – 11583, Isovalerylcarnitine, Phosphocreatine, 2-Aminoadipic acid, Gluconic acid, O-Acetylcarnitine, aspartic acid, Deamido-NAD+, glutamic acid, Isobutyrylcarnitine, Carnitine, Pyridoxal, Citric acid, Adenosine, ATP, valine, XC0061, Isoleucine, γ-Butyrobetaine, Lactic acid, alanine, phenylalanine, Gluconolactone, leucine, Glutathione (GSSG)_divalent, tyrosine, NAD+, XC0016, UTP, creatine, Theobromine, CTP, GTP, 3-Methylhistidine, Succinic acid, Glycerol 3-phosphate, glutamine, 5-Oxoproline, Thiamine, Butyrylcarnitine, 4-Acetamidobutanoic acid, UDP-Glucose, UDP-Galactose, threonine, N-Acetylglycine, proline, ADP, Choline, Malic acid, S-Adenosylmethionine, Pantothenic acid, Cysteinesulfinic acid, 6-Aminohexanoic acid, Homocysteic acid, Hydroxyproline, Methionine sulfoxide, 3-Guanidinopropionic acid, Glucose 6-phosphate, Phenaceturic acid, Threonic acid, tryptophan, Pyridoxine, N-Acetylaspartic acid, 4-Guanidinobutyric acid, serine, Citrulline, Betaine, N-Acetylasparagine, 2-Hydroxyglutaric acid, arginine, Glutathione (GSH),

creatinine, Dihydroxyacetone phosphate, histidine, glycine, Glucose 1-phosphate, N-Formylglycine, Ketoprofen, lysine, beta-alanine, N-Acetylglutamic acid, 2-Amino-2-(hydroxymethyl)-1,3-propanediol, Ornithine, Phosphorylcholine, Glycerophosphocholine, Terephthalic acid, Glyceraldehyde 3-phosphate, Gly-Asp, Taurine, Fructose 1,6-diphosphate, 3-Aminoisobutyric acid, Spermidine, GABA, Triethanolamine, Glycerol, N-Acetylserine, N-Acetylornithine, Diethanolamine, AMP, Cysteine glutathione disulfide, Streptomycin sulfate +H2O divalent, trans-Glutaconic acid, Nicotinic acid, Isobutylamine, Betaine aldehyde +H2O, Urocanic acid, 1-Aminocyclopropane-1-carboxylic acid Homoserinelactone, 5-Aminovaleric acid, 3-Hydroxybutyric acid, Ethanolamine, Isovaleric acid, N-Methylglutamic acid, Cystathionine, Spermine, Carnosine, 1-Methylnicotinamide, N-Acetylneuraminic acid, Sarcosine, GDP, N-Methylalanine, palmitic acid, 1,2-dioleoyl-sn-glycero-3-phospho-rac-glycerolcholesterol 5α,6α epoxidelanosterol, lignoceric acid, 1oleoyl_rac_GL, cholesterol_epoxide, erucic acid, T-LCA, oleoyl-L-carnitine, oleanolic acid, 3-phosphoglycerate, 5-hydroxynorvaline, 5-methoxytryptamine, adenosine-5-monophosphate, alpha-ketoglutarate, asparagine, benzoic acid, hypoxanthine, maltose, maltotriose, methionine sulfoxide, nornicotine, phenol, Phosphoethanolamine, pyrophosphate, pyruvic acid, quinic acid, taurine, uric acid, inosine, lactamide, 5-hydroxynorvaline NIST, cholesterol, deoxypentitol, 2-hydroxyestrone, 2-hydroxyestradiol, 2-metholyestrone, 2-metholxyestradiol, 2-hydroxyestrone-3-methyl ether, 4-hydroxyestrone, 4-metholxyestrone, 4-methoxyestradiol, 16alpha-hydroxyestrone, 17-epiestriol, estriol, 16-Ketoestradiol, 16-epiestriol, acylcarnitine C18:1, amino acids citrulline and trans-4-hydroxyproline, glycerophospholipids PC aa C28:1, PC ae C30:0 and PC ae C30:2, and sphingolipid SM (OH) C14:1. See e.g., Halama et al., Nesting of colon and ovarian cancer cells in the endothelial niche is associated with alterations in glycan and lipid metabolism, Scientific Reports volume 7, Article number: 39999 (2017); Hur et al., Systems approach to characterize the metabolism of liver cancer stem cells expressing CD133, Sci Rep., 7: 45557, doi: 10.1038/srep45557, (2017); Eliassen et al., Urinary Estrogens and Estrogen Metabolites and Subsequent Risk of Breast Cancer among Premenopausal Women, Cancer Res; 72(3); 696–706 (2011); Gangi et al., Metabolomic profile in pancreatic cancer patients: a consensus-based approach to identify highly discriminating metabolites, Oncotarget,Feb 2;

7(5): 5815–5829 (2016); Kumar et al., Serum and Plasma Metabolomic Biomarkers for Lung Cancer, Bioinformation, 13(6): 202–208, doi: 10.6026/97320630013202 (2017); Schmidt et al., Pre-diagnostic metabolite concentrations and prostate cancer risk in 1077 cases and 1077 matched controls in the European Prospective Investigation into Cancer and Nutrition, BMC Med.,15: 122, doi: 10.1186/s12916-017-0885-6 (2017); each of which is incorporated herein by reference in its entirety.

[329] In some embodiments, the one or more additional classes of biomarkers include a peptide (e.g., a peptide that is distinct from the various protein biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a peptide is derived from a protein (e.g., the peptide includes an amino acid sequence present in a protein biomarker or a different protein). Non-limiting examples of peptides indicative of cancer include the following peptides and peptides derived from the following proteins: CEACAM, CYFRA21-1, CA125, PKLK, ProGRP, NSE, TPA 6, TPA 7, TPA 8, NRG, NRG 100, CNDP, APOB100, SCC, VEGF, EGFR, PIK3CA, HER2, BRAF, ROS, RET, NRAS, MET, MEK1, HER2, C4.4A, PSF3, FAM83B, ECD, CTNNB, VIM, S100A4, S100A7, COX2, MUC1, KLKB1, SAA, HP-β chain, C9, Pgrmc1, Ciz1, Transferrin, α-1 antitrypsin, apolipo protein 1, complement c3a, Caveolin-1, Kallikrein 6, Glucose regulated protein- 8, α defensing -1,-2,-3, Serum C-peptide, Alpha -2- HS glycol protein, Tryptic KRT 8 peptide, Plasma glycol protein, Catenin, Defensin α 6, MMPs, Cyclin D, S100 P, Lamin A/C filament protein, Heat shock protein, aldehyde dehydrogenase, Txl-2, (thioredoxin like protein-2), P53, nm23, u-PA, VEGF, Eph B4, CRABP2, WT-1, Rab-3D, Mesothelin, ERα, ANXA4, PSAT1, SPB5, CEA5, CEA6, A1AT, SLPI, APOA4, VDBP, HE4, IL-1, -6, -7, -8, -10, -11, -12, -16, -18, -21, -23, -28A, -33, LIF, TNFR1–2, HVEM (TNFRSF14), IL1R-a, IL1R-b, IL-2R, M-CSF, MIP-1a, TNF-α, CD40, RANTES, CD40L, MIF, IFN-β, MCP-4 (CCL13), MIG (CXCL9), MIP-1δ (CCL15), MIP3a (CCL20), MIP-4 (CCL18), MPIF-1, SDF-1a + b (CXCL12), CD137/4–1BB, lymphotactin (XCL1), eotaxin-1 (CCL11), eotaxin-2 (CCL24), 6Ckine/CCL21), BLC (CXCL13), CTACK (CCL27), BCA-1

(CXCL13), HCC4 (CCL16), CTAP-3 (CXCL7), IGF1, VEGF, VEGFR3, EGFR, ErbB2, CTGF, PDGF AA, BB, PDGFRb, bFGF, TGFbRIII, β-cellulin, IGFBP1–4, 6, BDNF, PEDF, angiopoietin-2, renin, lysophosphatidic acid, β2-microglobulin, sialyl TN, ACE, CA 19–9, CEA, CA 15–3, CA-50, CA 72–4, OVX1, mesothelin, sialyl TN, MMP-2, -3, -7, -9, VAP-1, TIMP1–2, tenascin C, VCAM-1, osteopontin, KIM-1, NCAM, tetranectin, nidogen-2, cathepsin L, prostasin, matriptase, kallikreins 2, 6, 10, cystatin C, claudin, spondin2, SLPI, bHCG, urinary gonadotropin peptide, inhibin, leptin, adiponectin, GH, TSH, ACTH, PRL, FSH, LH, cortisol, TTR, osteocalcin, insulin, ghrelin, GIP, GLP-1, amylin, glucagon, peptide YY, follistatin, hepcidin, CRP, Apo A1, CIII, H, transthyretin, SAA, SAP, complement C3,4, complement factor H, albumin, ceruloplasmin, haptoglobin, β-hemoglobin, transferrin, ferritin, fibrinogen, thrombin, von Willebrand factor, myoglobin, immunosuppressive acidic protein, lipid- associated sialic acid, S100A12 (EN-RAGE), fetuin A, clusterin, α1-antitrypsin, a2- macroglobulin, serpin1 (human plasminogen activator inhibitor-1), Cox-1, Hsp27, Hsp60, Hsp80, Hsp90, lectin-type oxidized LDL receptor 1, CD14, lipocalin 2, ITIH4, sFasL, Cyfra21–1, TPA, perforin, DcR3, AGRP, creatine kinase-MB, human milk fat globule 1–2, NT-Pro-BNP, neuron-specific enolase, CASA, NB/70K, AFP, afamin, collagen, prohibitin, keratin-6, PARC, B7-H4, YK-L40, AFP-L3, DCP, GPC3, OPN, GP73, CK19, MDK, A2, 5-HIAA, CA15-3, CA19-9, CA27.29, CA72-4, calcitonin, CGA, BRAF V600E, BAP, BCT-ABL fusion protein, KIT, KRAS, PSA, Lactate dehydrogenase, NMP22, PAI-1, uPA, fibrin D-dimer, S100, TPA, thyroglobulin, CD20, CD24, CD44, RS/DJ-1, p53, alpha-2-HS-glycoprotein, lipophilin B, beta-globin, hemopexin, UBE2N, PSMB6, PPP1CB, CPT2, COPA, MSK1/2, Pro-NPY, Secernin-1, Vinculin, NAAA, PTK7, TFG, MCCC2, TRAP1, IMPDH2, PTEN, POSTN, EPLIN, eIF4A3, DDAH1, ARG2, PRDX3&4, P4HB, YWHAG, Enoyl CoA-hydrase, PHB, TUBB, KRT2, DES, HSP71, ATP5B, CKB, HSPD1, LMNA, EZH2, AMACR, FABP5, PPA2, EZR, SLP2, SM22, Bax, Smac/Diablo phosphorylated Bcl2, STAT3 and Smac/Diablo expression, PHB, PAP, AMACR, PSMA, FKBP4, PRDX4, KRT7/8/18, GSTP1, NDPK1, MTX2, GDF15, PCa-24, Caveolin-2, Prothrombin, Antithrombin-III, Haptoglobin, Serum amyloid A-1 protein, ZAG, ORM2, APOC3, CALML5, IGFBP2, MUC5AC, PNLIP, PZP, TIMP1, AMBP, inter-alpha-trypsin inhibitor heavy chain H1, inter-alpha-trypsin inhibitor heavy chain H2, inter-alpha-trypsin inhibitor

heavy chain H3, V-type proton ATPase subunit B, kidney isoform, Hepatocyte growth factor-like protein, Serum amyloid P-component, Acylglycerol kinase, Leucine-rich repeat-containing protein 9, Beta-2-glycoprotein 1, Plasma protease C1 inhibitor, Lipoxygenase homology domain-containing protein 1, Protocadherin alpha-13. See, e.g., Kuppusamy et al., Volume 24, Issue 6, September 2017, Pages 1212-1221; Elzek and Rodland, Cancer Metastasis Rev. 2015 Mar; 34(1): 83–96; Noel and Lokshin, Future Oncol. 2012 Jan; 8(1): 55–71; Tsuchiya et al., World J Gastroenterol. 2015 Oct 7; 21(37): 10573–10583; Lou et al., Biomark Cancer. 2017; 9: 1–9; Park et al., Oncotarget. 2017 Jun 27; 8(26): 42761–42771; Saraswat et al., Cancer Med. 2017 Jul; 6(7): 1738–1751; Zamay et al., Cancers (Basel). 2017 Nov; 9(11): 155; Tanase et al., Oncotarget. 2017 Mar 14; 8(11): 18497–18512, each of which is incorporated herein by reference in its entirety.

[330] In some embodiments, the one or more additional classes of biomarkers include nucleic acid lesions or variations (e.g., a nucleic acid lesion or variation that is distinct from the various genetic biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. Non-limiting examples of nucleic acid lesions or variations include copy number changes, DNA methylation changes, and/or other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements). Translocations and genomic rearrangements have been correlated with various cancers (e.g., prostate, glioma, lung cancer, non-small cell lung cancer, melanoma, and thyroid cancer) and used as biomarkers for years (e.g., Demeure et al., 2014, World J Surg., 38:1296-305; Hogenbirk et al., 2016, PNAS USA, 113:E3649-56; Gasi et al., 2011, PLoS One, 6:e16332; Ogiwara et al., 2008, Oncogene, 27:4788-97; US Patent No. 9,745,632; and US Patent No. 6,576,420). In addition, changes in copy number have been used as biomarkers for various cancers including, without limitation, head and neck squamous cell carcinoma, lymphoma (e.g., non-Hodgkin's lymphoma) and colorectal cancer (Kumar et al., 2017, Tumour Biol, 39:1010428317740296; Kumar et al., 2017, Tumour Biol., 39:1010428317736643; Henrique

et al., 2014, Expert Rev. Mol. Diagn., 14:419-22; and US Patent No. 9,816,139). DNA methylation and changes in DNA methylation (e.g., hypomethylation, hypermethylation) also are used as biomarkers in cancer. For example, hypomethylation has been associated with hepatocellular carcinoma (see, for example, Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22), esophageal carcinogenesis (see, for example, Alvarez et al., 2011, PLoS Genet., 7:e1001356) and gastric and liver cancer (see, for example, US Patent No. 8,728,732), and hypermethylation has been associated with colorectal cancer (see, for example, US Patent No. 9,957,570;). In addition to genome-wide changes in methylation, specific methylation changes within particular genes can be indicative of specific cancers (see, for example, US Patent No. 8,150,626). Li et al. (2012, J. Epidemiol., 22:384-94) provides a review of the association between numerous cancers (e.g., breast, bladder, gastric, lung, prostate, head and neck squamous cell, and nasopharyngeal) and aberrant methylation. Additionally or alternatively, additional types of nucleic acids or features of nucleic acids have been associated with various cancers. Non-limiting examples of such nucleic acids or features of nucleic acids include the presence or absence of various microRNAs (miRNAs) have been used in the diagnosis of colon, prostate, colorectal, and ovarian cancers (see, for example, D'Souza et al., 2018, PLos One, 13:e0194268; Fukagawa et al., 2017, Cancer Sci., 108:886-96; Giraldez et al., 2018, Methods Mol. Biol., 1768:459-74; US Patent Nos. 8,343,718; 9,410,956; and 9,074,206). For a review on the specific association of miR-22 with cancer, see Wang et al. (2017, Int. J. Oncol., 50:345-55); the abnormal expression of long non-coding RNAs (lncRNAs) also have been used as a biomarker in cancers such as prostate cancer, colorectal cancer, cervical cancer, melanoma, non-small cell lung cancer, gastric cancer, endometrial carcinoma, and hepatocellular carcinoma (see, for example, Wang et al., 2017, Oncotarget, 8:58577086; Wang et al., 2018, Mol. Cancer, 17:110; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4812-9; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:993-1002; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4820-7; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:2304-9; Xie et al., 2018, EBioMedicine, 33:57-67; and US Patent No. 9,410,206); the presence or absence of circular RNA (circRNA) has been used as a biomarker in lung cancer, breast cancer, gastric cancer, colorectal cancer, and liver cancer (e.g., Geng et al., 2018, J. Hematol. Oncol., 11:98) and melanoma (e.g., Zhang et al.,

2018, Oncol. Lett., 16:1219-25); changes in telomeric DNA (e.g., in length or in heterozygosity) or centromeric DNA (e.g., changes in expression of centromeric genes) also have been associated with cancers (e.g., prostate, breast, lung, lymphoma, and Ewing's sarcoma) (see, for example, Baretton et al., 1994, Cancer Res., 54:4472-80; Liscia et al., 1999, Br. J. Cancer, 80:821-6; Proctor et al., 2009, Biochim. Biophys. Acta, 1792:260-74; and Sun et al., 2016, Int. J. Cancer, 139:899-907); various mutations (e.g., deletions), rearrangements and/or copy number changes in mitochondrial DNA (mtDNA) have been used prognostically and diagnostically for various cancers (e.g., prostate cancer, melanoma, breast cancer, lung cancer, and colorectal cancer). See, for example, Maragh et al., 2015, Cancer Biomark., 15:763-73; Shen et al., 2010, Mitochondrion, 10:62-68; Hosgood et al., 2010, Carcinogen., 31:847-9; Thyagarajan et al., 2012, Cancer Epid. Biomarkers & Prev., 21:1574-81; and US Patent No. 9,745,632; and the abnormal presence, absence or amount of messenger RNAs (mRNAs) also have been correlated with various cancers including, without limitation, breast cancer, Wilms' tumors, and cervical cancer (see, for example, Guetschow et al., 2012, Anal. Bioanaly. Chem., 404:399-406; Schwienbacher et al., 2000, Cancer Res., 60:1521-5; and Ngan et al., 1997, Genitourin Med., 73:54-8). Each of these citations is incorporated herein by reference in its entirety.

Single Class of Biomarkers or Aneuploidy

[331] In one aspect, provided herein are methods and materials for detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for diagnosing or identifying the presence of a disease in a subject (e.g., identifying the subject as having cancer) by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for identifying a subject as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in

one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for treating a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for identifying a treatment for a subject who has been diagnosed or identified as having a disease (e.g., cancer) or who has been identified as being at risk (e.g., increased risk) of having or developing a disease (e.g., cancer) by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for identifying a subject who will or is likely to respond to a treatment by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for further diagnostic testing by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject. In another aspect, provided herein are methods and materials for identifying a subject as a candidate for increased monitoring by detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject.

[332] In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in the detection or diagnosis of cancer (e.g., a high frequency or incidence of correctly identifying a subject as having cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of

aneuploidy in one or more samples obtained from a subject provide a sensitivity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting a single type of cancer. In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high sensitivity in detecting two or more types of cancers. Any of a variety of cancer types can be detected using methods and materials provided herein (see, e.g., the section entitled "Cancers"). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject include liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject include pancreatic cancer. In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject include cancers of the female reproductive tract (e.g., cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer). In some embodiments, cancers that can be detected using methods and materials that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject include bladder cancer or upper-tract urothelial carcinomas.

[333] In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject

[334] In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in the detection or diagnosis of cancer (e.g., a low frequency or incidence of incorrectly identifying a subject as having cancer when that subject does not have cancer). In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide a specificity of at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or higher. As will be understood by those of ordinary skill in the art, a specificity of 99% means that only 1% of subjects that do not have cancer are incorrectly identified as having cancer. In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting a single cancer (e.g., there is a low probability of incorrectly identifying that subject as having that single cancer type). In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers (e.g., genetic biomarkers or protein biomarkers) or the presence of aneuploidy in one or more samples obtained from a subject provide high specificity in detecting two or more cancers (e.g., there is a low probability of incorrectly identifying that subject as having those two or more cancer types).

[335] In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers include detecting the presence of one or more members of a panel of genetic biomarkers.

[336] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in each of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS.

[337] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and/or SMAD4. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in each of the following genes: KRAS (e.g., genetic biomarkers in codons 12 and/or 61), TP53, CDKN2A, and SMAD4.

[338] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in each of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS,

FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in each of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in TP53

[339] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of genetic biomarkers include detecting one or more genetic biomarkers in each of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL.

[340] In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and myeloperoxidase (MPO). In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or

more members of a panel of protein biomarkers include detecting one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting each of the following protein biomarkers: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and CA15-3. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting one or more (e.g., 1, 2, 3, or 4) of the following protein biomarkers: CA19-9, CEA, HGF, and/or OPN. In some embodiments, methods provided herein that include detecting the presence of one or more members of a panel of protein biomarkers include detecting each of the following protein biomarkers: CA19-9, CEA, HGF, and OPN.

[341] In some embodiments, methods provided herein that include detecting the presence of aneuploidy include detecting aneuploidy on one or more of chromosome arms 5q, 8q, and/or 9p. In some embodiments, methods provided herein that include detecting the presence of aneuploidy include detecting aneuploidy on one or more of chromosome arms 4p, 7q, 8q, and/or 9q.

[342] In some embodiments, methods provided herein that include detecting the presence of one or more members of a single class of biomarkers include detecting the presence of one or more members of a class of biomarkers including, without limitation: copy number changes, DNA methylation changes, other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements), peptides, or metabolites.

[343] In some embodiments, methods provided herein include detecting the presence of one or more metabolites. In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more metabolites indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more metabolites indicative of cancer. Non-limiting examples of metabolites indicative of cancer include: 5-methylthioadenosine (MTA), Glutathione reduced (GSH), N-acetylglutamate, Lactose, N-acetylneuraminate, UDP-

acetylglucosamine, UDP-Acetylgalactosamine, UDP-glucuronate, Pantothenate, Arachidonate (20:4n6), Choline, Cytidine 5′-diphosphocholine, Dihomo-linolenate (20:3n3), Docosapentaenoate (DPA 22:5n3), Eicosapentaenoate (EPA 20:5n3), Glycerophosphorylcholine (GPC), Docosahexaenoate (DHA 22:6n3), Linoleate (18:2n6), Cytidine 5′-monophosphate (5′-CMP), Gamma-glutamylglutamate, X – 14577, X – 11583, Isovalerylcarnitine, Phosphocreatine, 2-Aminoadipic acid, Gluconic acid, O-Acetylcarnitine, aspartic acid, Deamido-NAD+, glutamic acid, Isobutyrylcarnitine, Carnitine, Pyridoxal, Citric acid, Adenosine, ATP, valine, XC0061, Isoleucine, γ-Butyrobetaine, Lactic acid, alanine, phenylalanine, Gluconolactone, leucine, Glutathione (GSSG)_divalent, tyrosine, NAD+, XC0016, UTP, creatine, Theobromine, CTP, GTP, 3-Methylhistidine, Succinic acid, Glycerol 3-phosphate, glutamine, 5-Oxoproline, Thiamine, Butyrylcarnitine, 4-Acetamidobutanoic acid, UDP-Glucose, UDP-Galactose, threonine, N-Acetylglycine, proline, ADP, Choline, Malic acid, S-Adenosylmethionine, Pantothenic acid, Cysteinesulfinic acid, 6-Aminohexanoic acid, Homocysteic acid, Hydroxyproline, Methionine sulfoxide, 3-Guanidinopropionic acid, Glucose 6-phosphate, Phenaceturic acid, Threonic acid, tryptophan, Pyridoxine, N-Acetylaspartic acid, 4-Guanidinobutyric acid, serine, Citrulline, Betaine, N-Acetylasparagine, 2-Hydroxyglutaric acid, arginine, Glutathione (GSH), creatinine, Dihydroxyacetone phosphate, histidine, glycine, Glucose 1-phosphate, N-Formylglycine, Ketoprofen, lysine, beta-alanine, N-Acetylglutamic acid, 2-Amino-2-(hydroxymethyl)-1,3-propanediol, Ornithine, Phosphorylcholine, Glycerophosphocholine, Terephthalic acid, Glyceraldehyde 3-phosphate, Gly-Asp, Taurine, Fructose 1,6-diphosphate, 3-Aminoisobutyric acid, Spermidine, GABA, Triethanolamine, Glycerol, N-Acetylserine, N-Acetylornithine, Diethanolamine, AMP, Cysteine glutathione disulfide, Streptomycin sulfate +H2O divalent, trans-Glutaconic acid, Nicotinic acid, Isobutylamine, Betaine aldehyde +H2O, Urocanic acid, 1-Aminocyclopropane-1-carboxylic acid Homoserinelactone, 5-Aminovaleric acid, 3-Hydroxybutyric acid, Ethanolamine, Isovaleric acid, N-Methylglutamic acid, Cystathionine, Spermine, Carnosine, 1-Methylnicotinamide, N-Acetylneuraminic acid, Sarcosine, GDP, N-Methylalanine, palmitic acid, 1,2-dioleoyl-sn-glycero-3-phospho-rac-glycerolcholesterol 5α,6α epoxidelanosterol, lignoceric acid, 1oleoyl_rac_GL, cholesterol_epoxide, erucic acid, T-LCA, oleoyl-L-carnitine, oleanolic acid, 3-

phosphoglycerate, 5-hydroxynorvaline, 5-methoxytryptamine, adenosine-5-monophosphate, alpha-ketoglutarate, asparagine, benzoic acid, hypoxanthine, maltose, maltotriose, methionine sulfoxide, nornicotine, phenol, Phosphoethanolamine, pyrophosphate, pyruvic acid, quinic acid, taurine, uric acid, inosine, lactamide, 5-hydroxynorvaline NIST, cholesterol, deoxypentitol, 2-hydroxyestrone, 2-hydroxyestradiol, 2-metholyestrone, 2-metholxyestradiol, 2-hydroxyestrone-3-methyl ether, 4-hydroxyestrone, 4-metholxyestrone, 4-methoxyestradiol, 16alpha-hydroxyestrone, 17-epiestriol, estriol, 16-Ketoestradiol, 16-epiestriol, acylcarnitine C18:1, amino acids citrulline and trans-4-hydroxyproline, glycerophospholipids PC aa C28:1, PC ae C30:0 and PC ae C30:2, and sphingolipid SM (OH) C14:1. See e.g., Halama et al., Nesting of colon and ovarian cancer cells in the endothelial niche is associated with alterations in glycan and lipid metabolism, Scientific Reports volume 7, Article number: 39999 (2017); Hur et al., Systems approach to characterize the metabolism of liver cancer stem cells expressing CD133, Sci Rep., 7: 45557, doi: 10.1038/srep45557, (2017); Eliassen et al., Urinary Estrogens and Estrogen Metabolites and Subsequent Risk of Breast Cancer among Premenopausal Women, Cancer Res; 72(3); 696–706 (2011); Gangi et al., Metabolomic profile in pancreatic cancer patients: a consensus-based approach to identify highly discriminating metabolites, Oncotarget,Feb 2; 7(5): 5815–5829 (2016); Kumar et al., Serum and Plasma Metabolomic Biomarkers for Lung Cancer, Bioinformation, 13(6): 202–208, doi: 10.6026/97320630013202 (2017); Schmidt et al., Pre-diagnostic metabolite concentrations and prostate cancer risk in 1077 cases and 1077 matched controls in the European Prospective Investigation into Cancer and Nutrition, BMC Med.,15: 122, doi: 10.1186/s12916-017-0885-6 (2017); each of which is incorporated herein by reference in its entirety.

[344] In some embodiments, methods provided herein include detecting the presence of one or more peptides (e.g., one or more peptides that are distinct from the various protein biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more peptides indicative of cancer. In some embodiments, a peptide is derived from a protein (e.g., the

peptide includes an amino acid sequence present in a protein biomarker or a different protein). Non-limiting examples of peptides indicative of cancer include the following peptides and peptides derived from the following proteins: CEACAM, CYFRA21-1, CA125, PKLK, ProGRP, NSE, TPA 6, TPA 7, TPA 8, NRG, NRG 100, CNDP, APOB100, SCC, VEGF, EGFR, PIK3CA, HER2, BRAF, ROS, RET, NRAS, MET, MEK1, HER2, C4.4A, PSF3, FAM83B, ECD, CTNNB, VIM, S100A4, S100A7, COX2, MUC1, KLKB1, SAA, HP-β chain, C9, Pgrmc1, Ciz1, Transferrin, α-1 antitrypsin, apolipo protein 1, complement c3a, Caveolin-1, Kallikrein 6, Glucose regulated protein- 8, α defensing -1,-2,-3, Serum C-peptide, Alpha -2- HS glycol protein, Tryptic KRT 8 peptide, Plasma glycol protein, Catenin, Defensin α 6, MMPs, Cyclin D, S100 P, Lamin A/C filament protein, Heat shock protein, aldehyde dehydrogenase, Txl-2, (thioredoxin like protein-2), P53, nm23, u-PA, VEGF, Eph B4, CRABP2, WT-1, Rab-3D, Mesothelin, ERα, ANXA4, PSAT1, SPB5, CEA5, CEA6, A1AT, SLPI, APOA4, VDBP, HE4, IL-1, -6, -7, -8, -10, -11, -12, -16, -18, -21, -23, -28A, -33, LIF, TNFR1–2, HVEM (TNFRSF14), IL1R-a, IL1R-b, IL-2R, M-CSF, MIP-1a, TNF-α, CD40, RANTES, CD40L, MIF, IFN-β, MCP-4 (CCL13), MIG (CXCL9), MIP-1δ (CCL15), MIP3a (CCL20), MIP-4 (CCL18), MPIF-1, SDF-1a + b (CXCL12), CD137/4–1BB, lymphotactin (XCL1), eotaxin-1 (CCL11), eotaxin-2 (CCL24), 6Ckine/CCL21), BLC (CXCL13), CTACK (CCL27), BCA-1 (CXCL13), HCC4 (CCL16), CTAP-3 (CXCL7), IGF1, VEGF, VEGFR3, EGFR, ErbB2, CTGF, PDGF AA, BB, PDGFRb, bFGF, TGFbRIII, β-cellulin, IGFBP1–4, 6, BDNF, PEDF, angiopoietin-2, renin, lysophosphatidic acid, β2-microglobulin, sialyl TN, ACE, CA 19–9, CEA, CA 15–3, CA-50, CA 72–4, OVX1, mesothelin, sialyl TN, MMP-2, -3, -7, -9, VAP-1, TIMP1–2, tenascin C, VCAM-1, osteopontin, KIM-1, NCAM, tetranectin, nidogen-2, cathepsin L, prostasin, matriptase, kallikreins 2, 6, 10, cystatin C, claudin, spondin2, SLPI, bHCG, urinary gonadotropin peptide, inhibin, leptin, adiponectin, GH, TSH, ACTH, PRL, FSH, LH, cortisol, TTR, osteocalcin, insulin, ghrelin, GIP, GLP-1, amylin, glucagon, peptide YY, follistatin, hepcidin, CRP, Apo A1, CIII, H, transthyretin, SAA, SAP, complement C3,4, complement factor H, albumin, ceruloplasmin, haptoglobin, β-hemoglobin, transferrin, ferritin, fibrinogen, thrombin, von Willebrand factor, myoglobin, immunosuppressive acidic protein, lipid-associated sialic acid, S100A12 (EN-RAGE), fetuin A, clusterin, α1-antitrypsin, a2-

macroglobulin, serpin1 (human plasminogen activator inhibitor-1), Cox-1, Hsp27, Hsp60, Hsp80, Hsp90, lectin-type oxidized LDL receptor 1, CD14, lipocalin 2, ITIH4, sFasL, Cyfra21–1, TPA, perforin, DcR3, AGRP, creatine kinase-MB, human milk fat globule 1–2, NT-Pro-BNP, neuron-specific enolase, CASA, NB/70K, AFP, afamin, collagen, prohibitin, keratin-6, PARC, B7-H4, YK-L40, AFP-L3, DCP, GPC3, OPN, GP73, CK19, MDK, A2, 5-HIAA, CA15-3, CA19-9, CA27.29, CA72-4, calcitonin, CGA, BRAF V600E, BAP, BCT-ABL fusion protein, KIT, KRAS, PSA, Lactate dehydrogenase, NMP22, PAI-1, uPA, fibrin D-dimer, S100, TPA, thyroglobulin, CD20, CD24, CD44, RS/DJ-1, p53, alpha-2-HS-glycoprotein, lipophilin B, beta-globin, hemopexin, UBE2N, PSMB6, PPP1CB, CPT2, COPA, MSK1/2, Pro-NPY, Secernin-1, Vinculin, NAAA, PTK7, TFG, MCCC2, TRAP1, IMPDH2, PTEN, POSTN, EPLIN, eIF4A3, DDAH1, ARG2, PRDX3&4, P4HB, YWHAG, Enoyl CoA-hydrase, PHB, TUBB, KRT2, DES, HSP71, ATP5B, CKB, HSPD1, LMNA, EZH2, AMACR, FABP5, PPA2, EZR, SLP2, SM22, Bax, Smac/Diablo phosphorylated Bcl2, STAT3 and Smac/Diablo expression, PHB, PAP, AMACR, PSMA, FKBP4, PRDX4, KRT7/8/18, GSTP1, NDPK1, MTX2, GDF15, PCa-24, Caveolin-2, Prothrombin, Antithrombin-III, Haptoglobin, Serum amyloid A-1 protein, ZAG, ORM2, APOC3, CALML5, IGFBP2, MUC5AC, PNLIP, PZP, TIMP1, AMBP, inter-alpha-trypsin inhibitor heavy chain H1, inter-alpha-trypsin inhibitor heavy chain H2, inter-alpha-trypsin inhibitor heavy chain H3, V-type proton ATPase subunit B, kidney isoform, Hepatocyte growth factor-like protein, Serum amyloid P-component, Acylglycerol kinase, Leucine-rich repeat-containing protein 9, Beta-2-glycoprotein 1, Plasma protease C1 inhibitor, Lipoxygenase homology domain-containing protein 1, Protocadherin alpha-13. See, e.g., Kuppusamy et al., Volume 24, Issue 6, September 2017, Pages 1212-1221; Elzek and Rodland, Cancer Metastasis Rev. 2015 Mar; 34(1): 83–96; Noel and Lokshin, Future Oncol. 2012 Jan; 8(1): 55–71; Tsuchiya et al., World J Gastroenterol. 2015 Oct 7; 21(37): 10573–10583; Lou et al., Biomark Cancer. 2017; 9: 1–9; Park et al., Oncotarget. 2017 Jun 27; 8(26): 42761–42771; Saraswat et al., Cancer Med. 2017 Jul; 6(7): 1738–1751; Zamay et al., Cancers (Basel). 2017 Nov; 9(11): 155; Tanase et al., Oncotarget. 2017 Mar 14; 8(11): 18497–18512, each of which is incorporated herein by reference in its entirety.

[345] In some embodiments, methods provided herein include detecting the presence of one or more nucleic acid lesions or variations (e.g., one or more nucleic acid lesions or variations that are distinct from the various genetic biomarkers described herein as being useful in one or more methods). In some embodiments, a subject is determined to be at elevated risk of having or developing cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. In some embodiments, a subject is determined as having cancer if the biological sample contains one or more nucleic acid lesions or variations indicative of cancer. Non-limiting examples of nucleic acid lesions or variations include copy number changes, DNA methylation changes, and/or other nucleic acids (e.g., mRNAs, miRNAs, lncRNAs, circRNA, mtDNA, telomeric DNA, translocation and genomic rearrangements). Translocations and genomic rearrangements have been correlated with various cancers (e.g., prostate, glioma, lung cancer, non-small cell lung cancer, melanoma, and thyroid cancer) and used as biomarkers for years (e.g., Demeure et al., 2014, World J Surg., 38:1296-305; Hogenbirk et al., 2016, PNAS USA, 113:E3649-56; Gasi et al., 2011, PLoS One, 6:e16332; Ogiwara et al., 2008, Oncogene, 27:4788-97; US Patent No. 9,745,632; and US Patent No. 6,576,420). In addition, changes in copy number have been used as biomarkers for various cancers including, without limitation, head and neck squamous cell carcinoma, lymphoma (e.g., non-Hodgkin's lymphoma) and colorectal cancer (Kumar et al., 2017, Tumour Biol, 39:1010428317740296; Kumar et al., 2017, Tumour Biol., 39:1010428317736643; Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22; and US Patent No. 9,816,139). DNA methylation and changes in DNA methylation (e.g., hypomethylation, hypermethylation) also are used as biomarkers in cancer. For example, hypomethylation has been associated with hepatocellular carcinoma (see, for example, Henrique et al., 2014, Expert Rev. Mol. Diagn., 14:419-22), esophageal carcinogenesis (see, for example, Alvarez et al., 2011, PLoS Genet., 7:e1001356) and gastric and liver cancer (see, for example, US Patent No. 8,728,732), and hypermethylation has been associated with colorectal cancer (see, for example, US Patent No. 9,957,570;). In addition to genome-wide changes in methylation, specific methylation changes within particular genes can be indicative of specific cancers (see, for example, US Patent No. 8,150,626). Li et al. (2012, J. Epidemiol., 22:384-94) provides a review of the association between numerous cancers (e.g.,

breast, bladder, gastric, lung, prostate, head and neck squamous cell, and nasopharyngeal) and aberrant methylation. Additionally or alternatively, additional types of nucleic acids or features of nucleic acids have been associated with various cancers. Non-limiting examples of such nucleic acids or features of nucleic acids include the presence or absence of various microRNAs (miRNAs) have been used in the diagnosis of colon, prostate, colorectal, and ovarian cancers (see, for example, D'Souza et al., 2018, PLos One, 13:e0194268; Fukagawa et al., 2017, Cancer Sci., 108:886-96; Giraldez et al., 2018, Methods Mol. Biol., 1768:459-74; US Patent Nos. 8,343,718; 9,410,956; and 9,074,206). For a review on the specific association of miR-22 with cancer, see Wang et al. (2017, Int. J. Oncol., 50:345-55); the abnormal expression of long non-coding RNAs (lncRNAs) also have been used as a biomarker in cancers such as prostate cancer, colorectal cancer, cervical cancer, melanoma, non-small cell lung cancer, gastric cancer, endometrial carcinoma, and hepatocellular carcinoma (see, for example, Wang et al., 2017, Oncotarget, 8:58577086; Wang et al., 2018, Mol. Cancer, 17:110; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4812-9; Yu et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:993-1002; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:4820-7; Zhang et al., 2018, Eur. Rev. Med. Pharmacol. Sci., 22:2304-9; Xie et al., 2018, EBioMedicine, 33:57-67; and US Patent No. 9,410,206); the presence or absence of circular RNA (circRNA) has been used as a biomarker in lung cancer, breast cancer, gastric cancer, colorectal cancer, and liver cancer (e.g., Geng et al., 2018, J. Hematol. Oncol., 11:98) and melanoma (e.g., Zhang et al., 2018, Oncol. Lett., 16:1219-25); changes in telomeric DNA (e.g., in length or in heterozygosity) or centromeric DNA (e.g., changes in expression of centromeric genes) also have been associated with cancers (e.g., prostate, breast, lung, lymphoma, and Ewing's sarcoma) (see, for example, Baretton et al., 1994, Cancer Res., 54:4472-80; Liscia et al., 1999, Br. J. Cancer, 80:821-6; Proctor et al., 2009, Biochim. Biophys. Acta, 1792:260-74; and Sun et al., 2016, Int. J. Cancer, 139:899-907); various mutations (e.g., deletions), rearrangements and/or copy number changes in mitochondrial DNA (mtDNA) have been used prognostically and diagnostically for various cancers (e.g., prostate cancer, melanoma, breast cancer, lung cancer, and colorectal cancer). See, for example, Maragh et al., 2015, Cancer Biomark., 15:763-73; Shen et al., 2010, Mitochondrion, 10:62-68; Hosgood et al., 2010, Carcinogen., 31:847-9; Thyagarajan et al.,

2012, Cancer Epid. Biomarkers & Prev., 21:1574-81; and US Patent No. 9,745,632; and the abnormal presence, absence or amount of messenger RNAs (mRNAs) also have been correlated with various cancers including, without limitation, breast cancer, Wilms' tumors, and cervical cancer (see, for example, Guetschow et al., 2012, Anal. Bioanaly. Chem., 404:399-406; Schwienbacher et al., 2000, Cancer Res., 60:1521-5; and Ngan et al., 1997, Genitourin Med., 73:54-8). Each of these citations is incorporated herein by reference in its entirety.

Validation of Detected Genetic Biomarkers

[346] In some embodiments, methods provided herein can be used to verify that a genetic biomarker detected in circulating tumor DNA present in cell-free DNA indicates the presence of a cancer cell in the subject. In some embodiments, methods provided herein can be used to verify that a genetic alteration (e.g., one or more genetic alterations) detected in circulating tumor DNA present in cell-free DNA indicates the presence of a cancer cell in the subject. For example, certain genetic biomarkers (e.g., genetic alterations) that are present in cancer cells also occur in other non-cancer cells in the body. Such non-cancer cells include, without limitation, white blood cell clones arising during age-associated clonal hematopoiesis (e.g., clonal hematopoietic expansion (also known as clonal hematopoiesis of indeterminate potential or CHIP) or myelodysplasia). As a result, such clones, which may represent early forms of myelodysplasia, are a potential source of false positives in ctDNA-based assays. In such cases, detecting a genetic biomarker (e.g., a genetic alteration) in cell-free DNA can lead to a false diagnosis of cancer since the genetic biomarker (e.g., genetic alteration) arises from hematopoietic white blood cells, rather than from a cancer (e.g., a solid tumor). Methods provided herein can reduce or eliminate such false cancer diagnoses.

[347] Methods provided herein can be used to reduce or eliminate false cancer diagnoses by determining whether one or more genetic biomarkers (e.g., genetic alterations) detected in cell-free DNA originate from hematopoietic white blood cells rather than from a cancer cell. For example, DNA can be isolated or obtained from white blood cells of a subject, which DNA can be tested to determine the presence or absence of a genetic biomarker (e.g., a genetic alteration) that was identified in cell-free DNA from the subject, which genetic

biomarker (e.g., genetic alteration) is associated with cancer. In some embodiments, if the genetic biomarker (e.g., genetic alteration) is identified in the DNA from a white blood cell, it is indicative that the genetic biomarker (e.g., genetic alteration) identified in cell-free DNA originated from the white blood cells, and not from a cancer cell present in the subject. In some embodiments, if the genetic biomarker (e.g., genetic alteration) is not identified in the DNA from the white blood cells, it is indicative that the genetic biomarker (e.g., genetic alteration) identified in cell-free DNA originated from a cancer cell present in the subject, and not from a white blood cell. Methods of testing DNA isolated or obtained from white blood cells for the presence or absence of a genetic biomarker (e.g., a genetic mutation) that is associated with cancer in order to determine whether that genetic biomarker (e.g., genetic alteration) originates from a cancer cell in the subject are generically described herein as "verifying a genetic alteration against white blood cells", "verifying a genetic alteration against DNA from white blood cells", "white blood cell verification", and similar phrases.

[348] Any genetic biomarker (e.g., genetic alteration) that is associated with cancer can be verified using methods described herein. Examples of genetic biomarkers (e.g., genes having genetic alterations) associated with cancer include, without limitation, ABCA7, ABL1, ABL2, ACVR1B, ACVR2A, AJUBA, AKT1, AKT2, ALB, ALDOB, ALK, AMBRA1, AMER1, AMOT, ANKRD46, APC, AR, ARHGAP35, ARHGEF12, ARID1A, ARID1B, ARID2, ARID4B, ARL15, ARMCX1, ASXL1, ASXL2, ATAD2, ATF1, ATG14, ATG5, ATM, ATRX, ATXN2, AXIN1, B2M, BAP1, BCL11A, BCL11B, BCL2, BCL3, BCL6, BCL9, BCLAF1, BCOR, BCR, BIRC6, BIRC8, BLM, BLVRA, BMPR1A, BRAF, BRCA1, BRCA2, BRD7, BRE, BRWD3, BTBD7, BTRC, C11orf70, C12orf57, C2CD5, C3orf62, C8orf34, CAMKV, CAPG, CARD11, CARS, CASP8, CBFA2T3, CBFB, CBLC, CBX4, CCAR1, CCDC117, CCDC88A, CCM2, CCNC, CCND1, CCND2, CCND3, CCR3, CD1D, CD79B, CDC73, CDCP1, CDH1, CDH11, CDK12, CDK4, CDK6, CDKN1A, CDKN1B, CDKN2A, CDX2, CEBPA, CELF1, CENPB, CEP128, CHD2, CHD4, CHD8, CHEK2, CHRDL1, CHUK, CIC, CLEC4C, CMTR2, CNN2, CNOT1, CNOT4, COL11A1, COPS4, COX7B2, CREB1, CREBBP, CSDE1, CSMD3, CTCF, CTDNEP1, CTNNB1, CUL1, CUL2, CYB5B, CYLD, DACH1, DCHS1, DCUN1D1, DDB2, DDIT3, DDX3X, DDX5, DDX6, DEK, DHX15, DHX16, DICER1, DIRC2, DIS3, DIXDC1, DKK2, DNAJB5,

DNER, DNM1L, DNMT3A, EED, EGFR, EIF1AX, EIF2AK3, EIF2S2, EIF4A1, EIF4A2, ELF3, ELK4, EMG1, EMR3, EP300, EPB41L4A, EPHA2, EPS8, ERBB2, ERBB3, ERRFI1, ETV4, ETV6, EVI1, EWSR1, EXO5, EXT1, EXT2, EZH2, F5, FANCM, FAT1, FBN2, FBXW7, FCER1G, FEV, FGF2, FGFR1, FGFR1OP, FGFR2, FGFR3, FH, FLT3, FN1, FOXA1, FOXP1, FUBP1, FUS, GALNTL5, GATA3, GGCT, GIGYF2, GK2, GLIPR2, GNAS, GNPTAB, GNRHR, GOLGA5, GOLM1, GOPC, GOT2, GPC3, GPS2, GPX7, GRK1, GSE1, GZMA, HDAC1, HERC1, HERC4, HGF, HIST1H2BO, HLA-A, HLA-B, HMCN1, HMGA1, HMGA2, HNRNPA1, HRAS, HSP90AB1, ID3, IDH1, IDH2, IFNGR2, IFT88, IKZF2, IL2, INO80C, INPP4A, INPPL1, IRF4, IWS1, JAK1, JAK2, JUN, KANSL1, KAT8, KATNAL1, KBTBD7, KCNMB4, KDM5C, KDM6A, KEAP1, KIAA1467, KIT, KLF4, KMT2A, KMT2B, KMT2C, KMT2D, KMT2E, KRAS, KRT15, LAMTOR1, LARP4B, LCK, LMO2, LPAR2, LYN, MAF, MAFB, MAML2, MAP2K1, MAP2K2, MAP2K4, MAP3K1, MAP4K3, MAPK1, MAX, MB21D2, MBD1, MBD6, MBNL1, MBNL3, MDM2, MDM4, MED12, MED23, MEN1, MET, MGA, MITF, MKLN1, MLH1, MLL, MLLT4, MOAP1, MORC4, MPL, MS4A1, MSH2, MSI1, MTOR, MYB, MYC, MYCL1, MYCN, MYD88, MYL6, MYO1B, MYO6, NAA15, NAA25, NAP1L2, NAP1L4, NCOA2, NCOA4, NCOR1, NEK9, NF1, NF2, NFE2L2, NFE2L3, NFKB2, NIPBL, NIT1, NKX3-1, NME4, NOTCH1, NOTCH2, NPM1, NR4A3, NRAS, NSD1, NTRK1, NUP214, NUP98, PALB2, PAX8, PBRM1, PCBP1, PCOLCE2, PDGFB, PHF6, PIK3CA, PIK3CB, PIK3R1, PIM1, PLAG1, PML, POLA2, POT1, PPARD, PPARG, PPM1D, PPP2R1A, PPP6C, PRKACA, PRKCI, PRPF40A, PSIP1, PTEN, PTH2, PTMS, PTN, PTPN11, RAB18, RAC1, RAF1, RANBP3L, RAPGEF6, RASA1, RB1, RBBP6, RBM10, RBM26, RC3H2, REL, RERE, RET, RFC4, RHEB, RHOA, RIMS2, RIT1, RNF111, RNF43, ROS1, RPL11, RPL5, RQCD1, RRAS2, RUNX1, RXRA, SARM1, SCAF11, SDHB, SDHD, SEC22A, SENP3, SENP8, SETD1B, SETD2, SF3A3, SF3B1, SFPQ, SIN3A, SKAP2, SMAD2, SMAD3, SMAD4, SMARCA4, SMARCB1, SMARCC2, SMO, SNCB, SOCS1, SOS1, SOX4, SOX9, SP3, SPEN, SPOP, SPSB2, SS18, STAG2, STK11, STK31, SUFU, SUFU, SUZ12, SYK, TAF1A, TARDBP, TAS2R30, TBL1XR1, TBX3, TCF12, TCF3, TCF7L2, TCL1A, TET2, TEX11, TFDP2, TFG, TGFBR2, THRAP3, TLX1, TM9SF1, TMCO2, TMED10, TMEM107, TMEM30A, TMPO, TNFAIP3,

TNFRSF9, TNRC6B, TP53, TP53BP1, TPR, TRAF3, TRIM8, TRIP12, TSC1, TSC2, TTK, TTR, TUBA3C, U2AF1, UBE2D3, UBR5, UNC13C, UNKL, UPP1, USO1, USP28, USP6, USP9X, VHL, VN1R2, VPS33B, WAC, WDR33, WDR47, WRN, WT1, WWP1, XPO1, YOD1, ZC3H13, ZDHHC4, ZFHX3, ZFP36L1, ZFP36L2, ZGRF1, ZMYM3, ZMYM4, ZNF234, ZNF268, ZNF292, ZNF318, ZNF345, ZNF600, ZNF750, and/or ZNF800. In some embodiments, genetic biomarkers (e.g., genes having genetic alterations) associated with cancer that can be verified against white blood cell DNA isolated or obtained from a subject include tumor suppressor genes or oncogenes. In some embodiments, one or more codons and/or their surrounding splice sites can be tested according to methods disclosed herein. Exemplary codons of tumor suppressor genes and oncogenes which may be tested include, without limitation, one or more of the following codons and their surrounding splice sites: codons 16-18 of AKT1; codons 1304-1311, 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58, 76-88 of CDKN2A; codons 31-39, 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, 143-148 of KRAS; codons 3-15, 54-63 of NRAS; codons 80-90, 343-348, 541-551, 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; codons 90-98, 125-132, 133-146, 145-154 of PTEN; and codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, 374-386 of TP53. In some embodiments, genetic biomarkers (e.g., genes having genetic alterations) associated with cancer that can be verified against white blood cell DNA isolated or obtained from a subject include one or more of the genetic biomarkers (e.g., genetic alterations) identified in Table 11 or Table 12. Testing DNA isolated or obtained from white blood cells may include amplification and/or sequencing of such DNA (e.g., using any of the methods described herein including, without limitation, Safe-SeqS methods). Using a technique such as Safe-SeqS provides corresponding advantages when testing DNA isolated or obtained from white blood cells as it does when testing cell-free DNA from the subject.

[349] In some embodiments, a single genetic biomarker (e.g., genetic alteration) is verified against DNA isolated or obtained from white blood cells. In some embodiments, more than

one genetic biomarkers (e.g., genetic alterations) are verified against DNA isolated or obtained from white blood cells. For example, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more genetic biomarkers (e.g., genetic alterations) can be verified against DNA isolated or obtained from white blood cells using methods described herein. In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) are verified against DNA isolated or obtained from white blood cells using a plurality of samples that are isolated or obtained from white blood cells. For example, one or more genetic biomarkers (e.g., genetic alterations) can be verified against DNA isolated or obtained from white blood cells by isolating DNA from two white blood cell samples isolated or obtained from the subject. Verifying genetic biomarkers (e.g., genetic alterations) against DNA isolated or obtained from white blood cells using a plurality of samples can increase the sensitivity of the testing, thus leading to a more accurate diagnosis.

[350] In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) (e.g., genetic alteration(s)) against DNA isolated or obtained from white blood cells in the absence of additional diagnostic testing methods. In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) (e.g., genetic alteration(s)) against DNA isolated or obtained from white blood cells in combination with additional diagnostic testing methods. In some embodiments, such additional diagnostic testing methods can include one or more of the diagnostic testing methods described herein. In some embodiments, such additional diagnostic testing methods can include testing a protein biomarker (e.g., one or more of the protein biomarkers disclosed herein). In some embodiments, such additional diagnostic testing methods can include testing a protein biomarker (e.g., one or more of the protein biomarkers disclosed herein) at a certain threshold level. Examples of protein biomarkers that can be combined with white blood cell verification include, without limitation, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3. Any of the variety of threshold levels for such protein biomarkers disclosed herein can be used in combination

with white blood cell verification of genetic biomarker(s) (e.g., genetic alteration(s)) found in cell-free DNA. Exemplary and non-limiting threshold levels for certain protein biomarkers include: CA19-9 (>92 U/ml), CEA (>7,507 pg/ml), CA125 (>577 U/ml), AFP (>21,321 pg/ml), Prolactin (>145,345 pg/ml), HGF (>899 pg/ml), OPN (>157,772 pg/ml), TIMP-1 (>176,989 pg/ml), Follistatin (>1,970 pg/ml), G-CSF (>800 pg/ml), and CA15-3 (>98 U/ml). In some embodiments, threshold levels for protein biomarkers can be higher (e.g., about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100%, or higher) than the exemplary threshold levels described herein. In some embodiments, threshold levels for protein biomarkers can be lower (e.g., about 10%, about 20%, about 30%, about 40%, about 50%, or lower) than the exemplary threshold levels described herein. In certain embodiments, a testing a single protein biomarker is combined with white blood cell verification of genetic biomarker(s) (e.g., genetic alteration(s))) found in cell-free DNA. In certain embodiments, testing more than one protein biomarker (two, three, four, five, six, seven, eight, nine, ten, eleven, or more protein biomarkers) is combined with white blood cell verification of genetic biomarker(s) (e.g., genetic alteration(s)) found in cell-free DNA.

[351] In some embodiments, a plurality of genetic biomarkers (e.g., a panel of genetic biomarkers) is verified against DNA isolated or obtained from white blood cells. In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes one or more of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS. In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes each of NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and GNAS. In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) that include one or more of (e.g., each of) NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) against DNA isolated or obtained from white blood cells in combination with additional diagnostic testing methods. Such

additional diagnostic testing methods include, without limitation, testing for the presence of one or more protein biomarkers and/or for the presence of aneuploidy. In some embodiments, the one or more protein biomarkers can be one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, or myeloperoxidase (MPO). In some embodiments, the one or more protein biomarkers can be one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, or CA15-3. In some embodiments, the one or more protein biomarkers can be one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, or CA15-3.

[352] In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes one or more of KRAS, TP53, CDKN2A, or SMAD4. In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes each of KRAS, TP53, CDKN2A, and SMAD4. In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) that include one or more of (e.g., each of) KRAS, TP53, CDKN2A, or SMAD4 can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) against DNA isolated or obtained from white blood cells in combination with additional diagnostic testing methods. Such additional diagnostic testing methods include, without limitation, testing for the presence of one or more protein biomarkers and/or for the presence of aneuploidy. In some embodiments, the one or more protein biomarkers can be one or more of (e.g., each of) CA19-9, CEA, HGF, or OPN.

[353] In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes one or more of NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A. In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes each of NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A. In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) that include one or more of (e.g., each of) NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43,

PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) against DNA isolated or obtained from white blood cells in combination with additional diagnostic testing methods. Such additional diagnostic testing methods include, without limitation, testing for the presence of one or more protein biomarkers and/or for the presence of aneuploidy (e.g., aneuploidy in one or more chromosomes or chromosomal arms that are associated with the presence of cancer). In some embodiments, the presence of aneuploidy can be detected on one or more of chromosomal arms 4p, 7q, 8q, or 9q.

[354] In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes one or more of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL. In some embodiments, a plurality of genetic biomarkers that is verified against DNA isolated or obtained from white blood cells includes each of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL. . In some embodiments, one or more genetic biomarkers (e.g., genetic alterations) that include one or more of (e.g., each of) TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL CDKN2A can be determined to originate from a cancer cell in the subject (or not) by verifying the genetic biomarker(s) against DNA isolated or obtained from white blood cells in combination with additional diagnostic testing methods. Such additional diagnostic testing methods include, without limitation, testing for the presence of one or more protein biomarkers and/or for the presence of aneuploidy (e.g., aneuploidy in one or more chromosomes or chromosomal arms that are associated with the presence of cancer). In some embodiments, the presence of aneuploidy can be detected on one or more of chromosomal arms 5q, 8q, or 9p.

[355] In some embodiments, a sample isolated or obtained from the subject that is used to isolate or obtain white blood cell DNA can be the same as the sample isolated or obtained from the subject that is used for testing genetic biomarkers in cell-free DNA and/or protein biomarkers. For example, the sample can be a blood sample (e.g., whole blood), which blood sample is subsequently separated into a plasma fraction and a white blood cell fraction.

Such separation can be achieved, for example, by density gradient centrifugation in which plasma is separated from white blood cells, which are typically found in the buffy coat. After such separation, DNA from the white blood cells in the buffy coat can be isolated and tested, while genetic biomarkers in cell-free DNA from the plasma fraction can also be isolated and tested. In some embodiments, the plasma fraction is allowed to clot in order to obtain a serum fraction. In some embodiments the sample is frozen, refrigerated, or otherwise stored prior to and/or after testing and/or fractionation. In some embodiments, one or more fractions from the sample are frozen, refrigerated, or otherwise stored prior to and/or after testing.

[356] In some embodiments, a sample isolated or obtained from the subject that is used to isolate or obtain white blood cell DNA can be different from the sample isolated or obtained from the subject that is used for testing genetic biomarkers in cell-free DNA and/or protein biomarkers. For example, a first sample can be isolated or obtained from the subject, which first sample is used for testing genetic biomarkers in cell-free DNA and/or protein biomarkers. Prior to, simultaneously, or after the first sample is isolated or obtained, a second sample can be isolated or obtained from the subject, which second sample is used to isolate or obtain DNA from white blood cells for verifying one or more genetic biomarkers (e.g., genetic alterations) identified in cell-free DNA. The second sample can be fractionated as described herein (e.g., by density gradient centrifugation). In some embodiments the first and/or second sample (or fractions thereof) can be frozen, refrigerated, or otherwise stored prior to and/or after testing and/or fractionation.

[357] In some embodiments, once a genetic biomarker (e.g., a genetic alteration) has been verified against DNA isolated or obtained from white blood cells and the genetic biomarker (e.g., a genetic alteration) is determined not to be present in DNA isolated from white blood cells (e.g., the genetic biomarker (e.g., a genetic alteration) is determined to originate from a cancer cell in the subject), the subject can undergo further diagnostic testing or increased monitoring (e.g., using one or more of the diagnostic testing and/or monitoring methods disclosed herein). In some embodiments, once a genetic biomarker (e.g., a genetic alteration) has been verified against DNA isolated or obtained from white blood cells and the genetic

biomarker (e.g., a genetic alteration) is determined not to be present in DNA isolated from white blood cells (e.g., the genetic biomarker (e.g., a genetic alteration) is determined to originate from a cancer cell in the subject), the subject can be administered a therapeutic intervention (e.g., one or more of the therapeutic interventions disclosed herein).

Sample Classification

[358] The present disclosure provides methods of identifying the presence of cancer in a subject based on one or more protein biomarkers (e.g., protein concentrations in whole blood or plasma). Various methods can be used to determine whether the subject has cancer and/or the likelihood that the subject has cancer. These methods involve various types of statistical techniques and methods described herein, including, e.g., a regression model, a logistic regression model, a neural network, a clustering model, principal component analysis, correlated component analysis, nearest neighbor classifier analysis, linear discriminant analysis, quadratic discriminant analysis, a support vector machine, a decision tree, Random Forest, a genetic algorithm, classifier optimization using bagging, classifier optimization using boosting, classifier optimization using the Random Subspace Method, a projection pursuit, and genetic programming and weighted voting, etc.

[359] In some embodiments, a regression analysis can be used to determine whether a subject has cancer. The regression analysis can be performed on a panel of protein biomarkers, a panel of genetic biomarkers (e.g., mutations), and/or a panel includes both protein biomarkers and genetic biomarkers. In some embodiments, the regression analysis is performed on the Ω score for one or more mutations (e.g., top mutation) and/or a panel of protein biomarkers.

[360] In some embodiments, the regression analysis is performed based on a mathematic model has the form:

$$V=\alpha+\Sigma\beta_i f(X_i)$$

[361] In this form of the model, V is a value indicating the likelihood score that a subject has cancer. In some embodiments, the likelihood score is indicative of the probability that a

test subject has cancer. X_i represents the value of each biomarker (e.g., Ω score, protein concentrations in plasma etc.). β_i is a coefficient for $f(X_i)$, which is a variable corresponds to value of the biomarker. The function $f(x)$ is a function that gives a corresponding value of x. In some embodiments, $f(x)=x$. Thus, the mathematic model can have the form $V=\alpha+\Sigma\beta_i X_i$. In some other embodiments, $f(x)$ may be a function for normalization or standardization. In some embodiments, the formula may include additional parameters to account for age, sex, and race category.

[362] In some embodiments, V is a value indicating the likelihood score for a subject has cancer. In some embodiments, V is an actual probability (a number varying between 0 and 1). In other embodiments, V is a value from which a probability can be derived.

[363] In some embodiments, the mathematical model is a regression model, for example, a logistic regression model or a linear regression model. The regression model can be used to test various sets of biomarkers.

[364] In the case of linear regression models, the model can be used to analyze expression data from a test subject and to provide a result indicative of a quantitative measure of the test subject, for example, the likelihood that the subject has cancer.

[365] In general, a linear regression equation is expressed as

$$Y=\alpha+\beta_1X_1+\beta_2X_2+ \ldots +\beta_kX_k+\varepsilon$$

[366] Y, the dependent variable, indicates a quantitative measure of a biological feature (e.g., likelihood of having cancer or not having cancer). The dependent variable Y depends on k explanatory variables (the measured characteristic values for the biomarkers), plus an error term that encompasses various unspecified omitted factors. In the above-identified model, the parameter β_1 gauges the effect of the first explanatory variable X_1 on the dependent variable Y. β_2 gives the effect of the explanatory variable X_2 on Y.

[367] A logistic regression model is a non-linear transformation of the linear regression. The logistic regression model is often referred to as the "logit" model and can be expressed as

$$\ln [p/(1-p)]=\alpha+\beta_1X_1+\beta_2X_2+ \ldots +\beta_kX_k+\varepsilon$$

where,

α is a constant;

ε is an error term;

ln is the natural logarithm, $\log_{(e)}$, where e=2.71828 . . . ,

p is the probability that the event Y occurs,

p/(1−p) is the "odds, "

ln [p/(1−p)] is the log odds, or "logit."

[368] It will be appreciated by those of skill in the art that α and ε can be folded into a single constant, and expressed as α. In some embodiments, a single term α is used, and ε is omitted. The "logistic" distribution is an S-shaped distribution function. The logit distribution constrains the estimated probabilities (p) to lie between 0 and 1.

[369] In some embodiments, the logistic regression model is expressed as

$$Y=\alpha+\Sigma\beta_i X_i$$

[370] Here, Y is a value (e.g., a likelihood score) indicating whether the set of biomarkers for a given subject should classify with the case group (e.g., groups of subjects with cancer), as opposed to the control group (e.g., groups of subjects without cancer). The probability that the set of biomarkers classifies with the case group, as opposed to the control group, thus, the probability that the subject has cancer can be derived from Y. The higher the score, the higher the probability that the subject has cancer.

[371] Xi is the value of ith biomarker. In some embodiments, it can be the protein concentrations in plasma, gender, age, or a score derived from genetic markers (e.g., Ω score). βi is a logistic regression equation coefficient for the biomarker, α is a logistic regression equation constant that can be zero, and βi and α are the result of applying logistic regression analysis to the case group and the control group.

[372] In some embodiments, the logistic regression model is fit by maximum likelihood estimation (MLE). The coefficients (e.g., α, β1, β2, . . .) are determined by maximum likelihood. A likelihood is a conditional probability (e.g., P(Y|X), the probability of Y given X). The likelihood function (L) measures the probability of observing the particular set of

dependent variable values (Y1, Y2, . . . , Yn) that occur in the sample data set. In some embodiments, it is written as the product of the probability of observing Y1, Y2, . . . , Yn:

$$L=Prob(Y1, Y2, \ldots, Yn) = Prob(Y1) * Prob(Y2)* \ldots Prob(Yn)$$

[373] The higher the likelihood function, the higher the probability of observing the Ys in the sample. MLE involves finding the coefficients (α, $\beta 1$, $\beta 2$, . . .) that make the log of the likelihood function ($LL<0$) as large as possible or -2 times the log of the likelihood function ($-2LL$) as small as possible. In MLE, some initial estimates of the parameters α, $\beta 1$, $\beta 2$, and so forth are made. Then, the likelihood of the data given these parameter estimates is computed. The parameter estimates are improved, the likelihood of the data is recalculated. This process is repeated until the parameter estimates remain substantially unchanged (for example, a change of less than 0.01 or 0.001). Examples of logistic regression and fitting logistic regression models are found in Hastie, The Elements of Statistical Learning, Springer, N.Y., 2001, pp. 95-100.

[374] Once the logistic regression equation coefficients and the logistic regression equation constant are determined, the model can be readily applied to a test subject to obtain Y. In some embodiments, Y can be used to calculate probability (p) by solving the function $Y = \ln(p/(1-p))$.

[375] In some embodiments, explanatory variables are normalized or standardized before fitting into the model. Standardized coefficients (or beta coefficients) are the estimates resulting from a regression analysis that have been standardized so that the variances of dependent and explanatory variables are 1. Therefore, standardized coefficients represent how many standard deviations a dependent variable will change, per standard deviation increase in the explanatory variable. For univariate regression, the absolute value of the standardized coefficient equals the correlation coefficient. Standardization of the coefficient is usually performed to identify which of the explanatory variables have a greater effect on the dependent variable in a multiple regression analysis. In some embodiments, variables are standardized or normalized before fitting into a logistic regression model. Standardized logistic regression coefficients (or standardized beta coefficients) are the estimates resulting

from performing a logistic regression analysis on variables that have been standardized. In some embodiments, only explanatory variables are standardized, and in some other embodiments, only dependent variables are standardized. Further, in some embodiments, both explanatory variables and dependent variables are standardized. In some embodiments, the standardized regression coefficient equals the corresponding unstandardized coefficient multiplied by the ratio std(X_i)/std(Y), where "std" denotes standard deviation.

[376] In some embodiments, the omega score (e.g., the omega score for the top mutation) can be used as an explanatory variable in a logistic regression. In some embodiments, the logistic regression can include one or more other explanatory variables (e.g., concentrations of proteins). In some embodiments, the protein biomarkers can be selected based on Mann-Whitney-Wilcoxon test. In some embodiments, the selected protein biomarkers have higher median values in cancer samples than in normal samples. In some embodiments, a forward selection is used to select explanatory variables from all biomarkers (including genetic biomarkers and protein biomarkers).

[377] Applying a mathematical model to the data can generate one or more classifiers. The classifiers are mathematical model with appropriate parameters (e.g., β coefficient in regression model). These parameters can be determined by applying a mathematical model to a training data set, e.g., a data set that includes both control subjects and a group of subjects that have cancer.

[378] A classifier can be evaluated for its ability to properly characterize each subject in a dataset (e.g., a training dataset or a validation dataset) using methods known to a person of ordinary skill in the art. Various statistical criteria can be used, for example, area under the curve (AUC), percentage of correct predictions, sensitivity, and/or specificity. In some embodiments, the classifier is evaluated by cross validation, Leave One OUT Cross Validation (LOOCV), n-fold cross validation, and jackknife analysis. In some embodiments, each classifier is evaluated for its ability to properly characterize those subjects in a dataset not used to generate the classifier (a "test dataset").

[379] In some embodiments, the method used to evaluate the classifier for its ability to properly characterize each subject in a dataset is a method that evaluates the classifier's sensitivity (true positive fraction) and 1-specificity (true negative fraction). In some

embodiments, the method used to test the classifier is a Receiver Operating Characteristic (ROC), which provides several parameters to evaluate both the sensitivity and the specificity of the result of the equation generated. In some embodiments, the ROC area (area under the curve) is used to evaluate the equations. A ROC area greater than 0.5, 0.6, 0.7, 0.8, 0.9 is preferred. A perfect ROC area score of 1.0 is indicative of both 100% sensitivity and 100% specificity. In some embodiments, classifiers are selected on the basis of the evaluation score. In some embodiments, the evaluation scoring system used is a receiver operating characteristic (ROC) curve score determined by the area under the ROC curve. In some embodiments, classifiers with scores of greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55, or 0.5 are chosen. In some embodiments, where specificity is important to the use of the classifier, a sensitivity threshold can be set, and classifiers ranked on the basis of the specificity are chosen. For example, classifiers with a cutoff for specificity of greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55 0.5 or 0.45 can be chosen. Similarly, the specificity threshold can be set, and classifiers ranked on the basis of sensitivity (e.g., greater than 0.95, 0.9, 0.85, 0.8, 0.7, 0.65, 0.6, 0.55 0.5 or 0.45) can be chosen. Thus, in some embodiments, only the top ten ranking classifiers, the top twenty ranking classifiers, or the top one hundred ranking classifiers are selected. The ROC curve can be calculated by various statistical tools, including, but not limited to, Statistical Analysis System (SAS®), R, and COREXpress® statistical analysis software.

[380] As would be understood by a person of ordinary skill in the art, the utility of the combinations and classifiers determined by a mathematical model will depend upon some characteristics (e.g., race, age group, gender, medical history) of the population used to generate the data for input into the model. One can select the individually identified biomarkers or subsets of the individually identified genes, and test all possible combinations of the selected biomarkers to identify useful combinations of biomarker sets.

[381] In some embodiment, a subject's likelihood score (e.g., the Y value in a logistic regression) can be used to determine whether a subject is likely to have cancer. Thus, if the likelihood score is greater than a pre-determined reference threshold, the subject is likely to have cancer. In some embodiment, if the likelihood s score is less than a reference threshold, the subject is not likely to have cancer. A person skilled in the art will appreciate that the

appropriate reference threshold for each classifier can be different, and can be optimized for various statistical measures (e.g., sensitivity, specificity, percentage of correct predictions). In some embodiments, the reference threshold is determined by experiments or in a clinical trial.

[382] In some embodiments, multiple classifiers are created that are satisfactory for the given purpose (e.g., all have sufficient AUC and/or sensitivity and/or specificity). In some embodiments, a formula is generated that utilizes more than one classifier. For example, a formula can be generated that utilizes classifiers in series. Other possible combinations and weightings of classifiers would be understood and are encompassed herein.

[383] In some embodiments, the probability that a subject has cancer can be derived from the likelihood score. Thus, if the probability is greater than a pre-determined threshold, for example, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, the subject will be administered with a treatment for cancer. In some embodiments, if the probability is less than a pre-determined threshold, for example, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, the subject will not be administered with a treatment for cancer. In some embodiments, the pre-determined threshold for treatment is 0.4, 0.5, or 0.6, and the pre-determined threshold for not treating, or for discontinuation of treatment, is 0.4, 0.5, or 0.6. In some embodiments, the pre-determined threshold is determined by experiments or in a clinical trial.

[384] A person skilled in the art will also appreciate that the sensitivity and the specificity of the method depend on the reference threshold (or the cut-off point). When the reference threshold is raised, the sensitivity will decrease, but the specificity will increase. In some embodiments, the reference threshold can be optimized for the sensitivity, the specificity, or the percentage of correct predictions.

Determining Tissue of Origin

[385] The present disclosure provides methods of determining cancer type, or the origin of a cancer cell or a tumor cell. Mathematical models can be applied to various biomarkers as described herein (e.g., protein concentrations for various biomarkers, genetic mutations in various biomarkers).

[386] Mathematical models useful in accordance with the disclosure include those using both supervised and unsupervised learning techniques. In some embodiments, the mathematical model chosen uses supervised learning in conjunction with a training dataset to evaluate each possible combination of biomarkers. Various mathematical models can be used, for example, a regression model, a logistic regression model, a neural network, a clustering model, principal component analysis, correlated component analysis, nearest neighbor classifier analysis, linear discriminant analysis, quadratic discriminant analysis, a support vector machine, a decision tree, Random Forest, a genetic algorithm, classifier optimization using bagging, classifier optimization using boosting, classifier optimization using the Random Subspace Method, a projection pursuit, and genetic programming and weighted voting, etc.

[387] In some embodiments, a supervised learning model is used to determine the origin of a cancer cell or a tumor cell. The supervised learning model refers to a model that learns a function that maps an input to an output based on example input-output pairs. It can infer a function from labeled training data consisting of a set of training examples. In supervised learning, each example is a pair consisting of an input object (typically a vector, e.g., a vector of protein biomarkers) and a desired output value (also called the supervisory signal, e.g., cancer type or tissue of origin). A supervised learning algorithm analyzes the training data and produces an inferred function, which can be used for mapping the biomarkers obtained from a test subject. Many supervised machine learning methods can be used. The methods include, but are not limited to, Support Vector Machines, regression analysis, linear regression, logistic regression, naive Bayes, linear discriminant analysis, decision trees, k-nearest neighbor algorithm, neural networks (e.g., Multilayer perceptron).

[388] In some embodiments, an unsupervised learning model is used to determine the origin of a cancer cell or a tumor cell. The unsupervised machine learning refers to the machine learning task of inferring a function that describes the structure of "unlabeled" data (i.e. data that has not been classified or categorized). This is performed under the assumption that relevant biomarkers will have more similarity if the samples have the same origin. The unsupervised machine learning can identify these shared characteristics and apply these models to biomarkers obtained from a test subject, thereby determining the origin of a cancer

cell or a tumor cell in the subject. Many unsupervised machine learning methods can be used. The methods include, but are not limited to, clustering (e.g., k-means clustering, mixture model clustering, and hierarchical clustering, etc.), anomaly detection, unsupervised neural networks (e.g., autoencoders, deep belief nets, Hebbian learning, generative adversarial networks, and self-organizing map, etc.).

[389] In some embodiments, Random Forest is used. Random Forest refers to a learning method for classification, regression and other tasks, that operate by constructing a multitude of decision trees at training time and outputting the class that is the mode of the classes (classification) or mean prediction (regression) of the individual trees. Random Forest can be implemented by various programs, e.g., by the Random Forest package (Liaw, Andy, and Matthew Wiener. "Classification and regression by randomForest." R news 2.3 (2002): 18-22). In some embodiments, Random Forest identifies the presence of cancer in a subject based on one or more protein biomarkers (e.g., protein concentrations in whole blood or plasma). In some embodiments, more than ten rounds of 10-fold cross validation can be performed.

[390] In some embodiments, support vector machines (SVM) can be used to determine tissue of origin. SVM starts with a set of training examples, each marked as belonging to one or the other of two categories (e.g., cancer type). The SVM training algorithm builds a model that assigns new examples to one category or the other, making it a non-probabilistic binary linear classifier (e.g., cancer from a particular origin, and cancer that is not from the particular origin). An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible.

[391] These mathematical models can be applied to various biomarkers, or panels of biomarkers (e.g., protein biomarkers) as described herein to determine the origin of the cancer cell. In some embodiments, these methods are only applied to subjects who have been predicted to have cancer.

[392] In some embodiments, once a subject is determined to have or is determined as being likely to have cancer, a tissue of origin for the cancer is determined as shown in Figure 68. For example, a decision can be made at each branch of the tree shown in Figure 68, and once

a terminus is reached (e.g. there are no more decisions to be made), the tissue of origin can be predicted or determined as shown. The tree shown in Figure 68 provides a framework for a practitioner to predict or determine the tissue of origin of a cancer (e.g., breast cancer, colorectal cancer, liver cancer, lung cancer, ovarian cancer, pancreatic cancer, and gastro-intestinal cancer).

[393] The tree shown in Figure 68 is exemplary and non-limiting. For example, at some decision points, the level of a protein biomarker (e.g. one or more protein biomarkers) can be determined (e.g., the level of a protein biomarker present in a sample obtained from a subject), and the level of that protein biomarker(s) can be compared to the level indicated on the tree shown in Figure 68. In some embodiments, the level of a protein biomarker is determined (e.g., the level of a protein biomarker present in a sample obtained from a subject), and the level of that protein biomarker is compared to the level that differs from the level indicated on the tree shown in Figure 68. In some embodiments, the different level of a protein biomarker (e.g. one or more of the protein biomarkers) on the tree shown in Figure 68 is about 10% different from (e.g., about 10% greater than or 10% less than), about 15% different from (e.g., about 15% greater than or 15% less than), about 20% different from (e.g., about 20% greater than or 20% less than), about 25% different from (e.g., about 25% greater than or 25% less than), about 30% different from (e.g., about 30% greater than or 30% less than), about 35% different from (e.g., about 35% greater than or 35% less than), about 40% different from (e.g., about 40% greater than or 40% less than), about 45% different from (e.g., about 45% greater than or 45% less than), about 50% different from (e.g., about 50% greater than or 50% less than) the level of that protein biomarker shown at one or more decision points on the tree shown in Figure 68. At some decision points, the gender (e.g., the biological gender) of the subject is determined and compared to the gender at one or more decision points indicated on the tree shown in Figure 68. At some decision points, the subject can be determined to be a woman. At some decision points, the subject can be determined to be a man.

[394] In some embodiments, once a subject is determined to have or is determined as being likely to have cancer, a tissue of origin for the cancer is determined according to the list of rules shown in Figure 69 and the table below. For example, the level of a protein biomarker

(e.g. one or more protein biomarkers) can be determined (e.g., the level of a protein biomarker present in a sample obtained from a subject), and the level of that protein biomarker(s) can be compared to the level indicated in the rules shown in Figure 69 and the table below. As one non-limiting example, the rule [condition = CA125>102.76 & sFas<=830.345 & gender %in% c('F'), prediction = ovarian] means that if a woman (%in% c('F')) has CA125 > 102.76, and sFas<=830.345, then the woman has or is predicted to have ovarian cancer. A person skilled in the art will be able to detect the level of one or more protein biomarkers in a subject and/or determine the gender (e.g., biological gender) of a subject, and determine that the subject has or is likely to have a cancer type listed on Figure 69. In some embodiments, once a subject is determined to have or is determined as being likely to have cancer, a tissue of origin for the cancer is determined to be colorectal when the level of one or more protein biomarkers in a subject and/or the gender (e.g., biological gender) of a subject does not follow any of the specific rules shown in Figure 69 and the table below. In some embodiments, the level of a protein biomarker is determined (e.g., the level of a protein biomarker present in a sample obtained from a subject), and the level of that protein biomarker is compared to the level that differs from the level indicated in the rules shown in Figure 69 and the table below. In some embodiments, the different level of a protein biomarker (e.g. one or more of the protein biomarkers) in the rules shown in Figure 69 is about 10% different from (e.g., about 10% greater than or 10% less than), about 15% different from (e.g., about 15% greater than or 15% less than), about 20% different from (e.g., about 20% greater than or 20% less than), about 25% different from (e.g., about 25% greater than or 25% less than), about 30% different from (e.g., about 30% greater than or 30% less than), about 35% different from (e.g., about 35% greater than or 35% less than), about 40% different from (e.g., about 40% greater than or 40% less than), about 45% different from (e.g., about 45% greater than or 45% less than), about 50% different from (e.g., about 50% greater than or 50% less than) the level of that protein biomarker shown at one or more decision points in the rules shown in Figure 69 and the table below. In some embodiments, the gender (e.g., the biological gender) of the subject is determined and compared to the gender in one or more of the rules shown in Figure 69 and the table below. In some embodiments, the subject can be determined to be a woman (e.g., "gender %in%

c('F')"). In some embodiments, the subject can be determined to be a man (e.g., "gender %in% c('M')"). For the table below, exemplary and non-limiting rules and cancer type predictions are indicated. "Else" indicates that if none of the other exemplary rules are met, the cancer can be predicted to be colorectal.

Exemplary Rules	**Prediction**
CA125>102.76 & sFas<=830.345 & gender %in% c('F')	Ovarian
CA199>37.65 & CYFRA211<=14640.67 & CD44>15.67 & Midkine>289.485 & PAR>4580.45 & sHER2>6935.375	Pancreatic
AFP>17774.49 & TIMP2<=61777.34 & Galectin3<=16.72 & Mesothelin<=27.71	Liver
CA199<=71.53 & Leptin>12927.9 & sFas>411.525 & TIMP1<=59700.835 & TIMP2<=37667.97 & gender %in% c('F')	Breast
CA125<=104.41 & CA153<=16.22 & CA199<=117.275 & HGF<=465.81 & Leptin<=7244.265 & SHBG>29.53	CRC
Prolactin>37214.25 & sFas>1046.435 & TIMP1<=93517.645 & DKK1<=1.095 & sHER2<=6054.825 & gender %in% c('M')	Lung
CA153<=15.285 & IL8>39.235 & IL8<=163.64 & sFas<=1098.015 & Myeloperoxidase>19.325 & sHER2<=5172.43	Stomach/Esophageal
AFP<=2867.07 & CA153>9.505 & Prolactin>37962.925 & sFas>688.47 & Myeloperoxidase<=11.935 & Thrombospondin2<=3273.685	Lung
AFP<=36492.58 & CA125<=10.475 & Prolactin<=275955.405 & sFas<=1351.39 & AXL>1999.77 & sHER2<=10172.47	CRC
CEA<=1892.955 & sFas<=1076.05 & TIMP2>40306.87 & CD44<=26.915 & sHER2<=9959.43 & gender %in% c('F')	Ovarian
Leptin<=5186.325 & OPN>94670.57 & TIMP1>75617.725 & SHBG<=141.115 & sHER2<=8369.265 & Thrombospondin2<=17040.89	Stomach/Esophageal
AFP<=40375.115 & CA153<=20.835 & CEA>3057.27 & Leptin<=237948.935 & OPN<=250628.405 & TIMP2<=68136.905	CRC
AFP<=299906.424 & sFas>1100.55 & TIMP1<=85064.65 & TIMP2<=53195.905 & DKK1<=1.285 & gender %in% c('F')	Breast
Leptin>8839.01 & sFas<=1745.34 & TIMP1>63205.505 & CD44<=19.735 & Mesothelin<=39.705 & gender %in% c('F')	CRC

AFP<=5369.16 & CA153<=16.21 & CEA>1374.755 & Myeloperoxidase<=368.56 & Midkine<=4401.495 & sHER2<=10713.16	CRC
TIMP2<=61631.2 & Myeloperoxidase>23.725 & SHBG<=96.985 & DKK1<=1.335 & Midkine<=348.515 & sHER2<=5523.84	Stomach/Esophageal
CA125<=56.21 & HGF<=928.54 & Prolactin>65977.55 & sFas<=2849.195 & Mesothelin>13.68 & AXL<=2093.75	Lung
CA199<=36.795 & CEA<=115717.2 & HE4<=15657.71 & Leptin>15287.95 & sFas>716.205 & gender %in% c('F')	Breast
Else	CRC

[395] For Figures 68 and 69 and the table shown above, the units of certain protein biomarkers are indicated in the key below:

CA19-9	U/ml
CEA	pg/ml
CA125	U/ml
AFP	pg/ml
Prolactin	pg/ml
HGF	pg/ml
OPN	pg/ml
TIMP-1	pg/ml
TIMP-2	pg/ml
Mesothelin	ng/ml
Midkine	pg/ml
Kallikrein-6	pg/ml
CD44	ng/ml
Angiopoietin-2	pg/ml
Endoglin	pg/ml
Follistatin	pg/ml
G-CSF	pg/ml
GDF15	ng/ml
DKK1	ng/ml
NSE	ng/ml
OPG	ng/ml
AXL	pg/ml
sHER2/sEGFR2/sErbB2	pg/ml
Thrombospondin-2	pg/ml
sEGFR	pg/ml
PAR	pg/ml
sPECAM-1	pg/ml
CA15-3	U/ml
Leptin	pg/ml
IL-6	pg/ml

IL-8	pg/ml
sFas	pg/ml
FGF2	pg/ml
CYFRA 21-1	pg/ml
HE4	pg/ml
TGFa	pg/ml
Galectin-3	ng/ml
Myeloperoxidase	ng/ml
SHBG	nM

Detecting Genetic Biomarkers

[396] Any of a variety of techniques can be used to detect the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject. Non-limiting examples of such techniques include a PCR-based multiplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a PCR-based singleplex PCR assay, a Sanger sequencing assay, a next-generation sequencing assay, a quantitative PCR assay, a ligation assay, and a microarray assay. Those of ordinary skill in the art will be aware of other suitable techniques for detecting the presence of one or more genetic biomarkers (e.g., mutations) present in a sample obtained from a subject.

[397] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using a method that can increase the sensitivity of massively parallel sequencing instruments with an error reduction technique. For example, such techniques can permit the detection of rare mutant alleles in a range of 1 mutant template among 100 to 1,000,000 wild-type templates (e.g., 500 to 1,000,000 wild-type templates). In some embodiments, such techniques can permit the detection of rare mutant alleles when they are present as a low fraction of the total number of templates (e.g., when rare mutant alleles when are present at a fraction of less than about 1%, less than about 0.1%, less than about 0.01%, less than about 0.001%, less than about 0.00001% of total templates, or lower, or any fraction between these exemplary fractions). In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample obtained from a subject is detected by amplifying DNA

(e.g., DNA obtained from cells in a sample or cell-free DNA) to form families of amplicons in which each member of a family is derived from a single template molecule in the cell-free DNA, wherein each member of a family is marked by a common oligonucleotide barcode, and wherein each family is marked by a distinct oligonucleotide barcode. For example, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample obtained from a subject can be detected by molecularly assigning a unique identifier (UID) to each template molecule, amplifying each uniquely tagged template molecule to create UID-families, and redundantly sequencing the amplification products. In some embodiments, the oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers that collectively contain a plurality of oligonucleotide barcodes. In some embodiments, the oligonucleotide barcode is endogenous to the template molecule, and an adapter including a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the oligonucleotide barcode. See, e.g., Kinde I, Wu J, Papadopoulos N, Kinzler KW, Vogelstein B (2011) Detection and quantification of rare mutations with massively parallel sequencing. Proc Natl Acad Sci U S A 108:9530-9535, the contents of which are incorporated herein by reference in their entirety.

[398] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, or plasma sample) obtained from a subject is detected using sequencing technology (e.g., a next-generation sequencing technology). A variety of sequencing technologies are known in the art. For example, a variety of technologies for detection and characterization of circulating tumor DNA in cell-free DNA is described in Haber and Velculescu, Blood-Based Analyses of Cancer: Circulating Tumor Cells and Circulating Tumor DNA, Cancer Discov., Jun;4(6):650-61. doi: 10.1158/2159-8290.CD-13-1014, 2014, incorporated herein by reference in its entirety. Non-limiting examples of such techniques include SafeSeqs (Kinde et. al, Detection and quantification of rare mutations with massively parallel sequencing, Proc Natl Acad Sci USA;108, 9530-5, 2011), OnTarget (Forshew et al., Noninvasive identification and monitoring of cancer mutations by targeted deep sequencing of plasma DNA, Sci Transl Med; 4:136ra68, 2012), and TamSeq (Thompson et al., Winnowing DNA for rare sequences: highly specific sequence and methylation based enrichment. PLoS ONE,

7:e31597, 2012), each of which is incorporated herein by reference in its entirety. In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected using droplet digital PCR (ddPCR), a method that is known to be highly sensitive for mutation detection. In some embodiments, the presence of one or more mutations present in a sample obtained from a subject is detected using other sequencing technologies, including but not limited to, chain-termination techniques, shotgun techniques, sequencing-by-synthesis methods, methods that utilize microfluidics, other capture technologies, or any of the other sequencing techniques known in the art that are useful for detection of small amounts of DNA in a sample (e.g., ctDNA in a cell-free DNA sample).

[399] In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using array-based methods. For example, the step of detecting a genetic alteration (e.g., one or more genetic alterations) in cell-free DNA can be performed using a DNA microarray. In some embodiments, a DNA microarray can detect one more of a plurality of genetic biomarkers (e.g., cancer cell mutations). In some embodiments, cell-free DNA is amplified prior to detecting the genetic biomarker (e.g., the genetic alteration). Non-limiting examples of array-based methods that can be used in any of the methods described herein, include: a complementary DNA (cDNA) microarray (Kumar et al. (2012) J. Pharm. Bioallied Sci. 4(1): 21-26; Laere et al. (2009) Methods Mol. Biol. 512: 71-98; Mackay et al. (2003) Oncogene 22: 2680-2688; Alizadeh et al. (1996) Nat. Genet. 14: 457-460), an oligonucleotide microarray (Kim et al. (2006) Carcinogenesis 27(3): 392-404; Lodes et al. (2009) PLoS One 4(7): e6229), a bacterial artificial chromosome (BAC) clone chip (Chung et al. (2004) Genome Res. 14(1): 188-196; Thomas et al. (2005) Genome Res. 15(12): 1831-1837), a single-nucleotide polymorphism (SNP) microarray (Mao et al. (2007) Curr. Genomics 8(4): 219-228; Jasmine et al. (2012) PLoS One 7(2): e31968), a microarray-based comparative genomic hybridization array (array-CGH) (Beers and Nederlof (2006) Breast Cancer Res. 8(3): 210; Pinkel et al. (2005) Nat. Genetics 37: S11-S17; Michels et al. (2007) Genet. Med. 9: 574-584), a molecular inversion probe (MIP) assay (Wang et al. (2012) Cancer Genet 205(7-8): 341-55; Lin et al. (2010) BMC Genomics 11: 712). In some embodiments, the cDNA microarray is an

Affymetrix microarray (Irizarry (2003) Nucleic Acids Res 31:e15; Dalma-Weiszhausz et al. (2006) Methods Enzymol. 410: 3-28), a NimbleGen microarray (Wei et al. (2008) Nucleic Acids Res 36(9): 2926-2938; Albert et al. (2007) Nat. Methods 4: 903-905), an Agilent microarray (Hughes et al. (2001) Nat. Biotechnol. 19(4): 342-347), or a BeadArray array (Liu et al. (2017) Biosens Bioelectron 92: 596-601). In some embodiments, the oligonucleotide microarray is a DNA tiling array (Mockler and Ecker (2005) Genomics 85(1): 1-15; Bertone et al. (2006) Genome Res 16(2): 271-281). Other suitable array-based methods are known in the art.

[400] In some embodiments, once a subject has been determined to have a cancer (e.g., an ovarian cancer, an endometrial cancer, a bladder cancer, or an UTUC), the subject may be additionally monitored or selected for increased monitoring. In some embodiments, methods provided herein can be used to select a subject for increased monitoring at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for increased monitoring can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for increased monitoring can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for increased monitoring can be administered a one or more additional diagnostic tests compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered two diagnostic tests, whereas a subject that has not been selected for increased monitoring is administered only a single diagnostic test (or no diagnostic tests). In some embodiments, a subject that has been selected for increased monitoring can also be selected for further diagnostic testing. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the

progression of the tumor or cancer in the subject and/or to assess the development of additional genetic biomarkers (e.g., cancer cell mutations) and/or aneuploidy), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell). In some embodiments, a therapeutic intervention is administered to the subject that is selected for increased monitoring after a genetic biomarker (e.g., a cancer cell mutation) and/or aneuploidy is detected. Any of the therapeutic interventions disclosed herein or known in the art can be administered. For example, a subject that has been selected for increased monitoring can be further monitored, and a therapeutic intervention can be administered if the presence of the cancer cell is maintained throughout the increased monitoring period. Additionally or alternatively, a subject that has been selected for increased monitoring can be administered a therapeutic intervention, and further monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for increased monitoring has been administered a therapeutic intervention, the increased monitoring will reveal one or more genetic biomarkers (e.g., one or more additional cancer cell mutations) and/or aneuploidy. In some embodiments, such one or more genetic biomarkers (e.g., one or more additional cancer cell mutations) and/or aneuploidy will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

[401] In some embodiments, once a subject has been determined to have a cancer (e.g., an ovarian cancer, an endometrial cancer, a bladder cancer, or an UTUC), the subject may be administered further tests or selected for further diagnostic testing. In some embodiments, methods provided herein can be used to select a subject for further diagnostic testing at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for further diagnostic testing can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for further diagnostic testing can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency

compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for further diagnostic testing can be administered a one or more additional diagnostic tests compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered two diagnostic tests, whereas a subject that has not been selected for further diagnostic testing is administered only a single diagnostic test (or no diagnostic tests). In some embodiments, the diagnostic testing method can determine the presence of the same type of cancer as the cancer that was original detected. Additionally or alternatively, the diagnostic testing method can determine the presence of a different type of cancer as the cancer that was original detected. In some embodiments, the diagnostic testing method is a scan. In some embodiments, the scan is a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, a DEXA scan. In some embodiments, the diagnostic testing method is a physical examination, such as an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, a pelvic exam, a positron emission tomography and computed tomography (PET-CT) scan. In some embodiments, a subject that has been selected for further diagnostic testing can also be selected for increased monitoring. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the subject and/or to assess the development of additional genetic biomarkers (e.g., additional cancer cell mutations) and/or aneuploidy), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell). In some embodiments, a therapeutic intervention is administered to the subject that is selected for further diagnostic testing after a genetic biomarker (e.g., a

cancer cell mutation) and/or aneuploidy is detected. Any of the therapeutic interventions disclosed herein or known in the art can be administered. For example, a subject that has been selected for further diagnostic testing can be administered a further diagnostic test, and a therapeutic intervention can be administered if the presence of the cancer cell is confirmed. Additionally or alternatively, a subject that has been selected for further diagnostic testing can be administered a therapeutic intervention, and can be further monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for further diagnostic testing has been administered a therapeutic intervention, the additional testing will reveal one or more additional genetic biomarkers (e.g., cancer cell mutations) and/or aneuploidy. In some embodiments, such one or more additional genetic biomarkers (e.g., cancer cell mutations) and/or aneuploidy will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

[402] In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using any of the variety of bottleneck sequencing system methods described in International Patent Application Publication Number WO 2017/132438, the contents of which are incorporated by reference herein in their entirety. Bottleneck Sequencing System (BotSeqS) is a next-generation sequencing method that simultaneously quantifies rare somatic point mutations across the mitochondrial and nuclear genomes. BotSeqS combines molecular barcoding with a simple dilution step immediately prior to library amplification. BotSeqS can be used to show age and tissue-dependent accumulations of rare mutations and demonstrate that somatic mutational burden in normal tissues can vary by several orders of magnitude, depending on biologic and environmental factors. BotSeqS has been used to show major differences between the mutational patterns of the mitochondrial and nuclear genomes in normal tissues. BotSeqS has shown that the mutation spectra of normal tissues were different from each other, but similar to those of the cancers that arose in them.

[403] According to some embodiments of BotSeqS, a method is provided for obtaining the sequence of a DNA. Adaptors are ligated to ends of random fragments of a DNA population to form a library of adaptor-ligated fragments, such that upon amplification of a fragment in the library of adaptor-ligated fragments, each end of the fragment has a distinct end. The library of adaptor- ligated fragments is diluted to form diluted, adaptor-ligated fragments. At least a portion of the diluted, adaptor-ligated fragments is amplified to form families from a single strand of an adaptor-ligated fragment. Family members are sequenced to obtain nucleotide sequence of a plurality of family members of an adaptor-ligated fragment.

[404] According to some embodiments of BotSeqS, a method is provided for sequencing DNA. Adaptors are ligated to ends of a population of fragmented double-stranded DNA molecules to form a library of adaptor-ligated fragments, such that upon amplification of a fragment in the library of adaptor-ligated fragments, each end of the fragment has a distinct end. The library of adaptor-ligated fragments is diluted to form diluted, adaptor-ligated fragments. At least a portion of the diluted, adaptor-ligated fragments is amplified to form families from a single strand of an adaptor-ligated fragment. Family members are sequenced to obtain nucleotide sequence of a plurality of family members of an adaptor-ligated fragment. Nucleotide sequence of a member of a first family is aligned to a reference sequence. A difference between the member of the first family and the reference sequence is identified. The difference is identified as a potential rare or potential non-clonal mutation if it is found in a second family from an opposite strand of the single strand of the adaptor-ligated fragment.

[405] According to some embodiments of BotSeqS, a method is provided for sequencing DNA. A double-stranded DNA population from a sample is randomly fragmented to form a library of fragments. Adaptors are ligated to ends of the fragments to form a library of adaptor-ligated fragments, such that upon amplification of a fragment in the library of adaptor-ligated fragments, each end of the fragment has a distinct end. The library of adaptor-ligated fragments is diluted to form diluted, adaptor-ligated fragments. At least a portion of the diluted, adaptor-ligated fragments is amplified to form families from a single strand of an adaptor-ligated fragment. Family members are sequenced to obtain nucleotide sequence of a plurality of family members of an adaptor-ligated fragment. Nucleotide

sequence of a member of a first family is aligned to a reference sequence. A difference between the member of the first family and the reference sequence is identified. The difference is identified as a potential rare or potential non-clonal mutation if it is found in a second family from an opposite strand of the single strand of the adaptor-ligated fragment.

[406] In some embodiments of detecting the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject, rare somatic point mutations are quantified across the mitochondrial and nuclear genomes. One or more embodiments of such methods are referred to informally as BotSeqS, which is short for Bottleneck Sequencing System. Using molecular barcoding (exogenous or endogenous) and a simple dilution step immediately prior to library amplification, the method permits, for example, determining mutational burden based on age or tissue type of normal tissues. Various BotSeqS methods described herein can also be used to demonstrate the effect of mutagens and environmental insults on mutation rate. Various BotSeqS methods described herein are designed to accurately detect rare point mutations in any molecularly-barcoded library in a completely unbiased fashion.

[407] BotSeqS was can be used with any molecular barcoding strategy, such as endogenous position-demarcated barcodes, described in Kinde, I, et al., Detection and quantification of rare mutations with massively parallel sequencing. Proceedings of the National Academy of Sciences of the United States of America 108, 9530-9535 (2011), and exogenously added matched barcodes (Kinde, I, et al., Detection and quantification of rare mutations with massively parallel sequencing. Proceedings of the National Academy of Sciences of the United States of America 108, 9530-9535 (2011); Jabara et al., Accurate sampling and deep sequencing of the HIV-1 protease gene using a Primer ID. Proceedings of the National Academy of Sciences of the United States of America 108, 20166-20171 (2011); Schmitt, M.W. et al. Detection of ultra-rare mutations by next-generation sequencing. Proceedings of the National Academy of Sciences of the United States of America 109, 14508-14513 (2012); Hiatt et al., Single molecule molecular inversion probes for targeted, high-accuracy detection of low-frequency variation. Genome research 23, 843-854 (2013); Kivioja, T. et al. Counting absolute numbers of molecules using unique molecular identifiers. Nature methods

9, 72-74 (2012); Kinde, I. et al. Evaluation of DNA from the Papanicolaou test to detect ovarian and endometrial cancers. Science translational medicine 5, 167ral64 (2013); Kumar, A. et al. Deep sequencing of multiple regions of glial tumors reveals spatial heterogeneity for mutations in clinically relevant genes. Genome biology 15, 530 (2014); Keys, J.R. et al. Primer ID Informs Next-Generation Sequencing Platforms and Reveals Preexisting Drug Resistance Mutations in the HIV-1 Reverse Transcriptase Coding Domain. AIDS Res Hum Retroviruses 31, 658-668 (2015)). In some embodiments, BotSeqS measures very rare mutations, genome-wide in a completely unbiased fashion, whereas SafeSeqS measures relatively frequent but not clonal mutations (i.e., "sub-clonal") at pre-defined targeted loci.

[408] Conceptually, BotSeqS can be envisioned as achieving low coverage of randomly sampled genomic loci, whereas Safe-SeqS works through ultra-high coverage of a targeted locus.

[409] Low genomic coverage which can be seen as a feature of various BotSeqS methods described herein, permits rare mutations to constitute a major portion of the signal at that genomic position, contributing to the sensitivity of the method. The applications of such methods are varied. They can be used to measure very rare somatic mutations. They can be used to assess somatic mosaicism, cell lineage development, theories on aging, environmental carcinogen exposure, and cancer risk assessment. Many of these applications are demonstrated in the examples herein.

[410] Various filters can be applied to the data that are generated with various BotSeqS sequencing methods. One filter that can be applied is for mtDNA only; Watson AND Crick duplicate families only, excluding templates that include high frequency mutations (i.e., homopolymers, >1 mutation per template) and excluding templates that map to repeatMasker. Another filter that can be applied is for nuclear DNA only; Watson AND Crick duplicate families only, excluding templates that include high frequency mutations (i.e., homopolymers, >1 mutation per template) and excluding templates that map to repetitive DNA or structural variants. Another filter that can be applied is for mtDNA only, single-base substation only, average quality score of greater than or equal to 30, Read 1 >=2 Watson duplicates with >=90% mutation fraction only, Read 2 >=2 Crick duplicates with >=90% mutation fraction only, Exclude all variants called in WGS, Exclude all variants in

dbSNP142, Exclude calls that map to repeatMasker, Exclude visual artifacts and high frequency mutations (i.e., homopolymers, cycle 6 and 7, > 1 change per template > 1 template per change). Yet another filter that can be applied is Nuclear DNA only, Single-base substitution only, Average quality score >= 30, Read 1 >=2 PCR duplicates with >=90% mutation fraction only, Read 2 >=2 PCR duplicates with >=90% mutation fraction only, Exclude all variants called in WGS, Exclude all variants in dbSNP130 and dbSNP142, Exclude calls that map to repetitive DNA or structural variants, Exclude visual artifacts and high frequency mutations (i.e., homopolymers, cycle 6 and 7, > 1 change per template).

[411] Various databases were used to align and filter the data, including: dbSNP build 130, Database of Genome Variants, Segmental Duplications, Fragments of Interrupted Repeats, Simple Tandem Repeats, Repeat Masker, dbSNP build 142, updated Database of Genome Variants, updated Database of Genome Variants, updated Segmental Duplications, updated Fragments of Interrupted Repeats, updated Simple Tandem Repeats, updated Repeat Masker. The GRCh37/hgl9 genome assembly from the USCS Human genome Browser was used.

[412] Fragments of double stranded DNA can be made from longer chain polymers, using any technique known in the art, including but not limited to enzyme digestion, sonication, and shearing. Alternately, some sources of DNA are already fragmented at suitable sizes. Such sources include without limitation saliva, sputum, urine, plasma, and stool. If the source of DNA is already appropriately sized, then the fragments do not need be further fragmented. Desirably, the fragmentation process, whether endogenous or by human action, is random. The desirable size of fragments may depend on the length of sequencing reads. Fragments may be less than 2 kbp, less than 1500 bp, less than 1 kbp, less than 500 bp, less than 400 bp, less than 200 bp, or less than 100 bp. Fragments may desirably be greater than twice the read length, for example. Fragments may be at least 50 bp, at least 100 bp, at least 150 bp, at least 200 bp, at least 300 bp, at least 400 bp, at least 500 bp, for example.

[413] In some embodiments, fragments are ligated to adaptors. In some embodiments, each end of a fragment has different adaptors. This can be a laborious process, that may involve much screening and processing to obtain fragments with two distinct adaptors on each end. One way to accomplish this goal is to use Y, U, or hairpin shaped adaptors which contain or can be processed to contain sequence non-complementary sequences on the Watson and

Crick strands. If there is a non-complementary region in an adaptor, amplification of the adaptor-ligated fragment will generate double stranded fragments with different adaptor orientation on fragments derived from each strand, when amplified.

[414] Dilution of libraries of adaptor-ligated fragments can be done using any level of dilution that is appropriate for the source. Less concentrated samples can undergo less dilution and more concentrated samples can undergo more dilution. Complexity of a sample will also factor into the desired degree of dilution. Any dilution series may be used as is convenient, such as two-fold dilutions, five-fold dilutions, ten-fold dilutions, etc. In some embodiments, a dilution level is chosen that will yield ~ 5-10 members of a family per adapter-ligated fragment. This is influenced by how many fragments are sequenced. For example, at one specific dilution, sequencing -20 million clusters will yield 1-4 members, but sequencing 75 million clusters yield 5-10 (see FIG. 55). The more molecules that are sequenced, the higher the number of members that will be found per family. Upon sequencing family members derived from the diluted, adaptor-ligated fragments, one desirably obtains nucleotide sequence of 4-100 family members of an adaptor-ligated fragment.

[415] Dilution may beneficially achieve a relatively low level of coverage of the genome. That is, the genome may be sampled rather than exhaustively and repetitively sequenced. In some embodiments, the dilution is sufficient so that fewer than 10 families from nuclear DNA include 20 or more overlapping nucleotides in the non-adaptor portion. In some embodiments, the dilution is sufficient so that fewer than 5 families from nuclear DNA include 20 or more overlapping nucleotides in the non-adaptor portion. In some embodiments, the dilution is sufficient so that fewer than 10 families comprise the potential rare or potential non-clonal difference detected between a test sequence and a reference sequence. In some embodiments, the dilution is sufficient so that fewer than 5 families comprise the potential rare or potential non- clonal difference detected between a test sequence and a reference sequence.

[416] In some embodiments, dilution accomplishes three features. First, dilution can achieve lower coverage of representative loci to one or a few molecules to "uncover" rare mutations. Second, dilution can increase the chances that both strands of the initial molecules

will be sequenced redundantly. Third, dilution can facilitate the random sampling of the genome with minimal amount of sequencing.

[417] Amplification can be performed by any technique known in the art. Typically, polymerase chain reaction will be used. Other techniques, whether linear or logarithmic may be used.

[418] Typically, primers will be used in the amplification that are complementary to adaptor sequences.

[419] Sequencing can be accomplished by any known technique in the art. A next generation sequencing method may be used. The sequences of the fragments can be aligned to a reference sequence. They can be grouped into families on the basis of an endogenous or an exogenous barcode. An endogenous barcode typically comprises the N nucleotides that are adjacent to the adaptor. The value of N can be chosen as is convenient and provides sufficient diversity/complexity. Exogenous barcodes can be added in a separate ligation step, by amplification primers, or they can be part of the adaptors. In some embodiments, the barcodes are random. In some embodiments, from 2 to 1000 family members are sequenced. In some embodiments, fewer than 100 family members are sequenced. In some embodiments, at least 4 family members are sequenced. In some embodiments, 4 to 10 family members are sequenced.

[420] According to various method described herein, one need not separate physically or analyze separately the nuclear and mitochondrial genomes. This permits one to compare rates in the two genomes in the same cells.

[421] Exogenous barcoding may be used to identify individual fragments, samples, tissues, patients, etc. Although the examples provided herein employed endogenous barcoding, this may be supplemented with or replaced by exogenous barcoding. In some embodiments, the complexity of the barcode population is greater than the complexity of the population of fragments to be barcoded such that the barcode represents a particular fragment. Barcodes can be added to a population of fragments using any technique known in the art, including without limitation, by amplification or ligation, or as part of adaptor molecules that are added by ligation. Differences that can be detected between a determined nucleotide sequence and a reference nucleotide sequence include without limitation mutations, such as point mutations,

indels (e.g., insertions or deletions of 1-6 bases), and/or substitutions. If the same mutation is found in two different families, then a higher degree of certainty is attached to it (e.g., it is more likely that it arose in the biological sample, rather than in the experimental processing). The two families can have identical sequences deriving from the double stranded fragments, but can have a different orientation with respect to the adaptor sequences. To achieve a higher degree of certainty, one can require that at least two members of each of two families have the sequence difference. To achieve a higher degree of certainty, one can require that 90% or more of the members of a family have the sequence difference.

[422] As a means of filtering out germline or clonal mutations, libraries of fragments that have not been amplified and which are from the same sample can be sequenced. Germline and clonal mutations will be evident from inspection because of their repeated occurrences.

[423] BotSeqS methods are simply-implemented NGS-based approaches that can accurately measure rare point mutations in an unbiased, genome-wide manner. Using BotSeqS, several important goals were achieved: (i) estimates of rare mutation frequencies across the whole genome were defined; (ii) rare mutations in both the nuclear and mitochondrial genomes of the same population of cells were simultaneously evaluated; (iii) rare mutation frequencies among various normal tissues of individuals of different age, DNA repair capacity, or exposure histories were compared; and (iv) the spectra of rare mutations in normal tissues was identified, allowing their comparison to those of clonal mutations in cancers.

[424] Data presented herein show that mutations increase with age, a result that is broadly consistent with the literature (Kennedy, S.R., Loeb, L.A. & Herr, A.J. Somatic mutations in aging, cancer and neurodegeneration. Mech Ageing Dev 133, 118-126 (2012); Vijg, J. Somatic mutations, genome mosaicism, cancer and aging. Current opinion in genetics & development 26, 141-149 (2014). The rate of increase of mutations is not as great in brain as it is in colon or kidney, presumably because the colon and kidney are both self-renewing tissues throughout adult life while the brain is not. On the other hand, the fact that the mutation frequency increased at all after childhood was surprising, given that the major cell types in pre-frontal cortex are generally thought to be post-mitotic (Spalding et al., Retrospective birth dating of cells in humans. Cell 122, 133-143 (2005)). Without being bound by theory, there are several potential explanations for this increase. A small number of

cells that are replicating more actively than neurons or glia could be responsible for the increase. Such cells could include microglia or infiltrating lymphocytes or other inflammatory cells. Alternatively, these mutations could represent the results of spontaneous DNA damage independent of DNA replication. A recent single-cell sequencing study of human neurons suggested that spontaneous damage occurs during transcription (Lodato, M.A. et al. Somatic mutation in single human neurons tracks developmental and transcriptional history. Science 350, 94-98 (2015)). However, in contrast to single-cell sequencing, BotSeqS measures mutations that are found on both strands. Thus for the explanation of spontaneous DNA damage to be plausible, the mutations identified by BotSeqS would have to have been subject to DNA repair. Consistent with this possibility, DNA repair processes are known to be active in post-mitotic neurons and glia (Madabhushi, R., Pan, L. & Tsai, L.H. DNA damage and its links to neurodegeneration. Neuron 83, 266-282 (2014)).

[425] A third possibility is that these mutations are artifacts of the procedure we used to detect them. It is fascinating that this formal possibility is essentially impossible to exclude because the mutations that were are likely found in only one cell of the tissue studied, and the DNA from that cell is no longer available for subsequent evaluation. Additionally, there is no other technique available to observe such mutations with the sensitivity achieved by various BotSeqS methods described herein. The sensitivity is currently limited only by the amount of sequencing devoted to the project. It is easy to detect mutations occurring at 6×10^{-8} per bp using a small fraction of a HiSeq™ 2500 flow cell. It is estimated that mutations could be detected at $< 10^{-9}$ per bp using an entire flow cell. The only other method that approaches this sensitivity has been described by Loeb and colleagues (Schmitt, M.W. et al. Detection of ultra-rare mutations by next-generation sequencing. Proceedings of the National Academy of Sciences of the United States of America 109, 14508-14513 (2012); Kennedy, S.R. et al. Detecting ultralow-frequency mutations by Duplex Sequencing. Nature protocols 9, 2586-2606 (2014)), but this is applicable only to pre-defined regions (~0.001%) of the genome. In the absence of direct confirmation, one is forced to use correlations and other approaches to support the accuracy of the technology described herein. These correlations include the following, as detailed in Table 51: similar mutation frequencies and spectra identified in

different DNA aliquots of the same samples; similar mutation frequencies and spectra identified in the same tissues of different individuals of similar age; expected increases in mutation frequencies with age; tissue-specific differences in age-dependent increases in mutation frequencies; higher mutation frequencies in normal tissues deficient in mismatch repair or exposed to environmental mutagens; and mutation spectra in normal tissues consistent with those previously observed in cancers from the same tissues. Other *in silico* and experimental approaches used to evaluate the accuracy of BotSeqS are described in the Example 7.

[426] It was also possible to compare mutation frequencies in the mitochondrial and nuclear genomes of the same tissues. In normal individuals in the absence of exposure to mutagens, the mutation frequency was much higher in the mitochondria than in the nuclear genome (median ratio of 26.2). This is consistent with the relatively poor efficiency of DNA repair in the mitochondria compared to the nuclear genome. Equally important, however, is that the ratio of mitochondrial to nuclear mutation frequencies was vastly lower (median of 1.3) in the normal kidneys of individuals exposed to either cigarette smoke or AA. This finding is not consistent with the known, less efficient repair of DNA in mitochondria. Moreover, there was a shift towards the AA mutational signature, A:T to T: A transversions, in the nuclear DNA of normal kidneys in individuals exposed to AA, but virtually none in the mtDNA. Without being bound by theory, one possibility is that the higher mutation prevalence in the mtDNA could be masking the effect of environmental mutagens on the mitochondrial genome compared to its effect on the nuclear genome. Another possibility is that there are unexpected and pronounced differences in the ways through which these mutagens cause DNA damage in these two organelles.

[427] Another novel finding of the data presented herein is the finding that mutation spectra differed among normal tissues, even in the absence of exposures to known mutagens. Whether such differences reflect varying exposures to as yet unidentified commonly encountered mutagens, or tissue-specific repair processes, is not known. In some embodiments, the rare mutation spectra in normal tissues were found to be similar to the clonal mutations found in cancers. Though varying mutation spectra in cancers has often been attributed to cancer-specific processes, the data presented herein suggest that at least a

subset of these mutations actually reflect tissue-specific processes. This concept is consistent with the idea that a substantial fraction of the mutations found in cancers occur in normal stem cells (Tomasetti, C. & Vogelstein, B. Cancer etiology. Variation in cancer risk among tissues can be explained by the number of stem cell divisions. Science 347, 78-81 (2015); Tomasetti, C, Vogelstein, B. & Parmigiani, G. Half or more of the somatic mutations in cancers of self-renewing tissues originate prior to tumor initiation. Proceedings of the National Academy of Sciences of the United States of America 110, 1999-2004 (2013). Various BotSeqS approaches described herein, which can easily measure very rare mutations in any tissue or cell type of interest, will be applicable to questions of broad biomedical interest.

[428] In some embodiments, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using any of the variety of methods described in U.S. Patent Application Number 9,476,095, the contents of which are incorporated by reference herein in their entirety. The identification of mutations that are present in a small fraction of DNA templates is advantageous for progress in several areas of biomedical research. Though massively parallel sequencing instruments are in principle well-suited to this task, the error rates in such instruments are generally too high to allow confident identification of rare variants. Provided herein is an approach that can substantially increase the sensitivity of massively parallel sequencing instruments for this purpose. One example of this approach, called "Safe-SeqS" for (Safe-Sequencing System) includes (i) assignment of a unique identifier (UID) to each template molecule; (ii) amplification of each uniquely tagged template molecule to create UID-families; and (iii) redundant sequencing of the amplification products. PCR fragments with the same UID are truly mutant ("super-mutants") if ≧95% of them contain the identical mutation. This approach is useful for, e.g., determining the fidelity of a polymerase, the accuracy of oligonucleotides synthesized in vitro, and the prevalence of mutations in the nuclear and mitochondrial genomes of normal cells.

[429] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using a unique identifier (UID) nucleic acid sequence attached to a first end of each of a plurality of analyte nucleic acid fragments to form uniquely identified analyte nucleic acid fragments, the nucleotide sequence of a uniquely identified analyte nucleic acid fragment is redundantly determined, wherein determined nucleotide sequences which share a UID form a family of members, and a nucleotide sequence is identified as accurately representing an analyte nucleic acid fragment when at least 1% of members of the family contain the sequence.

[430] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using a unique identifier sequence (UID) attached to a first end of each of a plurality of analyte DNA fragments using at least two cycles of amplification with first and second primers to form uniquely identified analyte DNA fragments. In such embodiments, the UIDs can be in excess of the analyte DNA fragments during amplification, the first primers can include a first segment complementary to a desired amplicon; a second segment containing the UID; and a third segment containing a universal priming site for subsequent amplification, the second primers can include a universal priming site for subsequent amplification, each cycle of amplification can attach one universal priming site to a strand, the uniquely identified analyte DNA fragments can be amplified to form a family of uniquely identified analyte DNA fragments from each uniquely identified analyte DNA fragment, and nucleotide sequences of a plurality of members of the family can be determined.

[431] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using endogenous unique identifier sequences (UIDs). For example, fragmented analyte DNA can be obtained that includes fragments of 30 to 2000 bases, inclusive. Each end of a fragment can form an endogenous UID for the fragment. Adapter oligonucleotides can be

attached to ends of the fragments to form adapted fragments. Fragments representing one or more selected genes can optionally be enriched by means of capturing a subset of the fragments using capture oligonucleotides complementary to selected genes in the analyte DNA or by amplifying fragments complementary to selected genes. The adapted fragments can be amplified using primers complementary to the adapter oligonucleotides to form families of adapted fragments. Nucleotide sequences can be determined for a plurality of members of a family. Nucleotide sequences of the plurality of members of the family can be compared. A nucleotide sequence can be identified as accurately representing an analyte DNA fragment when at least a 1% of members of the family contain the sequence.

[432] In some embodiments, provided herein are compositions including populations of primer pairs, wherein each pair includes a first and second primer for amplifying and identifying a gene or gene portion. The first primer can include a first portion (e.g., of 10-100 nucleotides) complementary to the gene or gene portion and a second portion of (e.g., of 10 to 100 nucleotides) including a site for hybridization to a third primer. The second primer can include a first portion of (e.g., of 10-100 nucleotides) complementary to the gene or gene portion and a second portion (e.g., of 10 to 100 nucleotides) including a site for hybridization to a fourth primer. In some embodiments, interposed between the first portion and the second portion of the second primer is a third portion consisting of 2 to 4000 nucleotides forming a unique identifier (UID). The unique identifiers in the population can have at least 4 different sequences. The first and second primers can be complementary to opposite strands of the gene or gene portion. A kit may include the population of primers and the third and fourth primers complementary to the second portions of each of the first and second primers.

[433] In some embodiments of methods provided herein, the presence of one or more genetic biomarkers (e.g., mutations) present in a sample (e.g., a cervical, endometrial, urine, saliva, ctDNA, blood, serum, and/or plasma sample) obtained from a subject is detected using an approach called "Safe-SeqS" (from Safe-Sequencing System). In one embodiment, Safe-SeqS involves two basic steps (FIG. 61): the first step is assignment of a Unique Identifier (UID) to each nucleic acid template molecule to be analyzed, and the second step is the amplification of each uniquely tagged template, so that many daughter molecules with the identical sequence are generated (defined as a UID-family). If a mutation pre-existed in the

template molecule used for amplification, that mutation should be present in a certain proportion, or even all, of daughter molecules containing that UID (barring any subsequent replication or sequencing errors). A UID-family in which every family member (or a certain predetermined proportion) has an identical mutation is called a "super-mutant." Mutations not occurring in the original templates, such as those occurring during the amplification steps or through errors in base-calling, should not give rise to super-mutants (e.g., will not be present at the pre-determined frequency in a UID family.) In some embodiments, amplification is not necessary.

[434] Any of the variety of Safe-SeqS approaches can be employed for any purpose where a very high level of accuracy and sensitivity is desired to be obtained from sequence data. As described herein, the approach can be used to assess the fidelity of a polymerase, the accuracy of in vitro synthesized nucleic acid synthesis, and the prevalence of mutations in nuclear or mitochondrial nucleic acids of normal cells. The approach may be used to detect and/or quantify mosaics and somatic mutations.

[435] In some embodiments of Safe-SeqS approaches provided herein, fragments of nucleic acids may be obtained using a random fragment forming technique such as mechanical shearing, sonicating, or subjecting nucleic acids to other physical or chemical stresses. Fragments may not be strictly random, as some sites may be more susceptible to stresses than others. Endonucleases that randomly or specifically fragment may also be used to generate fragments. In some embodiments of any of the variety of Safe-SeqS approaches, fragments of nucleic acids may be obtained using a technique that does not result in random fragments. Size of fragments may vary, but desirably will be in ranges between 30 and 5,000 basepairs, between 100 and 2,000, between 150 and 1,000, or within ranges with different combinations of these endpoints. Nucleic acids may be, for example, RNA or DNA. Modified forms of RNA or DNA may also be used.

[436] In some embodiments of Safe-SeqS approaches provided herein, attachment of an exogenous UID to an analyte nucleic acids fragment may be performed by any means known in the art, including enzymatic, chemical, or biologic. One means employs a polymerase chain reaction. Another means employs a ligase enzyme. The enzyme may be mammalian or

bacterial, for example. Ends of fragments may be repaired prior to joining using other enzymes such as Klenow Fragment of T4 DNA Polymerase. Other enzymes which may be used for attaching are other polymerase enzymes. An UID may be added to one or both ends of the fragments. A UID may be contained within a nucleic acid molecule that contains other regions for other intended functionality. For example, a universal priming site may be added to permit later amplification. Another additional site may be a region of complementarity to a particular region or gene in the analyte nucleic acids. A UID may be from 2 to 4,000, from 100 to 1000, from 4 to 400, bases in length, for example. In some embodiments, a UID is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000 nucleotides or more in length, or can be of any length between these lengths. In embodiments in which two or more UIDs are used, the UIDs can be of the same or different lengths.

[437] In some embodiments of Safe-SeqS approaches provided herein, UIDs may be made using random addition of nucleotides to form a short sequence to be used as an identifier. At each position of addition, a selection from one of four deoxyribonucleotides may be used. Alternatively, a selection from one of three, two, or one deoxyribonucleotides may be used. Thus, the UID may be fully random, somewhat random, or non-random in certain positions. Another manner of making UIDs utilizes pre-determined nucleotides assembled on a chip. In this manner of making, complexity is attained in a planned manner. In some embodiments, it may be advantageous to attach a UID to each end of a fragment, increasing the complexity of the UID population on fragments.

[438] A cycle of polymerase chain reaction for adding exogenous UID refers to the thermal denaturation of a double stranded molecule, the hybridization of a first primer to a resulting single strand, the extension of the primer to form a new second strand hybridized to the original single strand. A second cycle refers to the denaturation of the new second strand from the original single strand, the hybridization of a second primer to the new second strand, and the extension of the second primer to form a new third strand, hybridized to the

new second strand. Multiple cycles may be employed to increase efficiency, for example, when the analyte is dilute or inhibitors are present.

[439] In the case of endogenous UIDs, adapters can be added to the ends of fragments by any of a variety of methods including, without limitation, ligation. In some embodiments, complexity of the analyte fragments can be decreased by a capture step, either on a solid phase or in liquid step. In some embodiments, the capture step employs hybridization to probes representing a gene or set of genes of interest. In some embodiments, if on a solid phase, non-binding fragments are separated from binding fragments. Suitable solid phases known in the art include filters, membranes, beads, columns, etc. In some embodiments, if in a liquid phase, a capture reagent can be added which binds to the probes, for example through a biotin-avidin type interaction. After capture, desired fragments can be eluted for further processing. The order of adding adapters and capturing is not critical. Another non-limiting means of reducing the complexity of the analyte fragments involves amplification of one or more specific genes or regions. One exemplary way to accomplish this is to use inverse PCR. Primers can be used which are gene-specific, thus enriching while forming libraries. Optionally, the gene-specific primers can contain grafting sequences for subsequent attachment to a massively parallel sequencing platform.

[440] Because In some embodiments, endogenous UIDs provide a limited number of unique possibilities, depending on the fragment size and sequencing read length, combinations of both endogenous and exogenous UIDs can be used. In some embodiments, introducing additional sequences when amplifying increase the available UIDs and thereby increase sensitivity. For example, before amplification, the template can be split into 96 wells, and 96 different primers can be used during the amplification; this would effectively increase the available UIDs 96-fold, because up to 96 templates with the same endogenous UID could be distinguished. This technique can also be used with exogenous UIDs, such that each well's primers adds a unique, well-specific sequence to the amplification products, which can also improve the specificity of detection of rare templates.

[441] In some embodiments of Safe-SeqS approaches provided herein, amplification of fragments containing a UID can be performed according to known techniques to generate

families of fragments. Polymerase chain reaction can be used. Other amplification methods can also be used, as is convenient. Inverse PCR may be used, as can rolling circle amplification. Amplification of fragments typically is done using primers that are complementary to priming sites that are attached to the fragments at the same time as the UIDs. In some embodiments, priming sites are distal to the UIDs, so that amplification includes the UIDs. In some embodiments, amplification forms a family of fragments, each member of the family sharing the same UID. Because the diversity of UIDs is typically greatly in excess of the diversity of the fragments, each family should derive from a single fragment molecule in the analyte. Primers used for the amplification may be chemically modified to render them more resistant to exonucleases. Non-limiting examples of such modifications include the use of phosphorothioate linkages between one or more 3′ nucleotides, and boranophosphates.

[442] In some embodiments of Safe-SeqS approaches provided herein, family members are sequenced and compared to identify any divergencies within a family. In some embodiments, sequencing is performed on a massively parallel sequencing platform, many of which are commercially available. If the sequencing platform employs a sequence for "grafting," i.e., attachment to the sequencing device, such a sequence can be added during addition of UIDs or adapters or separately. A grafting sequence may be part of a UID primer, a universal primer, a gene target-specific primer, the amplification primers used for making a family, or separate. Redundant sequencing refers to the sequencing of a plurality of members of a single family.

[443] A threshold can be set for identifying a genetic biomarker (e.g., a mutation) in an analyte. If the "mutation" appears in all members of a family, then it derives from the analyte. If it appears in less than all members, then it may have been introduced during the analysis. Thresholds for calling a mutation may be set, for example, at 1%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 98%, or 100%. Thresholds can be set based on the number of members of a family that are sequenced and the particular purpose and situation.

[444] In some embodiments of Safe-SeqS approaches provided herein, populations of primer pairs are used to attach exogenous UIDs. For example, the first primer can include a first portion (e.g., of 10-100 nucleotides) complementary to the gene or gene portion and a second portion (e.g., of 10 to 100 nucleotides) including a site for hybridization to a third primer. In some embodiments the first portion and/or the second potion of the first primer is 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides in length, or any length in between. The second primer can include a first portion (e.g., of 10-100 nucleotides) complementary to the gene or gene portion and a second portion (e.g., of 10 to 100 nucleotides) including a site for hybridization to a fourth primer. In some embodiments the first portion and/or the second potion of the second primer is 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides in length, or any length in between. In some embodiments, interposed between the first portion and the second portion of the second primer is a third portion (e.g., of 2 to 4,000 nucleotides, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000 nucleotides, or any number of nucleotides between these values) forming a unique identifier (UID). . In some embodiments, interposed between the first portion and the second portion of both the first and second primer is a third portion (e.g., of 2 to 4,000 nucleotides, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000 nucleotides, or any number of nucleotides between these values), each of which forms a unique identifier (UID). In some embodiments, the third portion of the first primer is the same length as the third portion of the second primer. In some embodiments, the third portion of the first primer is a different length than the third portion of the second primer. In some embodiments, the unique identifiers in the population have at least 4, at least 16, at least 64, at least 256, at least 1,024, at least 4,096, at least 16,384, at least 65,536, at least 262,144, at least 1,048,576, at least 4,194,304 at least 16,777,216, or at least 67,108,864 different sequences. In some embodiments, the first and second primers are complementary to opposite strands of the gene or gene portion. A kit can be made containing both the primers for attaching exogenous UIDs as well as amplification primers, i.e., the third and

fourth primers complementary to the second portions of each of the first and second primers. The third and fourth primers can optionally contain additional grafting or indexing sequences. The UID may include randomly selected sequences, pre-defined nucleotide sequences, or both randomly selected sequences and pre-defined nucleotides. If both, these can be joined together in blocks or interspersed.

[445] In some embodiments of Safe-SeqS approaches provided herein, the methods of analysis can be used to quantitate as well as to determine a sequence. For example, the relative abundance of two analyte DNA fragments may be compared using methods described herein.

[446] The results described herein demonstrate that the Safe-SeqS approach can substantially improve the accuracy of massively parallel sequencing (Tables 52 and 53). Safe-SeqS can be implemented through either endogenous or exogenously introduced UIDs (or both), and can be applied to virtually any sample preparation workflow or sequencing platform. As demonstrated herein, Safe-SeqS can easily be used to identify rare mutants in a population of DNA templates, to measure polymerase error rates, and to judge the reliability of oligonucleotide syntheses. One of the advantages of the strategy is that it yields the number of templates analyzed as well as the fraction of templates containing variant bases. Previously described in vitro methods for the detection of small numbers of template molecules (e.g., Dressman D, Yan H, Traverso G, Kinzler K W, & Vogelstein B (2003) Transforming single DNA molecules into fluorescent magnetic particles for detection and enumeration of genetic variations. Proc Natl Acad Sci USA 100:8817-8822; Li J, et al. (2008) Replacing PCR with COLD-PCR enriches variant DNA sequences and redefines the sensitivity of genetic testing. Nat Med 14:579-584) allow the fraction of mutant templates to be determined but cannot determine the number of mutant and normal templates in the original sample.

[447] It is of interest to compare Safe-SeqS to other approaches for reducing errors in next generation sequencing. Sophisticated algorithms to increase the accuracy of base-calling have been developed (e.g., (Erlich Y, Mitra P, delaBastide M, McCombie W R, & Hannon G J (2008) Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. Nat

Methods 5:679-682; Rougemont J, et al. (2008) Probabilistic base calling of Solexa sequencing data. BMC Bioinformatics 9:431; Druley T E, et al. (2009) Quantification of rare allelic variants from pooled genomic DNA, Nat Methods 6:263-265; Vallania F L, et al. (2010) High-throughput discovery of rare insertions and deletions in large cohorts. Genome Res 20:1711-1718)). These can certainly reduce false positive calls, but their sensitivity is still limited by artifactual mutations occurring during the PCR steps required for library preparation as well as by (a reduced number of) base-calling errors. For example, the algorithm employed in the current study used very stringent criteria for base-calling and was applied to short read-lengths, but was still unable to reduce the error rate to less than an average of 2.0×10^{-4} errors/bp. This error frequency is at least as low as those reported with other algorithms. To improve sensitivity further, these base-calling improvements can be used together with Safe-SeqS. Travers et al. have described another powerful strategy for reducing errors (Eid J, et al. (2009) Real-time DNA sequencing from single polymerase molecules. Science 323:133-138). With this technology, both strands of each template molecule are sequenced redundantly after a number of preparative enzymatic steps. However, this approach can only be performed on a specific instrument. Moreover, for many clinical applications, there are relatively few template molecules in the initial sample and evaluation of nearly all of them is required to obtain the requisite sensitivity. In some embodiments, approaches described herein that employ exogenously introduced UIDs (FIG. 63) address this concern by coupling the UID assignment step with a subsequent amplification in which few molecules are lost.

[448] Strong evidence supporting the fact that mutations identified by conventional analyses in the current study represent artifacts rather than true mutations in the original templates is provided by the observation that the mutation prevalence in all but one experiment was similar—2.0×10^{-4} to 2.4×10^{-4} mutations/bp (Tables 52 and 53). The exception was the experiment with oligonucleotides synthesized from phosphoramidites, in which the error of the synthetic process was apparently higher than the error rate of conventional Illumina analysis when used with stringent base-calling criteria. In contrast, the mutation prevalence of Safe-SeqS varied much more, from 0.0 to 1.4×10^{-5} mutations/bp, depending on the template and experiment. Moreover, the mutation prevalence measured by

Safe-SeqS in the most controlled experiment, in which polymerase fidelity was measured (Table 53A), was almost identical to that predicted from previous experiments in which polymerase fidelity was measured by biological assays. Measurements of mutation prevalence in the DNA from normal cells provided herein are consistent with some previous experimental data. However, estimates of these prevalences vary widely and may depend on cell type and sequence analyzed (see SI text). It therefore cannot be said with certainty that the few mutations revealed by Safe-SeqS represented errors occurring during the sequencing process rather than true mutations present in the original DNA templates. Potential sources of error in the Safe-SeqS process are described in the SI text.

[449] Another potential application of Safe-SeqS is the minimization of PCR contamination, a serious problem for clinical laboratories. With endogenous or exogenous UID assignment, the UIDs of mutant templates can simply be compared to those identified in prior experiments; the probability that the same mutation from two independent samples would have the same UID in different experiments is negligible when mutations are infrequent. Additionally, with exogenous UIDs, a control experiment with the same template but without the UID assigning PCR cycles (FIG. 63) can ensure that no DNA contamination is present in that template preparation; no template should be amplified in the absence of UID assignment cycles and thus no PCR product of the proper size should be observed.

[450] It was demonstrated that the exogenous UIDs strategy can be used to analyze a single amplicon in depth. This technology may not be applicable to situations wherein multiple amplicons must be analyzed from a sample containing a limited number of templates. Multiplexing in the UID assignment cycles (FIG. 63) may provide a solution to this challenge. A second potential concern is that clinical samples may contain inhibitors that reduce the efficiency of this step. This problem can presumably be overcome by performing more than two cycles in UID assignment PCR step (FIG. 63), though this has the potential to complicate the determination of the number of templates analyzed. The specificity of Safe-SeqS is currently limited by the fidelity of the polymerase used in the UID assignment PCR step, i.e., 8.8×10^{-7} mutations/bp in its current implementation with two cycles. Increasing the number of cycles in the UID assignment PCR step to five would decrease the overall

specificity to ~2×10^{-6} mutations/bp. However, this specificity can be increased by requiring more than one super-mutant for mutation identification—the probability of introducing the same artifactual mutation twice or three times would be exceedingly low ($[2\times10^{-6}]^2$ or $[2\times10^{-6}]^3$, respectively). In sum, there are several simple ways to perform Safe-SeqS variations and analysis variations to realize the needs of specific experiments.

[451] Luria and Delbrück, in their classic paper in 1943, wrote that their "prediction cannot be verified directly, because what we observe, when we count the number of resistant bacteria in a culture, is not the number of mutations which have occurred but the number of resistant bacteria which have arisen by multiplication of those which mutated, the amount of multiplication depending on how far back the mutation occurred." Various Safe-SeqS procedures described here can verify such predictions because the number as well as the time of occurrence of each mutation can be estimated from the data, as noted in the experiments on polymerase fidelity. In addition to templates generated by polymerases in vitro, the same approach can be applied to DNA from bacteria, viruses, and mammalian cells. It is therefore expected that this strategy will provide definitive answers to a variety of important biomedical questions.

[452] In some embodiments, a genetic biomarker (e.g., one or more genetic biomarkers) is detected using any of the variety of methods described in U.S. Patent Application Publication No. 2018/0208999, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include analysis of the count, the fragmentation patterns, and size of cell-free nucleic acids, e.g., plasma DNA and serum DNA, including nucleic acids from pathogens, such as viruses. Various embodiments are directed to applications (e.g., classification of biological samples) of the analysis of the count, the fragmentation patterns, and size of cell-free nucleic acids, e.g., plasma DNA and serum DNA, including nucleic acids from pathogens, such as viruses. Some embodiments, of the application can determine if a subject has a particular condition. For example, a method can determine if a subject has cancer or a tumor, or other pathology. Embodiments of another application can be used to assess the stage of a condition, or the progression of a condition over time. For example, a method may be used to determine a stage of cancer in a subject, or the progression of cancer in a subject

over time (e.g., using samples obtained from a subject at different times). According to one embodiment, sequence reads obtained from a sequencing of the mixture of cell free nucleic acid molecules can be used to determine an amount of the sequence reads aligning to a reference genome corresponding to the virus. The amount of sequence reads aligning to the reference genome can be compared to a cutoff value to screen for the pathology. According to another embodiment, sizes of viral nucleic acid molecules (e.g., those aligning to a reference genome corresponding to the virus) can be used. A statistical value of a size distribution of the nucleic acid molecules from the virus can be determined. A level of pathology in the subject can be determined by processing the statistical value against a cutoff value. According to another embodiment, a first amount of cell-free nucleic acid molecules that end within one or more first windows of a reference genome corresponding to the virus is determined. Each first window comprising at least one of a first set of genomic positions at which ends of cell-free nucleic acid molecules are present at a rate above a first threshold in subjects with a cancer (or other pathology) associated with the virus. A relative abundance can be computed by normalizing the first amount using a second amount of cell-free nucleic acid molecules, which includes cell-free nucleic acid molecules ending at a second set of genomic positions outside of the one or more first windows including the first set of genomic positions. A level of cancer in the subject can be determined by processing the relative abundance against a cutoff value. Embodiments can combine various techniques. For example, a first assay can be count-based, size-based, or fragmentation-based. A second assay can be one of the other techniques. As examples a majority voting can be used, or cutoff values can be determined for both techniques, thereby determining a set of data points from the two techniques that correspond to a particular level of pathology.

[453] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0203974, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a computer-implemented method, involving receiving a data set in a computer comprising a processor and a computer-readable medium, where the computer-readable medium comprises instructions that, when executed by the processor, cause the computer to e.g. identify somatic mutations in the biological test

sample; and generate a somatic mutational profile that comprises the somatic mutations; and detecting the presence of the cancer in the patient based on the exposure weights of the mutational signatures. Additionally or alternatively, detection of a genetic biomarker can include using a non-negative matrix factorization (NMF) approach to construct a signature matrix that can be used to identify latent signatures in a patient. In other embodiments, the methods may use principal components analysis (PCA) or vector quantization (VQ) approaches to construct a signature matrix. In one example, the patient sample is a cell-free nucleic acid sample (e.g., cell-free DNA (cfDNA) and/or cell-free RNA (cfRNA)). The construction of a signature matrix using non-negative matrix factorization can be generalized to multiple features relevant to cancer detection and/or classification. In some embodiments, a signature matrix comprises a plurality of signatures where the probability of the occurrence for each of a plurality of features are represented. Examples of relevant features include, but are not limited to, an upstream sequence context of a base substitution mutation, a downstream sequence context of a base substitution mutation, an insertion, a deletion, a somatic copy number alteration (SCNA), a translocation, a genomic methylation status, a chromatin state, a sequencing depth of coverage, an early versus late replicating region, a sense versus antisense strand, an inter mutation distance, a variant allele frequency, a fragment start/stop, a fragment length, and a gene expression status, or any combination thereof. In one embodiment, the upstream and/or downstream sequence context can comprise a region of a nucleic acid that ranges in length from about 2 to about 40 bp, such as from about 3 to about 30 bp, such as from about 3 to about 20 bp, or such as from about 2 to about 10 bp of sequence context of a base substitution mutation. In one embodiment, the upstream and/or downstream sequence context may be a triplet sequence context, a quadruplet sequence context, a quintuplet sequence context, a sextuplet sequence context, or a septuplet sequence context of base substitution mutations. In some embodiments, the upstream and/or downstream sequence context can be the triplet sequence context of a base substitution mutation. In one embodiment, the methods are used to identify latent somatic mutational signatures in a subject's (e.g., an asymptomatic subject) cfDNA sample for early detection of cancer. In another embodiment, the methods are used to infer tissue of origin for a patient's cancer based on latent mutational signatures identified in the patient's cfDNA sample. In yet another embodiment, the methods are used to

identify latent mutational signatures in a patient's cfDNA sample that can be used to classify the patient for different types of therapies. In yet another embodiment, non-negative matrix factorization is applied to learn error modes in a somatic variant (mutation) calling assay. For example, systematic errors (e.g., errors contributed during library preparation, PCR, hybridization capture, and/or sequencing) that underlie the assay can be identified and assigned unique signatures that can be used to distinguish between the contribution from true somatic variants and artifactual variants arising from the technical processes in the assay. In yet another embodiment, non-negative matrix factorization can be used to identify mutational signatures that are associated with healthy aging. Mutation processes that are associated with aging are assigned mutational signatures that can be used to distinguish between healthy somatic mutations associated with patient age and somatic mutations contributed from, and indicative of, a cancer process in the patient. In another embodiment, one or more mutational signatures can be monitored over time and used for diagnosing, monitoring, and/or classifying cancer. For example, the observed mutational profile in cfDNA from patient samples at two or more time points can be evaluated. In some embodiments, two or more mutational signature processes can be evaluated as a combination of different mutational signatures. In still another embodiment, one or more mutational signatures can be monitored over time (e.g., at a plurality of time points) to monitor the effectiveness of a therapeutic regimen or other cancer treatment. Somatic mutations (i.e., driver mutations and passenger mutations) in a cancer genome are typically the cumulative consequence of one or more mutational processes of DNA damage and repair. Although not wishing to be bound by theory, it is believed that the strength and duration of exposure to each mutational process (e.g., environmental factors and DNA repair processes) results in a unique profile of somatic mutations in a subject (e.g., a cancer patient). These unique combinations of mutation types form a unique "mutational signature" for the cancer patient. Furthermore, as is well known in the art, a somatic mutation, or mutational profile can depend on the particular sequence context of the mutation. For example, UV damage typically results in a base change of C to T, when the base change occurs within a sequence context of (−T|C|−) C(A|T|C|G). In this example, C is the mutated base and the bases upstream (T or C) and downstream (A, T, C, or G) of C affect the probability of a mutation under UV radiation. In another example, spontaneous deamination of 5-methylcytosine

typically results in a base change of C to T, when the base change occurs within a sequence context of (A|T|C|G)C(−|−|−|G). Accordingly, in one embodiment, the sequence context of identified mutations can be utilized as a feature for analyzing somatic mutations in the detection and/or classification of cancer.

[454] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/119399, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing a sequencing library from a DNA-containing test sample, including methods for rescuing one or more partially ligated DNA fragments to enhance library preparation conversion efficiencies. The methods can further be used to improve recovery of duplex sequence information from double-stranded DNA. Additionally or alternatively, detection of a genetic biomarker can include a method for preparing a double- stranded DNA sequencing library, the method comprising the following steps: (a) obtaining a test sample comprising a plurality of double-stranded DNA (dsDNA) fragments, wherein the dsDNA fragments comprise a forward strand and a reverse strand; (b) ligating double-strand DNA adapters to both ends of the dsDNA fragments; and (c) extending unligated 3 '-ends of the dsDNA fragments with a DNA polymerase to create dsDNA fragment-adapter templates to prepare a sequencing library. In some embodiments, the dsDNA fragment-adapter templates are further amplified prior to sequencing. In other embodiments, one or more steps of the method may be carried out in a single reaction step. For example, steps (b) through (c) may be carried out in a single reaction tube utilizing a reaction mixture comprising a first set of dsDNA adapters, a ligase, a polymerase (optionally having strand-displacement activity), a terminal deoxynucleotidyl transferase, and a second set of ssDNA oligonucleotides or primers (e.g., including sequencing adapters and/or a universal primer). Optionally, the dsDNA molecules can be purified, and optionally fragmented, from test sample prior to ligation step (b). Additionally or alternatively, detection of a genetic biomarker can include a method for preparing a double-stranded DNA sequencing library, the method comprising the following steps: (a) obtaining a test sample comprising a plurality of double-stranded DNA (dsDNA) fragments, the dsDNA fragments comprising a forward strand and a reverse strand; (b) adding double-stranded adapters to the dsDNA fragments and ligating the double-strand adapters to

both ends of the dsDNA fragments; (c) extending unligated 3 '-ends of the dsDNA fragments with a polymerase to create dsDNA fragment-adapter templates, wherein the polymerase further comprises strand displacement activity; (d) adding a poly-adenine tail to the 3 '-ends of the dsDNA fragment-adapter templates; (e) adding a set of ssDNA oligonucleotides (or primers) and hybridizing the ssDNA oligonucleotides to the dsDNA fragment-adapter templates; and (f) extending the set of ssDNA oligonucleotides to create a dsDNA sequencing library. In some embodiments, one or more steps of the method may be carried out in a single reaction step. For example, steps (b) through (f) may be carried out in a single reaction tube utilizing a reaction mixture comprising a first set of dsDNA adapters, a ligase, a polymerase (optionally having strand-displacement activity), a terminal deoxynucleotidyl transferase, and a second set of ssDNA oligonucleotides or primers (e.g., including sequencing adapters and/or a universal primer). Optionally, the dsDNA molecules can be purified, and optionally fragmented, from test sample prior to ligation step (b).

[455] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/119438, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of analyzing sequencing data to detect CNVs in a nucleic acid sample. Detecting CNVs in a nucleic acid sample obtained from a human subject can be informative for determining a presence of cancer in the subject. In one embodiment, detecting CNVs in a nucleic acid sample obtained from a human subject can be used for early detection of cancer in the subject. In various embodiments, the methods determine coverage at individual nucleotide bases determined from targeted sequencing reads. Sources of coverage variation can be corrected at the base level. For each gene of a targeted gene panel, the determined base level coverage across bases of the gene can be considered to more effectively detect CNVs of each gene. Generally, baseline coverage biases that exist at each base position can be modeled using training data gathered from healthy individuals. Therefore, when analyzing a test sample obtained from a subject, the base level coverage can be determined for each base position in view of the expected coverage biases obtained through modeling. Specifically, if the coverage bias at a base position for a test sample obtained from the subject differs from the expected coverage bias obtained through modeling, coverage biases can be

normalized and removed. For a gene in a targeted gene panel, base level coverages across the base positions of the gene are analyzed to determine whether the coverage for the gene differs from an expected level of coverage for the gene as previously determined using training data gathered from healthy individuals. If so, a CNV can be called. The calling of a CNV can indicate a presence of cancer in the subject or that the subject is susceptible to an increased likelihood of developing cancer.

[456] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/111872, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include preparing sequencing libraries based on a plurality of RNA molecules which are tagged and amplified by tagging the molecule with an oligonucleotide hybridising to a polyC tail introduced by the terminal transferase activity of the reverse transcriptase, e.g. MMLV RT, and ligating the oligonucleotide to the RNA molecule using a ligase, e.g. T4 RNA ligase, and producing cDNA molecules based on mRNA and strand displacing reverse transcriptases, e.g. MMLV RT, and producing a second cDNA strand in order to produce a dsDNA library for sequencing. In some embodiments, the methods comprise sequencing at least a portion of a sequencing library to obtain sequencing data or sequence reads from a test sample (e.g., a biological sample from a subject). In one embodiment, the method for preparing a sequencing library from a test sample comprising RNA comprises the steps: (a) obtaining a test sample comprising RNA sequences, and purifying the RNA sequences from the test sample; (b) synthesizing first complementary DNA (cDNA) strands based on the RNA sequences and C-tailing 3 '-ends of cDNA strands; (c) annealing a complementary template switching oligonucleotide to the C-tail of the cDNA and ligating the complementary template switching oligonucleotide to the 5 '-ends of the RNA sequences to produce RNA templates; and (d) synthesizing a plurality of cDNA strands from the RNA templates using a strand- displacement reverse transcriptase. In some embodiments, one or more steps of the method may be carried out in a single reaction step. For example, steps (b) through (d) may be carried out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand- displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA

ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase). In some embodiments, the method for preparing a sequencing library from a test sample comprising RNA, comprises the steps: (a) obtaining a test sample comprising one or more RNA sequences, and purifying the one or more RNA sequences from the test sample; (b) annealing a first RNA primer to the one or more RNA sequences; (c) extending the first RNA primer in a first nucleic acid extension reaction using reverse transcriptase, wherein the reverse transcriptase comprises reverse transcription and terminal transferase activities, to generate a plurality of DNA sequences complementary to the one or more RNA templates, and wherein the complementary DNA (cDNA) sequences further comprise a plurality of non-templated bases at the 3 '-end of the cDNA sequences; (d) annealing a complementary nucleic acid sequence to the non-templated bases at the 3 '-end of the cDNA sequence, wherein the complementary nucleic acid sequence further comprises a unique molecular identifier (UMI) or a unique sequence tag; (e) ligating the complementary nucleic acid sequence to the 5 '-end of the one or more RNA sequences to generate one or more RNA templates, wherein the one or more RNA templates comprise the original one or more RNA sequences covalently linked to the complementary nucleic acid sequence comprising the UMI or unique sequence tag; (f) annealing one or more second RNA primers to the one or more RNA template; and (g) extending the one or more second RNA primers in a second nucleic acid extension reaction using a strand-displacement reverse transcriptase to generate a plurality of DNA sequence complementary to the one or more RNA templates, wherein the plurality of complementary DNA (cDNA) sequences each comprise the complementary DNA sequence and a UMI or unique sequence tag. In some embodiments, one or more steps of the method may be carried out in a single reaction step. For example, in some embodiments, steps (b) through (g) may be carried out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand-displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase). In one embodiment, the method involves preparing a sequencing library from a test sample comprising RNA molecules, the method comprising the steps: (a) obtaining a test sample comprising one or more RNA sequences, and purifying the one or more RNA sequences from

the test sample; (b) annealing a first RNA primer to the one or more RNA sequences; (c) extending the first RNA primer in a first nucleic acid extension reaction using a reverse transcriptase, wherein the reverse transcriptase comprises reverse transcription and terminal transferase activities, to generate a plurality of DNA sequences complementary to the one or more RNA sequences, wherein the terminal transferase activity adds a cytosine (C) tail to the 3 '- end of the complementary DNA (cDNA) sequences; (d) annealing a template switching oligonucleotide to the 3 '-cytosine tail of the cDNA sequence, wherein the template switching oligonucleotide comprises a unique molecular identifier (UMI) or a unique sequence tag; (e) ligating the template switching oligonucleotide to the 5 '-end of the one or more RNA sequences with T4 RNA ligase to generate one or more RNA templates, wherein the one or more RNA templates comprise the original one or more RNA sequences covalently linked to the template switching oligonucleotide and the UMI or unique sequence tag; (f) annealing a plurality of second RNA primers to the one or more RNA templates; and (g) extending the plurality of second RNA primers in a second nucleic acid extension reaction using a strand-displacement reverse transcriptase to generate a plurality of DNA sequence complementary to the one or more RNA templates, wherein the plurality of complementary DNA (cDNA) each comprise the complementary DNA sequence and a UMI or unique sequence tag. In some embodiments, one or more steps of a method can be carried out in a single reaction step. For example, steps (b) through (g) may be carried out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand-displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase).

[457] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/085862, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for identifying somatic mutational signatures for detecting, diagnosing, monitoring and/or classifying cancer in a patient known to have, or suspected of having cancer. In various embodiments, the methods use a non-negative matrix factorization (NMF) approach to construct a signature matrix that can be used

to identify latent signatures in a patient sample for detection and classification of cancer. In other embodiments, the methods may use principal components analysis (PCA) or vector quantization (VQ) approaches to construct a signature matrix. In one example, the patient sample is a cell-free nucleic acid sample (e.g., cell-free DNA (cfDNA) and/or cell-free RNA (cfRNA)). The construction of a signature matrix using non-negative matrix factorization can be generalized to multiple features relevant to cancer detection and/or classification. In some embodiments, a signature matrix comprises a plurality of signatures where the probability of the occurrence for each of a plurality of features are represented. Examples of relevant features include, but are not limited to, an upstream sequence context of a base substitution mutation, a downstream sequence context of a base substitution mutation, an insertion, a deletion, a somatic copy number alteration (SCNA), a translocation, a genomic methylation status, a chromatin state, a sequencing depth of coverage, an early versus late replicating region, a sense versus antisense strand, an inter mutation distance, a variant allele frequency, a fragment start/stop, a fragment length, and a gene expression status, or any combination thereof. In one embodiment, the upstream and/or downstream sequence context can comprise a region of a nucleic acid that ranges in length from about 2 to about 40 bp, such as from about 3 to about 30 bp, such as from about 3 to about 20 bp, or such as from about 2 to about 10 bp of sequence context of a base substitution mutation. In one embodiment, the upstream and/or downstream sequence context may be a triplet sequence context, a quadruplet sequence context, a quintuplet sequence context, a sextuplet sequence context, or a septuplet sequence context of base substitution mutations. In some embodiments, the upstream and/or downstream sequence context can be the triplet sequence context of a base substitution mutation. In one embodiment, the methods are used to identify latent somatic mutational signatures in a subject's (e.g., an asymptomatic subject) cfDNA sample for early detection of cancer. In another embodiment, the methods are used to infer tissue of origin for a patient's cancer based on latent mutational signatures identified in the patient's cfDNA sample. In yet another embodiment, the methods are used to identify latent mutational signatures in a patient's cfDNA sample that can be used to classify the patient for different types of therapies. In yet another embodiment, non-negative matrix factorization is applied to learn error modes in a somatic variant (mutation) calling assay. For example, systematic errors (e.g., errors contributed during library preparation, PCR,

hybridization capture, and/or sequencing) that underlie the assay can be identified and assigned unique signatures that can be used to distinguish between the contribution from true somatic variants and artifactual variants arising from the technical processes in the assay. In yet another embodiment, non-negative matrix factorization can be used to identify mutational signatures that are associated with healthy aging. Mutation processes that are associated with aging are assigned mutational signatures that can be used to distinguish between healthy somatic mutations associated with patient age and somatic mutations contributed from, and indicative of, a cancer process in the patient. In another embodiment, one or more mutational signatures can be monitored over time and used for diagnosing, monitoring, and/or classifying cancer. For example, the observed mutational profile in cfDNA from patient samples at two or more time points can be evaluated. In some embodiments, two or more mutational signature processes can be evaluated as a combination of different mutational signatures. In still another embodiment, one or more mutational signatures can be monitored over time (e.g., at a plurality of time points) to monitor the effectiveness of a therapeutic regimen or other cancer treatment. In one embodiment, the sequence context of identified mutations can be utilized as a feature for analyzing somatic mutations in the detection and/or classification of cancer.

[458] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0163201, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing sequencing libraries comprising a plurality of RNA molecules. In one embodiment, the method for preparing a sequencing library from a test sample comprising RNA, comprises the steps: (a) obtaining a test sample comprising RNA sequences, and purifying the RNA sequences from the test sample; (b) synthesizing first complementary DNA (cDNA) strands based on the RNA sequences and C-tailing 3′-ends of cDNA strands; (c) annealing a complementary template switching oligonucleotide to the C-tail of the cDNA and ligating the complementary template switching oligonucleotide to the 5′-ends of the RNA sequences to produce RNA templates; and (d) synthesizing a plurality of cDNA strands from the RNA templates using a strand-displacement reverse transcriptase. In some embodiments, one or more steps of the method may be carried out in a single reaction step. For example, steps (b) through (d) may be carried

out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand-displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase). In one embodiment, the method comprises the steps: (a) obtaining a test sample comprising one or more RNA sequences, and purifying the one or more RNA sequences from the test sample; (b) annealing a first RNA primer to the one or more RNA sequences; (c) extending the first RNA primer in a first nucleic acid extension reaction using reverse transcriptase, wherein the reverse transcriptase comprises reverse transcription and terminal transferase activities, to generate a plurality of DNA sequences complementary to the one or more RNA templates, and wherein the complementary DNA (cDNA) sequences further comprise a plurality of non-templated bases at the 3′-end of the cDNA sequences; (d) annealing a complementary nucleic acid sequence to the non-templated bases at the 3′-end of the cDNA sequence, wherein the complementary nucleic acid sequence further comprises a unique molecular identifier (UMI) or a unique sequence tag; (e) ligating the complementary nucleic acid sequence to the 5′-end of the one or more RNA sequences to generate one or more RNA templates, wherein the one or more RNA templates comprise the original one or more RNA sequences covalently linked to the complementary nucleic acid sequence comprising the UMI or unique sequence tag; (f) annealing one or more second RNA primers to the one or more RNA template; and (g) extending the one or more second RNA primers in a second nucleic acid extension reaction using a strand-displacement reverse transcriptase to generate a plurality of DNA sequence complementary to the one or more RNA templates, wherein the plurality of complementary DNA (cDNA) sequences each comprise the complementary DNA sequence and a UMI or unique sequence tag. In some embodiments, one or more steps of the method may be carried out in a single reaction step. For example, in some embodiments, steps (b) through (g) may be carried out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand-displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase). In one embodiment, a method involves preparing a sequencing library from a test sample

comprising RNA molecules, the method comprising the steps: (a) obtaining a test sample comprising one or more RNA sequences, and purifying the one or more RNA sequences from the test sample; (b) annealing a first RNA primer to the one or more RNA sequences; (c) extending the first RNA primer in a first nucleic acid extension reaction using a reverse transcriptase, wherein the reverse transcriptase comprises reverse transcription and terminal transferase activities, to generate a plurality of DNA sequences complementary to the one or more RNA sequences, wherein the terminal transferase activity adds a cytosine (C) tail to the 3′-end of the complementary DNA (cDNA) sequences; (d) annealing a template switching oligonucleotide to the 3′-cytosine tail of the cDNA sequence, wherein the template switching oligonucleotide comprises a unique molecular identifier (UMI) or a unique sequence tag; (e) ligating the template switching oligonucleotide to the 5′-end of the one or more RNA sequences with T4 RNA ligase to generate one or more RNA templates, wherein the one or more RNA templates comprise the original one or more RNA sequences covalently linked to the template switching oligonucleotide and the UMI or unique sequence tag; (f) annealing a plurality of second RNA primers to the one or more RNA templates; and (g) extending the plurality of second RNA primers in a second nucleic acid extension reaction using a strand-displacement reverse transcriptase to generate a plurality of DNA sequence complementary to the one or more RNA templates, wherein the plurality of complementary DNA (cDNA) each comprise the complementary DNA sequence and a UMI or unique sequence tag. In some embodiments, one or more steps of a method can be carried out in a single reaction step. For example, steps (b) through (g) may be carried out in a single reaction tube utilizing a reaction mixture comprising RNA primers (e.g., random hexamer RNA primers, polyT primers, or a combination thereof), a strand-displacement reverse transcriptase (e.g., MMLV reverse transcriptase), an RNA ligase (e.g., T4 RNA ligase), and optionally, a polynucleotide kinase (e.g., T4 polynucleotide kinase).

[459] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/081130, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method comprising obtaining a first biological sample from the subject, wherein the first biological sample comprises cell-free nucleic acid from the

subject and potentially cell-free nucleic acid from a pathogen. In some embodiments, the method comprises performing a first assay comprising measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample. In some embodiments, the method comprises obtaining a second biological sample from the subject, wherein the second biological sample comprises cell-free nucleic acid from the subject and potentially cell-free nucleic acid from a pathogen. In some embodiments, the method comprises performing a second assay comprising massively parallel sequencing of the cell-free nucleic acid in the second biological sample to generate sequence reads. In some embodiments, the method comprises determining an amount of the sequence reads that align to a reference genome of the pathogen. In some embodiments, the method comprises determining an amount of the cell-free nucleic acid molecules that have a size within a given range and align to a reference genome of the pathogen based on the massively parallel sequencing. In some embodiments, the method comprises screening for the tumor based on performing a first assay comprising measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample, and performing a second assay comprising massively parallel sequencing of the cell-free nucleic acid in the second biological sample to generate sequence reads. In some embodiments, the first biological sample and the second biological sample are the same. In some embodiments, the method further comprises determining a percentage of the sequence reads that align to a reference genome of the pathogen. In some embodiments, the method further comprises comparing the percentage of the sequence reads that align to a reference genome of the pathogen to a cutoff value. In some embodiments, the method further comprises determining a size ratio of a first proportion of the cell-free nucleic acid molecules from the second biological sample that align to the reference genome of the pathogen with a size within the given range and a second proportion of the cell-free nucleic acid molecules from the second biological sample that align to a reference genome of the subject with a size within the given range. In some embodiments, the method further comprises determining a size index, wherein the size index is an inverse of the size ratio, and comparing the size index to a second cutoff value. In some embodiments, the tumor is nasopharyngeal cancer. In some embodiments, the pathogen is Epstein-Barr Virus (EBV). In some embodiments, measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample comprises

amplification. In some embodiments, the amplification comprises polymerase chain reaction (PCR). In some embodiments, the PCR comprises quantitative PCR (qPCR). In some embodiments, the first biological sample and the second biological sample are plasma. In some embodiments, the method comprises obtaining a first biological sample from the subject, wherein the first biological sample comprises cell-free nucleic acid from the subject and potentially cell-free nucleic acid from a pathogen. In some embodiments, the method comprises performing a first assay comprising measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample, wherein the first assay comprises a positive predictive value for a presence of the tumor in the subject. In some embodiments, the method comprises performing a second assay on a second biological sample from the subject, wherein the second biological sample comprises cell-free nucleic acid from the subject and potentially cell-free nucleic acid from the pathogen, and wherein a positive predictive value for a presence of the tumor in the subject of the first assay and the second assay is at least 5 -fold greater than the positive predictive value of the first assay. In some embodiments, the positive predictive value for a presence of the tumor in the subject of the first assay and the second assay is at least 7.5-fold greater than the positive predictive value of the first assay. In some embodiments, the positive predictive value for a presence of the tumor in the subject of the first assay and the second assay is at least 15%. In some embodiments, the positive predictive value for a presence of the tumor in the subject of the first assay and the second assay is at least 25%. In some embodiments, the first biological sample and the second biological sample are the same. In some embodiments, the first biological sample and the second biological sample are plasma. In some embodiments, the tumor is nasopharyngeal cancer. In some embodiments, the pathogen is Epstein-Barr Virus (EBV). In some embodiments, measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample comprises amplification. In some embodiments, the amplification comprises polymerase chain reaction (PCR). In some embodiments, the PCR comprises quantitative PCR (qPCR). In some embodiments, the second assay comprises massively parallel sequencing of the cell-free nucleic acid in the second biological sample to generate sequence reads. In some embodiments, the second assay comprises of determining an amount of the sequence reads that align to a reference genome of the pathogen. In some embodiments,

the second assay comprises determining an amount of the cell-free nucleic acid molecules in the second biological sample that have a size within a given range and align to a reference genome of the pathogen. In some embodiments, the method comprises obtaining a first biological sample from the subject, wherein the first biological sample comprises cell-free nucleic acid from the subject and potentially cell-free nucleic acid from a pathogen. In some embodiments, the method comprises performing a first assay comprising measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample, wherein the first assay has a false positive rate for a presence of the tumor in the subject. In some embodiments, the method comprises performing a second assay on a second biological sample from the subject, wherein the second biological sample comprises cell-free nucleic acid from the subject and potentially cell-free nucleic acid from the pathogen, wherein a false positive rate for a presence of the tumor in the subject of the first assay and the second assay is at least 5-fold lower than the false positive rate of the first assay. In some embodiments, the false positive rate for a presence of the tumor in the subject of the first assay and the second assay is at least 10-fold lower than the false positive rate of the first assay. In some embodiments, the false positive rate for a presence of the tumor in the subject of the first assay and the second assay is less than 1%. In some embodiments, the first biological sample and the second biological sample are the same. In some embodiments, the first biological sample and the second biological sample are plasma. In some embodiments, the tumor is nasopharyngeal cancer. In some embodiments, the pathogen is Epstein-Barr Virus (EBV). In some embodiments, measuring a copy number of the cell-free nucleic acid from the pathogen in the first biological sample comprises amplification. In some embodiments, the amplification comprises polymerase chain reaction (PCR). In some embodiments, the PCR comprises quantitative PCR (qPCR). In some embodiments, the second assay comprises massively parallel sequencing of the cell-free nucleic acid in the second biological sample to generate sequence reads. In some embodiments, the second assay comprises of determining an amount of the sequence reads that align to a reference genome of the pathogen. In some embodiments, the second assay comprises determining an amount of the cell-free nucleic acid molecules in the second biological sample that have a size within a given range and align to a reference genome of the pathogen. In some embodiments, the method comprises analyzing a biological

sample, including a mixture of cell-free nucleic acid molecules, to determine a level of pathology in a subject from which the biological sample is obtained, the mixture including nucleic acid molecules from the subject and potentially nucleic acid molecules from a pathogen. In some embodiments, the method comprises analyzing a first plurality of cell-free nucleic acid molecules from a biological sample of the subject, wherein the analyzing comprises determining a genomic position in a reference genome corresponding to at least one end of the first plurality of cell-free nucleic acid molecules, the reference genome corresponding to the pathogen. In some embodiments, the method comprises determining a first amount of the first plurality of cell-free nucleic acid molecules that end within one of first windows, each first window comprising at least one of a first set of genomic positions at which ends of cell-free nucleic acid molecules are present at a rate above a first threshold in subjects with a pathology associated with the pathogen. In some embodiments, the method comprises computing a relative abundance of the first plurality of cell-free nucleic acid molecules ending within one of the first windows by normalizing the first amount using a second amount of the first plurality of cell-free nucleic acid molecules from the biological sample, wherein the second amount of the first plurality of cell-free nucleic acid molecules includes cell-free nucleic acid molecules ending at a second set of genomic positions outside of the first windows including the first set of genomic positions. In some embodiments, the method comprises determining the level of pathology in the subject by processing the relative abundance against one or more cutoff values. In some embodiments, the relative abundance against one or more cutoff values includes determining whether the relative abundance is greater than the one or more cutoff values. In some embodiments, the method further comprises determining the second amount of the first plurality of cell-free nucleic acid molecules that end within one of second windows, each second window comprising at least one of the second set of genomic positions at which ends of cell-free nucleic acid molecules are present at a rate above a second threshold in subjects without a pathology resulting from pathogen, wherein normalizing the first amount includes computing the relative abundance using the first amount and the second amount. In some embodiments, the method further comprises identifying the second set of genomic positions. In some embodiments, the identifying comprises analyzing, by a computer system, the cell-free nucleic acid molecules of a reference sample from a reference subject that

does not have the pathology. In some embodiments, analyzing each of the plurality of cell-free nucleic acid molecules comprises determining a genomic position in the reference genome corresponding to at least one end of the cell-free nucleic acid molecule. In some embodiments, the reference subject is healthy. In some embodiments, the relative abundance comprises a ratio of the first amount and the second amount. In some embodiments, the method further comprises identifying the first set of genomic positions at which ends of cell-free nucleic acid molecules occur at the rate above a first threshold. In some embodiments, identifying the first set of genomic positions comprises analyzing, by a computer system, a second plurality of cell-free nucleic acid molecules from at least one first additional sample to identify ending positions of the second plurality of cell-free nucleic acid molecules, wherein the at least one first additional sample is known to have the pathology associated with the pathogen and is of a same sample type as the biological sample. In some embodiments, the method further comprises, for each genomic window of a plurality of genomic windows, computing a corresponding number of the second plurality of cell-free nucleic acid molecules ending on the genomic window, and comparing the corresponding number to a reference value to determine whether the rate of cell-free nucleic acid molecules ending on one or more genomic positions within the genomic window is above the first threshold. In some embodiments, a first genomic window of the plurality of genomic windows has a width of at least one genomic position, and wherein each of the genomic positions within the first genomic window are identified as having the rate of cell-free nucleic acid molecules ending on the genomic position be above the first threshold when the corresponding number exceeds the reference value. In some embodiments, the first set of genomic positions have the highest N values for the corresponding numbers, wherein N is at least 100.

[460] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 20180119216, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing and analyzing a single-stranded sequencing library from a double-stranded DNA (e.g., double-stranded cfDNA) sample. In some embodiments, the sample includes double-stranded DNA (dsDNA) molecules, and damaged dsDNA (e.g., nicked dsDNA) molecules. In some embodiments, the

sample includes single-stranded DNA (ssDNA) molecules. The methods facilitate the collection of information, including strand-pairing and connectivity information, from dsDNA, ssDNA and damaged DNA (e.g., nicked DNA) molecules in a sample, thereby providing enhanced diagnostic information as compared to sequencing libraries that are prepared using conventional methods. Additionally or alternatively, detection of a genetic biomarker can include preparing a single stranded DNA (ssDNA) library for sequencing. For example, detection of a genetic biomarker can include using a ssDNA library preparation wherein both the forward (sense) and reverse (antisense) strands of a double stranded DNA fragment are tagged with an identical, or substantially identical, unique sequence tag (e.g., a partition-specific barcode or UMI) that allows for the complementary strands from a dsDNA molecule to be identified and analyzed. In one embodiment, the method comprises preparing a single-stranded DNA library for sequencing, the method comprising the following steps: (a) obtaining a test sample comprising double stranded DNA (dsDNA) and isolating dsDNA from the test sample; (b) partitioning the dsDNA sample into a plurality of individual reaction compartments; (c) adding a reaction mixture to each of said individual reaction compartments, said reaction mixture including a plurality of oligonucleotide comprising a unique sequence tag; (d) denaturing dsDNA to produce single-strand DNA (ssDNA) fragments; and (e) ligating unique sequence tags to the ssDNA fragments. In another embodiment, a method is provided for preparing a cell-free DNA library for sequencing, the method comprising the following steps: (a) obtaining a test sample comprising cell-free double stranded DNA (dsDNA) and isolating dsDNA from the test sample; (b) partitioning the dsDNA sample into a plurality of individual reaction droplets; (c) adding a reaction mixture to each of said individual droplets, said reaction mixture including a plurality of DNA capture beads, wherein each of said DNA capture beads includes a plurality of attached oligonucleotides comprising unique sequence tag; (d) heating the droplets to denature the dsDNA or chemically denaturing the dsDNA to produce single-strand DNA (ssDNA) fragments and to release the unique sequence tags from the beads; and (e) ligating the unique sequence tags to 3′ ends of the ssDNA fragments. In some embodiments, said beads are selected from the group comprising streptavidin-coated beads, solid phase reversible immobilization (SPRI) bead, and magnetic beads. In another embodiment, a method is provided for preparing a single-stranded DNA library for sequencing,

the method comprising the following steps: (a) providing a plurality of partitions, wherein individual partitions of the plurality comprise: (i) a portion of a test sample comprising, e.g., damaged and/or undamaged, double stranded DNA (dsDNA) isolated from one or more individuals; and (ii) a plurality of oligonucleotides, wherein the plurality of oligonucleotides comprise a partition-specific barcode; (b) incubating the partitions under conditions suitable to denature the double-stranded DNA into single-stranded DNA; and (c) ligating the single-stranded DNA to the oligonucleotides, wherein the ligating covalently links the partition-specific barcode to the single-stranded DNA and produces partition-specific barcoded single-stranded DNA. In some embodiments, the method further comprises combining the plurality of partitions. In some embodiments, the method further comprises hybridizing oligonucleotide primer to the partition-specific barcoded single-stranded DNA and extending the primer, thereby producing partition-specific barcoded double-stranded DNA. In some embodiments, the method comprises amplifying the partition-specific barcoded single-stranded DNA and/or the partition-specific barcoded double-stranded DNA. In some embodiments, the method further comprises dephosphorylating the double stranded DNA isolated from one or more individuals. In some embodiments, the method comprises dephosphorylating the double stranded DNA isolated from one or more individuals and then partitioning the double stranded DNA isolated from one or more individuals, thereby providing the plurality of partitions.

[461] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0087105, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing and analyzing a sequencing library from a mixed cell-free DNA (cfDNA) sample, wherein the mixed sample includes double-stranded DNA (dsDNA), damaged dsDNA (e.g., nicked dsDNA), and single-stranded DNA (ssDNA) molecules. The subject methods facilitate the collection of information from dsDNA, ssDNA and damaged DNA (e.g., nicked DNA) molecules in a sample, thereby providing enhanced diagnostic information as compared to sequencing libraries that are prepared from dsDNA alone. In some embodiments, the method comprise preparing a combined cell-free DNA (cfDNA) sequencing library from a mixed cfDNA sample by: ligating a universal adapter comprising a unique sequence tag to at least one single-stranded

DNA (ssDNA) molecule in the mixed cfDNA sample; extending the universal adapter to generate an ssDNA-derived double-stranded DNA (dsDNA) molecule; and generating a combined cfDNA sequencing library from the ssDNA-derived dsDNA molecule. In some embodiments, a method further comprises ligating a sequencing Y-adapter to the ssDNA-derived dsDNA molecule before generating the combined cfDNA sequencing library. In some embodiments, the sequencing Y-adapter comprises a unique sequence tag. In some embodiments, the first and second unique sequence tags are different. In some embodiments, the method further comprises: extending the second sequencing Y-adapter to generate a second nick-derived dsDNA molecule; ligating a third sequencing Y-adapter to the second nick-derived dsDNA molecule; and generating a combined cfDNA sequencing library from the first and the second nick-derived dsDNA molecules. In some embodiments, the method for preparing a combined cfDNA sequencing library from a mixed cfDNA sample comprises: ligating a first sequencing Y-adapter to a first end of a nicked dsDNA molecule in the mixed cfDNA sample, wherein the nicked dsDNA molecule comprises a nicked strand and an unnicked strand; ligating a second sequencing Y-adapter to a second end of the nicked dsDNA molecule in the mixed cfDNA sample; denaturing the sequencing Y-adapter-ligated nicked dsDNA molecule to generate a first ssDNA molecule derived from the unnicked strand, a second ssDNA molecule derived from the nicked strand, and a third ssDNA molecule derived from the nicked strand; extending the second sequencing Y-adapter to generate a first nick-derived dsDNA molecule; ligating a third sequencing Y-adapter to the first nick-derived dsDNA molecule; and generating a combined cfDNA sequencing library from the first nick-derived dsDNA molecule. In some embodiments, the first sequencing Y-adapter comprises a first unique sequence tag, the second sequencing Y-adapter comprises a second unique sequence tag, and the third sequencing Y-adapter comprises a third unique sequence tag. In some embodiments, the first, second and third unique sequence tags are the same. In some embodiments, the first, second and third unique sequence tags are different. In some embodiments, the first and second unique sequence tags are the same, and the third unique sequence tag is different. In some embodiments, the first and third unique sequence tags are the same, and the second unique sequence tag is different. In some embodiments, the second and third unique sequence tags are the same, and the first unique sequence tag is different.

[462] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0002749, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, compositions, reactions mixtures, kits, and systems for sequencing both RNA and DNA from a single source sample. In some embodiments, RNA is treated so as to differentiate RNA sequences from DNA sequences derived from the same sample. In some embodiments, the RNA and DNA are cell-free polynucleotides. In some embodiments, the methods improve the sensitivity and/or base calling accuracy of sequencing methodologies in the identification of mutations (e.g. rare sequence variants). In some embodiments, the method comprises: (a) obtaining a sample comprising both RNA and DNA; (b) reverse transcribing the RNA to produce cDNA/RNA hybrid molecules; (c) degrading the RNA of the hybrid molecules to produce single-stranded cDNA; (d) preferentially joining a tag oligonucleotide comprising a tag sequence to the single-stranded cDNA in a reaction comprising a single-stranded DNA ligase to produce tagged cDNA; and (e) sequencing the DNA and the tagged cDNA; wherein the reverse transcribing, preferentially joining, and sequencing are performed in the presence of the DNA. In some embodiments, the RNA and DNA are cell-free nucleic acids. Nucleic acids (including cell-free nucleic acids) can be isolated from any of a variety of sources, such as blood, a blood fraction (e.g. serum or plasma), urine, and other bodily fluids. In some embodiments, the reverse transcribing comprises extension of primers comprising a random sequence (e.g. one or more nucleotides selected at random from a set of two or more different nucleotides at one or more positions, with each of the different nucleotides selected at one or more positions represented in a pool of oligonucleotides comprising the random sequence). In some embodiments, the reverse transcribing comprises extension of the cDNA of the hybrid along a template-switch oligonucleotide (TSO), which may comprise a universal switch primer sequence. In some embodiments, the tag oligonucleotide is joined to a 3′ end of the single-stranded cDNA. In some embodiments, the tag oligonucleotide comprises a primer binding sequence. In some embodiments, the sequencing comprises amplifying the tagged cDNA to produce double-stranded tagged cDNA. In some embodiments, amplifying the tagged cDNA comprises extending a primer hybridized to the primer binding sequence. In some embodiments, the

sequencing comprises joining sequencing adapters to the tagged cDNA and the DNA. In some embodiments, the tag oligonucleotide comprises a unique molecular identifier (UMI), wherein each of a plurality of tagged cDNA molecules is distinguishable from others in the plurality of tagged cDNA molecules based on the UMI (e.g. as determined by the sequence of the UMI, optionally in combination with the sequence of the cDNA). In some embodiments, the sample is blood, a blood fraction, plasma, serum, saliva, sputum, urine, semen, transvaginal fluid, cerebrospinal fluid, or stool. In some embodiments, the sample is blood or a blood fraction (e.g. serum or plasma). In some embodiments, the method further comprises using a processor to group RNA-derived sequences separately from DNA-derived sequences based on the presence or absence of the tag sequence, or a complement of the tag sequence. In some embodiments, the method further comprises identifying presence or absence of a condition of a subject (e.g. cancer) based on the RNA-derived sequences and the DNA-derived sequences. In some embodiments, the method further comprises treating the subject based on the RNA-derived sequences and the DNA-derived sequences. In some embodiments, the method comprises: (a) obtaining a sample comprising both RNA and DNA; (b) joining a tag oligonucleotide comprising a tag sequence to the RNA in a reaction comprising an RNA ligase to produce tagged RNA; (c) reverse transcribing the tagged RNA to produce tagged cDNA; and (d) sequencing the DNA and the tagged cDNA; wherein the joining, reverse transcribing, and sequencing are performed in the presence of the DNA. In some embodiments, the RNA and DNA are cell-free nucleic acids. In some embodiments, the method further comprises fragmenting the RNA to produce fragmented RNA prior to joining the tag sequence. In some embodiments, the fragmented RNA have an average size within a pre-defined range (e.g. an average or median length from about 10 to about 1,000 nucleotides in length, such as between 10-800, 10-500, 50-500, 90-200, or 50-150 nucleotides; or an average or median length of less than 1500, 1000, 750, 500, 400, 300, 250, or fewer nucleotides in length). In some embodiments, fragmenting the RNA comprises subjecting the RNA and DNA to conditions that preferentially fragment the RNA. In some embodiments, fragmenting the RNA comprises sonication, chemical fragmentation, or heating. In some embodiments, the method further comprises dephosphorylating 3′ ends of fragmented RNA. In some embodiments, the tag oligonucleotide is joined to a 3′ end of the RNA. In some embodiments, the tag oligonucleotide

comprises a primer binding sequence. In some embodiments, the reverse transcribing comprises extending a primer hybridized to the primer binding sequence. In some embodiments, the reverse transcribing comprises extension of the tagged cDNA along a template-switch oligonucleotide (TSO), which may comprise a universal switch primer sequence. In some embodiments, the sequencing comprises amplifying the tagged cDNA to produce double-stranded tagged cDNA. In some embodiments, the sequencing comprises joining sequencing adapters to the tagged cDNA and the DNA. In some embodiments, the tag oligonucleotide comprises a unique molecular identifier (UMI), wherein each of a plurality of tagged cDNA molecules is distinguishable from others in the plurality of tagged cDNA molecules based on the UMI (e.g. as determined by the sequence of the UMI, optionally in combination with the sequence of the cDNA). In some embodiments, the sample is blood, a blood fraction, plasma, serum, saliva, sputum, urine, semen, transvaginal fluid, cerebrospinal fluid, or stool. In some embodiments, the sample is blood or a blood fraction (e.g. serum or plasma). In some embodiments, the reverse transcribing comprises extension of primers comprising a random sequence. In some embodiments, the method further comprises using a processor to group RNA-derived sequences separately from DNA-derived sequences based on the presence or absence of the tag sequence, or a complement of the tag sequence. In some embodiments, the method further comprises identifying presence or absence of a condition of a subject (e.g. cancer) based on the RNA-derived sequences and the DNA-derived sequences. In some embodiments, the method further comprises treating the subject based on the RNA-derived sequences and the DNA-derived sequences.

[463] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/218512, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for enriching a plurality of target nucleic acids in a sample, the methods comprising providing an endonuclease system, wherein each of the plurality of target nucleic acids comprises a first variant and a second variant, wherein the endonuclease system comprises a plurality of clustered regularly interspaced short palindromic repeat (CRISPR) RNAs (crRNAs), or derivatives thereof, each crRNA comprising a targeting sequence, and a plurality of CRISPR-associated (Cas) proteins, or variants thereof, each Cas

protein capable of binding to a protospacer adjacent motif (PAM) site on a target nucleic acid, wherein the first variant of each target nucleic acid comprises a PAM site adjacent to a region complementary to a crRNA targeting sequence, and wherein the second variant does not comprise the PAM site or does not comprise the region complementary to the crRNA targeting sequence adjacent to the PAM site, and contacting the sample with the endonuclease system, thereby depleting the first variant and enriching the second variant of each of the plurality of target nucleic acids in the sample. In some embodiments, the first variant of each target nucleic acid comprises a PAM site adjacent to a region complementary to a crRNA targeting sequence, and the second variant does not comprise the PAM site. In some embodiments, the first variant of each target nucleic acid comprises a PAM site adjacent to a region complementary to a crRNA targeting sequence, and the second variant does not comprise the region complementary to the crRNA targeting sequence adjacent to the PAM site. In some embodiments, the first variant of each target nucleic acid comprises a PAM site adjacent to a region complementary to a crRNA targeting sequence, and the second variant does not comprise the region complementary to the crRNA targeting sequence. In some embodiments, the methods comprise amplifying the enriched second variants of the plurality of target nucleic acids to produce an enriched sequencing library. In some embodiments, the methods comprise sequencing the enriched sequencing library to detect structural rearrangements or mutations in the target nucleic acids in the sample.

[464] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/127741, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for high fidelity sequencing and identification of rare nucleic acid variants. The systems and methods may be used to identify rare variants in cell-free nucleic acid samples such as tumor specific mutations among a sample comprising a normal genomic nucleic acid majority. The systems and methods allow for the confident identification of mutations occurring at frequencies below 1 : 10,000 in a sample. Identification of such rare variants results from optimization of several steps in the sequencing process followed by analysis of sequencing reads based on aligned read pairs referred to as ensembles. The systems and methods may find applications outside of rare variant

identification such as sequencing optimization for a desired level of performance or sensitivity. The methods include sequencing nucleic acid. Steps of the method may include obtaining sequencing reads of a nucleic acid, identifying an ensemble comprising two or more sequencing reads with shared start coordinates and read lengths, determining a number of sequenced molecules comprised by the ensemble, identifying a candidate variant in the ensemble, and determining a likelihood of the candidate variant being a true variant using a likelihood estimation model and the determined number of sequenced molecules. In certain embodiments, the step of obtaining sequencing reads may further comprise preparing a sequencing library from the nucleic acid, amplifying the sequencing library, and sequencing the sequencing library using next generation sequencing (NGS). In certain embodiments, adapters may be ligated to the nucleic acid under conditions configured to allow adapter stacking. The preparation of the sequencing library may comprise ligating adapters to the nucleic acid at a temperature of about 16 degrees Celsius using a reaction time of about 16 hours. The amplification step may comprise PCR amplification and the methods may further comprise selecting an over-amplification factor and a PCR cycle number required to detect variants at a specified concentration in a sample using an in-silico model. In various embodiments, the methods include designing a hybrid capture panel to target a genomic region based on factors comprising, guanine-cytosine (GC) content, mutation frequency in a target population, and sequence uniqueness and capturing the amplified nucleic acid using the hybrid capture panel before the sequencing step. The capturing step may include using a first hybrid capture panel targeting a sense strand of a target loci and a second hybrid capture panel targeting an antisense strand of the target loci. In certain embodiments, a synthetic nucleic acid control, also referred to as control sequence, control spike-in, or positive control, may be added to the nucleic acid before amplification of the sequencing library and error rate may then be determined using sequencing reads of the synthetic nucleic acid control. The synthetic nucleic acid control may comprise a known sequence having low diversity across a species from which the nucleic acid is derived and having a plurality of non-naturally occurring mismatches to the known sequence and, in certain embodiments, the plurality of non-naturally occurring mismatches can be 4. The synthetic nucleic acid control may include a guanine-cytosine (GC) content distribution that is representative of the target loci of the hybrid capture panel or may

include a plurality of nucleic acids comprising varying overlaps with a pull down probe of the hybrid capture panel. Error rate or candidate variant frequency may be determined using sequencing reads of the synthetic nucleic acid control.

[465] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,902,992, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for detecting copy number variation comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide are optionally attached to unique barcodes; b) filtering out reads that fail to meet a set threshold; c) mapping sequence reads obtained from step (a) to a reference sequence; d) quantifying/counting mapped reads in two or more predefined regions of the reference sequence; e) determining a copy number variation in one or more of the predefined regions by (i) normalizing the number of reads in the predefined regions to each other and/or the number of unique barcodes in the predefined regions to each other; and (ii) comparing the normalized numbers obtained in step (i) to normalized numbers obtained from a control sample. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a rare mutation in a cell-free or substantially cell free sample obtained from a subject comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; b) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; c) filtering out reads that fail to meet a set threshold; d) mapping sequence reads derived from the sequencing onto a reference sequence; e) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; f) for each mappable base position, calculating a ratio of (a) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (b) a number of total sequence reads for each mappable base position; g) normalizing the ratios or frequency of variance for each mappable base position and determining potential rare variant(s) or mutation(s); h) and

comparing the resulting number for each of the regions with potential rare variant(s) or mutation(s) to similarly derived numbers from a reference sample. Additionally or alternatively, detection of a genetic biomarker can include a method of characterizing the heterogeneity of an abnormal condition in a subject, the method comprising generating a genetic profile of extracellular polynucleotides in the subject, wherein the genetic profile comprises a plurality of data resulting from copy number variation and/or other rare mutation (e.g., genetic alteration) analyses. In some embodiments, the prevalence/concentration of each rare variant identified in the subject is reported and quantified simultaneously. In other embodiments, a confidence score, regarding the prevalence/concentrations of rare variants in the subject, is reported. In some embodiments, extracellular polynucleotides comprise DNA. In other embodiments, extracellular polynucleotides comprise RNA. Polynucleotides may be fragments or fragmented after isolation. Additionally or alternatively, detection of a genetic biomarker can include a method for circulating nucleic acid isolation and extraction. In some embodiments, extracellular polynucleotides are isolated from a bodily sample that may be selected from a group consisting of blood, plasma, serum, urine, saliva, mucosal excretions, sputum, stool and tears. In some embodiments, the methods also comprise a step of determining the percent of sequences having copy number variation or other rare genetic alteration (e.g., sequence variants) in said bodily sample. In some embodiments, the percent of sequences having copy number variation in said bodily sample is determined by calculating the percentage of predefined regions with an amount of polynucleotides above or below a predetermined threshold. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a rare mutation in a cell-free or a substantially cell free sample obtained from a subject comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotides generate a plurality of sequencing reads; b) filtering out reads that fail to meet a set threshold; c) mapping sequence reads derived from the sequencing onto a reference sequence; d) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; e) for each mappable base position, calculating a ratio of (a) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (b) a number of total sequence reads for each mappable base position; f) normalizing the ratios or frequency

of variance for each mappable base position and determining potential rare variant(s) or other genetic alteration(s); and g) comparing the resulting number for each of the regions. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a. providing at least one set of tagged parent polynucleotides, and for each set of tagged parent polynucleotides; b. amplifying the tagged parent polynucleotides in the set to produce a corresponding set of amplified progeny polynucleotides; c. sequencing a subset (including a proper subset) of the set of amplified progeny polynucleotides, to produce a set of sequencing reads; and d. collapsing the set of sequencing reads to generate a set of consensus sequences, each consensus sequence corresponding to a unique polynucleotide among the set of tagged parent polynucleotides. In certain embodiments, the method further comprises: e. analyzing the set of consensus sequences for each set of tagged parent molecules.

[466] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/064629, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a bait set panel comprising one or more bait sets that selectively enrich for one or more nucleosome-associated regions of a genome, said nucleosome-associated regions comprising genomic regions having one or more genomic base positions with differential nucleosomal occupancy, wherein the differential nucleosomal occupancy is characteristic of a cell or a tissue type of origin or a disease state. In some embodiments, each of the one or more nucleosome-associated regions of a bait set panel comprise at least one of: (i) significant structural variation, comprising a variation in nucleosomal positioning, said structural variation selected from the group consisting of: an insertion, a deletion, a translocation, a gene rearrangement, methylation status, a micro-satellite, a copy number variation, a copy number-related structural variation, or any other variation which indicates differentiation; and (ii) instability, comprising one or more significant fluctuations or peaks in a genome partitioning map indicating one or more locations of nucleosomal map disruptions in a genome. In some embodiments, the one or more bait sets of a bait set panel are configured to capture nucleosome-associated regions of the genome based on a function of a plurality of reference nucleosomal occupancy profiles (i) associated with one or more disease states and one or more non-disease states; (ii) associated with a known

somatic mutation, such as SNV, CNV, indel, or re-arrangement; and/or (iii) associated with differential expression patterns. In an embodiment, the one or more bait sets of a bait set panel selectively enrich for one or more nucleosome-associated regions in a cell-free deoxyribonucleic acid (cfDNA) sample. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching a nucleic acid sample for nucleosome-associated regions of a genome comprising (a) bringing a nucleic acid sample in contact with a bait set panel, said bait set panel comprising one or more bait sets that selectively enrich for one or more nucleosome-associated regions of a genome; and (b) enriching the nucleic acid sample for one or more nucleosome-associated regions of a genome. Additionally or alternatively, detection of a genetic biomarker can include a method for generating a bait set comprising (a) identifying one or more regions of a genome, said regions associated with a nucleosome profile, and (b) selecting a bait set to selectively capture said regions. In an embodiment, a bait set in a bait set panel selectively enriches for one or more nucleosome- associated regions in a cell-free deoxyribonucleic acid sample. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching for multiple genomic regions comprising bringing a predetermined amount of a nucleic acid sample in contact with a bait panel comprising (i) a first bait set that selectively hybridizes to a first set of genomic regions of the nucleic acid sample, provided at a first concentration ratio that is less than a saturation point of the first bait set, and (ii) a second bait set that selectively hybridizes to a second set of genomic regions of the nucleic acid sample, provided at a second concentration ratio that is associated with a saturation point of the second bait set; and enriching the nucleic acid sample for the first set of genomic regions and the second set of genomic regions. Additionally or alternatively, detection of a genetic biomarker can include a method for improving accuracy of detecting an insertion or deletion (indel) from a plurality of sequence reads derived from cell- free deoxyribonucleic acid (cfDNA) molecules in a bodily sample of a subject, which plurality of sequence reads are generated by nucleic acid sequencing, comprising (a) for each of the plurality of sequence reads associated with the cell-free DNA molecules, providing: a predetermined expectation of an indel being detected in one or more sequence reads of the plurality of sequence reads; a predetermined expectation that a detected indel is a true indel present in a given cell-free DNA molecule of the cell-free DNA molecules, given that an indel

has been detected in the one or more of the sequence reads; and a predetermined expectation that a detected indel is introduced by non-biological error, given that an indel has been detected in the one or more of the sequence reads; (b) providing quantitative measures of one or more model parameters characteristic of sequence reads generated by nucleic acid sequencing; (c) detecting one or more candidate indels in the plurality of sequence reads associated with the cell-free DNA molecules; and (d) for each candidate indel, performing a hypothesis test using one or more of the model parameters to classify said candidate indel as a true indel or an introduced indel, thereby improving accuracy of detecting an indel. Additionally or alternatively, detection of a genetic biomarker can include a kit comprising (a) a sample comprising a predetermined amount of DNA; and (b) a bait set panel comprising (i) a first bait set that selectively hybridizes to a first set of genomic regions of a nucleic acid sample comprising a predetermined amount of DNA, provided at a first concentration ratio that is less than a saturation point of the first bait set and (ii) a second bait set that selectively hybridizes to a second set of genomic regions of the nucleic acid sample, provided at a second concentration ratio that is associated with a saturation point of the second bait set. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching for multiple genomic regions, comprising: (a) bringing a predetermined amount of nucleic acid from a sample in contact with a bait mixture comprising (i) a first bait set that selectively hybridizes to a first set of genomic regions of the nucleic acid from the sample, which first bait set is provided at a first concentration that is less than a saturation point of the first bait set, and (ii) a second bait set that selectively hybridizes to a second set of genomic regions of the nucleic acid sample, which second bait set is provided at a second concentration that is associated with a saturation point of the second bait set; and (b) enriching the nucleic acid sample for the first set of genomic regions and the second set of genomic regions. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching multiple genomic regions, comprising: (a) bringing a predetermined amount of nucleic acid from a sample in contact with a bait mixture comprising: (i) a first bait set that selectively hybridizes to a first set of genomic regions of the nucleic acid from the sample, which first bait set is provided at a first concentration that is less than a saturation point of the first bait set, and (ii) a second bait set that selectively hybridizes to a second set of genomic regions of the nucleic

acid from the sample, which second bait set is provided at a second concentration that is at or above a saturation point of the second bait set; and (b) enriching the nucleic acid from the sample for the first set of genomic regions and the second set of genomic regions, thereby producing an enriched nucleic acid.

[467] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,790,559, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for detecting copy number variation comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide are optionally attached to unique barcodes; b) filtering out reads that fail to meet a set threshold; c) mapping sequence reads obtained from step (a) to a reference sequence; d) quantifying/counting mapped reads in two or more predefined regions of the reference sequence; e) determining a copy number variation in one or more of the predefined regions by (i) normalizing the number of reads in the predefined regions to each other and/or the number of unique barcodes in the predefined regions to each other; and (ii) comparing the normalized numbers obtained in step (i) to normalized numbers obtained from a control sample. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a rare mutation in a cell-free or substantially cell free sample obtained from a subject comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotides generate a plurality of sequencing reads; b) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; c) filtering out reads that fail to meet a set threshold; d) mapping sequence reads derived from the sequencing onto a reference sequence; e) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; f) for each mappable base portion, calculating a ratio of (a) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (b) a number of total sequence reads for each mappable base position, g) normalizing the ratios or frequency of variance for

each mappable base position and determining potential rare variant(s) or mutation(s); h) and comparing the resulting number for each of the regions with potential rare variant(s) or mutation(s) to similarly derived numbers from a reference sample. Additionally or alternatively, detection of a genetic biomarker can include a method of characterizing the heterogeneity of an abnormal condition in a subject, the method comprising generating a genetic profile of extracellular polynucleotides in the subject, wherein the genetic profile comprises a plurality of data resulting from copy number variation and/or other rare mutation (e.g., genetic alteration) analyses. Additionally or alternatively, detection of a genetic biomarker can include a system comprising a computer readable medium for performing the following steps: selecting predefined regions in a genome; enumerating number of sequence reads in the predefined regions; normalizing the number of sequence reads across the predefined regions, and determining percent of copy number variation in the predefined regions. In some embodiments, the entirety of the genome or at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the genome is analyzed. In some embodiments, computer readable medium provides data in percent cancer DNA or RNA in plasma or serum to the end user. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a rare mutation in a cell-free or a substantially cell free sample obtained from a subject comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotides generate a plurality of sequencing reads; b) filtering out reads that fail to meet a set threshold; c) mapping sequence reads derived from the sequencing onto a reference sequence; d) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; e) for each mappable base position, calculating a ratio of (a) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (b) a number of total sequence reads tor each mappable base position; f) normalizing the ratios or frequency of variance for each mappable base position and determining potential rare variant(s) or other genetic alteration(s); and g) comparing the resulting number for each of the regions. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a. providing at least one set of tagged parent polynucleotides, and for each set of tagged parent polynucleotides; b. amplifying the tagged parent polynucleotides in the set to produce a

corresponding set of amplified progeny polynucleotides; c. sequencing a subset (including a proper subset) of the set of amplified progeny polynucleotides, to produce a set of sequencing reads; and d. collapsing the set of sequencing reads to generate a set of consensus sequences, each consensus sequence corresponding to a unique polynucleotide among the set of tagged parent polynucleotides. In certain embodiments, the method further comprises; e. analyzing the set of consensus sequences for each set of tagged parent molecules. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a. providing at least one set of tagged parent polynucleotides, and for each set of tagged parent polynucleotides; b. amplifying the tagged parent polynucleotides in the set to produce a corresponding set of amplified progeny polynucleotides; c. sequencing a subset (including a proper subset) of the set of amplified progeny polynucleotides, to produce a set of sequencing reads; d. collapsing the set of sequencing reads to generate a set of consensus sequences, each consensus sequence corresponding to a unique polynucleotide among the set of tagged parent polynucleotides; and e. filtering out from among the consensus sequences those that fail to meet a quality threshold. In one embodiment, the quality threshold considers a number of sequence reads from amplified progeny polynucleotides collapsed into a consensus sequence. In another embodiment, the quality threshold considers a number of sequence reads from amplified progeny polynucleotides collapsed into a consensus sequence. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a. providing at least one set of tagged parent polynucleotides, wherein each set maps to a different reference sequence in one or more genomes, and, for each set of tagged parent polynucleotides; i. amplifying the first polynucleotides to produce a set of amplified polynucleotides; ii. sequencing a subset of the set of amplified polynucleotides, to produce a set of sequencing reads; and iii. collapsing the sequence reads by: 1. grouping sequences reads sequenced from amplified progeny polynucleotides into families, each family amplified from the same tagged parent polynucleotide. In one embodiment collapsing further comprises: 2. determining a quantitative measure of sequence reads in each family. In another embodiment the method further comprises (including a) including a): b. determining a quantitative measure of unique families; and c. based on (1) the quantitative measure of unique families and (2) the quantitative measure of sequence read in each group, inferring a measure of unique tagged parent

polynucleotides in the set. In another embodiment, inferring is performed using statistical or probabilistic models. In another embodiment, the method further comprises using a control or set of control samples to correct for amplification or representation biases between the two sets. In another embodiment, the method further comprises determining copy number variation between the sets. In another embodiment the method further comprises (including a, b, c): d. determining a quantitative measure of polymorphic forms among the families; and e. based on the determined quantitative measure of polymorphic forms, inferring a quantitative measure of polymorphic forms in the number of inferred unique tagged parent polynucleotides. In another embodiment wherein polymorphic forms include but are not limited to: substitutions, insertions, deletions, inversions, microsatellite changes, transversions, translocations, fusions, methylation, hypermethylation, hydroxymethylation, acetylation, epigenetic variants, regulatory-associated variants or protein binding sites. In another embodiment wherein the sets derive from a common sample, the method further comprising: a. inferring copy number variation for the plurality of sets based on a comparison of the inferred number of tagged parent polynucleotides in each set mapping to each of a plurality of reference sequences. In another embodiment, the original number of polynucleotides in each set is further inferred. Additionally or alternatively, detection of a genetic biomarker can include a system comprising a computer readable medium for performing the aforesaid methods. Additionally or alternatively, detection of a genetic biomarker can include a method of communicating sequence information about at least one individual polynucleotide molecule comprising: a. providing at least one individual polynucleotide molecule; b. encoding sequence information in the at least one individual polynucleotide molecule to produce a signal; c. passing at least part of the signal through a channel to produce a received signal comprising nucleotide sequence information about the at least one individual polynucleotide molecule, wherein the received signal comprises noise and/or distortion; d. decoding the received signal to produce a message comprising sequence information about the at least one individual polynucleotide molecule, wherein decoding reduces noise and/or distortion in the message; and e. providing the message to a recipient. In one embodiment, the noise comprises incorrect nucleotide cells. In another embodiment, distortion comprises uneven amplification of the individual polynucleotide molecule compared with other individual polynucleotide molecules. In another

embodiment distortion results from amplification or sequencing bias. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a rare mutation in a cell-free or substantially cell free sample obtained from a subject comprising: a) sequencing extracellular polynucleotides from a bodily sample from a subject, wherein each of the extracellular polynucleotide generate a plurality of sequencing reads; b) performing multiplex sequencing on regions or whole-genome sequencing if enrichment is not performed; c) filtering out reads that fail to meet a set threshold; d) mapping sequence reads derived from the sequencing onto a reference sequence; e) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; f) for each mappable base position, calculating a ratio of (a) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (b) a number of total sequence reads for each mappable base position; g) normalizing the ratios or frequency of variance for each mappable base position and determining potential rare variant(s) or mutation(s); and h) and comparing the resulting number for each of the regions with potential rare variant(s) or mutation(s) to similarly derived numbers from a reference sample. Additionally or alternatively, detection of a genetic biomarker can include a method of characterizing the heterogeneity of an abnormal condition in a subject, the method comprising generating a genetic profile of extracellular polynucleotides in the subject, wherein the genetic profile comprises a plurality data resulting from copy number variation and rare mutation analyses. Additionally or alternatively, detection of a genetic biomarker can include a method comprising determining copy number variation or performing rare mutation analysis in a cell-free or substantially cell free sample obtained from a subject using multiplex sequencing. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a) providing at least one set of tagged parent polynucleotides, and for each set of tagged parent polynucleotides; b) amplifying the tagged parent polynucleotides in the set to produce a corresponding set of amplified progeny polynucleotides; c) sequencing a subset (including a proper subset) of the set of amplified progeny polynucleotides, to produce a set of sequencing reads; d) collapsing the set of sequencing reads to generate a set of consensus sequences, each consensus sequence corresponding to a unique polynucleotide among the set

of tagged parent polynucleotides; and e) filtering out from among the consensus sequences those that fail to meet a quality threshold.

[468] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,700,286, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a cancer detection assay in plasma/serum measuring by adding and comparing the amount of DNA and RNA of certain genes in the plasma/serum of cancer patients that are the reflection of a gene amplification and a gene over expression. Thus, gene amplification (seen by more DNA) and gene over expression (more RNA) are linked. Additionally or alternatively, detection of a genetic biomarker can include a method for the diagnosis or the follow up of the evolution of cancers which comprises measuring together gene over expression (RNA) and gene amplification (DNA) in the bodily fluids of patients suspected to harbor cancer on any gene that is both amplified and over expressed in cancer cells and comparing to healthy controls. More particularly, RNA and DNA are extracted from a bodily fluid, such as plasma, serum, sputum, saliva, etc., purified and amplified, and the over expressed RNA and amplified DNA are analyzed and compared to a unique house keeping gene. In some embodiments, the nucleic acids are amplified by reversed transcriptase chain reaction (RT-PCR) and are analyzed by gel coloration, by radioactive immunological technique (RIA), by enzyme linked immunosorbant test (ELISA) or by a microchip test (gene array), and possibly quantified by any method for nucleic acid quantification. In some embodiments, the quantification of RNA and DNA is carried out by real time PCR, such as "TAQMAN™", or on capillaries "LIGHTCYCLER™", or real time PCR and RT PCR of any company. In some embodiments, the genes analyzed may be compared to a reference nucleic acid extract (DNA and RNA) corresponding to the expression (RNA) and quantity (DNA) of a unique house keeping gene, or to a reference RNA corresponding to the expression of a house keeping coding gene, or to a reference DNA corresponding to a unique gene, or may be estimated in reference to a standard curve obtained with nucleic acids of a cell line.

[469] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0195131, which is hereby incorporated by reference in its entirety. For

example, detection of a genetic biomarker can include methods to detect fusion genes, which may be used to detect a disease, such as cancer. Additionally or alternatively, detection of a genetic biomarker can include methods for enrichment of breakpoint fragments, such as to detect and characterize fusion genes, which may be associated with a disease, such as cancer. Additionally or alternatively, detection of a genetic biomarker can include a method for providing a diagnostic or therapeutic intervention to a subject having or suspected of having cancer, comprising (a) providing a biological sample comprising cell-free nucleic acid molecules from a subject; (b) contacting the cell-free nucleic acid molecules from the biological sample with a probe set under hybridization conditions sufficient to produce probe-captured polynucleotides, which probe set comprises a plurality of polynucleotide probes, wherein each of the plurality of polynucleotide probes has (i) sequence complementarity with a fusion gene and (ii) affinity for the fusion gene that is greater than a polynucleotide having sequence complementary with the fusion gene and containing only unmodified nucleotides; (c) isolating the probe-captured polynucleotides from the mixture, to produce a sample enriched with isolated polynucleotides comprising breakpoint fragments of the fusion gene; (d) sequencing the isolated polynucleotides to produce sequences; (e) detecting polynucleotides comprising breakpoints of fusion genes based on the sequences; and (f) providing the diagnostic or therapeutic intervention based on the detection of breakpoint fragments. Additionally or alternatively, detection of a genetic biomarker can include a method for capturing a breakpoint fragment of a fusion gene, comprising (a) providing a biological sample containing or suspected of containing a cell-free nucleic acid molecule comprising the breakpoint fragment of the fusion gene; and (b) contacting the biological sample with a polynucleotide probe under conditions sufficient to (i) permit hybridization between the polynucleotide probe and the breakpoint fragment to provide a probe-captured polynucleotide in a mixture, which polynucleotide probe has sequence complementarity with the breakpoint fragment and has affinity for the fusion gene that is greater than a polynucleotide having sequence complementary with the fusion gene and containing only unmodified nucleotides; and (ii) enrichment or isolation of the probe-captured polynucleotide from the mixture, wherein the polynucleotide probe has sequence complementarity with the breakpoint fragment. Additionally or alternatively, detection of a genetic biomarker can include a probe set

comprising a plurality of polynucleotide probes, wherein each of the polynucleotide probes has (i) sequence complementarity with a fusion gene as part of a cell-free nucleic acid molecule and (ii) affinity for the fusion gene that is greater than a polynucleotide having sequence complementary with the fusion gene and containing only unmodified nucleotides. Additionally or alternatively, detection of a genetic biomarker can includes a high affinity polynucleotide, comprising a sequence that is configured to specifically hybridize to a nucleic acid sequence associated with a fusion gene in a cell-free nucleic acid molecule. Additionally or alternatively, detection of a genetic biomarker can include a high affinity polynucleotide configured to specifically hybridize to a fusion gene. In one embodiment, the high affinity polynucleotide comprises one or more locked nucleic acid nucleotides. In another embodiment the high affinity polynucleotide has a melting temperature that is at least any of 1° C., 2° C., 3° C., 4° C., 5° C., 10° C., 15° C. or 20° C. higher than a polynucleotide with the same sequence comprising only natural nucleotides. In another embodiment, the high affinity polynucleotide has a melting temperature that is at least any of 2%, 4%, 6%, 8%, or 10% higher than a polynucleotide with the same sequence comprising only natural nucleotides. In another embodiment, the high affinity polynucleotide is configured to specifically hybridize to a cancer fusion gene. Additionally or alternatively, detection of a genetic biomarker can include a high affinity polynucleotide probe comprising a high affinity polynucleotide configured to specifically hybridize to a fusion gene. In one embodiment, the high affinity polynucleotide comprises one or more locked nucleic acid nucleotides. In another embodiment, the probe comprises a functionality selected from a detectable label, a binding moiety or a solid support. In another embodiment, the probe is configured to hybridize to a breakpoint fragment of a fusion gene. In another embodiment, the breakpoint fragment has a length between about 140 nucleotides and about 180 nucleotides. In another embodiment the fragment is cell-free deoxyribonucleic acid (DNA) or genomic DNA. In another embodiment, the high affinity polynucleotide is bound to a solid support. Additionally or alternatively, detection of a genetic biomarker can include a method for capturing a breakpoint fragment of a fusion gene comprising contacting the breakpoint fragment with a high affinity polynucleotide probe under stringent hybridization conditions and allowing hybridization, wherein the polynucleotide probe is bound to a solid support and wherein the polynucleotide probe has a nucleotide

sequence that is substantially or perfectly complementary to a nucleotide sequence of the breakpoint fragment. In one embodiment, the high affinity polynucleotide comprises one or more locked nucleic acid nucleotides. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching a sample for polynucleotides comprising a breakpoint of a fusion gene, comprising: a) contacting a probe set of claim 20 with a mixture of polynucleotides under hybridization conditions to produce probe-captured polynucleotides; and b) isolating the probe-captured polynucleotides from the mixture, to produce a sample enriched with polynucleotides comprising breakpoint fragments of the fusion gene. In one embodiment, the high affinity polynucleotide comprises one or more locked nucleic acid nucleotides. In another embodiment, the polynucleotides comprise cell-free DNA or fragmented genomic DNA. In another embodiment, the method further comprises isolating captured polynucleotides from the probes. In another embodiment, the method further comprises sequencing the isolated polynucleotides. Additionally or alternatively, detection of a genetic biomarker can include a method of diagnosing cancer in a subject comprising: a) providing a sample comprising polynucleotides from a subject; b) contacting the cell-free DNA (cfDNA) from the sample with a probe set of claim 20 under hybridization conditions to produce probe-captured polynucleotides; c) isolating the probe-captured polynucleotides from the mixture, to produce a sample enriched with polynucleotides comprising breakpoint fragments of the fusion gene; d) sequencing the isolated polynucleotides to produce sequences; e) detecting polynucleotides comprising breakpoints of fusion genes based on the sequences; and f) diagnosing cancer based on the detection of breakpoint fragments. In one embodiment, the high affinity polynucleotide comprises one or more locked nucleic acid nucleotides.

[470] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0120291, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for analyzing a disease state of a subject, comprising (a) using a genetic analyzer to generate genetic data from nucleic acid molecules in biological samples of the subject obtained at (i) two or more time points or (ii) substantially the same time point, wherein the genetic data relates to genetic information of the subject, and wherein the biological samples include a cell-free biological sample; (b) receiving

the genetic data from the genetic analyzer; (c) with one or more programmed computer processors, using the genetic data to produce an adjusted test result in a characterization of the genetic information of the subject; and (d) outputting the adjusted test result into computer memory. In some embodiments, the genetic data comprises current sequence reads and prior sequence reads, and wherein (c) comprises comparing the current sequence reads with the prior sequence reads and updating a diagnostic confidence indication accordingly with respect to the characterization of the genetic information of the subject, which diagnostic confidence indication is indicative of a probability of identifying one or more genetic variations in a biological sample of the subject. In some embodiments, the method further comprises obtaining a subsequent characterization and leaving as is a diagnostic confidence indication in the subsequent characterization for de novo information. In some embodiments, the method further comprises determining a frequency of one or more genetic variants detected in a collection of sequence reads included in the genetic data and producing the adjusted test result at least in part by comparing the frequency of the one or more genetic variants at the two or more time points. In some embodiments, the method further comprises determining an amount of copy number variation at one or more genetic loci detected in a collection of sequence reads included in the genetic data and producing the adjusted test result at least in part by comparing the amount at the two or more time points. In some embodiments, the method further comprises using the adjusted test result to provide (i) a therapeutic intervention or (ii) a diagnosis of a health or disease to the subject. In some embodiments, the genetic data comprises a first set of genetic data and a second set of genetic data, wherein the first set of genetic data is at or below a detection threshold and the second set of genetic data is above the detection threshold. In some embodiments, the detection threshold is a noise threshold. In some embodiments, the method further comprises, in (c), adjusting a diagnosis of the subject from negative or uncertain to positive when the same genetic variants are detected in the first set of genetic data and the second set of genetic data in a plurality of sampling instances or time points. In some embodiments, the method further comprises, in (c), adjusting a diagnosis of the subject from negative or uncertain to positive in a characterization from an earlier time point when the same genetic variants are detected in the first set of genetic data at an earlier time point and in the second set of genetic data at a later time point. Additionally or alternatively, detection of a

genetic biomarker can include a method of detecting a trend in the amount of cancer polynucleotides in a biological sample from a subject over time, comprising determining, using or more programmed computer processors, a frequency of the cancer polynucleotides at each of a plurality of time points; determining an error range for the frequency at each of the plurality of time points to provide at least a first error range at a first time point and a second error range at a second time point subsequent to the first time point; and determining whether (1) the first error range overlaps with the second error range, which overlap is indicative of stability of frequency of the cancer polynucleotides at a plurality of time points, (2) the second error range is greater than the first error range, thereby indicating an increase in frequency of the cancer polynucleotides at a plurality of time points, or (3) the second error range is less than the first error range, thereby indicating a decrease in frequency of the cancer polynucleotides at a plurality of time points. Additionally or alternatively, detection of a genetic biomarker can include a method to detect one or more genetic variations and/or amount of genetic variation in a subject, comprising sequencing nucleic acid molecules in a cell-free nucleic acid sample of the subject with a genetic analyzer to generate a first set of sequence reads at a first time point; comparing the first set of sequence reads with at least a second set of sequence reads obtained at least at a second time point before the first time point to yield a comparison of first set of sequence reads and the at least the second set of sequence reads; using the comparison to update a diagnostic confidence indication accordingly, which diagnostic confidence indication is indicative of a probability of identifying one or more genetic variations in a cell-free nucleic acid sample of the subject; and detecting a presence or absence of the one or more genetic variations and/or amount of genetic variation in nucleic acid molecules in a cell-free nucleic acid sample of the subject based on the diagnostic confidence indication. In some embodiments, the method further comprises obtaining the cell-free nucleic acid Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a mutation in a cell-free nucleic acid sample of a subject, comprising: (a) determining consensus sequences by comparing current sequence reads obtained from a genetic analyzer with prior sequence reads from a prior time period to yield a comparison, and updating a diagnostic confidence indication based on the comparison, wherein each consensus sequence corresponds to a unique polynucleotide among a set of tagged parent polynucleotides

derived from the cell-free nucleic acid sample, and (b) based on the diagnostic confidence, generating a genetic profile of extracellular polynucleotides in the subject, wherein the genetic profile comprises data resulting from copy number variation or mutation analyses. Additionally or alternatively, detection of a genetic biomarker can include a method to detect abnormal cellular activity, comprising: providing at least one set of tagged parent polynucleotides derived from a biological sample of a subject; amplifying the tagged parent polynucleotides in the set to produce a corresponding set of amplified progeny polynucleotides; using a genetic analyzer to sequence a subset of the set of amplified progeny polynucleotides to produce a set of sequencing reads; and collapsing the set of sequencing reads to generate a set of consensus sequences by comparing current sequence reads with prior sequence reads from at least one prior time period and updating a diagnostic confidence indication accordingly, which diagnostic confidence indication is indicative of a probability of identifying one or more genetic variations in a biological sample of the subject, wherein each consensus sequence corresponds to a unique polynucleotide among the set of tagged parent polynucleotides. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a mutation in a cell-free or substantially cell free sample of a subject comprising: (a) sequencing extracellular polynucleotides from a bodily sample of the subject with a genetic analyzer; (b) for each of the extracellular polynucleotides, generating a plurality of sequencing reads; (c) filtering out reads that fail to meet a set threshold; (d) mapping sequence reads derived from the sequencing onto a reference sequence; (e) identifying a subset of mapped sequence reads that align with a variant of the reference sequence at each mappable base position; (f) for each mappable base position, calculating a ratio of (i) a number of mapped sequence reads that include a variant as compared to the reference sequence, to (ii) a number of total sequence reads for each mappable base position; and (g) using one or more programmed computer processors to compare the sequence reads with other sequence reads from at least one previous time point and updating a diagnostic confidence indication accordingly, which diagnostic confidence indication is indicative of a probability of identifying the variant. Additionally or alternatively, detection of a genetic biomarker can include a method for operating a genetic test equipment, comprising: providing initial starting genetic material obtained from a bodily sample obtained from a subject; converting double stranded

polynucleotide molecules from the initial starting genetic material into at least one set of non-uniquely tagged parent polynucleotides, wherein each polynucleotide in a set is mappable to a reference sequence; and for each set of tagged parent polynucleotides: (i) amplifying the tagged parent polynucleotides in the set to produce a corresponding set of amplified progeny polynucleotides; (ii) sequencing the set of amplified progeny polynucleotides to produce a set of sequencing reads; (iii) collapsing the set of sequencing reads to generate a set of consensus sequences, wherein collapsing uses sequence information from a tag and at least one of: (1) sequence information at a beginning region of a sequence read, (2) an end region of the sequence read and (3) length of the sequence read, wherein each consensus sequence of the set of consensus sequences corresponds to a polynucleotide molecule among the set of tagged parent polynucleotides; and (iv) analyzing the set of consensus sequences for each set of tagged parent molecules; (v) comparing current sequence reads with prior sequence reads from at least one other time point; and (vi) updating a diagnostic confidence indication accordingly, which diagnostic confidence indication is indicative of a probability of identifying one or more genetic variations in a bodily sample of the subject. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting one or more genetic variants in a subject, comprising: (a) obtaining nucleic acid molecules from one or more cell-free biological samples of said subject; (b) assaying said nucleic acid molecules to produce a first set of genetic data and a second set of genetic data, wherein said first set of genetic data and/or said second set of genetic data is within a detection threshold; (c) comparing said first set of genetic data to said second set of genetic data to identify said one or more genetic variants in said first set of genetic data or said second set of genetic data; and (d) based on said one or more genetic variants identified in (c), using one or more programmed computer processors to update a diagnostic confidence indication for identifying said one or more genetic variants in a cell-free biological sample of said subject. Additionally or alternatively, detection of a genetic biomarker can include a method for calling a genetic variant in cell-free deoxyribose nucleic acids (cfDNA) from a subject comprising: (a) using a DNA sequencing system to sequence cfDNA from a sample taken at a first time point from a subject; (b) detecting a genetic variant in the sequenced cfDNA from the first time point, wherein the genetic variant is detected at a level below a diagnostic limit; (c) using the DNA sequencing system to sequence cfDNA from

a sample taken from the subject at one or more subsequent time points; (d) detecting the genetic variant in the sequenced cfDNA from the one or more subsequent time points, wherein the genetic variant is detected at level below the diagnostic limit; (e) calling the samples as positive for the genetic variant based on detecting the genetic variant below the diagnostic limit in samples taken at a plurality of the time points. Additionally or alternatively, detection of a genetic biomarker can include a method for calling a genetic variant in cell-free deoxyribose nucleic acids (cfDNA) from a subject comprising: (a) using a deoxyribonucleic acid (DNA) sequencing system to sequence cfDNA from a sample from a subject; (b) detecting a genetic variant in the sequenced cfDNA, wherein the genetic variant is detected at a level below a diagnostic limit; (c) using the DNA sequencing system to sequence cfDNA from the sample taken from the subject, wherein the sample is re-sequenced one or more times; (d) detecting the genetic variant in the sequenced cfDNA from the one or more re-sequenced samples, wherein the genetic variant is detected at level below the diagnostic limit; and (e) calling the samples as positive for the genetic variant based on detecting the genetic variant below the diagnostic limit in re-sequenced samples.

[471] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0240972, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include systems and methods for determining gene fusion by determining a fused read containing sequencing data of at least a portion of a fused chromosome DNA molecule; determining a predetermined point on the genome with least one mapped portion of the fused read clipped at the predetermined point (a breakpoint); identifying two mapped read portions from two breakpoints (breakpoint pair) as a potential fusion candidate; creating one or more fusion sets based on breakpoint pairs and clustering the fusion sets into one or more fusion clusters; and identifying each fusion cluster meeting a predetermined criterion as a gene fusion. Additionally or alternatively, detection of a genetic biomarker can include a method for processing genetic sequence read data from a sample, the method comprising: determining a fused read containing sequencing data of at least a portion of a fused chromosome DNA molecule; determining a predetermined point on the genome with least one mapped portion of the fused read clipped at the predetermined point (a

breakpoint); identifying two mapped read portions from two breakpoints (breakpoint pair) as a potential fusion candidate; creating one or more fusion sets based on breakpoint pairs and clustering the fusion sets into one or more fusion clusters; and identifying each fusion cluster meeting a predetermined criterion as a gene fusion. In some embodiments, the method comprises assigning a unique molecule or read identifier (read ID) to each read. In some embodiments, the method comprises clipping each mapped portion of the reads from one or both sides. In some embodiments, the breakpoints are independent of the reads in identity and are identified by a sign, a chromosome and a position. In some embodiments, the breakpoints keep statistics including a number of reads and molecules that are clipped or split at the breakpoint, and a number of wild-type reads and molecules that pass over the breakpoint. In some embodiments, the method comprises selecting every two mapped read portions with common read IDs that belong to two breakpoints with appropriate signs as a potential fusion candidate. In some embodiments, the potential fusion candidate location in the original read before mapping shows the read portion as originally located next to each other. In some embodiments, the method comprises checking if read portions are mapped on one strand for differences in the breakpoints' signs. In some embodiments, the method comprises tracking fusion set statistics Additionally or alternatively, detection of a genetic biomarker can include a system to analyze genetic information, comprising a DNA sequencer; a processor coupled to the DNA sequencer, the processor running computer code to process genetic sequence read data from a sample, the computer code comprising instructions for: determining a fused read containing sequencing data of a portion of a fused chromosome DNA molecule; determining at least a predetermined point on the genome with least one mapped portion of the fused read clipped at the predetermined point (a breakpoint); identifying two mapped read portions from two breakpoints (breakpoint pair) as a potential fusion candidate; creating one or more fusion sets based on breakpoint pairs and clustering the fusion sets into one or more fusion clusters; and identifying each fusion cluster meeting a predetermined criterion as a gene fusion. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: sequencing DNA molecules with a DNA sequencer to generate a collection of sequences; mapping the collection of sequences to a reference genome; identifying fused reads from the mapped collection, wherein a fused read contains sub-sequences, wherein a first sub-

sequence maps to a first genetic locus and a second sub-sequence maps to a second, distinct genetic locus; for each fused read, identifying a first breakpoint at the first genetic locus and a second breakpoint at the second genetic locus, wherein a breakpoint is a point on the reference genome where a sequence of a fused read is clipped, and wherein the first and second breakpoints form a breakpoint pair; generating sets of fused reads, each set comprising fused reads having the same breakpoint pair; clustering sets of fused reads, wherein each cluster is formed from sets of fused reads having first breakpoints within a first predetermined nucleotide distance and second breakpoints within a second predetermined nucleotide distance; and determining a gene fusion for one or more clusters, wherein a gene fusion for a cluster has, as a first fusion gene breakpoint, a breakpoint selected from the first breakpoints in the cluster and, as a second fusion gene breakpoint, a breakpoint selected from the second breakpoints in the cluster, and wherein the first and second fusion gene breakpoints are each selected based on selection criteria. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: sequencing a plurality of DNA molecules with a DNA sequencer; tagging each of the plurality of sequences molecules with an identifier; mapping each tagged sequence to a reference genome; identifying clipped reads from the mapped tagged sequences, wherein a clipped read is a tagged sequence containing a mapped portion and a clipped portion, wherein the mapped portion maps to a genetic locus and the clipped portion does not map to the genetic locus; determining a breakpoint of each clipped read, wherein a breakpoint is a point on the reference genome where a sequence of a clipped read is clipped; creating breakpoint sets, each breakpoint set comprising identifiers of clipped reads having the same breakpoint; creating sets of breakpoint pairs by comparing pairs of breakpoint sets, each set of breakpoint pairs including identifiers present in both members of a compared pair of breakpoint sets; clustering sets of breakpoint pairs, wherein each cluster includes sets of breakpoint pairs having a first breakpoint of the pair within a first predetermined genetic distance and a second breakpoint of the pair within a second predetermined genetic distance; and determining a gene fusion for one or more of the clusters, wherein a gene fusion for a cluster has, as a first fusion gene breakpoint, a breakpoint selected from the first breakpoints in the cluster and, as a second fusion gene breakpoint, a breakpoint selected from the second breakpoints in the cluster, and wherein the first and second fusion gene breakpoints are each selected based on a selection

criteria. In some embodiments, the selection criteria include the breakpoint having the most fused reads in the cluster. Additionally or alternatively, detection of a genetic biomarker can include a method for identifying a fusion gene breakpoint, the method comprising: determining a fused read containing sequencing data of at least a portion of a fused chromosome DNA molecule; determining a predetermined point on the genome with least one mapped portion of the fused read clipped at the predetermined point (a breakpoint); identifying two mapped read portions from two breakpoints (breakpoint pair) as a potential fusion candidate; creating one or more fusion sets based on breakpoint pairs and clustering the fusion sets into one or more fusion clusters; identifying each fusion cluster meeting a predetermined criterion as a gene fusion, and identifying a breakpoint of the gene fusion as the fusion gene breakpoint. Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosing a condition in a subject, the method comprising: determining a fused read containing sequencing data of at least a portion of a fused chromosome DNA molecule; determining a predetermined point on the genome with least one mapped portion of the fused read clipped at the predetermined point (a breakpoint); identifying two mapped read portions from two breakpoints (breakpoint pair) as a potential fusion candidate; creating one or more fusion sets based on breakpoint pairs and clustering the fusion sets into one or more fusion clusters; and identifying each fusion cluster meeting a predetermined criterion as a gene fusion, wherein said gene fusion is indicative of the condition.

[472] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0240973, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method comprising: (a) obtaining sequencing reads of deoxyribonucleic acid (DNA) molecules of a cell-free bodily fluid sample of a subject; (b) generating from the sequence reads a first data set comprising for each genetic locus in a plurality of genetic loci a quantitative measure related to sequencing read coverage ("read coverage"); (c) correcting the first data set by performing saturation equilibrium correction and probe efficiency correction; (d) determining a baseline read coverage for the first data set, wherein the baseline read coverage relates to saturation equilibrium and probe efficiency; and (e) determining a copy number state for each genetic locus in the plurality of

genetic loci relative to the baseline read coverage. In some embodiments, the first data set comprises, for each genetic locus in a plurality of genetic loci, a quantitative measure related to (i) guanine-cytosine content ("GC content") of the genetic locus. In some embodiments, the method comprises, prior to (c), removing from the first data set genetic loci that are high-variance genetic loci, wherein removing comprises: (i) fitting a model relating the quantitative measures related to guanine-cytosine content and the quantitative measures of sequencing read coverage of the genetic loci; and (ii) removing from the genetic loci at least 10% of the genetic loci, wherein the removing the genetic loci comprises removing genetic loci that most differ from the model, thereby providing the first data set of baselining genetic loci. In some embodiments, the method comprises removing at least 45% of the genetic loci. In some embodiments, determining a copy number state comprises comparing the read coverage of the genetic loci to the baseline read coverage. In some embodiments, the cell-free bodily fluid is selected from the group consisting of serum, plasma, urine, and cerebrospinal fluid. In some embodiments, the read coverage is determined by mapping the sequencing reads to a reference genome. In some embodiments, obtaining the sequencing reads comprises ligating adaptors to the DNA molecules from the cell-free bodily fluid from the subject. In some embodiments, the DNA molecules are duplex DNA molecules and the adaptors are ligated to the duplex DNA molecules such that each adaptor differently tags complementary strands of the DNA molecule to provide tagged strands. In some embodiments, determining the quantitative measure related to the probability that a strand of DNA derived from the genetic locus is represented within the sequencing reads comprises sorting sequencing reads into paired reads and unpaired reads, wherein (i) each paired read corresponds to sequence reads generated from a first tagged strand and a second differently tagged complementary strand derived from a double-stranded polynucleotide molecule in said set, and (ii) each unpaired read represents a first tagged strand having no second differently tagged complementary strand derived from a double-stranded polynucleotide molecule represented among said sequence reads in said set of sequence reads. In some embodiments, the method further comprises determining quantitative measures of (i) said paired reads and (ii) said unpaired reads that map to each of one or more genetic loci to determine a quantitative measure related to total double-stranded DNA molecules in said sample that map to each of said one or more genetic loci based on said quantitative measure

related to paired reads and unpaired reads mapping to each locus. In some embodiments, the adaptors comprise barcode sequences. In some embodiments, determining the read coverage comprises collapsing the sequencing reads based on position of the mapping of the sequencing reads to the reference genome and the barcode sequences. In some embodiments, the genetic loci comprise one or more oncogenes. In some embodiments, a method comprises determining that at least a subset of the baselining genetic loci has undergone copy number alteration in the tumor cells of the subject by determining relative quantities of variants within the baselining genetic loci for which the germline genome of the subject is heterozygous. In some embodiments, the relative quantities of the variants are not approximately equal. In some embodiments, baselining genetic loci for which the relative quantities of the variants are not approximately equal are removed from the baselining genetic loci, thereby providing allelic-frequency corrected baselining genetic loci. In some embodiments, the allelic-frequency corrected baselining genetic loci are used as the baselining loci in the methods of any one of the preceding claims. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: receiving into memory sequencing reads of deoxyribonucleic acid (DNA) molecules of a cell-free bodily fluid sample of a subject; executing code with a computer processor to perform the following steps: generating from the sequence reads a first data set comprising for each genetic locus in a plurality of genetic loci a quantitative measure related to sequencing read coverage ("read coverage"); correcting the first data set by performing saturation equilibrium correction and probe efficiency correction; determining a baseline read coverage for the first data set, wherein the baseline read coverage relates to saturation equilibrium and probe efficiency; and determining a copy number state for each genetic locus in the plurality of genetic loci relative to the baseline read coverage. Additionally or alternatively, detection of a genetic biomarker can include a system comprising: a network; a database comprising computer memory configured to store nucleic acid (e.g., DNA) sequence data which are connected to the network; a bioinformatics computer comprising a computer memory and one or more computer processors, which computer is connected to the network; wherein the computer further comprises machine-executable code which, when executed by the one or more computer processors, copies nucleic acid (e.g., DNA) sequence data stored on the database, writes the copied data to memory in the bioinformatics computer

and performs steps including: generating from the nucleic acid (e.g., DNA) sequence data a first data set comprising for each genetic locus in a plurality of genetic loci a quantitative measure related to sequencing read coverage ("read coverage"); correcting the first data set by performing saturation equilibrium correction and probe efficiency correction; determining a baseline read coverage for the first data set, wherein the baseline read coverage relates to saturation equilibrium and probe efficiency; and determining a copy number state for each genetic locus in the plurality of genetic loci relative to the baseline read coverage. In some embodiments, the database is connected to a DNA sequencer.

[473] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0260590, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method comprising: (a) sequencing polynucleotides from cancer cells from a biological sample of a subject; (b) identifying and quantifying somatic mutations in the polynucleotides; (c) developing a profile of tumor heterogeneity in the subject indicating the presence and relative quantity of a plurality of the somatic mutations in the polynucleotides, wherein different relative quantities indicates tumor heterogeneity; and (d) determining a therapeutic intervention for a cancer exhibiting the tumor heterogeneity, wherein the therapeutic intervention is effective against a cancer having the profile of tumor heterogeneity determined. In some embodiments, the cancer cells are spatially distinct. In some embodiments, the therapeutic intervention is more effective against a cancer presenting with the plurality of somatic mutations than it is against a cancer presenting with any one, but not all, of the somatic mutations. In some embodiments, the method further comprises: (e) monitoring changes in tumor heterogeneity in the subject over time and determining different therapeutic interventions over time based on the changes. In some embodiments, the method further comprises: (e) displaying the therapeutic intervention. In some embodiments, the method further comprises: (e) implementing the therapeutic intervention. In some embodiments, the method further comprises: (e) generating a phylogeny of tumor evolution based on the tumor profile; wherein determining the therapeutic intervention takes into account the phylogeny. In some embodiments, determining is performed with the aid of computer-executed algorithm. In some embodiments, sequence reads

generated by sequencing are subject to noise reduction before identifying and quantifying. In some embodiments, noise reduction comprises molecular tracking of sequences generated from a single polynucleotide in the sample. In some embodiments, determining a therapeutic intervention takes into account the relative frequencies of the tumor-related genetic alterations. In some embodiments, the therapeutic intervention comprises administering, in combination or in series, a plurality of drugs, wherein each drug is relatively more effective against a cancer presenting with a different one of somatic mutations that occur at different relative frequency. In some embodiments, a drug that is relatively more effective against a cancer presenting with a somatic mutation occurring at higher relative frequency is administered in higher amount. In some embodiments, the drugs are delivered at doses that are stratified to reflect the relative amounts of the variants in the DNA. In some embodiments, cancers presenting with at least one of the genetic variants is resistant to at least one of the drugs. In some embodiments, determining a therapeutic intervention takes into account the tissue of origin of the cancer. In some embodiments, the therapeutic intervention is determined based on a database of interventions shown to be therapeutic for cancers having tumor heterogeneity characterized by each of the somatic mutations. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing a therapeutic intervention for a subject having a cancer having a tumor profile from which tumor heterogeneity can be inferred, wherein the therapeutic intervention is effective against cancers with the tumor profile. In some embodiments, the tumor profile indicates relative frequency of a plurality of more somatic mutations. In some embodiments, the method further comprises monitoring changes in the relative frequencies in the subject over time and determining different therapeutic interventions over time based on the changes. In some embodiments, the therapeutic intervention is more effective against a cancer presenting with each of the somatic mutations than it is against a cancer presenting with any one, but not all, of the somatic mutations. In some embodiments, the therapeutic intervention comprises administering, in combination or in series, a plurality of drugs, wherein each drug is relatively more effective against a cancer presenting with a different one of somatic mutations that occur at different relative frequency. In some embodiments, a drug that is relatively more effective against a cancer presenting with a somatic mutation occurring at higher relative frequency is administered in higher amount. In some

embodiments, the drugs are delivered at doses that are stratified to reflect the relative amounts of the variants in the DNA. In some embodiments, cancers presenting with at least one of the genetic variants is resistant to at least one of the drugs. Additionally or alternatively, detection of a genetic biomarker can include a system comprising a computer readable medium comprising machine-executable code that, upon execution by a computer processor, implements a method comprising: (a) receiving into memory sequence reads of polynucleotides mapping to a genetic locus; (b) determining, among said sequence reads, identity of bases that are different than a base of a reference sequence at the locus of the total number of sequence reads mapping to a locus; (c) reporting the identity and relative quantity of the determined bases and their location in the genome; and (d) inferring heterogeneity of a given sample based on information in (c). In some embodiments, the method implemented further comprises receiving into memory sequence reads derived from samples at a plurality of different times and calculating a difference in relative amount and identity of a plurality of bases between the two samples. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: (a) performing biomolecular analysis of biomolecular polymers from disease cells (e.g., spatially distinct disease cells) from a subject; (b) identifying and quantifying biomolecular variants in the biomolecular macromolecules; (c) developing a profile of disease cell heterogeneity in the subject indicating the presence and relative quantity of a plurality of the variants in the biomolecular macromolecules, wherein different relative quantities indicates disease cell heterogeneity; and (d) determining a therapeutic intervention for a disease exhibiting the disease cell heterogeneity, wherein the therapeutic intervention is effective against a disease having the profile of disease cell heterogeneity determined. In some embodiments, the disease cells are spatially distinct disease cells. In some embodiments, the therapeutic intervention is determined based on a database of interventions shown to be therapeutic for cancers having tumor heterogeneity characterized by each of the somatic mutations. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting disease cell heterogeneity in a subject comprising: a) quantifying polynucleotides that bear a sequence variant at each of a plurality of genetic loci in polynucleotides from a sample from the subject, wherein the sample comprises polynucleotides from somatic cells and from disease cells; b) determining for each locus a measure of copy number variation (CNV)

for polynucleotides bearing the sequence variant; c) determining for each locus a weighted measure of quantity of polynucleotides bearing a sequence variant at the locus as a function of CNV at the locus; and d) comparing the weighted measures at each of the plurality of loci, wherein different weighted measures indicate disease cell heterogeneity. In some embodiments, the disease cells are tumor cells. In some embodiments, polynucleotides comprise cfDNA. Additionally or alternatively, detection of a genetic biomarker can include a method of inferring a measure of burden of DNA from cells undergoing cell division in a sample comprising measuring copy number variation induced by proximity of one or more genomic loci to cells' origins of replication, wherein increased CNV indicates cells undergoing cell division. In some embodiments, the burden is measured in cell-free DNA. In some embodiments, the measure of burden relates to the fraction of tumor cells or genome-equivalents of DNA from tumor cells in the sample. In some embodiments, CNV due to proximity to origins of replication is inferred from a set of control samples or cell-lines. In some embodiments, a hidden-markov model, regression model, principal component analysis-based model, or genotype-modified model is used to approximate variations due to origins of replications. In some embodiments, the measure of burden is presence or absence of cells undergoing cell division. In some embodiments, proximity is within 1 kb of an origin of replication. Additionally or alternatively, detection of a genetic biomarker can include a method of increasing sensitivity and/or specificity of determining gene-related copy-number variations by ameliorating the effect of variations due to proximity to origins of replications. In some embodiments, the method comprises measuring CNV at a locus, determining amount of CNV due to proximity of the locus to an origin of replication, and correcting the measured CNV to reflect genomic CNV, e.g., by subtracting amount of CNV attributable to cell division. In some embodiments, the genomic data is obtained from cell-free DNA. In some embodiments, the measure of burden relates to the fraction of tumor cells or genome-equivalents of DNA in a sample. In some embodiments, variations due to origins of replication are inferred from a set of control samples or cell-lines. In some embodiments, a hidden-markov model, regression model, principal component analysis-based model, or genotype-modified model is used to approximate variations due to origins of replications.

[474] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0061072, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for detection of single-nucleotide variations (SNVs) from somatic sources in a cell-free biological sample of a subject, such as in a mixture of nucleic acid molecules from somatic and germline sources. In some embodiments, the systems and methods detect single-nucleotide variations (SNVs) from somatic sources in a cell-free biological sample of a subject by generating training data with class labels; forming a machine learning unit having one output for each of adenine (A), cytosine (C), guanine (G), and thymine (T) base calls, respectively; training the machine learning unit with a training set of biological samples; and applying the machine learning unit to detect the SNVs from somatic sources in the cell-free biological sample, wherein the cell-free biological sample may comprise a mixture of nucleic acid molecules (e.g., deoxyribonucleic acid (DNA)) from somatic and germline sources, e.g., cells comprising somatic mutations and germline DNA.

[475] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0058332, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method to detect a somatic or germline variant, comprising providing a predetermined genomic DNA (gDNA) to an assay mixture, capturing a sample of a subject's genetic information using a gene analyzer, and detecting genetic variants from the genetic information; and classifying a variant as from a germ line source if present in gDNA derived molecules having lengths longer than cell-free DNA (cfDNA) derived molecules. In some embodiments, the gDNA has a fragment length of more than about 200 bases. In some embodiments, the gDNA has a fragment length of at least 400 bases or at least 500 bases. In some embodiments, gDNA fragment length is higher than the cfDNA fragment length distribution. In some embodiments, the gDNA is added to the assay mixture. In some embodiments, the gDNA is left in the assay mixture after a filtering operation. In some embodiments, the gDNA is left in the assay mixture after a centrifugation operation. In some embodiments, approximately 1% to 5% gDNA is added to the assay mixture. In some

embodiments, at least 1% gDNA is added to the assay mixture. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing a sample comprising both genomic DNA (gDNA) and cell-free DNA (cfDNA) from a subject; determining subject germline genotype at least one genetic locus from the gDNA; determining a quantitative measure of at least one genetic variant at each genetic locus in the cfDNA; determining whether the quantitative measure of the genetic variant is or is not consistent with germline genotype; and calling the genetic variant as a germline variant if the quantitative measure is consistent with germline genotype, or as a somatic mutant if the quantitative measure is not consistent with the germline genotype. Additionally or alternatively, detection of a genetic biomarker can include a method comprising determining a quantitative measure of a genetic variant detected in cell-free DNA (cfDNA) from a subject; determining that the measure is consistent with a heterozygous genotype in the subject; determining a probable genotype of the subject at the locus from genomic DNA (gDNA); comparing the genotype at the locus from gDNA with the variant detected in the cfDNA; and calling the variant as a somatic mutation if the variant detected in the cfDNA is not consistent with the genotype at the locus from gDNA. In some embodiments, calling the variant as a somatic mutation if the genotype at the locus from gDNA is determined to be homozygous. In some embodiments, calling the variant as a somatic mutation if the genotype at the locus from gDNA is determined to be heterozygous with a confidence selected from the group consisting of: at least 70%, at least 80%, at least 90%, at least 95%, or at least 99%. In some embodiments, determining a quantitative measure of a genetic variant comprises sequencing the cfDNA. In some embodiments, determining the probable genotype of the subject comprises sequencing genomic DNA from the subject. In some embodiments, the sequencing is selected from the group consisting of: targeted sequencing, single molecule real-time sequencing, exon sequencing, electron microscopy-based sequencing, panel sequencing, transistor-mediated sequencing, direct sequencing, random shotgun sequencing, Sanger dideoxy termination sequencing, whole-genome sequencing, sequencing by hybridization, pyrosequencing, capillary electrophoresis, gel electrophoresis, duplex sequencing, cycle sequencing, single-base extension sequencing, solid-phase sequencing, high-throughput sequencing, massively parallel signature sequencing, emulsion PCR, co-amplification at lower denaturation

temperature-PCR (COLD-PCR), multiplex PCR, sequencing by reversible dye terminator, paired-end sequencing, near-term sequencing, exonuclease sequencing, sequencing by ligation, short-read sequencing, single-molecule sequencing, sequencing-by-synthesis, real-time sequencing, reverse-terminator sequencing, nanopore sequencing, 454 sequencing, Solexa Genome Analyzer sequencing, SOLiD™ sequencing, MS-PET sequencing, and a combination thereof.

[476] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/119452, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, compositions and systems for analyzing a nucleic acid population comprising at least two forms of nucleic acid selected from double-stranded DNA, single-stranded DNA and single-stranded RNA. In some embodiments the method comprises (a) linking at least one of the forms of nucleic acid with at least one tag nucleic acid to distinguish the forms from one another, (b) amplifying the forms of nucleic acid at least one of which is linked to at least one nucleic acid tag, wherein the nucleic acids and linked nucleic acid tag, if present, are amplified, to produce amplified nucleic acids, of which those amplified from the at least one form are tagged; (c) assaying sequence data of the amplified nucleic acids at least some of which are tagged; and (d) decoding tag nucleic acid molecules of the amplified nucleic acids to reveal the forms of nucleic acids in the population providing an original template for the amplified nucleic acids linked to the tag nucleic acid molecules for which sequence data has been assayed. In some embodiments, the method further comprises enriching for at least one of the forms relative to one or more of the other forms. In some embodiments, at least 70% of the molecules of each form of nucleic acid in the population are amplified in step (b). In some embodiments, at least three forms of nucleic acid are present in the population and at least two of the forms are linked to different tag nucleic acid forms distinguishing each of the three forms from one another. In some embodiments each of the at least three forms of nucleic acid in the population is linked to a different tag. In some embodiments, each molecule of the same form is linked to a tag comprising the same identifying information tag (e.g., a tag with the same or comprising the same sequence). In some embodiments, molecules of the same form are linked to different types of tags. In some

embodiments step (a) comprises: subjecting the population to reverse transcription with a tagged primer, wherein the tagged primer is incorporated into cDNA generated from RNA in the population. In some embodiments, the reverse transcription is sequence-specific. In some embodiments, the reverse transcription is random. In some embodiments, the method further comprises degrading RNA duplexed to the cDNA. In some embodiments, the method further comprises separating single-stranded DNA from double- stranded DNA and ligating nucleic acid tags to the double-stranded DNA. In some embodiments, the single-stranded DNA is separated by hybridization to one or more capture probes. In some embodiments, the method further comprises differentially tagging single-stranded DNA with a single-stranded tag using a ligase that functions on single stranded nucleic acids, and double- stranded DNA with double-stranded adapters using ligase that functions on double-stranded nucleic acids. In some embodiments, the method further comprises before assaying, pooling tagged nucleic acids comprising different forms of nucleic acid. In some embodiments, the method further comprises analyzing the pools of partitioned DNA separately in individual assays. The assays can be the same, substantially similar, equivalent, or different. In any of the above methods, the sequence data can indicate presence of a somatic or germline variant, or a copy number variation or a single nucleotide variation, or an indel or gene fusion. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a nucleic acid population comprising nucleic acids with different extents of modification. Additionally or alternatively, detection of a genetic biomarker can include methods for screening for characteristics (e.g., 5' methylcytosine) associated with a disease. The method comprises contacting the nucleic acid population with an agent (such as a methyl binding domain or protein) that preferentially binds to nucleic acids bearing the modification; separating a first pool of nucleic acids bound to the agent from a second pool of nucleic acids unbound to the agent, wherein the first pool of nucleic acids are overrepresented for the modification, and the nucleic acids in the second pool are underrepresented for the modification; linking the nucleic acids in the first pool and/or second pool to one or more nucleic acid tags that distinguish the nucleic acids in the first pool and the second pool to produce a population of tagged nucleic acids; amplifying the tagged nucleic acids, wherein the nucleic acids and the linked tags are amplified; assaying sequence data of the amplified nucleic acids and linked tags; decoding the

tags to reveal whether the nucleic acids for which sequence data has been assayed were amplified from templates in the first or second pool. Additionally or alternatively, detection of a genetic biomarker can include a method for analyzing a nucleic acid population in which at least some of the nucleic acids include one or more modified cytosine residues. The method comprises linking capture moieties, e.g., biotin, to nucleic acids in the population to serve as templates for amplification; performing an amplification reaction to produce amplification products from the templates; separating the templates linked to capture moieties from amplification products; assaying sequence data of the templates linked to capture moieties by bisulfite sequencing; and assaying sequence data of the amplification products. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a nucleic acid population comprising nucleic acids with different extents of 5-methylcytosine. The method comprises (a) contacting the nucleic acid population with an agent that preferentially binds to 5-methylated nucleic acids; (b) separating a first pool of nucleic acids bound to the agent from a second pool of nucleic acids unbound to the agent, wherein the first pool of nucleic acids are overrepresented for 5-methylcytosine, and the nucleic acids in the second pool are underrepresented for 5- methylation; (c) linking the nucleic acids in the first pool and/or second pool to one or more nucleic acid tags that distinguish the nucleic acids in the first pool and the second pool, wherein the nucleic acid tags linked to nucleic acids in the first pool comprise a capture moiety (e.g., biotin); (d) amplifying the labelled nucleic acids, wherein the nucleic acids and the linked tags are amplified; (e) separating amplified nucleic acids bearing the capture moiety from amplified nucleic acids that do not bear the capture moiety; and (f) assaying sequence data of the separated, amplified nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a nucleic acid population comprising at least two forms of nucleic acid selected from double-stranded DNA, single- stranded DNA and single-stranded RNA, the method, wherein each of the at least two forms comprises a plurality of molecules, comprising: linking at least one of the forms of nucleic acid with at least one tag nucleic acid to distinguish the forms from one another, amplifying the forms of nucleic acid at least one of which is linked to at least one nucleic acid tag, wherein the nucleic acids and linked nucleic acid tag, are amplified, to produce amplified nucleic acids, of which those amplified from the at least one form are tagged;

assaying sequence data of the amplified nucleic acids at least some of which are tagged; wherein the assaying obtains sequence information sufficient to decode the tag nucleic acid molecules of the amplified nucleic acids to reveal the forms of nucleic acids in the population providing an original template for the amplified nucleic acids linked to the tag nucleic acid molecules for which sequence data has been assayed. In one embodiment the method further comprises the step of decoding the tag nucleic acid molecules of the amplified nucleic acids to reveal the forms of nucleic acids in the population providing an original template for the amplified nucleic acids linked to the tag nucleic acid molecules for which sequence data has been assayed. In another embodiment, the method further comprises enriching for at least one of the forms relative to one or more of the other forms. In another embodiment, at least 70% of the molecules of each form of nucleic acid in the population are amplified. In another embodiment, at least three forms of nucleic acid are present in the population and at least two of the forms are linked to different tag nucleic acid forms distinguishing each of the three forms from one another. In another embodiment each of the at least three forms of nucleic acid in the population is linked to a different tag. In another embodiment, each molecule of the same form is linked to a tag comprising the same tag information. In another embodiment, molecules of the same form are linked to different types of tags. In another embodiment, the method further comprises subjecting the population to reverse transcription with a tagged primer, wherein the tagged primer is incorporated into cDNA generated from RNA in the population. In another embodiment, the reverse transcription is sequence-specific. In another embodiment wherein the reverse transcription is random. In another embodiment, the method further comprises degrading RNA duplexed to the cDNA. In another embodiment, the method further comprises separating single-stranded DNA from double- stranded DNA and ligating nucleic acid tags to the double-stranded DNA. In another embodiment, the single-stranded DNA is separated by hybridization to one or more capture probes. In another embodiment, the method further comprises circularizing single-stranded DNA with a circligase and ligating nucleic acid tags to the double-stranded DNA. In another embodiment, the method comprises, before assaying, pooling tagged nucleic acids comprising different forms of nucleic acid. In another embodiment, the nucleic acid population is from a bodily fluid sample. In another embodiment, the bodily fluid sample is blood, serum, or plasma. In another embodiment, the nucleic acid

population is a cell free nucleic acid population. In another embodiment, the bodily fluid sample is from a subject suspected of having a cancer. In another embodiment the sequence data indicates presence of a somatic or germline variant. In another embodiment, the sequence data indicates presence of a copy number variation. In another embodiment, the sequence data indicates presence of a single nucleotide variation (SNV), indel or gene fusion. In another embodiment, the sequence data indicates presence of a single nucleotide variation (SNV), indel or gene fusion. Additionally or alternatively, detection of a genetic biomarker can include a method, comprising: providing a population of nucleic acid molecules obtained from a bodily sample of a subject; fractionating the population of nucleic acid molecules based on one or more characteristics to generate plurality of groups of nucleic acid molecules, wherein the nucleic acid molecules of each of the plurality of groups comprise distinct identifiers; pooling the plurality of groups of nucleic acid molecules; sequencing the pooled plurality of groups of nucleic acid molecules to generate plurality of sets sequence reads; and fractionating the sequence reads based on the identifiers. Additionally or alternatively, detection of a genetic biomarker can include a method for analyzing the fragmentation pattern of cell-free DNA comprising: providing a population of cell-free DNA from a biological sample; fractionating the population of cell-free DNA, thereby generating subpopulations of cell- free DNA; sequencing at least one subpopulation of cell-free DNA, thereby generating sequence reads; aligning the sequence reads to a reference genome; and, determining the fragmentation pattern of the cell-free DNA in each subpopulation by analyzing any number of the: length of each sequence read mapping to each base position in the reference genome; number of sequence reads mapping to the base position in the reference genome as a function of length of the sequence reads; number of sequence reads starting at each base position in the reference genome; or, number of sequence reads ending at each base position in the reference genome. In another embodiment, the one or more characteristics comprise a chemical modification selected from the group consisting of: methylation, hydroxymethylation, formylation, acetylation, and glycosylation.

[477] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/009723, which is hereby incorporated by reference in its entirety. For example, detection

of a genetic biomarker can include methods, systems, and compositions for performing nucleosome profiling using cell-free nucleic acids (e.g., cfDNA). This can be used to identify new driver genes, determine copy number variation (CNV), identify somatic mutations and structural variations such as fusions and indels, as well as identify regions that can be used in a multiplexed assay to detect any of the above variations. Additionally or alternatively, detection of a genetic biomarker can include various uses of cell-free nucleic acids (e.g., DNA or RNA). Such uses include detecting, monitoring and determining treatment for a subject having or suspected of having a health condition, such as a disease (e.g., cancer). The methods provided may use sequence information in a macroscale and global manner, with or without somatic variant information, to assess a fragmentome profile that can be representative of a tissue of origin, disease, progression, etc. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method for determining a presence or absence of a genetic aberration in deoxyribonucleic acid (DNA) fragments from cell-free DNA obtained from a subject, the method comprising: (a) constructing, by a computer, a multi-parametric distribution of the DNA fragments over a plurality of base positions in a genome; and (b) without taking into account a base identity of each base position in a first locus, using the multi-parametric distribution to determine the presence or absence of the genetic aberration in the first locus in the subject. In some embodiments, the genetic aberration comprises a sequence aberration. In some embodiments, the sequence aberration comprises a single nucleotide variant (SNV). In some embodiments, the sequence aberration comprises an insertion or deletion (indel), or a gene fusion. In some embodiments, the sequence aberration comprises two or more different members selected from the group consisting of (i) a single nucleotide variant (SNV), (ii) an insertion or deletion (indel), and (iii) a gene fusion. In some embodiments, the genetic aberration comprises a copy number variation (CNV). In some embodiments, the multi-parametric distribution comprises a parameter indicative of a length of the DNA fragments that align with each of the plurality of base positions in the genome. In some embodiments, the multi-parametric distribution comprises a parameter indicative of a number of the DNA fragments that align with each of the plurality of base positions in the genome. In some embodiments, the multi-parametric distribution comprises a parameter indicative of a number of the DNA fragments that start or end at each of the plurality of base

positions in the genome. In some embodiments, n the multi-parametric distribution comprises parameters indicative of two or more of: (i) a length of the DNA fragments that align with each of the plurality of base positions in the genome, (ii) a number of the DNA fragments that align with each of the plurality of base positions in the genome, and (iii) a number of the DNA fragments that start or end at each of the plurality of base positions in the genome. In some embodiments, the multi-parametric distribution comprises parameters indicative of (i) a length of the DNA fragments that align with each of the plurality of base positions in the genome, (ii) a number of the DNA fragments that align with each of the plurality of base positions in the genome, and (iii) a number of the DNA fragments that start or end at each of the plurality of base positions in the genome. Additionally or alternatively, detection of a genetic biomarker can include a method of generating a classifier for determining a likelihood that a subject belongs to one or more classes of clinical significance, the method comprising: a) providing a training set comprising, for each of the one or more classes of clinical significance, populations of cell-free DNA from each of a plurality of subjects of a species belonging to the class of clinical significance and from each of a plurality of subjects of the species not belonging to the class of clinical significance; b) sequencing cell-free DNA fragments from the populations of cell-free DNA to produce a plurality of DNA sequences; c) for each population of cell-free DNA, mapping the plurality of DNA sequences to each of one or more genomic regions in a reference genome of the species, each genomic region comprising a plurality of genetic loci; d) preparing, for each population of cell-free DNA, a dataset comprising, for each of a plurality of the genetic loci, values indicating a quantitative measure of at least one characteristic selected from: (i) DNA sequences mapping to the genetic locus, (ii) DNA sequences starting at the locus, and (iii) DNA sequences ending at the genetic locus, to yield a training set; and e) training a computer-based machine learning system on the training set, thereby generating a classifier for determining a likelihood that the subject belongs to one or more classes of clinical significance. Additionally or alternatively, detection of a genetic biomarker can include a method of determining an abnormal biological state in a subject, the method comprising: a) sequencing cell-free DNA fragments from cell-free DNA from the subject to produce DNA sequences; b) mapping the DNA sequences to each of one or more genomic regions in a reference genome of a species of the subject, each genomic region comprising a plurality of

genetic loci; c) preparing a dataset comprising, for each of a plurality of the genetic loci, values indicating a quantitative measure of at least one feature selected from: (i) DNA sequences mapping to the genetic locus, (ii) DNA sequences starting at the locus, and (iii) DNA sequences ending at the genetic locus; and d) based on the dataset, determining a likelihood of the abnormal biological state. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method for generating an output indicative of a presence or absence of a genetic aberration in deoxyribonucleic acid (DNA) fragments from cell-free DNA obtained from a subject, the method comprising: (a) constructing, by a computer, a distribution of the DNA fragments from the cell-free DNA over a plurality of base positions in a genome; and (b) for each of one or more genetic loci, calculating, by a computer, a quantitative measure indicative of a ratio of (1) a number of the DNA fragments with dinucleosomal protection associated with a genetic locus from the one or more genetic loci, and (2) a number of the DNA fragments with mononucleosomal protection associated with the genetic locus, or vice versa; and (c) determining, using the quantitative measure for each of the one or more genetic loci, said output indicative of a presence or absence of the genetic aberration in the one or more genetic loci in the subject. In some embodiments, the distribution comprises one or more multi-parametric distributions. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method for deconvolving a distribution of deoxyribonucleic acid (DNA) fragments from cell-free DNA obtained from a subject, the method comprising: (a) constructing, by a computer, a distribution of a coverage of the DNA fragments from the cell-free DNA over a plurality of base positions in a genome; and (b) for each of one or more genetic loci, deconvolving, by a computer, the distribution of the coverage, thereby generating fractional contributions associated with one or more members selected from the group consisting of a copy number (CN) component, a cell clearance component, and a gene expression component. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented classifier for determining genetic aberrations in a test subject using deoxyribonucleic acid (DNA) fragments from cell-free DNA obtained from the test subject, comprising: (a) an input of a set of distribution scores for each of one or more populations of cell-free DNA obtained from each of a plurality of subjects, wherein each distribution score is generated based at least on one or more of: (i) a length of the DNA

fragments that align with each of a plurality of base positions in a genome, (ii) a number of the DNA fragments that align with each of a plurality of base positions in a genome, and (iii) a number of the DNA fragments that start or end at each of a plurality of base positions in a genome; and (b) an output of classifications of one or more genetic aberrations in the test subject. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method for creating a trained classifier, comprising: (a) providing a plurality of different classes, wherein each class represents a set of subjects with a shared characteristic; (b) for each of a plurality of populations of cell-free DNA obtained from each of the classes, providing a multi-parametric model representative of cell-free deoxyribonucleic acid (DNA) fragments from the populations of cell- free DNA, thereby providing a training data set; and (c) training, by a computer, a learning algorithm on the training data set to create one or more trained classifiers, wherein each trained classifier is configured to classify a test population of cell-free DNA from a test subject into one or more of the plurality of different classes. Additionally or alternatively, detection of a genetic biomarker can include a method of classifying a test sample from a subject, comprising: (a) providing a multi-parametric model representative of cell-free deoxyribonucleic acid (DNA) fragments from a test population of cell-free DNA from the subject; and (b) classifying the test population of cell-free DNA using a trained classifier. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method comprising: (a) generating, by a computer, sequence information from cell-free DNA fragments from a subject; (b) mapping, by a computer, the cell-free DNA fragments to a reference genome based on the sequence information; and (c) analyzing, by a computer, the mapped cell-free DNA fragments to determine, at each of a plurality of base positions in the reference genome, a plurality of measures selected from the group consisting of: (i) number of cell-free DNA fragments mapping to the base position, (ii) length of each cell-free DNA fragment mapping to the base position, (iii) number of cell-free DNA fragments mapping to the base position as a function of length of the cell-free DNA fragment; (iv) number of cell-free DNA fragments starting at the base position; (v) number of cell-free DNA fragments ending at the base position; (vi) number of cell-free DNA fragments starting at the base position as a function of length, and (vii) number of cell-free DNA fragments ending at the base position as a function of length. Additionally or alternatively,

detection of a genetic biomarker can include a computer-implemented method for deconvolving a distribution of deoxyribonucleic acid (DNA) fragments from cell-free DNA obtained from a subject, the method comprising: (a) constructing, by a computer, a distribution of a coverage of the DNA fragments from the cell-free DNA over a plurality of base positions in a genome; and (b) for each of one or more genetic loci, deconvolving, by a computer, the distribution of the coverage, thereby generating fractional contributions associated with one or more members selected from the group consisting of a copy number (CN) component, a cell clearance component, and a gene expression component. In some embodiments, the method further comprises comprising generating an output indicative of a presence or absence of a genetic aberration based at least on a portion of the fractional contributions.

[478] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/181146, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems that may be used for early cancer detection. In some embodiments, the method comprises (a) providing a sample comprising cfDNA from a subject, wherein the subject does not detectably exhibit a cancer; (b) capturing from the sample cfDNA molecules covered by a sequencing panel, wherein the sequencing panel comprises one or more regions from each of a plurality of different genes, wherein: (i) the sequencing panel is no greater than 50,000 nucleotides; (ii) the presence of a tumor marker in any one of the different genes indicates that the subject has the cancer; and (iii) at least 80% of subjects having the cancer have a tumor marker present in at least one of the plurality of different genes; and (c) sequencing the captured cfDNA molecules to a read depth sufficient to detect the tumor markers at a frequency in the sample as low as 0.01%. In some embodiments, a tumor marker is selected from the group consisting of a single base substitution, a copy number variation, an indel, a gene fusion, a transversion, a translocation, an inversion, a deletion, aneuploidy, partial aneuploidy, polyploidy, chromosomal instability, chromosomal structure alterations, chromosome fusions, a gene truncation, a gene amplification, a gene duplication, a chromosomal lesion, a DNA lesion, abnormal changes in nucleic acid chemical modifications, abnormal changes in epigenetic patterns and abnormal changes in nucleic acid methylation. In some embodiments, at least 85%, at least 90%, at least

93%, at least 95%, at least 97%), at least 98% or at least 99% of subjects having the cancer have a tumor marker present in at least one of the plurality of different genes. Some embodiments comprise sequencing the captured cfDNA molecules to a read depth sufficient to detect the tumor markers at a frequency in the sample as low as 0.005%, 0.001% or 0.0005%. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: a. providing a sample comprising cell-free nucleic acid (cfNA) molecules from a subject, wherein the subject does not detectably exhibit a cancer; b. capturing from the sample cfNA molecules covered by a sequencing panel, wherein the sequencing panel comprises one or more regions from each of a plurality of different genes, wherein: i. the sequencing panel is no greater than 50,000 nucleotides; ii. a presence of a tumor marker in any one of the different genes indicates that the subject has the cancer; and iii. at least 80% of subjects having the cancer have a tumor marker present in at least one of the plurality of different genes; and c. sequencing the captured cfNA molecules to a read depth sufficient to detect the tumor markers at a frequency in the sample as low as 1.0%, 0.75%, 0.5%, 0.25%, 0.1%, 0.075%, 0.05%, 0.025%, 0.01%, or 0.005%. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting cancer in a subject comprising: sequencing circulating cell-free DNA (cfDNA) from the subject at a depth of at least 50,000 reads per base to detect one or more genetic variants associated with cancer. In some embodiments, the sequencing is at a depth of at least 100,000 reads per base. In some embodiments, the sequencing is at a depth of about 120,000 reads per base. In some embodiments, the sequencing is at a depth of about 150,000 reads per base. In some embodiments, the sequencing is at a depth of about 200,000 reads per base. In some embodiments, the reads per base represent at least 5,000 original nucleic acid molecules, at least 10,000 original nucleic acid molecules, at least 20,000 original nucleic acid molecules, at least 30,000 original nucleic acid molecules, at least 40,000 original nucleic acid molecules, or at least 50,000 original nucleic acid molecules. In some embodiments, the method further comprises comparing sequence information from the cfDNA to sequence information obtained from a cohort of healthy individuals, a cohort of cancer patients, or germline DNA from the subject. In some embodiments, the method further comprises amplifying the cfDNA prior to sequencing, and determining a consensus sequence from sequence reads obtained from the sequencing to reduce errors from amplification or

sequencing. In some embodiments, determining the consensus sequence is performed on a molecule-by-molecule basis. In some embodiments, determining the consensus sequence is performed on a base by base basis. In some embodiments, detection of consensus sequence is based on assessing probabilities of each of the potential nucleotides based on the observed sequencing output, as well as sequencing and amplification error profile characteristics of an individual sample, a batch of samples, or a reference set of samples. In some embodiments, determining the consensus sequence is performed using molecular barcodes that tag individual cfDNA molecules derived from the subject. In some embodiments, a set of molecules with a consensus sequence deviant from the human reference is compared to those observed in other samples processed in the laboratory to determine and exclude any potential contaminating event. In some embodiments, determining the consensus sequence is optimized by comparing the consensus sequence to those obtained from the cohort of healthy individuals, the cohort of cancer patients, or the germline DNA from the subject. In some embodiments, the method further comprises tagging the cfDNA molecules with a barcode such that at least 20% of the cfDNA in a sample derived from the subject are tagged. In some embodiments, the tagging is performed by attaching adaptors comprising a barcode. In some embodiments, the adaptors comprise any or all of blunt end adaptors, restriction enzyme overhang adaptors, or adaptors with a single nucleotide overhang. In some embodiments, the adaptors with a single nucleotide overhang comprise C-tail adaptors, A-tail adaptors, T-tail adaptors, and/or G-tail adaptors. In some embodiments, the tagging is performed by PCR amplification using primers with barcodes. In some embodiments, the barcode is single stranded. In some embodiments, the barcode is double stranded. In some embodiments, the method further comprises dividing the cfDNA into partitions. In some embodiments, the cfDNA in each partition is uniquely tagged with respect to each other partition. In some embodiments, the cfDNA in each partition is non-uniquely tagged with respect to each other partition. In some embodiments, the cfDNA in each partition is not tagged. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a tumor in a subject suspected of having cancer or having cancer, comprising: (a) sequencing cell-free DNA (cfDNA) molecules derived from a cell-free DNA (cfDNA) sample obtained from the subject; (b) analyzing sequence reads derived from the sequencing to identify (i) circulating tumor DNA (ctDNA) among the cfDNA molecules

and (ii) one or more driver mutations in the cfDNA; and (c) using information about the presence, absence, or amount of the one or more driver mutations in the ctDNA molecules to identify (i) the tumor in the subject and (ii) actions for treatment of the tumor to be taken by the subject, wherein the method detects the tumor in the subject with a sensitivity of at least 85%, a specificity of at least 99%, and a diagnostic accuracy of at least 99%.

[479] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/136603, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for detecting or monitoring cancer evolution. Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method, comprising: (a) obtaining information about a plurality of subjects with cancer at a first time point, wherein the information comprises for each subject of the plurality of subjects at least a genetic profile of a tumor obtained by genotyping nucleic acids from a cell-free bodily fluid and any treatment provided to the subject before the first time point, and determining a first state of each of the plurality of subjects based on the information at the first time point to produce a set of first states; (b) obtaining the information about the plurality of subjects at one or more second time points subsequent to the first time point, and determining a second state of each of the plurality of subjects at each of the one or more second time points based on the information at a given one of the one or more second time points, to produce a set of subsequent states; and (c) using the set of first states from (a) and the set of subsequent states from (b) to generate a predictive algorithm that is configured to determine a probability that a given first state will result in a second state among a set of states at a later time point subsequent to the given first state. In some embodiments, the method further comprises (d) for the given first state among a set of states at an earlier time point, determining the probability that the given first state will result in the second state among the set of states at the later time point; and (e) generating an electronic output indicative of the probability determined in (d). Additionally or alternatively, detection of a genetic biomarker can include a computer-implemented method, comprising: (a) obtaining information about a plurality of subjects with cancer at a first time point, wherein the information comprises, for each subject of the plurality of subjects, at least a genetic profile of a tumor obtained by

genotyping at least 50 genes and any treatment provided to the subject before the first time point, and determining a first state of each of the plurality of subjects based on the information at the first time point, to produce a set of first states; (b) obtaining the information about the plurality of subjects at one or more second time points subsequent to the first time point, and determining a second state of each of the plurality of subjects at each of the one or more second time points based on the information at a given one of the one or more second time points, to produce a set of subsequent states; and (c) using the set of first states from (a) and the set of subsequent states from (b) to generate a predictive algorithm that is configured to determine a probability that a given first state will result in a second state among a set of states at a later time point subsequent to the given first state. In some embodiments, the method further comprises (d) for the given first state among a set of states at an earlier time point, determining the probability that the given first state will result in the second state among the set of states at the later time point; and (e) generating an electronic output indicative of the probability determined in (d). In some embodiments, obtaining the information comprises sequencing cell-free deoxyribonucleic acid (cfDNA) from the plurality of subjects and, optionally, performing a medical interview of each of the plurality of subjects. In some embodiments, treatment was provided to the subject before the first time point. In some embodiments, the methods comprise generating one or more decision trees, each decision tree comprising a root node, one or more decision branches, one or more decision nodes, and one or more terminal nodes, wherein a state at the root node represents the first time point, the one or more decision branches represent alternative treatments, and the one or more decision nodes and the one or more terminal nodes represent subsequent states. In some embodiments, the one or more decision branches comprise a plurality of decision branches. In some embodiments, the subsequent states comprise a viability state(s) of the subjects indicative of the subjects being alive or deceased. In some embodiments, the subsequent states comprise a subject survival rate. In some embodiments, each of the first states comprises a common set of one or more somatic mutations. In some embodiments, the information further comprises a subject profile. Additionally or alternatively, detection of a genetic biomarker can include a method, comprising: (a) obtaining information about a subject with a cancer at a first time point, wherein the information comprises at least one characteristic of the subject from a patient

profile, a tumor profile, or a treatment; (b) determining an initial state of the subject based on the information at the first time point; (c) determining a probability for each of a plurality of subsequent states at each of one or more subsequent time points based on the initial state of the subject, thereby providing a set of probabilities with regards to state outcomes; (d) generating a recommendation of a treatment for the cancer based at least in part on the set of probabilities with regards to state outcomes that optimizes for a probability that subject obtains a particular outcome; and (e) generating an electronic output indicative of the recommendation generated in (d). In some embodiments, the probability is at least in part a function of a treatment choice from among a plurality of treatment choices. In some embodiments, the one or more subsequent time points comprises a plurality of subsequent time points. In some embodiments, the method further comprises determining the probability at a plurality of subsequent time points. In some embodiments, the time points comprise at least three time points. In some embodiments, the time points comprise at least four time points. In some embodiments, the first time point is prior to the subject receiving the treatment and the subsequent time point is after the subject receiving the treatment. In some embodiments, a second treatment is administered after the subsequent time point based on the subsequent state at the subsequent time point. In some embodiments, the at least one characteristic of the subject is from the patient profile and is selected from the group consisting of: age, gender, genetic profile, enzyme levels, organ function, quality of life, frequency of medical interventions, remission status, and patient outcome. Additionally or alternatively, detection of a genetic biomarker can include a method, comprising: (a) establishing one or more communications links over a communication network with one or more medical service providers; (b) receiving over the communications network from the one or more medical service providers medical information about one or more subjects; (c) receiving from the medical service provider one or more samples comprising cell-free deoxyribonucleic acid (cfDNA) from each of the one or more subjects; (d) sequencing the cfDNA and identifying one or more genetic variants present in the cfDNA; (e) creating or supplementing a database with information for each of the one or more subjects, the information comprising both identified genetic variants and received medical information; and (f) using the database and a computer implemented algorithm, generating at least one predictive model that predicts, based on an initial state of a subject, the

probability of a subsequent state for each of a plurality of different therapeutic interventions. Additionally or alternatively, detection of a genetic biomarker can include a non-transitory computer-readable medium comprising machine executable code that, upon execution by one or more computer processors, implements a method comprising: (a) obtaining information about a plurality of subjects with cancer at a first time point, wherein the information comprises, for each subject of the plurality of subjects, at least a genetic profile of a tumor obtained by genotyping nucleic acids from a cell-free bodily fluid and any treatment provided to the subject before the first time point, and determining a first state of each of the plurality of subjects based on the information at the first time point, to produce a set of first states; (b) obtaining the information about the plurality of subjects at one or more second time points subsequent to the first time point, and determining a second state of each of the plurality of subjects at each of the one or more second time points based on the information at a given one of the one or more second time points, to produce a set of subsequent states; and (c) using the set of first states from (a) and the set of subsequent states from (b) to generate a predictive algorithm that is configured to determine a probability that a given first state will result in a second state among a set of states at a later time point subsequent to the given first state. Additionally or alternatively, detection of a genetic biomarker can include a method, comprising: (a) obtaining information about a subject comprising at least a genetic profile of a tumor and a treatment previously or currently provided to the subject, if any, and determining an initial state of the subject based on the information; (b) providing a decision tree, wherein a root node represents an initial subject state, decision branches represent alternative treatments available to the subject, chance nodes represent points of uncertainty, and decision nodes or terminal nodes represent subsequent states; (c) providing a course of treatment for the subject that maximizes a probability of the subject achieving a living state at a terminal node; and (d) administering the course of treatment to the subject. In some embodiments, the method further comprises: (e) at a second time point subsequent to the initial state, obtaining information about a subject comprising at least a genetic profile of a tumor and a treatment previously or currently provided to the subject, if any, and determining an second state of the subject among a plurality of subsequent states based on the information; (f) based on the second state, providing a subsequent course of treatment for the subject that maximizes probability of the subject

achieving a living state at a terminal node; and (g) administering the subsequent course of treatment to the subject. In some embodiments, the method further comprises: (e) at a second time point subsequent to the initial state, obtaining information about a subject comprising at least a genetic profile of a tumor and a treatment previously or currently provided to the subject, if any, and determining an second state of the subject among a plurality of subsequent states based on the information; (f) based on the second state, providing a subsequent course of treatment for the subject that maximizes probability of the subject achieving a living state at a terminal node; and (g) administering the subsequent course of treatment to the subject.

[480] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 10,017,759, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing a library of nucleic acid fragments, and more specifically to methods for preparing a library of nucleic acid fragments in a single tube using proteases for a variety of applications including, e.g., next generation DNA sequencing. Additionally, a method of preparing a library of tagged nucleic acid fragments including (a) contacting a population of cells directly with a lysis reagent to generate a cell lysate, wherein the lysis reagent has one or more proteases, and wherein the cell lysate contains a target nucleic acid; (b) inactivating the one or more proteases to form an inactivated cell lysate, and (c) directly applying at least one transposase and at least one transposon end composition containing a transferred strand to the inactivated cell lysate under conditions where the target nucleic acid and the transposon end composition undergo a transposition reaction to generate a mixture, wherein (i) the target nucleic acid is fragmented to generate a plurality of target nucleic acid fragments, and (ii) the transferred strand of the transposon end composition is joined to 5′ ends of each of a plurality of the target nucleic acid fragments to generate a plurality of 5′ tagged target nucleic acid fragments. In some embodiments, steps (a), (b), and (c) are performed in a single reaction mixture, e.g., in a tube. In some embodiments, the population of cells is a minimal population of cells. In some embodiments, the minimal population of cells contains one, two, three, four, or five cells. In some embodiments, the target nucleic acid is a double-stranded DNA, and wherein the target nucleic acid remains the double-stranded DNA prior to applying a transposase and a transposon end composition in step (c). In some

embodiments, the target nucleic acid is genomic DNA. In some embodiments, the target nucleic acid contains chromosomal DNA or a fragment thereof. In some embodiments, the target nucleic acid includes a genome or a partial genome. In some embodiments, the method further includes (d) incubating the mixture from step (c) directly with at least one nucleic acid modifying enzyme under conditions wherein a 3′ tag is joined to the 5′ tagged target nucleic acid fragments to generate a plurality of di-tagged target nucleic acid fragments. In some embodiments, steps (a), (b), (c), and (d) are performed in a single reaction tube. In some embodiments, the method further includes (e) amplifying one or more di-tagged target nucleic acid fragments to generate a library of tagged nucleic acid fragments with additional sequence at 5′ end and/or 3′ end of the di-tagged nucleic acid fragments. In some embodiments, steps (a), (b), (c), (d), and (e) are performed in a single reaction tube. In some embodiments, the amplifying includes use of one or more of a polymerase chain reaction (PCR), a strand-displacement amplification reaction, a rolling circle amplification reaction, a ligase chain reaction, a transcription-mediated amplification reaction, or a loop-mediated amplification reaction. In some embodiments, the amplifying includes a PCR using a single primer that is complementary to the 3′ tag of the di-tagged target DNA fragments. In some embodiments, the amplifying includes a PCR using a first and a second primer, wherein at least a 3′ end portion of the first primer is complementary to at least a portion of the 3′ tag of the di-tagged target nucleic acid fragments, and wherein at least a 3′ end portion of the second primer exhibits the sequence of at least a portion of the 5′ tag of the di-tagged target nucleic acid fragments. In some embodiments, a 5′ end portion of the first primer is non-complementary to the 3′ tag of the di-tagged target nucleic acid fragments, and a 5′ end portion of the second primer does not exhibit the sequence of at least a portion of the 5′ tag of the di-tagged target nucleic acid fragments. In some embodiments, the first primer includes a first universal sequence, and/or wherein the second primer includes a second universal sequence. In some embodiments, the method further includes sequencing the tagged nucleic acid fragments. In some embodiments, the sequencing of the tagged nucleic acid fragments includes use of one or more of sequencing by synthesis, bridge PCR, chain termination sequencing, sequencing by hybridization, nanopore sequencing, and sequencing by ligation. In some embodiments, the sequencing of the tagged nucleic acid fragments includes use of next generation sequencing. In some

embodiments, the method further includes analyzing copy number variation. In some embodiments, the method further includes analyzing single nucleotide variation.

[481] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,944,924, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include the use of application-specific capture primers in next generation sequencing. A method of modifying an immobilized capture primer can include: a) providing a solid support having an immobilized application-specific capture primer, the application-specific capture primer including: i) a 3′ portion including an application-specific capture region, and ii) a 5′ portion including a universal capture region; b) contacting an application-specific polynucleotide with the application-specific capture primer under conditions sufficient for hybridization to produce an immobilized application-specific polynucleotide, and c) removing the application-specific capture region of an application-specific capture primer not hybridized to an application-specific polynucleotide to convert the unhybridized application-specific capture primer to a universal capture primer. In some embodiments, a portion of the application-specific capture region is removed. In some embodiments, the application-specific capture primer comprises a plurality of different immobilized application-specific capture primers. In some embodiments, the application-specific polynucleotide comprises a plurality of different application-specific polynucleotides. In some embodiments, the application-specific capture region includes a target-specific capture region and the application-specific polynucleotide includes a target polynucleotide. In some embodiments, the application-specific capture region includes a transposon end (TE) region and the application-specific polynucleotide includes a TE oligonucleotide. In some embodiments, the method further includes applying an oligonucleotide before execution of step c) under conditions sufficient for oligonucleotide hybridization with the universal capture region of an application-specific capture primer to produce a double-stranded DNA region. In certain embodiments, the oligonucleotide is a P5 or P7 oligonucleotide. In some embodiments, the method further includes applying an oligonucleotide before execution of step c) under conditions sufficient for oligonucleotide hybridization with the application-specific capture region of an application-specific capture primer to produce a double-stranded DNA region. In some

embodiments, the method further includes contacting the application-specific capture primer with a nuclease, wherein the application-specific capture region of an application specific capture primer not hybridized with an application-specific polynucleotide to is removed by the nuclease. In some embodiments, the nuclease is an exonuclease. In some embodiments, the exonuclease is exonuclease I. In some embodiments, the exonuclease is exonuclease III. In some embodiments, the nuclease is an endonuclease.

[482] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,992598, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for amplicon preparation. The method includes: (a) contacting a nucleic acid sample including a plurality of target polynucleotides with at least one primer under conditions sufficient for hybridization, the at least one primer containing an adapter; (b) amplifying by polymerase chain reaction (PCR) the plurality of target polynucleotides to produce a plurality of amplicons; (c) directly contacting a plurality of target specific capture primers immobilized on a solid support with the plurality of amplicons under conditions sufficient for hybridization to produce a first plurality of immobilized amplicons, the solid support further including a plurality of universal capture primers; (d) extending the plurality of target specific capture primers to produce a plurality of immobilized extension products complementary to the target polynucleotides; (e) annealing the plurality of universal capture primers to the plurality of the immobilized extension products, and (f) amplifying by PCR the plurality of immobilized extension products to produce a second plurality of immobilized amplicons, wherein the population of immobilized amplicons includes a uniformity of 85% or more. The method can be used with 10 ng or less input nucleic acid and can further include sequencing the second plurality of immobilized amplicons. The method also can be used for determining the presence of a gene associated with a disorder or disease, including a cancer associated gene. Cell free DNA also can be employed in the method. Additionally, detection of a genetic biomarker can include a method for increasing detection sensitivity of a nucleic acid sequence variant, which includes: (a) contacting a nucleic acid sample including a plurality of target polynucleotides with gene specific forward and reverse primers under conditions sufficient for hybridization, each species of the gene specific forward primer

including a unique sequence index and an adapter; (b) amplifying by polymerase chain reaction (PCR) the plurality of target polynucleotides to produce a plurality of amplicons; (c) directly contacting a plurality of target specific capture primers immobilized on a solid support with the plurality of amplicons under conditions sufficient for hybridization to produce a first plurality of immobilized of amplicons, the solid support further including a plurality of universal capture primers; (d) extending the plurality of target specific capture primers to produce a plurality of immobilized extension products complementary to the target polynucleotides; (e) annealing the plurality of universal capture primers to the plurality of the immobilized extension products; (f) amplifying by PCR the plurality of immobilized extension products to produce a second plurality of immobilized amplicons, wherein the second plurality of immobilized amplicons includes a uniformity of 85% or more; (g) sequencing the second plurality of immobilized amplicons, and (h) eliminating random sequence errors for one or more target polynucleotide by comparing three or more nucleotide sequences at a variant position for a target polynucleotide species, wherein the target polynucleotide species are identified by the unique sequence index to thereby determine a true nucleotide sequence variant in the one or more target polynucleotides. The method can detect a mismatch rate of 0.3% or less for a variant nucleotide position.

[483] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,879,312, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for the selective enrichment of nucleic acids. Some embodiments include the selective enrichment of long nucleic acids comprising a target nucleic acid. Some embodiments include the selective enrichment of PCR products. Some embodiments of the methods comprise (a) contacting the population of nucleic acids with a nickase, thereby producing a population of nicked nucleic acids; (b) contacting the population of nicked nucleic acids with an exonuclease, thereby generating a nucleic acid having a single-stranded portion, wherein the single-strand portion comprises at least a portion of the target; (c) contacting a capture probe to the at least a portion of the target, wherein the probe hybridizes to the target; and (d) separating a nucleic acid hybridized to the capture probe from a nucleic acid not bound to the capture probe. In other embodiments, the methods comprise (a) obtaining

a population of nucleic acids, wherein at least some of the nucleic acids in the population comprise a target; (b) contacting the population of nucleic acids with a nickase, thereby producing a population of nicked nucleic acids; (c) contacting the population of nicked nucleic acids with an exonuclease, thereby generating a nucleic acid having a single-stranded portion, wherein the single-strand portion comprises at least a portion of the target; (d) contacting a capture probe to the at least a portion of the target, wherein the probe hybridizes to the target; and (e) separating a nucleic acid hybridized to the capture probe from a nucleic acid not bound to the capture probe. Some embodiments of the methods also include a step of releasing the hybridized nucleic acid from the capture probe. Other embodiments also include amplifying the target. Still further embodiments additionally include sequencing at least a portion of the target. In some embodiments, one or more process steps, for example step (a), can also include contacting the population of double stranded nucleic acids with a type II restriction endonuclease that includes an isoschizomer of the nickase; and recircularizing the cut double stranded nucleic acids under conditions that favor intramolecular recircularization of individual nucleic acids. In such embodiments, various type II restriction endonucleases, or combinations of type II restriction endonucleases, can be used. In some embodiments, for example, the restriction endonuclease includes BbvCI. In other embodiments, the nickase includes Nb.BbvCI and Nt.BbvCI. In some embodiments of the methods, the probe includes a capture moiety. In some such embodiments, the capture moiety includes biotin or streptavidin. In some embodiments, the step of separating a nucleic acid hybridized to the capture probe from a nucleic acid not bound to the capture probe also includes contacting the hybridized target and probe to a binding moiety. In some embodiments, the binding moiety includes avidin, and streptavidin. In some embodiments, the binding moiety also includes a bead, microsphere or other particle. Embodiments of the methods also include repeating one or more steps of the process. In certain embodiments, all of the method steps are repeated. In some embodiments of the methods, the target includes a first capture moiety, and the probe includes a second capture moiety. Some such embodiments also include contacting the first capture moiety to a first binding moiety, thereby providing for enrichment of the target, and contacting the second capture moiety to a second binding moiety, thereby providing for enrichment of the probe. In addition to the foregoing, some embodiments of the methods also provide for the

selective enrichment of a nucleic acid that comprise the steps of (a) providing a population of nucleic acids, wherein at least some of the nucleic acids in the population include a target hybridized with a capture probe; (b) locking the hybridized probe to the target; and (c) separating a nucleic acid locked to a probe from a nucleic acid that is not locked to a probe. In other embodiments, the methods comprise (a) obtaining a population of nucleic acids, wherein at least some of the nucleic acids in the population include a target; (b) hybridizing the target with a capture probe; (c) locking the probe hybridized probe to the target; and (d) separating a nucleic acid locked to a probe from a nucleic acid that is not locked to a probe. In addition to the foregoing, some embodiments of the methods, also include methods for selective enrichment of a nucleic acid that comprise (a) providing a population of nucleic acids, wherein at least some of the nucleic acids in the population include a target that comprises a portion of the 5′ end of a nucleic acid and a portion of the 3′ end of the nucleic acid, said target being hybridized to a selector probe that comprises a first and second oligonucleotide annealed together, wherein the first oligonucleotide is complementary to at least a portion of the 5′ end of the nucleic acid and complementary to at least a portion of the second oligonucleotide, and the second oligonucleotide is complementary to at least a portion of the 3′ end of the nucleic acid; (b) joining the selector probe to the target; and (c) separating a nucleic acid joined to the selector probe from a nucleic acid not joined to the selector probe. Other embodiments of the enrichment methods comprise the steps of (a) obtaining a population of nucleic acids, wherein at least some of the nucleic acids in the population include a target, the target including a portion of the 5′ end of a nucleic acid and a portion of the 3′ end of the nucleic acid; (b) obtaining a selector probe that comprises a first and second oligonucleotide annealed together, wherein the first oligonucleotide is complementary to at least a portion of the 5′ end of the nucleic acid and complementary to at least a portion of the second oligonucleotide, and the second oligonucleotide is complementary to at least a portion of the 3′ end of the nucleic acid; (c) contacting the selector probe to the target, wherein the probe hybridizes to the target; (d) joining the selector probe to the target; and (e) separating a nucleic acid joined to the selector probe from a nucleic acid not joined to the selector probe. In addition to the foregoing, some embodiments of the methods also include methods for selective enrichment of a nucleic acid that comprise (a) providing a population of single-stranded nucleic acids, wherein at least some

of the nucleic acids in the population include a target, the target comprising the 5′ end of a nucleic acid and the 3′ end of the nucleic acid, said target being hybridized to a selector probe that comprises a first and second oligonucleotide annealed together, wherein the first oligonucleotide comprises a 5′ portion complementary to the 3′ end of the nucleic acid, a spacer portion, and a 3′ portion complementary to the 5′ end of the nucleic acid, the second oligonucleotide being complementary to the spacer portion; (b) joining the selector probe to the target; and (c) separating a nucleic acid joined to the selector probe from a nucleic acid not joined to the selector probe. Other embodiments of the methods comprise (a) obtaining a population of single-stranded nucleic acids, wherein at least some of the nucleic acids in the population include a target, the target comprising the 5′ end of a nucleic acid and the 3′ end of the nucleic acid; (b) obtaining a selector probe that includes a first and second oligonucleotide annealed together, wherein the first oligonucleotide comprises a 5′ portion complementary to the 3′ end of the nucleic acid, a spacer portion, and a 3′ portion complementary to the 5′ end of the nucleic acid, the second oligonucleotide being complementary to the spacer portion; (c) contacting the selector probe to the target, wherein the probe hybridizes to the target; (d) joining the selector probe to the target; and (e) separating a nucleic acid joined to the selector probe from a nucleic acid not joined to the selector probe. Some embodiments also include methods for normalizing amplified nucleic acids that include selecting a first population of oligonucleotides having a ratio of oligonucleotides that includes capture moieties to oligonucleotides lacking capture moieties for a first population of oligonucleotides; obtaining a second population of oligonucleotides; amplifying target nucleic acids with the first and second populations of oligonucleotides; and separating amplified targets having incorporated oligonucleotide comprising capture moieties from amplified targets lacking incorporated oligonucleotide capture moieties. In some embodiments, the step of separating further comprises contacting the hybridized target and probe to a binding moiety. In some embodiments, the binding moiety includes avidin and streptavidin. In some embodiments, the binding moiety also includes a bead, microsphere or other particle.

[484] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,828,672, which is hereby incorporated by reference in its entirety. For example, detection of a genetic

biomarker can include reagents for nucleic acid preparation comprising a siderophore. In some embodiments, the siderophore is a bacterial siderophore. In some embodiments, the siderophore is a desferrioxamine B (DFO-B) mesylate salt. In some embodiments, the reagents may comprise a DNA polymerase. In some embodiments, the reagents may comprise dNTPs. In some embodiments, the reagents do not contain EDTA. Some embodiments provide methods for preparing a nucleic acid library, which comprise: providing a plurality of nucleic acid molecules from a sample; and manipulating the plurality of nucleic acid molecules in a reagent for nucleic acid preparation comprising a siderophore. In some embodiments, manipulating the plurality of nucleic acid molecules comprises hybridizing the plurality of nucleic acid molecules to a plurality of oligonucleotide probes. In some embodiments, the plurality of nucleic acid molecules and/or the plurality of oligonucleotide probes are immobilized on a support. In some embodiments, the plurality of nucleic acid molecules and/or the plurality of oligonucleotide probes are immobilized on the support through a binding partner pair to the support. In some embodiments, the support is a magnetic bead. In some embodiments, manipulating the plurality of nucleic acid molecules comprises removing oligonucleotide probes not specifically bound to the plurality of nucleic acid molecules. In some embodiments, the methods comprise modifying the oligonucleotide probes specifically bound to the plurality of nucleic acid molecules. In some embodiments, the methods comprise fragmenting the plurality of nucleic acid molecules. In some embodiments, the methods comprise adding adapters to the plurality of nucleic acid molecules. In some embodiments, the adapters are added to the plurality of nucleic acid molecules by amplification. Some embodiments provide methods for reducing oxidative damage to a nucleic acid molecule, which methods comprise preparing the nucleic acid molecule in the absence of EDTA. In some embodiments, preparing the nucleic acid molecule comprises preparing the nucleic acid molecule in the presence of a siderophore. In some embodiments, the siderophore is a bacterial siderophore. In some embodiments, the siderophore is a desferrioxamine B (DFO-B) mesylate salt. In some embodiments, preparing the nucleic acid molecule comprises exposing the nucleic acid molecule to Fe(III). In some embodiments, preparing the nucleic acid molecule comprises exposing the nucleic acid molecule to a magnetic bead. In some embodiments, the oxidative damage comprises a point mutation in the nucleic acid molecule. In some

embodiments, the point mutation is a C to A transversion. Some embodiments provide methods for increasing the Q (phred) score of a sequencing reaction, which methods comprise preparing a nucleic acid molecule in the absence of EDTA. In some embodiments, preparing the nucleic acid molecule comprises preparing the nucleic acid molecule in the presence of a siderophore. In some embodiments, the siderophore is a bacterial siderophore. In some embodiments, the siderophore is a desferrioxamine B (DFO-B) mesylate salt. In some embodiments, the Q score is greater than about 34. In some embodiments, the Q score is greater than about 38. In some embodiments, the Q score is greater than about 42. In some embodiments, the sequencing reaction is a deep sequencing application. In some embodiments, the deep sequencing application is cancer-related deep sequencing application. In some embodiments, the methods comprise sequencing the nucleic acid molecule in the absence of EDTA. Some embodiments provide kits comprising at least one container means, wherein the at least one container means comprises a reagent for nucleic acid preparation comprising a siderophore. In some embodiments, the siderophore is a desferrioxamine B (DFO-B) mesylate salt. In some embodiments, the reagent does not contain EDTA.

[485] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,708,655, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions, systems, and methods for detecting events using tethers anchored to or adjacent to nanopores. In some embodiments, a composition includes a nanopore including a first side, a second side, and an aperture extending through the first and second sides; and a permanent tether including a head region, a tail region, and an elongated body disposed therebetween. The head region can be anchored to or adjacent to the first side or second side of the nanopore. The elongated body including a reporter region can be movable within the aperture responsive to a first event occurring adjacent to the first side of the nanopore. In one non-limiting example, the head region can be anchored to a molecule, such as a protein, disposed on the first side or second side of the nanopore. In some embodiments, a method includes providing a nanopore including a first side, a second side, and an aperture extending through the first and second sides; and providing a permanent tether including a head region, a tail region, and an elongated body disposed therebetween. The head region can

be anchored to or adjacent to the first or second side of the nanopore, and the elongated body can include a reporter region. The method can include moving the reporter within the aperture responsive to a first event occurring adjacent to the first side of the nanopore. In some embodiments, the reporter region is translationally movable within the aperture responsive to the first event. Additionally, or alternatively, the reporter region can be rotationally movable within the aperture responsive to the first event. Additionally, or alternatively, the reporter region can be conformationally movable within the aperture responsive to the first event. In some embodiments, the head region is anchored to or adjacent to the first side or second side of the nanopore via a covalent bond. The head region can be anchored to the first side of the nanopore. The tail region can extend freely toward the second side of the nanopore. In some embodiments, the reporter region is translationally movable toward the first side of the nanopore responsive to the first event. The reporter region can be translationally movable toward the second side after the first event. The reporter region further can be translationally movable toward the first side responsive to a second event occurring adjacent to the first side of the nanopore, the second event being after the first event. The reporter region further can be translationally movable toward the second side after the second event. In some embodiments, the first event includes adding a first nucleotide to a polynucleotide. In embodiments that include a second event, the second event can include adding a second nucleotide to the polynucleotide. An electrical or flux blockade characteristic of the reporter region can be different than an electrical or flux blockade characteristic of another region of the elongated body. In some embodiments, a system can include a composition and measurement circuitry configured to measure a first current or flux through the aperture or to measure a first optical signal while the reporter region is moved responsive to the first event.

[486] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,670,530, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of determining a haplotype or partial haplotype of a DNA sample containing high molecular weight segments of genomic DNA. Such methods may be characterized by the following operations: (a) processing the DNA sample to produce an enriched DNA sample enriched for DNA from a first high molecular weight segment having a

plurality of alleles from a first haplotype; (b) sequencing DNA in the enriched DNA sample to produce a plurality of sequence reads, which are shorter in length than the first high molecular weight segment, where some of the sequence reads contain a first allele of the first haplotype and other of the sequence reads contain a second allele of the first haplotype; (c) aligning the sequence reads to a reference genome to produce aligned reads, where aligned reads from the first high molecular weight segment tend to cluster into islands on the reference genome; (d) determining distances separating adjacent ones of the aligned reads on the reference genome, where the separation distances between adjacent aligned reads fall into at least two groups distinguishable by the magnitude of their separation distances; (e) selecting a first group of the aligned reads having separation distances to adjacent aligned reads that are smaller than a cutoff value, thereby excluding aligned reads having greater separation distances, where at least a portion of the first group of the aligned reads belong to the same island on the reference genome; and (f) using alleles from the first group of aligned reads to define a first haplotype or first partial haplotype. In some embodiments, the methods have an additional operation of determining a complete haplotype from the first partial haplotype and other partial haplotypes. In some embodiments, selecting a first group of the aligned reads includes determining the cutoff value. As an example, the determining the cutoff value includes: (i) generating a mixture model from the separation distances between adjacent aligned reads, wherein the mixture model fits two distributions to the separation distances; and (ii) determining the cutoff value from a property of at least one of the two distributions. In some cases, each of the two distributions comprises its own central tendency (e.g., the mean of a Gaussian distribution). In certain embodiments, selecting a first group of the aligned reads includes determining the cutoff value. As an example, the determining the cutoff value includes: (i) generating a mixture model from the separation distances between adjacent aligned reads, wherein the mixture model fits two distributions to the separation distances; and (ii) determining the cutoff value from a property of at least one of the two distributions. In some cases, each of the two distributions comprises its own central tendency (e.g., the mean of a Gaussian distribution). In certain embodiments, generating a mixture model involves applying an expectation maximization procedure to the separation distances between adjacent aligned reads. In some implementations, determining the cutoff value includes an operation of identifying a fraction

of the probability mass of the distribution containing the shorter separation distances. For example, the fraction of the probability mass of the distribution containing the shorter separation distances may be about 80% or greater.

[487] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,587,273, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of selecting a representational sample of nucleic acid sequences from a complex mixture. The method includes: (a) contacting a complex mixture of nucleic acids under conditions sufficient for hybridization with a population of capture probes complementary to one or more nucleic acids comprising a predetermined portion of the sequence collectively present in the complex mixture to form hybridization complexes of the one or more nucleic acids with the population of probes, the population of capture probes being attached to a solid support, and (b) removing unhybridized nucleic acids to select a representational sample of nucleic acids having a complexity of less than 10% but more than 0.001% of the complex mixture, wherein the representational sample comprises a nucleic acid copy having a proportion of each sequence in the copy relative to all other sequences in the copy substantially the same as the proportions of the sequences in the predetermined portion of one or more nucleic acids within the complex mixture. Additionally or alternatively, detection of a genetic biomarker can include a method of selecting a representational sample of genomic sequences from a complete genome. In some embodiments, the method further provides a nucleic acid population that includes a representational sample having a complexity of less than 10% but more than 0.001% of a complex mixture, the representational sample comprising a nucleic acid copy having a proportion of each sequence in the copy relative to all other sequences in the copy substantially the same as the proportions of sequences in a predetermined portion of a sequence collectively present in one or more nucleic acids within the complex mixture.

[488] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,574,234, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions for analyzing nucleic acid sequences. In

some embodiments, the methods utilize clonal objects, such as DNA balls, that have been captured on beads. Some embodiments provide compositions having a bead and one clonal object, wherein the clonal object is affinity bound or hybridized to the bead, for example, through patch on the surface of the bead, such as an affinity binding patch or a hybridization patch. In some aspects, the patch includes a plurality of polynucleotides attached to a single region on the surface of the bead. Some embodiments also provide a population of beads having affinity bound or hybridized clonal objects. In particular embodiments, each of the clonal objects are affinity bound or hybridized to the beads through a patch on the surface of each bead, such as an affinity binding patch or a hybridization patch. The ratio of beads to bound or hybridized clonal objects in the population can be 1:1. In particular embodiments, no more than one clonal object is bound or hybridized to any given bead in the population. Using these methods, compositions can be fabricated wherein a bead and one clonal object are affinity bound or hybridized to each other through attachment to a patch on the surface of the bead. Some embodiments can provide a method of fabricating an affinity binding patch on a bead by providing a bead having a plurality of capture moieties; providing a solid surface having a plurality of capture-complement moieties, wherein the capture-complement moieties further comprise a cleavable moiety and an affinity ligand; specifically binding the capture moieties to the capture-complement moieties, thereby forming an immobilized bead on the solid surface; and cleaving the cleavable moiety so as to retain the affinity ligand on the bead, thereby fabricating an affinity binding patch on the bead. In particular embodiments, the capture moieties or the capture-complement moieties or both include capture sequences of polynucleotides. Accordingly, Some embodiments can provide a method of fabricating an affinity binding patch on a bead by providing a bead having a plurality of first polynucleotides attached to the surface of the bead, wherein the first polynucleotides each have a capture sequence; providing a solid surface having a plurality of second polynucleotides attached to the solid surface, wherein the second polynucleotides each have a capture-complement sequence, a cleavable moiety and an affinity ligand; hybridizing the capture sequences of the first polynucleotides to the capture-complement sequences of the second polynucleotides, thereby forming an immobilized bead on the solid surface; and cleaving the second polynucleotides at the cleavable moiety so as to retain the affinity ligand on the second plurality

of polynucleotides, thereby fabricating an affinity binding patch on the bead. In some aspects, the method further includes fabricating one clonal object bound to the affinity binding patch by contacting the affinity ligand with a binding agent, wherein the binding agent has two or more binding sites, and binding one clonal object to the binding agent through a second affinity ligand on the clonal object, wherein the one clonal object has a single tandemly repeated target nucleic acid molecule, thereby fabricating one clonal object bound to the affinity binding patch. Some embodiments can provide a method of fabricating a bead having one clonal object by providing a bead having a plurality of first capture moieties; providing a solid surface having a plurality of second capture moieties patterned into patches on the surface, wherein the second capture moieties each have a cleavable moiety, wherein one clonal object is bound to one patch on the surface via one or more of the second capture moieties, wherein the one clonal object has a single tandemly repeated target nucleic acid molecule; specifically binding the first capture moiety to the clonal object, thereby forming an immobilized bead on the solid surface, and cleaving the cleavable moiety so as to retain the clonal object, thereby fabricating a bead having one clonal object. In particular embodiments, the capture moieties comprise polynucleotides. Accordingly, Some embodiments can provide a method of fabricating a bead having one clonal object by providing a bead having a plurality of first polynucleotides; providing a solid surface having a plurality of second polynucleotides patterned into patches on the surface, wherein the second polynucleotides each have a cleavable moiety, wherein one clonal object is hybridized to one polynucleotide patch on the surface, wherein the one clonal object has a single tandemly repeated target nucleic acid molecule; hybridizing the first polynucleotides to the clonal object, thereby forming an immobilized bead on the solid surface, and cleaving the second polynucleotides at the cleavable moiety so as to retain the clonal object, thereby fabricating a bead having one clonal object. Some embodiments can provide a method of fabricating a hybridization patch on a bead by providing a bead having a plurality of first polynucleotides attached to the surface of the bead, wherein the first polynucleotides each have a first capture sequence, providing a solid surface having a plurality of second polynucleotides attached to the solid surface, wherein the second polynucleotides each have a first capture-complement sequence and a second capture-complement sequence, hybridizing the first capture sequences of the first polynucleotides to the first capture-complement

sequence of the second polynucleotides, thereby forming an immobilized bead on the solid surface, and extending the first polynucleotides of the immobilized bead using the second capture-complement sequence as a template, thereby fabricating a hybridization patch of extended first polynucleotides on the bead, the extended first polynucleotides having a second capture sequence. In some aspects, the method further includes fabricating one clonal object bound to the patch on the bead by providing a clonal object having the second capture-complement sequence, and hybridizing the second capture-complement sequence of the clonal object to the second capture sequences of the bead, thereby fabricating one clonal object bound to the patch on the bead. In some aspects of the method, extending the first polynucleotides includes the addition of one or more nucleoside triphosphates having an affinity ligand, thereby fabricating an affinity binding patch on the bead. Some embodiments include methods of amplifying a target nucleic acid molecule. Some embodiments provide a method of amplifying a target nucleic acid molecule by placing the compositions or populations of beads having affinity bound or hybridized clonal objects onto a solid surface having microwells, wherein only one bead can spatially fit into one microwell and amplifying the target nucleic acid molecules in the microwells, thereby forming amplicons. In some aspects, the method further includes sequencing the amplified target nucleic acid molecules using methods such as sequencing by synthesis, sequencing by ligation or sequencing by hybridization, thereby determining the nucleic acid sequence of the target nucleic acid molecule.

[489] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,453,258, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include determination of a sequence, for example a nucleic acid sequence, using a minimal dye set, minimal excitation light sources, and minimal optical emission filters while still allowing for differentiation of the incorporation of all four nucleotides in a sequencing reaction. Additionally or alternatively, detection of a genetic biomarker can include methods for determining the sequence of a polynucleotide comprising detecting in a sequencing reaction the incorporation of three different types of detectable nucleotide conjugates into a polynucleotide and determining the incorporation of a fourth type of nucleotide based on the detection pattern of the three different types of detectable nucleotides into the polynucleotide

thereby determining the sequence of a polynucleotide, wherein the incorporation of three different types of detectable nucleotide conjugates is detected from a signal state and wherein the incorporation of the fourth type of nucleotide is determined from a dark state. Additionally or alternatively, detection of a genetic biomarker can include methods for determining the sequence of a polynucleotide comprising applying to a polynucleotide sample for sequencing a solution comprising four modified nucleotide types wherein three modified nucleotide types are conjugated to one or more detection moieties and one or more linkers positioned between the nucleotide and the one or more detection moieties, and wherein a fourth nucleotide type lacks a detection moiety, detecting a pattern of incorporation of said modified nucleotides in a sequencing reaction thereby capturing a first detectable pattern, applying one or more compositions to the sequencing reaction thereby changing the first detectable pattern, detecting a second detectable pattern, and determining the sequence of the polynucleotide sample based on the detectable patterns. In some embodiments, the polynucleotide for sequencing comprises one or more of deoxyribonucleic acids, modified deoxyribonucleic acids, ribonucleic acids and modified ribonucleic acids. In some embodiments, the polynucleotide for sequencing is a genomic DNA library preparation. In some embodiments, the nucleotide conjugate comprises nucleotide types selected from the group consisting of dATP, dTTP, dUTP, dCTP, dGTP or non-natural nucleotide analogs thereof. In some embodiments, the non-natural nucleotide analog comprises a reversible terminator moiety and is selected from the group consisting of rbATP, rbTTP, rbCTP, rbUTP and rbGTP. In some embodiments, the nucleotide incorporation is sequence by synthesis, sequence by ligation, and sequence by hybridization or a combination thereof. In some embodiments, the three nucleotide type conjugates are detected by detecting a fluorescent moiety. In some embodiments, the fluorescent moiety is the same for the three nucleotide conjugates whereas in other embodiments the fluorescent moiety is one or more different fluorescent moieties. In some embodiments, the one or more different fluorescent moieties are detected by the same emission filter. In some embodiments, the fluorescent moiety comprises a fluorescent resonance energy transfer system moiety. In some embodiments, the incorporation of the fourth nucleotide is determined by lack of detection. In some embodiments, the detectable nucleic acid conjugates are detected by fluorescence. In some embodiments, the fluorescence is detected by a first and a second imaging event, in further

embodiments the first and second imaging events are separated in time. In some embodiments, the first imaging event detects a pattern of fluorescence that is different from the pattern of fluorescence detected by the second imaging event. In some embodiments, the incorporation of one or more nucleotides is determined by the difference in the pattern of fluorescence between the first and second imaging events. In some embodiments, the one or more nucleotide type conjugates further comprise one or more linker sequences, in further embodiments the one or more linker sequences comprise one or more of a cleavable linker and a spacer linker. In some embodiments, the cleavable linker comprises one or more cleavable linkage groups selected from the group consisting of a disulfide, a diol, a diazo, an ester, a sulfone, an azide, an alyl and a silyl ether, whereas in preferred embodiments the cleavable linkage group is a disulfide. In some embodiments, the spacer linker is one or more of polyethylene glycol or concatamers thereof and 2-{2-[3-(2-amino-ethylcarbornyl)-phenoxy]-1-azido-ethoxy}-ethoxy-acetic acid. In some embodiments, the one or more spacer linkers further comprise one or more cleavable linkage groups wherein the cleavable linkage group is selected from the group consisting of a disulfide, a diol, a diazo, an ester, a sulfone, an azide, an alyl and a silyl ether. In some embodiments, the spacer linker is polyethylene glycol or concatamers thereof whereas in other embodiments the spacer linker is 2-{2-[3-(2-amino-ethylcarbornyl)-phenoxy]-1-azido-ethoxy}-ethoxy-acetic acid. In some embodiments, the one or more nucleotide conjugates comprise a polyethylene glycol linker and a 2-{2-[3-(2-amino-ethylcarbornyl)-phenoxy]-1-azido-ethoxy}-ethoxy-acetic acid linker which may or may not further comprise a hapten and a fluorescent moiety. In some embodiments, the hapten is selected from the group consisting of biotin, digoxigenin and dinitrophenol. In some embodiments, the one or more nucleotide conjugates comprises a streptavidin-fluorescent moiety conjugate whereas in other embodiments, the one or more nucleotide conjugates comprises an anti-hapten antibody-fluorescent moiety conjugate selected from the group consisting of anti-digoxigenin and anti-dinitrophenol. In some embodiments the nucleotide conjugate comprising a polyethylene glycol linker and a 2-{2-[3-(2-amino-ethylcarbornyl)-phenoxy]-1-azido-ethoxy}-ethoxy-acetic acid linker further comprises two fluorescent moieties. In some embodiments, the two fluorescent moieties constitute a fluorescence resonance energy transfer system.

[490] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,441,267, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of determining the identity of a nucleotide at a detection position in a target sequence. The methods comprise providing a hybridization complex comprising the target sequence and a capture probe covalently attached to a microsphere on a surface of a substrate. The methods comprise determining the nucleotide at the detection position. The hybridization complex can comprise the capture probe, a capture extender probe, and the target sequence. In addition, the target sequence may comprise exogeneous adapter sequences. In an additional aspect, the method comprises contacting the micro spheres with a plurality of detection probes each comprising a unique nucleotide at the readout position and a unique detectable label. The signal from at least one of the detectable labels is detected to identify the nucleotide at the detection position. In an additional aspect, the detection probe does not contain detection label, but rather is identified based on its characteristic mass, for example via mass spectrometry. In addition, the detection probe comprises a unique label that is detected based on its characteristic mass. Additionally or alternatively, detection of a genetic biomarker can include methods wherein the target sequence comprises a first target domain directly 5′ adjacent to the detection position. The hybridization complex comprises the target sequence, a capture probe and an extension primer hybridized to the first target domain of the target sequence. The determination step comprises contacting the micro spheres with a polymerase enzyme, and a plurality of NTPs each comprising a covalently attached detectable label, under conditions whereby if one of the NTPs basepairs with the base at the detection position, the extension primer is extended by the enzyme to incorporate the label. As is known to those in the art, dNTPs and ddNTPs are the preferred substrates for DNA polymerases. NTPs are the preferred substrates for RNA polymerases. The base at the detection position is then identified. Additionally or alternatively, detection of a genetic biomarker can include methods wherein the target sequence comprises a first target domain directly 5′ adjacent to the detection position, wherein the capture probe serves as an extension primer and is hybridized to the first target domain of the target sequence. The determination step comprises contacting the micro spheres with a polymerase enzyme, and a plurality of NTPs each comprising a covalently

attached detectable label, under conditions whereby if one of the NTPs basepairs with the base at the detection position, the extension primer is extended by the enzyme to incorporate the label. The base at the detection position is thus identified. Additionally or alternatively, detection of a genetic biomarker can include methods wherein the target sequence comprises (5′ to 3′), a first target domain comprising an overlap domain comprising at least a nucleotide in the detection position and a second target domain contiguous with the detection position. The hybridization complex comprises a first probe hybridized to the first target domain, and a second probe hybridized to the second target domain. The second probe comprises a detection sequence that does not hybridize with the target sequence, and a detectable label. If the second probe comprises a base that is perfectly complementary to the detection position a cleavage structure is formed. The method further comprises contacting the hybridization complex with a cleavage enzyme that will cleave the detection sequence from the signalling probe and then forming an assay complex with the detection sequence, a capture probe covalently attached to a microsphere on a surface of a substrate, and at least one label. The base at the detection position is thus identified.

[491] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,060,431, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include array compositions comprising a substrate with a surface comprising discrete sites. The composition can further comprise a population of microspheres comprising at least a first and a second subpopulation; each subpopulation comprises a bioactive agent; and an identifier binding ligand that will bind a decoder binding ligand such that the identity of the bioactive agent can be elucidated. The microspheres are distributed on the surface. Some embodiments provide array compositions comprising a substrate with a surface comprising discrete sites, and a population of microspheres comprising at least a first and a second subpopulation. Each subpopulation comprises a bioactive agent and does not comprise an optical signature. Some embodiments provide methods of making an array composition as outlined above. The methods comprise forming a surface comprising individual sites on a substrate and distributing microspheres on said surface such that said individual sites contain microspheres. The microspheres comprise at least a first and a second subpopulation each

comprising a bioactive agent and do not comprise an optical signature. Some embodiments provide methods of making a composition comprising forming a surface comprising individual sites on a substrate and distributing microspheres on the surface such that the individual sites contain microspheres. The microspheres comprise at least a first and a second subpopulation each comprising a bioactive agent and an identifier binding ligand that will bind a decoder binding ligand such that the identification of the bioactive agent can be elucidated. Additionally or alternatively, detection of a genetic biomarker can include methods of decoding an array composition comprising providing an array composition as outlined above, and adding a plurality of decoding binding ligands to the array composition to identify the location of at least a plurality of the bioactive agents. Additionally or alternatively, detection of a genetic biomarker can include methods of determining the presence of a target analyte in a sample. The methods comprise contacting the sample with an array composition as outlined above, and determining the presence or absence of the target analyte. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing an array composition comprising a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent and at least a first and a second decoding attribute, and detecting each of said first and second decoding attributes to identify each of said bioactive agents. Additionally or alternatively, detection of a genetic biomarker can include a method of increasing the information obtained in a decoding step. The method includes the use of degenerate probes as DBL-IBL combinations. Additionally or alternatively, detection of a genetic biomarker can include the use of multiple decoding attributes on a bead. Additionally or alternatively, detection of a genetic biomarker can include a method of increasing the confidence of decoding. The method includes using the decoding as a quality control measure. Additionally or alternatively, detection of a genetic biomarker can include a method of decoding an array composition comprising providing an array composition comprising a population of microspheres comprising at least 50 subpopulations, wherein each subpopulation comprises a bioactive agent adding a plurality of decoding binding ligands to said population of microspheres to identify at least 50 of the bioactive agents. Additionally or alternatively, detection of a genetic biomarker can include a method of determining the presence of a target analyte in a sample comprising contacting said

sample with a composition comprising a population of microspheres comprising at least 50 subpopulations, wherein each subpopulation comprises a bioactive agent adding a plurality of decoding binding ligands to said population of microspheres to identify at least 50 of the bioactive agents and determining the presence or absence of said target analyte.

[492] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,060,431, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include microfluidic devices for the detection of a target analyte in a sample. The devices comprise a solid support that has any number of modules, including a sample inlet port and at least one sample handling well comprising a well inlet port and a well outlet port. The device generally further comprises a first microchannel to allow fluid contact between the sample inlet port and the sample handling well. The device also comprises a detection module comprising a substrate with a surface comprising discrete sites, and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on said surface. The detection module also comprises a detection inlet port to receive the sample. The device also comprises a second microchannel to allow fluid contact between the sample handling well and the detection inlet port. Additionally or alternatively, detection of a genetic biomarker can include a method of assembling a detector in a microfluidic device. The method includes providing a microfluidic device comprising a first microchannel to allow fluid contact between a sample inlet port and a sample handling well, a second microchannel to allow fluid contact between said sample handling well and a detection inlet port, and a detection module comprising a substrate with a surface comprising discrete sites. The method further includes flowing a fluid across the substrate. The fluid comprises a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent, whereby the beads flow across the discrete sites, and are deposited randomly in the discrete sites. The method additionally includes reversing the flow of the fluid. Additionally or alternatively, detection of a genetic biomarker can include a method of assembling a detector in a microfluidic device. The method includes providing a microfluidic device comprising a plurality of first micro channels, and a population of microspheres in

microchannels. The device further includes a receiving chamber connected to said microchannels. The method further includes flowing said microspheres through said microchannels into said receiving chamber.

[493] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,222,134, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, systems and compositions for detecting molecules. In particular, methods, systems and compositions for detecting multiple types of molecules on a solid support. Some embodiments relate to methods for detecting molecules. In some embodiments, such methods comprise the steps of (a) providing a solid support comprising molecules associated with a site on the solid support such that the molecules are detected in aggregate during a detection step, wherein the site comprises at least two different types of molecules; (b) detecting a signal corresponding to the aggregate of molecules at the site; (c) estimating the fraction of different types of molecules at the site or estimating the amount of signal corresponding to different types of molecules at the site; (d) calculating the amount of signal corresponding to different types of molecules at the site using the fraction estimate, thereby obtaining a signal estimate or calculating the fraction of different types of molecules at the site using the signal estimate, thereby obtaining a fraction estimate; and (e) iteratively updating the fraction estimate and signal estimate until the estimates converge, thereby detecting molecules associated with the site. In some embodiments of the above-described methods, the providing step further comprises providing a mixture of molecules to the solid support. In other embodiments, the providing step further comprises associating the molecules with the site. In still other embodiments, the providing step further comprises attaching the molecules at the site. In some embodiments of the above-described methods, the estimating step is performed by guessing the fraction of different types of molecules at the site or guessing the amount of signal corresponding to different types of molecules at the site. In other embodiments, the estimating step comprises performing a principal component analysis (PCA). In some embodiments of the above-described methods, the updating step comprises performing a numerical optimization algorithm. In some such methods, the numerical optimization algorithm is based on an iterative map search. In some such embodiments, the

numerical optimization algorithm is based on Fienup's iteration map. In some embodiments of the above-described methods, sequence data is obtained for one or more molecules. In some such methods, sequence data is obtained by a sequencing-by-synthesis process. In certain embodiments, the sequencing-by-synthesis process comprises a pyrosequencing process. In some embodiments of the above-described methods, the solid support comprises a bead. In some other embodiments, the solid support comprises a flow-cell. In preferred embodiments of the above-described methods, the molecules comprise nucleic acids. In some such methods, the nucleic acids are attached at the site. In some embodiments, the nucleic acids comprise a first subpopulation of nucleic acids and a second subpopulation of nucleic acids, wherein the nucleic acids of the first subpopulation each have an identical target region and the nucleic acids of the second subpopulation each have an identical region that is a variant of the target region. In some embodiments, the nucleotide sequence of the target region of the nucleic acids of the first subpopulation has at least 1 nucleotide that is different as compared to the nucleotide sequence of the variant of the target region of the nucleic acids of the second subpopulation. In some embodiments, the nucleotide sequence of the target region of the nucleic acids of the first subpopulation has at least 3 nucleotides that are different as compared to the nucleotide sequence of the variant of the target region of the nucleic acids of the second subpopulation. In some embodiments, a nucleotide sequence difference between the target region in the nucleic acids of the first subpopulation and the variant of the target region in the nucleic acids of the second subpopulation comprises at least one difference selected from the group consisting of a mutation, a polymorphism, an insertion, a deletion, a substitution, a simple tandem repeat polymorphism, and a single nucleotide polymorphism (SNP). In some embodiments, the nucleic acids comprise alleles of a genetic locus from a polyploid organism. In some other embodiments, the nucleic acids comprise alternative splicing forms of a nucleic acid. In yet other embodiments, the nucleic acids comprise alleles of a genetic locus from a diploid organism. Also described are molecule detection systems. The molecule detection systems can comprise a solid support comprising molecules associated with a site on the solid support such that the molecules are detected in aggregate, wherein the molecules comprise at least two different types of molecules, and a detector configured to detect the molecules associated with the site. In some embodiments, the molecules are attached at the site. In a

preferred embodiment, the molecules comprise nucleic acids. In some embodiments of the molecule detection systems, a site comprises about 2 to about 1011 molecules, about 2 to about 1010 molecules, about 2 to about 109 molecules, about 2 to about 108 molecules, about 2 to about 107 molecules, about 2 to about 106 molecules, about 2 to about 105 molecules, about 2 to about 104 molecules. In some embodiments, the molecules are associated with the site. In other embodiments, the molecules are attached at the site. In certain embodiments, the molecules comprise nucleic acids. Some embodiments of the above-described molecule detection systems can further comprise a fluid handling system configured to apply fluid to the site. Other embodiments of the above-described molecule detection systems can further comprise a light source configured to provide an excitation beam to the site. Some embodiments of the above-described molecule detection systems can further comprise a first data processing module configured to estimate the fraction of different types of molecules at the site or the amount of signal corresponding to different types of molecules at the site. In some embodiments, the first data processing module is also used for determining the variation associated with the estimate. In other embodiments, the determining step is performed using a separate data processing module. In some embodiments of such systems, the systems can further comprise a second data processing module configured to calculate the amount of signal corresponding to different types of molecules at the site using the fraction estimate or to calculate the fraction of different types of molecules at the site using the signal estimate. In other embodiments of such systems, the systems can further comprise a third data processing module configured to iteratively update the fraction estimate and signal estimate. In some embodiments of the above-described molecule detection systems, the systems are configured to identify the nucleotide sequence of a target region of a nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include methods of identifying a target region of a nucleic acid. The methods can comprise (a) associating a first subpopulation of nucleic acids with a site on a solid support, wherein nucleic acids of the first subpopulation comprise an identical target region; (b) associating a second subpopulation of nucleic acids with the site on the solid support, wherein nucleic acids of the second subpopulation comprise an identical target region that is a variant of the target region of the nucleic acids of the first subpopulation; (c) detecting a signal corresponding to one or more nucleotides of the target

region of first subpopulation nucleic acids and one or more nucleotides of the variant of the target region of second subpopulation nucleic acids; (d) estimating the fraction of first subpopulation nucleic acids and second subpopulation nucleic acids associated with the site or estimating the amount of signal corresponding to first subpopulation nucleic acids and second subpopulation nucleic acids associated with the site; (e) calculating the amount of signal corresponding to first subpopulation nucleic acids and second subpopulation nucleic acids associated with the site using the fraction estimate, or calculating the fraction of first subpopulation nucleic acids and second subpopulation nucleic acids associated with the site using the signal estimate; and (f) iteratively updating the fraction estimate and signal estimate until the estimates converge, thereby identifying a target region of a nucleic acid. In some embodiments of the above-described methods, step (a) comprises attaching first subpopulation nucleic acids and second subpopulation nucleic acids to the solid support. In some embodiments of the above-described methods, step (d) comprises performing a principal component analysis (PCA). In some embodiments of the above-described methods, step (f) comprises performing a numerical optimization algorithm. In some such embodiments, the numerical optimization algorithm is based on iterative map search. In some other embodiments, the numerical optimization algorithm is based on Fienup's iteration map. In some embodiments of the above-described methods, sequence data is obtained from both first and second subpopulation nucleic acids. In some such embodiments, sequence data is obtained by a sequencing-by-synthesis process. In some embodiments, the sequencing-by-synthesis process comprises a pyrosequencing process. Additionally or alternatively, detection of a genetic biomarker can include methods for identifying a biosignature. The methods can comprise the steps of (a) providing samples obtained from a plurality of subjects, wherein the samples comprise molecules; (b) tagging molecules from the samples so as to identify the subject from which each sample originated; (c) associating molecules from the samples with a site on a solid support such that the molecules are detected in aggregate during a detection step, wherein the site comprises at least two different types of molecules; (d) obtaining a biosignature for molecules associated with the site by: i) detecting a signal corresponding to the aggregate of the molecules at the site, ii) estimating the fraction of different types of molecules at the site or the amount of signal corresponding to different types of molecules at

the site, iii) calculating the amount of signal corresponding to different types of molecules at the site using the fraction estimate, or calculating the fraction of different types of molecules at the site using the signal estimate, and iv) iteratively updating the fraction estimate and signal estimate until the estimates converge, thereby obtaining a biosignature for molecules at the site; and (e) comparing the biosignature obtained in step (d) to a reference biosignature, thereby identifying the biosignature. In a preferred embodiment, the molecules are attached at the site. In a preferred embodiment of the above-described methods, the molecules comprise nucleic acids. In some such embodiments, the nucleic acids comprise a marker from a pathogen. In certain embodiments, the pathogen comprises a pathogen selected from the group consisting of a virus, a bacterium and a eukaryotic cell. In some embodiments, the eukaryotic cell can be a cancer cell. In some embodiments of the above-described methods, the sample comprises an abnormal cell type. In some embodiments of the above-described methods, the sample is obtained from a cancer patient. Also described is a solid support including a population of nucleic acids associated with a site on the solid support such that nucleic acids of the population of nucleic acids are detected in aggregate, the population of nucleic acids comprising a first subpopulation and a second subpopulation, wherein nucleic acids of the first subpopulation comprise an identical target region and nucleic acids of the second subpopulation comprise an identical region that is a variant of the target region. Additionally or alternatively, detection of a genetic biomarker can include beads comprising a first subpopulation of capture nucleic acids having a competitor molecule hybridized thereto and a second subpopulation of capture nucleic acids comprising a region that permits hybridization of a complementary molecule. Additionally or alternatively, detection of a genetic biomarker can include beads comprising capture nucleic acids hybridized with an amplified nucleic acid comprising a degenerate tag, the degenerate tag being hybridized to a capture nucleic acid. In some embodiments, the bead is present in a channel of a substrate. In other embodiments, the bead is present in a well of a multiwell substrate. In a preferred embodiment, the well is configured to hold a single bead having the amplified nucleic acids hybridized thereto.

[494] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,163,283, which is hereby incorporated by reference in its entirety. For example, detection of a genetic

biomarker can include compositions comprising a plurality of nucleic acids, each nucleic acid comprising an invariant sequence, a variable sequence and a label. Additionally or alternatively, detection of a genetic biomarker can include a method for decoding an array composition. The method includes providing an array composition comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising first and second subpopulations, each subpopulation comprising an identifier nucleic acid sequence comprising a primer sequence and a decoder sequence. The method further comprises adding to the array a first set of combinatorial decoding probes comprising a priming sequence, at least one decoding nucleotide and a label, and detecting the presence of the label.

[495] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,045,796, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting one or several typable loci contained within a given genome, where the method includes the steps of providing an amplified representative population of genome fragments having such typable loci, contacting the genome fragments with a plurality of nucleic acid probes having sequences corresponding to the typable loci under conditions wherein probe-fragment hybrids are formed; and detecting typable loci of the probe-fragment hybrids. In particular embodiments these nucleic acid probes are at most 125 nucleotides in length. However, probes having any of a variety of lengths or sequences can be used as set forth in more detail below. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting typable loci of a genome including the steps of providing an amplified representative population of genome fragments that has such typable loci, contacting the genome fragments with a plurality of nucleic acid probes having sequences corresponding to the typable loci under conditions wherein probe-fragment hybrids are formed; and directly detecting typable loci of the probe-fragment hybrids. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting typable loci of a genome including the steps of providing an amplified representative population of genome fragments having the typable loci; contacting the genome fragments with a plurality of immobilized nucleic acid probes having sequences corresponding to the typable loci under conditions wherein immobilized probe-fragment hybrids are formed; modifying the immobilized probe-

fragment hybrids; and detecting a probe or fragment that has been modified, thereby detecting the typable loci of the genome. Additionally or alternatively, detection of a genetic biomarker can include a method, including the steps of (a) providing a plurality of genome fragments, wherein the plurality of genome fragments has at least 100 ug of DNA having a complexity of at least 1 Gigabases; (b) contacting the plurality of genome fragments with a plurality of different immobilized nucleic acid probes, wherein at least 500 of the different nucleic acid probes hybridize with genome fragments to form probe-fragment hybrids; and (c) detecting typable loci of the probe-fragment hybrids. Additionally or alternatively, detection of a genetic biomarker can include a method can also include the steps of (a) providing a plurality of genome fragments, wherein the plurality of genome fragments has a concentration of at least 1 ug/ul of DNA having a complexity of at least 1 Gigabases; (b) contacting the plurality of genome fragments with a plurality of different immobilized nucleic acid probes, wherein at least 500 of the different nucleic acid probes hybridize with genome fragments to form probe-fragment hybrids; and (c) detecting typable loci of the probe-fragment hybrids. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying genomic DNA, including the steps of providing isolated double stranded genomic DNA, producing nicked DNA by contacting the double stranded genomic DNA with a nicking agent, contacting this nicked DNA with a strand displacing polymerase and a plurality of primers, so as to amplify the genomic DNA. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting typable loci of a genome. The method includes the steps of (a) in vitro transcribing a plurality of amplified gDNA fragments, thereby obtaining genomic RNA (gRNA) fragments; (b) hybridizing the gRNA fragments with a plurality of nucleic acid probes having sequences corresponding to the typable loci; and (c) detecting typable loci of the gRNA fragments that hybridize to the probes. Additionally or alternatively, detection of a genetic biomarker can include a method of producing a reduced complexity, locus-specific, amplified representative population of genome fragments. The method includes the steps of (a) replicating a native genome with a plurality of random primers, thereby producing an amplified representative population of genome fragments; (b) replicating a sub-population of the amplified representative population of genome fragments with a plurality of different locus-specific primers, thereby producing a locus-specific, amplified representative population of

genome fragments; and (c) isolating the sub-population, thereby producing a reduced complexity, locus-specific, amplified representative population of genome fragments. Additionally or alternatively, detection of a genetic biomarker can include a method for inhibiting ectopic extension of probes in a primer extension assay. The method includes the steps of (a) contacting a plurality of probe nucleic acids with a plurality of target nucleic acids under conditions wherein probe-target hybrids are formed; (b) contacting the plurality of probe nucleic acids with an ectopic extension inhibitor under conditions wherein probe-ectopic extension inhibitor hybrids are formed; and (c) selectively modifying probes in the probe-target hybrids compared to probes in the probe-ectopic extension inhibitor hybrids. Additionally or alternatively, detection of a genetic biomarker can include a method including the steps of (a) contacting a plurality of genome fragments with a plurality of different immobilized nucleic acid probes under conditions wherein immobilized probe-fragment hybrids are formed; (b) modifying the immobilized probes while hybridized to the genome fragments, thereby forming modified immobilized probes; (c) removing said genome fragments from said probe-fragment hybrids; and (d) detecting the modified immobilized probes after removing the genome fragments, thereby detecting typable loci of the genome fragments. Additionally or alternatively, detection of a genetic biomarker can include a method including the steps of (a) representationally amplifying a native genome, wherein an amplified representative population of genome fragments having the typable loci is produced under isothermal conditions; (b) contacting the genome fragments with a plurality of nucleic acid probes having sequences corresponding to the typable loci under conditions wherein probe-fragment hybrids are formed; and (c) detecting typable loci of the probe-fragment hybrids.

[496] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,765,419, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for detection of pyrophosphate, which can either be used alone or in connection with other technologies, such as pyrosequencing. In some embodiments, such methods and systems permit the detection of pyrophosphate with reduced background. Additionally or alternatively, detection of a genetic biomarker can include methods and systems for pyrosequencing of nucleic acids with reduced background.

Additionally or alternatively, detection of a genetic biomarker can include methods of delaying pyrophosphate detection. The methods can include the steps of providing a pyrophosphate sequestering agent, generating pyrophosphate in the presence of the sequestering agent, whereby the pyrophosphate is reversibly sequestered, releasing the pyrophosphate from the sequestering agent and detecting the pyrophosphate. Additionally or alternatively, detection of a genetic biomarker can include methods for sequencing a nucleic acid. The method can include the steps of providing nucleotides or nucleotide analogs in the presence of a pyrophosphate sequestering agent and a pyrophosphate detecting agent, incorporating one or more of the nucleotides or nucleotide analogs into a polynucleotide so as to extend the polynucleotide in the presence of the pyrophosphate sequestering agent, thereby generating sequestered pyrophosphate, removing the unincorporated nucleotides or nucleotide analogs from the presence of the pyrophosphate detecting agent, releasing the pyrophosphate from the sequestering agent in the presence of the pyrophosphate detecting agent and detecting released pyrophosphate, wherein released pyrophosphate indicates that one or more nucleotides or nucleotide analogs have been incorporated into the polynucleotide. Additionally or alternatively, detection of a genetic biomarker can include methods of modulating the availability of free pyrophosphate during sequencing of a nucleic acid molecule. These methods can include the steps of combining nucleotides or nucleotide analogs with a nucleic acid template; incubating the nucleic acid template and the nucleotides or nucleotide analogs together with a polymerase and a pyrophosphate sequestering agent under conditions sufficient to form a polynucleotide complementary to all or a portion of the nucleic acid template, wherein pyrophosphate generated during the incubating is reversibly sequestered by the sequestering agent, removing from the nucleic acid template the nucleotides or nucleotide analogs that have not been incorporated into the polynucleotide and releasing the pyrophosphate from the pyrophosphate sequestering agent by providing a release reagent. Additionally or alternatively, detection of a genetic biomarker can include arrays comprising a solid support having a plurality of sites distributed thereon, wherein at least a portion of the sites comprise a template nucleic acid and a pyrophosphate sequestering agent capable of reversibly sequestering pyrophosphate. In certain aspects, the sites comprise wells. In certain aspects, the template nucleic acid is attached to a particle or bead within the wells. In certain

aspects, the wells further comprise beads having a pyrophosphate detecting agent attached thereto. In certain aspects, the pyrophosphate sequestering agent is disposed between the template nucleic acid and the pyrophosphate detecting agent. In certain aspects, the pyrophosphate detecting agent comprises ATP sulfurylase and luciferase. In certain aspects, the wells further comprise packing beads. In some embodiments, pyrophosphate is reversibly sequestered by adsorption with the sequestering agent. In certain aspects, the sequestering agent comprises a cationic agent capable of sequestering pyrophosphate through chelation, complexation, or adsorption. In certain aspects, the cationic agent comprises an agent selected from the group consisting of a metal, metal salt, a metal oxide or other agent set forth below. In certain aspects, the metal or metal oxide comprises Ti or TiO2. In other aspects, the pyrophosphate sequestering agent comprises hydroxyapatite. In other aspects the sequestering agent comprises an ammonium or substituted ammonium salt, or a resin or bead that contains such groups. In certain aspects of the above embodiments, the pyrophosphate sequestering agent comprises particles or beads. In addition to the foregoing, in some embodiments of the methods and arrays, pyrophosphate can be released from the sequestering agent by providing a release reagent to the sequestering agent. In certain aspects, the release reagent comprises an anion capable of displacing the pyrophosphate from the sequestering agent, for example, by preferentially complexing or chelating the cation of the sequestering agent. In certain aspects, the release reagent comprises an agent selected from the group consisting of an acid or salt of an acid such as oxalic acid, an oxalate salt, sulfamic acid, a sulfamate salt, ethylene diamine tetraacetic acid (EDTA), ethylene glycol-bis-β-amino-ethyl ether N,N,N′,N′-tetra-acetic acid (EGTA) citric acid, tartaric acid, acetic or other carboxylic acids or their salts. In other aspects, the release reagent comprises phosphate. In other aspects, the release reagent comprises a bisphosphonate. In certain aspects, the release reagent is the enzyme ATP sulfurylase. In this particular aspect, the ATP sulfurylase is in solution rather than being bound to a bead or other surface. The ATP sulfurylase can release the pyrophosphate from the sequestering agent by transforming the pyrophosphate into ATP in the presence of adenysine phosphosulfate (APS). Typically, the ATP will have a lower binding affinity for the sequestering agent than does pyrophosphate. In some aspects, arrays can include sites that further comprise a polymerase and nucleotides or nucleotide analogs. In some embodiments, arrays can further comprises at

least one electrode capable of producing an electric field in the presence of the sites. Additionally or alternatively, detection of a genetic biomarker can include methods of making an array. The methods can include the steps of providing a solid support having a plurality of sites distributed thereon and providing a template nucleic acid and a pyrophosphate sequestering agent capable of reversibly sequestering pyrophosphate to at least a portion of the sites. In certain aspects, the step of providing the template nucleic acid to the plurality of sites occurs prior to providing the pyrophosphate sequestering agent. In certain aspects, the step of providing the template nucleic acid to the plurality of sites occurs subsequent to providing the pyrophosphate sequestering agent. In certain aspects, the step of providing the template nucleic acid to the plurality of sites occurs at the same time as providing the pyrophosphate sequestering agent. In some embodiments, arrays manufactured according to the methods above can be employed in the sequencing and/or pyrophosphate sequestering and release processes. For example, in some embodiments, the pyrophosphate is reversibly sequestered by adsorption with the sequestering agent. In certain aspects, the sequestering agent comprises a cationic agent capable of sequestering pyrophosphate through chelation, complexation, or adsorption. In certain aspects, the cationic agent comprises an agent selected from the group consisting of a metal, metal salt, a metal oxide or other agent set forth below. In certain aspects, the metal or metal oxide comprises Ti or TiO2. In other aspects, the pyrophosphate sequestering agent comprises hydroxyapatite. In other aspects, the sequestering agent comprises an ammonium or substituted ammonium salt, or a resin or bead that contains such groups. In certain aspects of the above embodiments, the pyrophosphate sequestering agent comprises particles or beads. In addition to the foregoing, in some embodiments, arrays manufactured according to the above methods can be utilized in processes in which pyrophosphate can be released from the sequestering agent by providing a release reagent to the sequestering agent. In certain aspects, the release reagent comprises an anion capable of displacing the pyrophosphate from the sequestering agent, for example, by preferentially complexing or chelating the cation of the sequestering agent. In certain aspects, the release reagent comprises an agent selected from the group consisting of an acid or salt of an acid such as oxalic acid, an oxalate salt, sulfamic acid, a sulfamate salt, ethylene diamine tetraacetic acid (EDTA), ethylene glycol-bis-β-amino-ethyl ether N,N, N′,N′-tetra-acetic acid (EGTA) citric

acid, tartaric acid, acetic or other carboxylic acids or their salts. In other aspects, the release reagent comprises phosphate. In other aspects, the release reagent comprises a bisphosphonate. In certain aspects, the release reagent is the enzyme ATP sulfurylase. In this particular aspect, the ATP sulfurylase is in solution rather than being bound to a bead or other surface. The ATP sulfurylase can release the pyrophosphate from the sequestering agent by transforming the pyrophosphate into ATP in the presence of adenysine phosphosulfate (APS). Typically, the ATP will have a lower binding affinity for the sequestering agent than does pyrophosphate.

[497] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,741,630, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of detecting a target analyte in a biological sample, comprising providing a composite array comprising a substrate having a surface; a first and a second assay location on said surface, wherein said assay locations comprise a population of microspheres, and wherein said microspheres comprise bioactive agents; a physical partition separating said first assay location from said second assay location; adding said biological sample to said first assay location under conditions sufficient to allow said target analyte to bind to said bioactive agents; and detecting the binding of said bioactive agents to said target analyte. In more specific embodiments, the binding of the bioactive agents to the target analyte can be detected by a change in an optical signature of the microspheres. Target analytes and bioactive agents can include a nucleic acid, for example. In some embodiments, the methods can further comprise detecting a target analyte in a second biological sample by adding said second biological sample to said second assay location and thereafter detecting the binding of said bioactive agents to said target analyte. In certain aspects, the substrate can include a microscope slide. Further methods include detecting a target nucleic acid in a biological sample, wherein said target nucleic acid includes one or more single nucleotide polymorphisms (SNPs) at one or more predetermined positions, comprising providing a composite array comprising a substrate having a surface; a population of microspheres, wherein said microspheres are linked to capture probes configured to bind to said target nucleic acid at said one or more predetermined positions; a first and second assay location on said surface, wherein said assay locations comprise said population of microspheres; a physical partition separating said first assay

location from said second assay location; adding said biological sample to said first assay location under conditions sufficient to allow said target nucleic acid to bind to said capture probes; and detecting the binding of said target nucleic acid to said capture probes. Additionally or alternatively, detection of a genetic biomarker can include array compositions comprising a rigid support; a molded layer with at least a first assay location comprising discrete sites, where the molded layer is adhered to the rigid support; a layer of bonding agent adhering the rigid support to the molded layer; and a population of microspheres comprising at least a first and a second subpopulation, where the first subpopulation comprises a first bioactive agent and the second subpopulation comprises a second bioactive agent where the microspheres are randomly distributed on the sites. Additionally or alternatively, detection of a genetic biomarker can include a method for making an array composition containing at least a first assay location having discrete sites comprising the steps of contacting a surface of a template structure, the surface comprising one or more sets of projections, with a moldable material; removing the moldable material from the surface of the template structure, whereby the removed moldable material forms a molded layer with at least a first assay location comprising discrete sites; adhering the molded layer to a rigid support; and randomly distributing microspheres on the molded layer such that individual discrete sites comprise microspheres, where the microspheres comprise at least a first and a second subpopulation, where the first subpopulation comprises a first bioactive agent and the second subpopulation comprises a second bioactive agent.

[498] n some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,901,897, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include composite array compositions comprising a first substrate with a surface comprising a plurality of assay locations, each assay location comprising a plurality of discrete sites. The substrate further comprises a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on each of the assay locations. Additionally or alternatively, detection of a genetic biomarker can include composite array compositions comprising a first substrate with a surface comprising a plurality of assay locations and a second substrate

comprising a plurality of array locations, each array location comprising discrete sites. The compositions further comprise a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on each of the array locations. Additionally or alternatively, detection of a genetic biomarker can include methods of decoding an array composition comprising providing an array composition as outlined above, and adding a plurality of decoding binding ligands to the composite array composition to identify the location of at least a plurality of the bioactive agents. Additionally or alternatively, detection of a genetic biomarker can include methods of determining the presence of one or more target analytes in one or more samples comprising contacting the sample with the composition, and determining the presence or absence of said target analyte. Additionally or alternatively, detection of a genetic biomarker can include a hybridization chamber. The hybridization chamber includes a base plate and a lid. A sealant is localized between the lid and base plate to provide for an airtight seal. When a two-component array system is used, the chamber also includes component ports in the lid to immobilize the array components. That is, array components are inserted through the port in the lid. The ports may include seals so that an airtight seal is maintained. The chamber also may include clamps and alignment pins. Additionally or alternatively, detection of a genetic biomarker can include a hybridization chamber wherein the base plate contains holes. The holes may be in a microplate array format. In one embodiment, at least two holes are joined by a channel. In one embodiment, a flexible membrane is placed on the base plate. When pressure i.e. a vacuum, is applied to the membrane, wells form in the membrane at the location of the holes in the base plate. The apparatus also includes a pneumatic device for the delivery of a vacuum or positive pressure to the membrane. Additionally or alternatively, detection of a genetic biomarker can include a method of mixing samples in an array formal. The method includes providing a vacuum to the membrane such that wells are formed. A solution is then applied to the membrane such that at least one of the wells is filled with liquid. Subsequently, the vacuum is applied intermittently to the membrane, which results in mixing of the liquid. Additionally or alternatively, detection of a genetic biomarker can include an apparatus comprising a hybridization chamber and any of the composite array compositions. Additionally or alternatively, detection of a genetic

biomarker can include performing methods of decoding an array composition in a hybridization chamber. Additionally or alternatively, detection of a genetic biomarker can include performing methods of determining the presence of one or more target analytes in one or more samples in a hybridization chamber.

[499] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,288,103, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting target sequences in a sample comprising providing a first solid support comprising at least a first and a second target sequence, contacting the first and second target sequences with first and second probes, respectively, wherein each of the first and second probes comprise a first universal priming site, a target specific domain substantially complementary to at least a portion of the target sequence, to form first and second hybridization complexes, respectively, removing unhybridized probes, contacting the first and second hybridization complexes with a first enzyme to form modified first and second probes, respectively contacting the modified first and second probes with at least a first primer that hybridizes to the universal priming site NTPs, and an extension enzyme, wherein the first and second modified probes are amplified to form first and second amplicons, respectively, and detecting the amplicons. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting target sequences in a sample comprising providing a first solid support comprising at least a first and a second target sequence, contacting the first and second target sequences with first and second probes, respectively, wherein each of the first and second probes comprise a first universal priming site, a target specific domain substantially complementary to at least a portion of the target sequence, to form first and second hybridization complexes, respectively, removing unhybridized probes, contacting the first and second probes with at least a first universal primer that hybridizes to the universal priming site, NTPs and an extension enzyme, wherein the first and second probes are extended to form first and second modified probes, respectively, contacting the first and second modified probes with at least third and fourth probes, respectively, wherein the modified first and second probes comprise a detection position, the third and fourth probes each comprise an interrogation position, and a second enzyme, wherein the second enzyme

only modifies the third and fourth probes if there is perfect complementarity between the bases at the interrogation position and the detection position, forming third and fourth modified probes, and detecting the third and fourth modified probes. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing a plurality of target nucleic acid sequences each comprising from 3′ to 5′ a first, second and third target domain, the first target domain comprising a detection position, the second target domain being at least one nucleotide contacting the target nucleic acid sequences with sets of probes for each target sequence, each set comprising a first probe comprising from 5′ to 3′ a first domain comprising a first universal priming sequence, and a second domain comprising a sequence substantially complementary to the first target domain of a target sequence, and an interrogation position within the 3′ four terminal bases, a second probe comprising a first domain comprising a sequence substantially complementary to the third target domain of a target sequence, to form a set of first hybridization complexes, contacting the first hybridization complexes with an extension enzyme and dNTPs, under conditions whereby if the base at the interrogation positions is perfectly complementary with the bases at the detection positions, extension of the first probes occurs through the second target domains to form second hybridization complexes, contacting the second hybridization complexes with a ligase to ligate the extended first probes to the second probes to form amplification templates. Additionally or alternatively, detection of a genetic biomarker can include a multiplex reaction method comprising providing a sample comprising at least first and second targets hybridizing the first and second targets with first and second probes, respectively forming first and second hybridization complexes, respectively, immobilizing the first and second hybridization complexes, washing to remove unhybridized nucleic acids, contacting the first and second hybridization complexes with an enzyme, whereby the first and second probes are modified forming modified first and second probes, respectively, whereby the modified first and second probes are modified to contain first and second interrogation nucleotides that are complementary to first and second detection nucleotides in the first and second targets, respectively, contacting the modified first and second probes with first and second allele specific primers, respectively, whereby the first and second allele specific primers hybridize to the modified first and second probes, respectively, 5′ to the first and second interrogation

nucleotides, dNTPs, polymerase, whereby the first and second allele specific primers are modified when a target domain of the allele specific primers is perfectly complementary to the modified target probes to form modified first and second allele specific probes, amplifying the modified first and second allele specific probes to form first and second amplicons, and detecting the first and second amplicons. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing a plurality of target nucleic acid sequences each comprising from 3′ to 5′ a first, second and third target domain, the first target domain comprising a detection position, the second target domain being at least one nucleotide, contacting the target nucleic acid sequences with sets of probes for each target sequence, each set comprising: a first probe comprising from 5′ to 3′, a first domain comprising a first universal priming sequence, and a second domain comprising a sequence substantially complementary to the first target domain of a target sequence, and an interrogation position within the 3′ four terminal bases, a second probe comprising a first domain comprising a sequence substantially complementary to the third target domain of a target sequence, to form a set of first hybridization complexes, contacting the first hybridization complexes with at least a first universal primer that hybridize to the first universal priming sequence, an extension enzyme and dNTPs, under conditions whereby if the base at the interrogation positions are perfectly complementary with the bases at the detection positions, extension of the first probes occurs through the second target domains to form second hybridization complexes, contacting the second hybridization complexes with a ligase to ligate the extended first probes to the second probes to form amplification templates.

[500] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,899,626, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of measuring the methylation level of DNA. The method can include the steps of providing data representing the standard deviation of methylation measurements of DNA, determining the methylation level of at least one locus in a sample DNA and comparing the methylation level of the at least one locus to the data to determine the standard deviation of the measurement. Additionally or alternatively, detection of a genetic biomarker can include a method of comparing the methylation level of DNA samples. The

method can include the steps of providing data representing the standard deviation of methylation measurements of DNA; determining the methylation level of at least one locus in a first sample DNA; determining the methylation level of the at least one locus in a second sample DNA; identifying the standard deviations of the methylation level of the at least one locus in the first sample DNA and in the second sample DNA from the data; and determining whether the methylation level of the at least one locus in the first sample DNA and in the second sample DNA are the same or different based on the standard deviations. Additionally or alternatively, detection of a genetic biomarker can include a DNA methylation level detection system, including a scanner for reading methylation levels for a plurality of loci in a sample DNA and a first module configured to compare the methylation levels against data representing the standard deviation of methylation measurements of DNA. Some embodiments relate to a method of measuring the methylation level of DNA including providing data representing the standard deviation of methylation measurements of DNA; determining the methylation level of at least one locus in a sample DNA; and comparing the methylation level of said at least one locus to said data to determine the standard deviation of said measurement. In some embodiments, at least one locus comprises a plurality of loci. In some embodiments, the methylation levels are determined using an array. In some embodiments, the plurality of loci comprises at least 100 loci measured simultaneously on said array. In some embodiments, the data correlates standard deviation of methylation level as a function of methylation level. In some embodiments, the data comprises different standard deviation values for different methylation levels. In some embodiments, the data comprises said different standard deviation values occurring along a parabola when correlated to said different methylation levels. In some embodiments, the data is produced by creating a training set comprising mixtures of DNA with varying methylation levels, wherein said training set comprises replicates of said mixtures; determining the methylation level of at least one locus in said mixtures of said training set; determining standard deviation values for said methylation levels determined for said replicates of said training set; and correlating said standard deviation values and said methylation levels determined for said training set. In some embodiments, the mixtures of the training set comprise different ratios of genomic DNA from a cell population with highly methylated DNA and a cell population with minimally methylated DNA. In some

embodiments, the methylation levels for the mixtures of said training set vary from 0 to 1. Some embodiments further include identifying at least three regions from 0 to 1, determining the median of the methylation levels for each of the regions and fitting a parabola to said median for each of said regions. In some embodiments, the standard deviation values comprise the 95th percentile standard deviation values. Some embodiments further include the steps of determining the methylation level of said at least one locus in a second sample DNA; identifying the standard deviations of said methylation level of said at least one locus in said sample DNA and in said second sample DNA from said data; and determining whether said methylation level of said at least one locus in said first sample DNA and in said second sample DNA are the same or different based on said standard deviations. Some embodiments relate to a DNA methylation level detection system including a scanner for reading methylation levels for a plurality of loci in a sample DNA; and a first module configured to compare said methylation levels against data representing the standard deviation of methylation measurements of DNA. In some embodiments, the methylation levels are determined using an array. In some embodiments, the plurality of loci comprises at least 100 loci measured simultaneously on said array. In some embodiments, the data correlates standard deviation of methylation level as a function of methylation level. In some embodiments, the data comprises different standard deviation values for different methylation levels. In some embodiments, the data comprises said different standard deviation values occurring along a parabola when correlated to said different methylation levels. In some embodiments, the data is produced by creating a training set comprising mixtures of DNA with varying methylation levels, wherein said training set comprises replicates of said mixtures; determining the methylation level of at least one locus in said mixtures of said training set; determining standard deviation values for said methylation levels determined for said replicates of said training set; and correlating said standard deviation values and said methylation levels determined for said training set. Some embodiments relate to a method of comparing the methylation level of DNA samples including providing data representing the standard deviation of methylation measurements of DNA; determining the methylation level of at least one locus in a first sample DNA; determining the methylation level of said at least one locus in a second sample DNA; identifying the standard deviations of said methylation level of said at least one locus in said first sample DNA and in

said second sample DNA from said data; and determining whether said methylation level of said at least one locus in said first sample DNA and in said second sample DNA are the same or different based on said standard deviations.

[501] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,776,531, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a probe composition, including (a) a substrate; (b) a probe molecule attached to the substrate; and (c) a stabilization polymer layer on the substrate, wherein said stabilization polymer layer coats the probe molecule. Additionally or alternatively, detection of a genetic biomarker can include a method of making a probe composition. The method includes the steps of (a) providing a substrate having an attached biopolymer probe; and (b) contacting the substrate with a stabilization polymer. Additionally or alternatively, detection of a genetic biomarker can include a method of shipping a solid-phase probe. The method includes the steps of (a) providing a substrate having an attached probe molecule, and further having a stabilization polymer layer; (b) placing the substrate in a package; and (c) shipping the package to a remote location.

[502] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,499,806, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include array compositions comprising a substrate with a surface comprising discrete sites, at least one fiducial, and a population of microspheres comprising at least a first and a second subpopulation. Each subpopulation comprises a bioactive agent, and the microspheres are distributed on said surface. Each subpopulation may optionally comprise a unique optical signature, an identifier binding ligand that will bind a decoder binding ligand such that the identification of the bioactive agent can be elucidated, or both. Additionally or alternatively, detection of a genetic biomarker can include compositions comprising a computer readable memory to direct a computer to function in a specified manner. The computer readable memory comprises an acquisition module for receiving a data image of a random array comprising a plurality of discrete sites, a registration module for registering a data image, and a comparison module for comparing registered data images. Each module

comprises computer code for carrying out its function. The registration module may utilize any number of fiducials, including a fiducial fiber when the substrate comprises a fiber optic bundle, a fiducial microsphere, or a fiducial template generated from the random array. Additionally or alternatively, detection of a genetic biomarker can include methods of making the array compositions comprising forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, and incorporating at least one fiducial onto the surface. When the array has complete rotational freedom, at least two fiducials are preferred in the array to allow for correction of rotation. Additionally or alternatively, detection of a genetic biomarker can include methods for comparing separate data images of a random array. The methods comprise using a computer system to register a first data image of the random array to produce a registered first data image, using the computer system to register a second data image of the random array to produce a registered second data image, and comparing the first and the second registered data images to determine any differences between them. Additionally or alternatively, detection of a genetic biomarker can include methods of decoding a random array composition comprising providing a random array composition. A first plurality of decoding binding ligands is added to the array composition and a first data image is created. A fiducial is used to generate a first registered data image. A second plurality of decoding binding ligands is added to the array composition and a second data image is created. The fiducial is used to generate a second registered data image. A computer system is used to compare the first and the second registered data image to identify the location of at least two bioactive agents. Additionally or alternatively, detection of a genetic biomarker can include methods of determining the presence of a target analyte in a sample. The methods comprise acquiring a first data image of a random array composition, and registering the first data image to create a registered first data image. The sample is then added to the random array and a second data image is acquired from the array. The second data image is registered to create a registered second data image. Then the first and the second registered data images are compared to determine the presence or absence of the target analyte. Optionally, the data acquisition may be at different wavelengths. Additionally or alternatively, detection of a genetic biomarker can include methods for preprocessing or prefiltering signal data comprising acquiring a data image from an array, and determining the similarity of a first

signal from at least one array site to a reference signal to determine whether the site comprises a candidate bead. Additionally or alternatively, detection of a genetic biomarker can include methods for registering an analytical image of a microsphere array comprising providing a hybridization intensity image. After the microsphere array is decoded, a registration grid is computed based on known locations of bioactive agents on the microspheres obtained from the decoding step. The sample is added to the microsphere array and a hybridization intensity image is acquired from the array. Bright bead types are distributed throughout the array to serve as fiducials. The registration grid is overlaid on to the image and then the registration grid is aligned so that the identity of the signal intensity at each grid location for each bead type within the array is ascertained. Once the correct position of the grid is obtained, each core is assigned a number so that the correct placement of the grid can be made for further sequential images.

[503] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,942,968, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a composition that includes a substrate with a surface comprising discrete sites, a reflective coating on the surface, and a population of microspheres distributed on the substrate. The microspheres comprise at least a first and a second subpopulation. Generally, at least one subpopulation comprises a bioactive agent. Additionally or alternatively, detection of a genetic biomarker can include a composition wherein the substrate comprises a first and a second surface, wherein the first surface comprises the discrete sites, and the reflective coating is on the second surface. The population of microspheres are distributed on the first surface. Additionally or alternatively, detection of a genetic biomarker can include a method of making a reflective array. The method includes providing a substrate with a surface comprising discrete sites, applying to the surface a coating of reflective material and distributing microspheres on the surface. Additionally or alternatively, detection of a genetic biomarker can include a method, wherein the substrate comprises a first and a second surface, wherein the first surface comprises discrete sites, the reflective material is on the second surface and the microspheres are distributed on the first surface. Additionally or alternatively, detection of a genetic biomarker can include a method comprising providing a

preformed unitary fiber optic bundle comprising a proximal and a distal end, the distal end comprising plurality of discrete sites comprising a population of microspheres, the population comprising at least first and second subpopulations, and imaging the fiber optic bundle from the distal end. A reflective coating may be applied to either the distal end or the proximal end of the fiber optic bundle. Additionally or alternatively, detection of a genetic biomarker can include an array composition comprising a substrate with a surface comprising discrete sites comprising alternatively shaped wells. The wells may contain a cross section that is shaped as a square, a hexagon, a star, a triangle, a pentagon or an octagon. Additionally or alternatively, detection of a genetic biomarker can include method comprising providing a substrate with a plurality of discrete sites, the sites comprising alternatively shaped wells and a population of microspheres, the population comprising at least first and second subpopulations, and imaging the substrate. Additionally or alternatively, detection of a genetic biomarker can include an array composition comprising a substrate with a surface comprising discrete sites and a population of microspheres distributed on the substrate, wherein the microspheres comprise a bioactive agent and a signal transducer element. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a non-labeled target analyte in a sample comprising providing a substrate with a plurality of discrete sites, distributing on the sites a population of microspheres comprising a bioactive agent and a signal transducer element, contacting the substrate with the sample, whereby upon binding of the target analyte to the bioactive agent, a signal from the signal transducer element is altered as an indication of the presence of the target analyte. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a chiral molecule in a sample comprising providing a substrate with a surface comprising at least first and second discrete sites at least first and second bioactive agents attached to the first and second discrete sites respectively, contacting the substrate with the sample, illuminating the substrate with polarized light, and detecting rotation of the light in at least one of the first and second discrete sites as an indication of the presence of the chiral molecule. Additionally or alternatively, detection of a genetic biomarker can include a method of determining the location of a microsphere in an array comprising providing a substrate with a first surface comprising at least a first and a second discrete site, wherein the first discrete site comprises a microsphere, but the second discrete site does not

comprising a microsphere, illuminating the substrate and detecting illumination of the substrate, whereby reduced illumination at the first discrete site relative to the second discrete site provides an indication of the presence of the first microsphere in the first discrete site. Additionally or alternatively, detection of a genetic biomarker can include a method of increasing signal output from an array comprising providing a substrate with a surface comprising at least first and second discrete sites and at least first and second labels attached to the first and second discrete sites respectively, cooling the substrate to at least below room temperature and detecting a signal from the first and second labels, whereby the signal is increased relative to a signal obtained from a substrate that is not cooled. Additionally or alternatively, detection of a genetic biomarker can include a method for background signal subtraction in an array comprising providing a substrate with a surface comprising at least first and second discrete sites and at least first and second labels attached to the first and second discrete sites respectively, detecting the signal from the first and second discrete sites in a plurality of different emissions, and subtracting the lowest signal from each of the first and second discrete sites from the remaining signals from the first and second discrete sites, respectively. Additionally or alternatively, detection of a genetic biomarker can include a method of correcting image non-uniformity comprising providing a substrate with a surface comprising at least first and second discrete sites, at least first and second labels attached to the first and second discrete sites respectively and at least a first internal reference point of known signal intensity, detecting a first and second signal from the first and second labels, respectively, detecting a signal from the internal reference point, and determining the variation between the signal from the internal reference point and the known signal intensity of the internal reference point as an indication of said image non-uniformity. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a target analyte in a sample comprising providing an array comprising a substrate with a surface comprising discrete sites, a reflective coating on said surface, and a population of microspheres distributed on the substrate. The microspheres comprise at least a first and a second subpopulation each comprising a different bioactive agent. The method further includes contacting the array with the sample, such that the target analyte binds to at least one of the bioactive agents and detecting the presence of the target analyte. In a preferred embodiment,

the target analyte is labeled. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a target analyte in a sample comprising providing an array comprising a substrate with a surface comprising discrete sites comprising alternatively shaped wells and a population of microspheres distributed on the substrate. The microspheres comprise at least a first and a second subpopulation each comprising a different bioactive agent. The method further includes contacting the array with the sample, such that the target analyte binds to at least one of the bioactive agents and detecting the presence of the target analyte. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a target analyte in a sample comprising providing a substrate with a surface comprising at least first and second discrete sites and a population of microspheres distributed on the substrate, wherein the microspheres comprise at least a first and a second subpopulation each comprising a different bioactive agent, contacting the substrate with the sample, such that the target analyte binds to at least one of the bioactive agents. In some embodiments, the method includes cooling the substrate to at least below room temperature and detecting a signal, whereby the signal is increased relative to a signal obtained from a substrate that is not cooled.

[504] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,890,764, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions comprising a substrate with a surface comprising discrete sites, and a population of microspheres distributed on the sites. At least one of the microspheres comprises a nanocrystal. The nanocrystal can be embedded in the microsphere, for example using the sol-gel polymerization process, or it can be attached to the microsphere. The microspheres optionally comprise bioactive agents and/or identifier binding ligands. In an additional aspect, the population of microspheres comprises at least a first and a second subpopulation comprising a first and a second bioactive agent, respectively, and a first and a second optical signature, respectively, capable of identifying each bioactive agent. At least one of the optical signatures comprises a nanocrystal. Additionally or alternatively, detection of a genetic biomarker can include methods of making a composition comprising forming a surface comprising individual sites on a substrate and distributing microspheres on the surface such

that the individual sites contain microspheres. The microspheres comprise an optical signature, and at least one optical signature comprises at least one nanocrystal. Additionally or alternatively, detection of a genetic biomarker can include a method of determining the presence of a target analyte in a sample comprising contacting the sample with a composition. The composition comprises a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation each comprising a bioactive agent and an optical signature capable of identifying the bioactive agent. The microspheres are distributed on the surface such that the discrete sites contain microspheres and wherein at least one of the optical signatures comprises at least one nanocrystal. The presence or absence of the target analyte is then determined. Additionally or alternatively, detection of a genetic biomarker can include methods of making a composition comprising adhering nanocrystals to porous silica, and sealing the pores of the silica using the sol-gel polymerization process.

[505] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0201992, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, apparatus, systems, and computer program products for determining nucleic acid fragment sequences using unique molecular indices (UMIs). In some implementations, the UMIs includes nonrandom UMIs (NRUMIs) or variable-length, nonrandom unique molecular indices (vNRUMIs). Additionally or alternatively, detection of a genetic biomarker can include methods for sequencing nucleic acid molecules from a sample. The method includes: (a) applying adapters to DNA fragments in the sample to obtain DNA-adapter products, wherein each adapter includes a nonrandom unique molecular index, and wherein nonrandom unique molecular indices of the adapters have at least two different molecular lengths and form a set of variable-length, nonrandom unique molecular indices (vNRUMIs); (b) amplifying the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads associated with the set of vNRUMIs; (d) identifying, among the plurality of reads, reads associated with a same variable-length, nonrandom unique molecular index (vNRUMI); and (e) determining a sequence of a DNA fragment in the sample

using the reads associated with the same vNRUMI. In some implementations, identifying the reads associated with the same vNRUMI includes obtaining, for each read of the plurality of reads, alignment scores with respect to the set of vNRUMIs, each alignment score indicating similarity between a subsequence of a read and a vNRUMI, wherein the subsequence is in a region of the read in which nucleotides derived from the vNRUMI are likely located. In some implementations, the alignment scores are based on matches of nucleotides and edits of nucleotides between the subsequence of the read and the vNRUMI. In some implementations, the edits of nucleotides include substitutions, additions, and deletions of nucleotides. In some implementations, each alignment score penalizes mismatches at the beginning of a sequence but does not penalize mismatches at the end of the sequence. In some implementations, obtaining an alignment score between a read and a vNRUMI includes: (a) calculating an alignment score between the vNRUMI and each one of all possible prefix sequences of the subsequence of the read; (b) calculating an alignment score between the subsequence of the read and each one of all possible prefix sequences of the vNRUMI; and (c) obtaining a largest alignment score among the alignment scores calculated in (a) and (b) as the alignment score between the read and the vNRUMI. In some implementations, the subsequence has a length that equals to a length of the longest vNRUMI in the set of vNRUMIs. In some implementations, identifying the reads associated with the same vNRUMI in (d) further includes: selecting, for each read of the plurality of reads, at least one vNRUMI from the set of vNRUMIs based on the alignment scores; and associating each read of the plurality of reads with the at least one vNRUMI selected for the read. In some implementations, selecting the at least one vNRUMI from the set of vNRUMIs includes selecting a vNRUMI having a highest alignment score among the set of vNRUMIs. In some implementations, the at least one vNRUMI includes two or more vNRUMIs. In some implementations, the method further includes selecting one of the two or more vNRUMI as the same vNRUMI of (d) and (e). In some implementations, the adapters applied in (a) are obtained by: (i) providing a set of oligonucleotide sequences having at least two different molecular lengths; (ii) selecting a subset of oligonucleotide sequences from the set of oligonucleotide sequences, all edit distances between oligonucleotide sequences of the subset of oligonucleotide sequences meeting a threshold value, the subset of oligonucleotide sequences forming the set of

vNRUMIs; and (iii) synthesizing the adapters each including a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and at least one vNRUMI of the set of vNRUMIs. In some implementations, the threshold value is 3. In some implementations, the set of vNRUMIs include vNRUMIs of 6 nucleotides and vNRUMIs of 7 nucleotides. In some implementations, the determining of (e) includes collapsing reads associated with the same vNRUMI into a group to obtain a consensus nucleotide sequence for the sequence of the DNA fragment in the sample. In some implementations, the consensus nucleotide sequence is obtained based partly on quality scores of the reads. In some implementations, the determining of (e) includes: identifying, among the reads associated with the same vNRUMI, reads having a same read position or similar read positions in a reference sequence, and determining the sequence of the DNA fragment using reads that (i) are associated with the same vNRUMI and (ii) have the same read position or similar read positions in the reference sequence. In some implementations, the set of vNRUMIs includes no more than about 10,000 different vNRUMIs. In some implementations, the set of vNRUMIs includes no more than about 1,000 different vNRUMIs. In some implementations, the set of vNRUMIs includes no more than about 200 different vNRUMIs. In some implementations, applying adapters to the DNA fragments in the sample includes applying adapters to both ends of the DNA fragments in the sample. Additionally or alternatively, detection of a genetic biomarker can include methods for preparing sequencing adapters, the methods including: (a) providing a set of oligonucleotide sequences having at least two different molecular lengths; (b) selecting a subset of oligonucleotide sequences from the set of oligonucleotide sequences, all edit distances between oligonucleotide sequences of the subset of oligonucleotide sequences meeting a threshold value, the subset of oligonucleotide sequences forming a set of variable-length, nonrandom unique molecular indexes (vNRUMIs); and (c) synthesizing a plurality of sequencing adapters, wherein each sequencing adapter includes a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and at least one vNRUMI of the set of vNRUMIs. In some implementations, (b) includes: (i) selecting an oligonucleotide sequence from the set of oligonucleotide sequences; (ii) adding the selected oligonucleotide to an expanding set of oligonucleotide sequences and removing the selected oligonucleotide from the set of oligonucleotide sequences to obtain a reduced set of oligonucleotide sequences; (iii)

selecting an instant oligonucleotide sequence from the reduced set that maximizes a distance function, wherein the distance function is a minimal edit distance between the instant oligonucleotide sequence and any oligonucleotide sequences in the expanding set, and wherein the distance function meeting the threshold value; (iv) adding the instant oligonucleotide to the expanding set and removing the instant oligonucleotide from the reduced set; (v) repeating (iii) and (iv) one or more times; and (vi) providing the expanding set as the subset of oligonucleotide sequences forming the set of vNRUMIs. Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing nucleic acid molecules from a sample, including (a) applying adapters to DNA fragments in the sample to obtain DNA-adapter products, wherein each adapter includes a nonrandom unique molecular index, and wherein nonrandom unique molecular indices of the adapters have at least two different molecular lengths and form a set of variable-length, nonrandom unique molecular indices (vNRUMIs); (b) amplifying the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads associated with the set of vNRUMIs; and (d) identifying, among the plurality of reads, reads associated with a same variable-length, nonrandom unique molecular index (vNRUMI). Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing nucleic acid molecules from a sample, including (a) applying adapters to DNA fragments in the sample to obtain DNA-adapter products, wherein each adapter includes a unique molecular index (UMI), and wherein unique molecular indices (UMIs) of the adapters have at least two different molecular lengths and form a set of variable-length unique molecular indices (vUMIs); (b) amplifying the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads associated with the set of vUMIs; and (d) identifying, among the plurality of reads, reads associated with a same variable-length unique molecular index (vUMI). Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing nucleic acid molecules from a sample, including (a) applying adapters to DNA fragments in the sample to obtain DNA-adapter products, wherein each adapter includes a unique molecular index (UMI) in a set of unique molecular indices (UMIs); (b) amplifying the DNA-adapter products to obtain a plurality of amplified

polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads associated with the set of UMIs; (d) obtaining, for each read of the plurality of reads, alignment scores with respect to the set of UMIs, each alignment score indicating similarity between a subsequence of a read and a UMI; (e) identifying, among the plurality of reads, reads associated with a same UMI using the alignment scores; and (e) determining a sequence of a DNA fragment in the sample using the reads associated with the same UMI. Additionally or alternatively, detection of a genetic biomarker can include a system, apparatus, and computer program products for determining DNA fragment sequences implementing the methods. Additionally or alternatively, detection of a genetic biomarker can include a computer program product including a non-transitory machine readable medium storing program code that, when executed by one or more processors of a computer system, causes the computer system to implement a method for determining sequence information of a sequence of interest in a sample using unique molecular indices (UMIs). The program code includes instructions to perform the methods above.

[506] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0201974, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions for targeted amplification of DNA and sample identification. Additionally or alternatively, detection of a genetic biomarker can include methods for obtaining nucleic acid sequence information from a biological sample comprising: (a) providing a biological sample comprising different target nucleic acids; (b) contacting the biological sample with a plurality of different probe sets to form hybridization complexes with the different target nucleic acids; (c) amplifying the nucleic acid from the biological samples to produce amplicons; wherein there is no purification of the nucleic acid from the biological sample prior to the contacting step (b); and (d) obtaining nucleic acid sequence information for a plurality of portions of the amplified sample. Additionally or alternatively, detection of a genetic biomarker can include a method of obtaining nucleic acid sequence information from a FFPE sample comprising: (a) providing a FFPE sample comprising different target nucleic acids embedded within a preserved tissue; (b) contacting the FFPE sample with a plurality of different probe sets to form hybridization

complexes with the different target nucleic acids; (c) amplifying the nucleic acid from the FFPE samples to produce amplicons; wherein there is no purification of the nucleic acid from the FFPE sample prior to the contacting step (b); and (d) obtaining nucleic acid sequence information for a plurality of the amplicons. In particular embodiments, there is no purification of the nucleic acid from the FFPE sample prior to the amplifying in step (c). Additionally or alternatively, detection of a genetic biomarker can include methods for amplification of nucleic acid from a FFPE sample comprising: (a) providing a FFPE sample comprising nucleic acid embedded within a preserved tissue, the nucleic acid having, from 3′ to 5′: contiguous first, second, and third target domains; (b) contacting the FFPE sample with a plurality of different probe sets to form hybridization complexes with the different target nucleic acids, wherein each probe set comprises: (i) a first probe comprising, from 5′ to 3′: a first priming sequence and a sequence that is substantially complementary to the first target domain; and (ii) a second probe comprising 5′ to 3′: a sequence substantially complementary to the third target domain, and a second priming sequence; (c) contacting the hybridization complexes with an extension enzyme and nucleotides, wherein the first probes are extended along the second target domains of hybridization complexes formed in (b); (d) ligating the extended first probes to the second probes to form amplification templates; and (e) amplifying the amplification templates with first and second primers that are complementary to the first priming sequence and the second priming sequence to produce amplicons and obtaining nucleic acid sequence information for a plurality of the amplicons. Additionally or alternatively, detection of a genetic biomarker can include a method for nucleic acid sample identification comprising: (a) providing a nucleic acid-containing cellular sample; (b) lysing cells of the sample with a lysis reagent to liberate nucleic acid from within the cells of the cellular sample, thereby forming a lysate; (c) amplifying the nucleic acid from the lysed samples; wherein there is no purification of the nucleic acid from the lysate prior to beginning the amplification step (c); and (d) obtaining nucleic acid sequence information for a plurality of portions of the amplified sample, and comparing the sequence information to a second set of sequence information. In certain aspects, the nucleic acid is DNA. In certain aspects, the sample is a blood sample. In certain aspects, the sample comprises dried blood. In certain aspects, the sample comprises a FFPE tissue sample. In certain aspects, the second set of sequence information comprises a whole

genome sequence. In certain aspects, the second set of sequence information comprises exome sequence information. In certain aspects, the amplifying comprises a targeted amplification reaction. In certain aspects, the targeted amplification reaction comprises extension and ligation of two probes. In certain aspects, the targeted amplification reaction comprises polymerase chain reaction using at least two amplification primers that are specific for a portion of the sample genome. Additionally or alternatively, detection of a genetic biomarker can include a method of tracking the identity of a biological sample during different stages of sample processing, comprising: (a) providing a nucleic acid-containing cellular sample; (b) separating a portion of the sample into a first portion and a second portion and obtaining a first set of nucleic acid sequence information from the first portion the biological sample according to the above embodiments, wherein the first set of nucleic acid sequence information comprises identity informative sequence information; (c) purifying nucleic acid from the second portion and obtaining a second set of sequence information; and (d) using computer-assisted logic, comparing the identity informative sequence information from the first set of nucleic acid sequence information sequence information to the second set of sequence information to confirm that the first and second sets of sequence information were obtained from the same source. Additionally or alternatively, detection of a genetic biomarker can include a method of confirming the source of two different biological samples comprising: (a) providing a first nucleic acid-containing cellular sample; (b) obtaining a first set of nucleic acid sequence information from the first portion the biological sample according to some of the above embodiments, wherein the first set of nucleic acid sequence information comprises identity informative sequence information; (c) providing a second nucleic acid sample comprising purified nucleic acid and obtaining a second set of sequence information; and (d) using computer-assisted logic, comparing the identity informative sequence information from the first set of nucleic acid sequence information sequence information to the second set of sequence information to confirm that the first and second sets of sequence information were obtained from the same individual.

[507] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0155774, which is hereby incorporated by reference in its entirety. For

example, detection of a genetic biomarker can include compositions, systems, and methods for sequencing polynucleotides using tethers anchored to polymerases adjacent to nanopores. Under one aspect, a composition includes a nanopore including a first side, a second side, and an aperture extending through the first and second sides. The composition also can include a plurality of nucleotides, wherein each of the nucleotides includes an elongated tag. The composition also can include first and second polynucleotides, the first polynucleotide being complementary to the second polynucleotide. The composition also can include a polymerase disposed adjacent to the first side of the nanopore, the polymerase configured to add nucleotides of the plurality of nucleotides to the first polynucleotide based on a sequence of the second polynucleotide. The composition also can include a permanent tether including a head region, a tail region, and an elongated body disposed therebetween, the head region being anchored to the polymerase, wherein the elongated body occurs in the aperture of the nanopore. The composition also can include a first moiety disposed on the elongated body, wherein the first moiety is configured to bind to the elongated tag of a first nucleotide upon which the polymerase is acting, as well as a reporter region disposed on the elongated body, wherein the reporter region is configured to indicate when the first nucleotide is complementary or is not complementary to a next nucleotide in the sequence of the second polynucleotide. Under another aspect, a method can include providing a nanopore including a first side, a second side, and an aperture extending through the first and second sides. The method further can include providing a plurality of nucleotides, wherein each of the nucleotides includes an elongated tag. The method further can include providing first and second polynucleotides, the first polynucleotide being complementary to the second polynucleotide. The method further can include providing a polymerase disposed adjacent to the first side of the nanopore, the polymerase configured to add nucleotides of the plurality of nucleotides to the first polynucleotide based on a sequence of the second polynucleotide, wherein the polymerase is anchored to a permanent tether including a head region, a tail region, and an elongated body disposed therebetween, the elongated body occurring in the aperture of the nanopore. The method further can include determining that a first nucleotide is being acted upon by the polymerase based on binding of the elongated tag to a first moiety disposed on the elongated body. The method further can include, with a reporter region disposed on the elongated body,

indicating when the first nucleotide is complementary or is not complementary to a next nucleotide in the sequence of the second polynucleotide.

[508] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0141020, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include substrates and methods useful for placing a single molecule onto a target area. In a first aspect is a substrate that includes a plurality of first and second capture primers immobilized to a feature on the substrate. At least one target polynucleotide, one end attached to one of the capture primers and the other end linked to a target molecule, wherein the target polynucleotide includes a target region flanked by first and second capture primer binding regions complementary to the first and second capture primers, the second capture primer binding region includes a base pair mismatch to the second capture primer, and a plurality of clonal amplicons complementary to the target polynucleotide immobilized to the feature. In some embodiments, the base pair mismatch is a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 base pair mismatch. In some embodiments, the base pair mismatch is a three base pair mismatch. In some embodiments, the substrate further includes a plurality of features. In some embodiments, the feature includes a single target molecule. In some embodiments, the feature is filled to capacity with the plurality of clonal amplicons. In some embodiments, the plurality of features includes a single target molecule. In some embodiments, two or more of the features include different single target molecules. In some embodiments, the features are filled to capacity with the plurality of clonal amplicons. Additionally or alternatively, detection of a genetic biomarker can include methods of placing a single target molecule on a feature of a substrate. In one aspect, the method is a method of placing a single target molecule on a feature of a substrate by hybridizing a plurality of first and second capture primers immobilized to a feature on a substrate with at least one target polynucleotide, where the target polynucleotide includes a target region flanked by first and second capture primer binding regions complementary to the first and second capture primers, and the second capture primer binding region includes a base pair mismatch to the second capture primer and being linked to a target molecule. The method further includes amplifying the at least one target polynucleotide at an average amplification rate that exceeds an average transport rate of a target

polynucleotide to a feature to produce a plurality of clonal amplicons complementary to the target polynucleotide. In some embodiments of the methods, the base pair mismatch is a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 base pair mismatch. In some embodiments of the methods, the base pair mismatch is a three base pair mismatch. In some embodiments of the methods, the substrate comprises a plurality of features. In some embodiments of the methods, the feature includes a single target molecule. In some embodiments of the methods, the feature is filled to capacity with the plurality of clonal amplicons. In some embodiments of the methods, the plurality of features includes a single target molecule. In some embodiments of the methods, the two or more of the features include different single target molecules. In some embodiments of the methods, the features are filled to capacity with the plurality of clonal amplicons. In some embodiments of the methods, the average amplification rate of subsequent amplicons produced at the feature exceeds the average amplification rate of a first amplicon. In some embodiments, the target polynucleotide includes one or more polynucleotides selected from the group consisting of RNA, DNA, and PNA. In some embodiments, the target polynucleotides include double stranded DNA (dsDNA). In some embodiments, the target polynucleotide comprises less than 1,000 nucleotides. In some embodiments, the target polynucleotide comprises between 10 to 25, 26 to 50, 51 to 100, 101 to 200, 201 to 300, 301 to 400, 401 to 500, 501 to 600, 601 to 700, 701 to 800, 801 to 900, or 901 to 1000 base pairs in length. In some embodiments, the target molecule includes a polypeptide, polynucleotide, carbohydrate, amino acid, nucleotide, monosaccharide, hapten, ligand, antigen, analyte, small molecule organic compound or inorganic compound. In some embodiments, the target molecule includes a polypeptide. In some embodiments, the polypeptide is selected from the group consisting of a nanopore, binding polypeptide and enzyme. In some embodiments, the nanopore pore is selected from the group consisting of MspA, OmpF, OmpG, NalP, WZA, ClyA toxin, α-hemolysin, anthrax toxin, leukocidins and DNA origami nanopore. In some embodiments, the binding polypeptide is selected from the group consisting of an antibody, a Fab, a Fab′, a F(ab′)2, a scFV, a diabody, a triabody, a minibody and a single-domain antibody (sdAB), T cell receptor, microcins, Neuropeptides, G-protein coupled receptors, antibody, epidermal growth factor receptor and HER2.

[509] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0095969, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, systems and apparatus for capturing, integrating, organizing, navigating and querying large-scale data from high-throughput biological and chemical assay platforms. Some embodiments provide methods, systems and interfaces for associating experimental data, features and groups of data related by structure and/or function with chemical, medical and/or biological terms in an ontology or taxonomy. Some embodiments also provide methods, systems and interfaces for filtering data by data source information, allowing dynamic navigation through large amounts of data to find the most relevant results for a particular query. A system of one or more computers can be configured to perform particular operations or actions by virtue of having software, firmware, hardware, or a combination of them installed on the system that in operation causes or cause the system to perform the actions. One or more computer programs can be configured to perform particular operations or actions by virtue of including instructions that, when executed by data processing apparatus, cause the apparatus to perform the operations including: (a) selecting, by the one or more processors, a plurality of gene sets from a database, wherein each gene set of the plurality of gene sets includes a plurality of genes and a plurality of experimental values associated with the plurality of genes, and wherein the plurality of experimental values are correlated with the biological, chemical or medical concept of interest in at least one experiment; (b) determining, for each gene set and by the one or more processors, one or more experimental gene scores for first one or more genes among the plurality of genes using one or more experimental values of the first one or more genes; (c) determining, for each gene set and by the one or more processors, one or more in silico gene scores for second one or more genes among the plurality of genes based at least in part on the first one or more genes' correlations with the second one or more genes, wherein the first one or more genes' correlations with the second one or more genes are indicated in other gene sets in the database beside the plurality of gene sets; (d) obtaining, by the one or more processors, summary scores for the first and second one or more genes based at least in part on the one or more experimental gene scores for the first one or more genes determined in (b) and the one or more in silico gene scores for

the second one or more genes determined in (c), wherein each summary score is aggregated across the plurality of gene sets; and (e) identifying, by the one or more processors, the genes that are potentially associated with the biological, chemical or medical concept of interest using the summary scores of the first and second one or more genes. Implementations may include one or more of the following features. In some implementations, (c) includes, for each gene set of the plurality of gene sets: (i) identifying a second plurality of gene sets from the database, each gene set of the second plurality of gene sets including a second plurality of genes and a second plurality of experimental values associated with the second plurality of genes, and where the second plurality of experimental values are correlated with a first gene among the first one or more genes. The method may also include (ii) aggregating the experimental values across the second plurality of gene sets to obtain a vector of aggregated values for the first gene among the first one or more genes. The method may also include (iii) applying (i) and (ii) to one or more other genes among the first one or more genes, thereby obtaining one or more vectors of experimental values for the one or more other genes among the first one or more genes. The method may also include (iv) aggregating vectors of aggregated values for the first gene and the one or more other genes among the first one or more genes, thereby obtaining one compressed vector including the one or more in silico gene scores for the second one or more genes. Additionally or alternatively, detection of a genetic biomarker can include a method where each of the aggregated vectors of (iv) for a particular gene among the first one or more genes is weighted in proportion to an experimental value of the particular gene. The method where each of the aggregated vectors of (iv) for a particular gene among the first one or more genes is weighted in proportion to a number of gene sets of the second plurality of gene sets identified for the particular gene. Some implementations provide the method further including, determining, before (d), one or more gene-group scores for third one or more genes. Some implementations provide the method where each gene-group score for a particular gene is determined using (i) gene memberships of one or more gene groups that each include a group of genes related to a group label, where the group of genes includes the particular gene, and (ii) at least some of the one or more experimental values of the first one or more genes. Some implementations provide the method where (d) includes obtaining the summary scores for the first and second one or more genes based at least in part on the gene-group scores for at least

some of the third one or more genes, as well as the one or more experimental scores for the first one or more genes determined in (b) and the one or more in silico scores for the second one or more genes determined in (c). Some implementations provide the method where determining the one or more gene-group scores for the third one or more genes includes: identifying, for a particular gene among the third one or more genes, the one or more gene groups that each include the particular gene. The method may also include determining, for each gene group, a percentage of members of the gene group that are among the first one or more genes. The method may also include aggregating, for each gene group, one or more experimental values of at least some of the first one or more genes that are members of the gene group, thereby obtaining a sum experimental value for the gene group. The method may also include determining, for the particular gene among the third one or more genes, a gene-group score using the percentage of members of the gene group that are among the first one or more genes and the sum experimental value for the gene group. Some implementations provide the method where determining the gene-group score using the percentage of members of the gene group that are among the first one or more genes and the sum experimental value for the gene group includes: obtaining, for each gene group, a product of the percentage of members and the sum experimental value, thereby obtaining one or more products for the one or more gene groups. The method may also include summing, across the one or more gene groups, the one or more products, thereby obtaining a summed product. The method may also include determining, for the particular gene among the third one or more genes, a gene-group score based on the summed product. In some implementations, the method further includes, before (d), determining interactome scores respectively for fourth one or more genes. In some implementations, each interactome score for a particular gene is determined using (i) connections between the particular gene and other genes connected to the particular gene in a network of genes and (ii) at least some of the one or more experimental values of the first one or more genes. In some implementations, (d) includes obtaining the summary scores for at least the first one or more genes and the second one or more genes based at least in part on the interactome scores for at least some of the fourth one or more genes, as well as the one or more experimental gene scores for the first one or more genes determined in (b) and the one or more in silico gene scores for the second one or more genes determined in (c). In some

implementations, the network of genes are based on interactions and relations among genes, proteins, and/or phospholipids. In some implementations, calculating the interactome score includes calculating the interactome score as Ni′:

[510] Ni′=Ni+Σ((Ni+Nn)*edge_weightn)

[511] wherein Ni is the summary score of the particular gene i, Nn is a summary score of gene n connected to the particular gene, and edge_weightn is the weight of the edge connecting the particular gene i and gene n. In some implementations, calculating the interactome score further includes: saving Ni′ that are smaller than a second threshold in a first pass dictionary; and repeating the calculation for all genes in the first pass dictionary, thereby updating the interactome scores. In some implementations, the method further includes training the model by optimizing an objective function. In some implementations, training the model includes applying a bootstrap technique to bootstrap samples. In some implementations, the objective function relates to at least one summary score distribution after bootstrapping. In some implementations, optimizing the objective function includes minimizing differences of summary scores between a training set and a validation set. In some implementations, optimizing the objective function includes maximizing a distance between a summary score distribution obtained from the plurality of gene sets and a summary score distribution obtained from random gene sets. In some implementations, summary scores are ranked and binned in buckets of a defined size, wherein penalty scores are assigned to the buckets, the penalty scores favoring higher ranked summary scores. In some implementations, the objective function is based only on top ranked summary scores. In some implementations, training the model includes using the objective function in an unsupervised machine learning approach to learn parameters of the model. In some implementations, the model has the form:

[512] F(θ)=k1*c1+k2*c2+ . . . +kn*cn

[513] wherein θ are parameters of the model, ci are components of the model, and ki are weight factors for the components. In some implementations, the method further includes partitioning one or more of the components of the model into sub-components based on sample weights of experimental data types. In some implementations, the summary scores of the first and second one or more genes are penalized based on how likely experimental values of the first and second one or more genes in one or more random gene sets are correlated with the

biological, chemical or medical concept of interest. In some implementations, each summary score of a particular gene is penalized by a penalty value that is inversely proportional to a p value of a rank product, wherein the rank product includes a product of ranks of the particular gene across the one or more random gene sets. One general aspect includes a computer program product including a non-transitory machine readable medium storing program code that, when executed by one or more processors of a computer system, causes the computer system to implement a method for identifying genes that are potentially associated with a biological, chemical or medical concept of interest, said program code including: (a) code for selecting a plurality of gene sets from a database, where each gene set of the plurality of gene sets includes a plurality of genes and a plurality of experimental values associated with the plurality of genes, and where the plurality of experimental values are correlated with the biological, chemical or medical concept of interest in at least one experiment. The program code also includes (b) code for determining, for each gene set, one or more experimental gene scores for first one or more genes among the plurality of genes using one or more experimental values of the first one or more genes. The program code also includes (c) code for determining, for each gene set, one or more in silico gene scores for second one or more genes among the plurality of genes based at least in part on the first one or more genes' correlations with the second one or more genes, where the first one or more genes' correlations with the second one or more genes are indicated in other gene sets in the database beside the plurality of gene sets. The program code also includes (d) code for obtaining summary scores for the first and second one or more genes based at least in part on the one or more experimental gene scores for the first one or more genes determined in (b) and the one or more in silico gene scores for the second one or more genes determined in (c), where each summary score is aggregated across the plurality of gene sets. The program code also includes (e) code for identifying the genes that are potentially associated with the biological, chemical or medical concept of interest using the summary scores of the first and second one or more genes.

[514] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0023119, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for preparing a sequencing

library that includes nucleic acids from a plurality of single cells. In one embodiment, the method includes providing isolated nuclei from a plurality of cells; subjecting the isolated nuclei to a chemical treatment to generate nucleosome-depleted nuclei while maintaining integrity of the isolated nuclei; distributing subsets of the nucleosome-depleted nuclei into a first plurality of compartments and contacting each subset with a transposome complex, where the transposome complex in each compartment includes a transposase and a first index sequence that is different from first index sequences in the other compartments; fragmenting nucleic acids in the subsets of nucleosome-depleted nuclei into a plurality of nucleic acid fragments and incorporating the first index sequences into at least one strand of the nucleic acid fragments to generate indexed nuclei that include indexed nucleic acid fragments, where the indexed nucleic acid fragments remain attached to the transposases; combining the indexed nuclei to generate pooled indexed nuclei; distributing subsets of the pooled indexed nuclei into a second plurality of compartments; incorporating into the indexed nucleic acid fragments in each compartment a second index sequence to generate dual-index fragments, where the second index sequence in each compartment is different from second index sequences in the other compartments; and combining the dual-index fragments, thereby producing a sequencing library that includes whole genome nucleic acids from the plurality of single cells. In one embodiment, the chemical treatment includes a treatment with a chaotropic agent capable of disrupting nucleic acid-protein interactions, such as lithium 3,5-diiodosalicylic acid. In one embodiment, the chemical treatment includes a treatment with a detergent capable of disrupting nucleic acid-protein interactions, such as sodium dodecyl sulfate (SDS). In one embodiment, the nuclei are treated with a cross-linking agent before subjecting the isolated nuclei to the chemical treatment, such as formaldehyde. The cross-linking agent can be at a concentration from about 0.2% to about 2%, and in one embodiment is about 1.5%. In one embodiment, the cross-linking by formaldehyde is reversed after distributing subsets of the pooled indexed nuclei and before incorporating into the indexed nucleic acid fragments in each compartment a second index sequence. In one embodiment, the reversal of the cross-linking includes incubation at about 55° C. to about 72° C. In one embodiment, the transposases are disassociated from the indexed nucleic acid fragments prior to the reversal of the cross-linking. In one embodiment, the transposases are disassociated from the indexed nucleic acid fragments

using sodium dodecyl sulfate (SDS). In one embodiment, the nuclei are treated with a restriction enzyme prior to fragmenting nucleic acids in the subsets of nucleosome-depleted nuclei into a plurality of nucleic acid fragments and incorporating the first index sequences. In one embodiment, the nuclei are treated with a ligase after treatment with the restriction enzyme. In one embodiment, the distributing subsets of the nucleosome-depleted nuclei, the distributing subsets of the pooled indexed nuclei, or the combination thereof, is performed by fluorescence-activated nuclei sorting. In one embodiment, the subsets of the nucleosome-depleted nuclei include approximately equal numbers of nuclei, and in one embodiment, the subsets of the nucleosome-depleted nuclei include from 1 to about 2000 nuclei. In one embodiment, the subsets of the pooled indexed nuclei include approximately equal numbers of nuclei, and in one embodiment, the subsets of the pooled indexed nuclei include from 1 to about 25 nuclei. In one embodiment, the subsets of the pooled indexed nuclei include at least 10 times fewer nuclei than the subsets of the nucleosome-depleted nuclei, or at least 100 times fewer nuclei than the subsets of the nucleosome-depleted nuclei. In one embodiment, the first plurality of compartments, the second plurality of compartments, or the combination thereof, is a multi-well plate, such as a 96-well plate or a 384-well plate. In one embodiment, the transposome complex is added to the compartments after the subsets of nucleosome-depleted nuclei are distributed into the compartments. In one embodiment, each of the transposome complexes includes a transposon, and each of the transposons includes a transferred strand. In one embodiment, the transferred strand includes the first index sequence and a first universal sequence. In one embodiment, the incorporation of the second index sequence into the indexed nucleic acid fragments includes contacting the indexed nucleic acid fragments in each compartment with a first universal primer and a second universal primer, each including an index sequence and each including a sequence identical to or complementary to a portion of the first universal sequence, and performing an exponential amplification reaction. In one embodiment, the exponential amplification reaction can be a polymerase chain reaction (PCR), and in one embodiment, the PCR can include 15 to 30 cycles.

[515] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0037950, which is hereby incorporated by reference in its entirety. For

example, detection of a genetic biomarker can include microarrays and methods of modifying immobilized capture primers. In one aspect, is a microarray including: a) a substrate including at least one well, a surface surrounding the well and an inner well surface; b) a first layer covering the inner well surface and including at least one first capture primer pair; and c) a second layer covering the first layer and the surface surrounding the well. In another aspect, is a microarray including: a) a substrate including at least one well, a surface surrounding the well and an inner well surface; and b) a layer covering the inner well surface and including at least one first capture primer pair and at least one second capture primer pair. In another aspect, is a method for amplifying a nucleic acid, including: a) producing a first layer on a substrate, wherein the substrate includes at least one well, a surface surrounding the well and an inner well surface, wherein the first layer covers the inner well surface; b) depositing at least one first capture primer pair in the first layer; c) producing a second layer on the substrate covering the first layer and the surface surrounding the well; d) contacting a sample including a plurality of target polynucleotides with the substrate under conditions sufficient for a target polynucleotide to hybridize with a capture primer of the at least one first capture primer pair, and e) performing a first kinetic exclusion assay (KEA) to produce a clonal population of amplicons from the target polynucleotide inside the well, thereby amplifying the target polynucleotide. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a nucleic acid, including: a) producing a first layer on a substrate, wherein the substrate includes at least one well, a surface surrounding the well and an inner well surface, wherein the first layer at least partially covers the inner well surface; b) depositing at least one first capture primer pair in the first layer, wherein the first capture primer pair includes a plurality of first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and a plurality of second capture primers including a 3′ portion including an Illumina® P7 primer nucleotide sequence; c) producing a second layer on the substrate covering the first layer and the surface surrounding the well; d) depositing at least one second capture primer pair in the second layer, wherein the second capture primer pair is 3′ phosphate-terminated and includes a plurality of first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and a plurality of second capture primers including a 3′ portion including an Illumina® P7 primer nucleotide sequence; e)

contacting a sample including a plurality of target polynucleotides with the substrate under conditions sufficient for a single target polynucleotide per well to hybridize with a primer of the at least one first capture primer pair, wherein the target polynucleotides are flanked by complementary universal primer regions each including a complementary Illumina® P5′ primer nucleotide sequence or a complementary Illumina® P7′ primer nucleotide sequence; f) performing a first KEA to produce a monoclonal population of amplicons from the single target polynucleotide inside the at least one well, thereby amplifying the target polynucleotide; g) contacting the substrate with a T4-kinase to deblock the primers of the second primer pair, and h) performing bridge amplification or a second KEA to enlarge the monoclonal population of amplicons of the single target polynucleotide beyond the well. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a nucleic acid, including: a) producing a first layer on a substrate, wherein the substrate includes at least one well, a surface surrounding the well and an inner well surface, wherein the first layer at least partially covers the inner well surface; b) depositing at least one first capture primer pair in the first layer, wherein the first capture primer pair includes a plurality of at least one first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and an Illumina® SBS3 primer nucleotide sequence and a plurality of at least one second capture primers including a 3′ portion including an Illumina® P7 primer nucleotide sequence and an Illumina® SBS8 primer nucleotide sequence; c) producing a second layer on the substrate covering the first layer and the surface surrounding the well; d) depositing at least one second capture primer pair in the second layer, wherein the at least one second capture primer pair includes a plurality of first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and a plurality of second capture primers including an 3′ portion including an Illumina® P7 nucleotide sequence; e) contacting a sample including a plurality of target polynucleotides with the substrate under conditions sufficient for a single target polynucleotide per well to hybridize with a primer of the at least one first capture primer pair, wherein the plurality of target polynucleotides are flanked by a complementary SBS each including a complementary Illumina® SBS3′ primer nucleotide sequence or a complementary Illumina® SBS8′ nucleotide sequence, and f) performing a KEA for an extended time to produce a monoclonal population of amplicons from the single target polynucleotide inside

and outside the at least one well, thereby amplifying the single target polynucleotide inside the well and enlarging the monoclonal population of target polynucleotides beyond the at least one well. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a nucleic acid, including: a) producing a first layer on a substrate, wherein the substrate includes at least one well, a surface surrounding the well, and an inner well surface, wherein the first layer at least partially covers the inner well surface; b) depositing at least one first capture primer pair in the first layer, wherein the first primer pair includes a plurality of first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and a plurality of second capture primers including a 3′ portion including an Illumina® P7 primer nucleotide sequence; c) producing a second layer on the substrate covering the first layer and the surface surrounding the well; d) contacting a sample including a plurality of target polynucleotides with the substrate under conditions sufficient for a single target polynucleotide per well to hybridize with a primer of the at least one first capture primer pair, wherein the plurality of polynucleotides are flanked by complementary universal primer regions each including a complementary Illumina® P5′ primer nucleotide sequence or a complementary Illumina® P7′ primer nucleotide sequence; e) performing a first KEA to produce a monoclonal population of amplicons from the single target polynucleotide inside the at least one well, thereby amplifying the target polynucleotide; f) depositing at least one second capture primer pair in the second layer, wherein the at least one second capture primer pair includes a plurality of first capture primers including a 3′ portion including an Illumina® P5 primer nucleotide sequence and a plurality of second capture primers including a 3′ portion including an Illumina® P7 primer nucleotide sequence, and g) performing bridge amplification or a second KEA to enlarge the monoclonal population of amplicons of the single target polynucleotide. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a nucleic acid, including: a) producing a layer on a substrate, wherein the substrate includes at least one well, a surface surrounding the well and an inner well surface, wherein the well has a diameter of about 1 μm or more and wherein the layer at least partially covers the inner well surface; b) depositing at least one first capture primer pair and at least one second capture primer pair in the layer, wherein the primer density of the at least one first capture primer pair is higher than the primer density of the at least second primer pair; c)

contacting a sample including a plurality of target polynucleotides with the substrate under conditions sufficient for a single target polynucleotide per well to hybridize with the second primer, and d) performing a KEA to produce a monoclonal population of amplicons from the single target polynucleotide hybridized to the second primer inside the well, thereby amplifying the single target polynucleotide. Additionally or alternatively, detection of a genetic biomarker can include a method for modifying an immobilized capture primer including: a) contacting a substrate including a plurality of immobilized capture primers with a plurality of template nucleic acids under conditions sufficient for hybridization to produce one or more immobilized template nucleic acids, wherein the plurality of immobilized capture primers includes a first plurality of primers including a 5′-terminal universal capture region Y and a second plurality of primers including a 3′-terminal universal capture region Z, and wherein each template nucleic acid is flanked by 5′-terminal and a 3′-terminal universal capture regions Y or Z and includes one or more restriction sites and the target-specific capture region between the 5′-terminal universal capture region and the one or more restriction sites or between the 3′-terminal universal capture region and the one or more restriction sites, and b) extending one or more immobilized capture primers to produce one or more immobilized extension products complementary to the one or more template nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for modifying an immobilized capture primer including: a) contacting a substrate including a plurality of immobilized capture primers with a plurality of template nucleic acids under conditions sufficient for hybridization to produce one or more immobilized template nucleic acid, wherein the plurality of immobilized capture primers includes a first plurality of primers including a 3′-terminal Illumina® P5 primer nucleotide sequence and a second plurality of primers including a 3′-terminal Illumina® P7 primer nucleotide sequence, and wherein each template nucleic acid is flanked by a 3′-terminal complementary Illumina® P5′ primer nucleotide sequence and a 5′-terminal complementary Illumina® P7′ primer nucleotide sequence, and includes two SapI restriction sites, a spacer region between the SapI restriction sites, and a target-specific capture region between the 3′terminal complementary Illumina® P5′ primer nucleotide sequence and the SapI restriction sites; and b) extending one or more immobilized capture primers to produce one or more immobilized extension products complementary to the one or more template nucleic

acids. c) amplifying the one or more immobilized extension products by bridge amplification or KEA to produce one or more monoclonal clusters of immobilized double-stranded template nucleic acids; d) contacting the one or more monoclonal cluster of immobilized double-stranded template nucleic acids with SapI to cut the two restriction sites in a plurality of immobilized double-stranded template nucleic acids to produce a plurality of immobilized double-stranded chimeric capture primers including the Illumina® P5 primer nucleotide sequence and the target-specific capture region and a plurality of immobilized double-stranded regenerated universal capture primers including the Illumina® P7 primer nucleotide sequence, and e) optionally, contacting the plurality of immobilized double-stranded chimeric capture primers and immobilized double-stranded regenerated universal capture primers with a 5′-3′ dsDNA-exonuclease to produce a plurality of immobilized single-stranded chimeric capture primers and a plurality of immobilized single-stranded regenerated universal capture primers.

[516] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0356030, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions, systems, and methods for detecting the presence of polymer subunits using chemiluminescence. Under one aspect, a composition includes a substrate; a first polynucleotide coupled to the substrate; a second polynucleotide hybridized to the first polynucleotide; and a catalyst coupled to a first nucleotide of the second polynucleotide, the catalyst being operable to cause a chemiluminogenic molecule to emit a photon. In some embodiments, the composition further includes a plurality of the chemiluminogenic molecules. The catalyst can cause each of the chemiluminogenic molecules to emit a corresponding photon. The composition further can include a plurality of reagent molecules, the catalyst causing each of the chemiluminogenic molecules to emit a corresponding photon by oxidizing that chemiluminogenic molecule using a reagent molecule. The oxidized chemiluminogenic molecule can have an excited state that decays by emitting the corresponding photon. A system can include any of the foregoing compositions and circuitry configured to detect the photon emitted by the chemiluminogenic molecule. In some embodiments, the circuitry further is configured to detect the presence of the first nucleotide based on detection of the photon. Under another aspect, a method can

include providing a substrate; providing a first polynucleotide coupled to the substrate; hybridizing a second polynucleotide to the first polynucleotide; coupling a first catalyst to a first nucleotide of the second polynucleotide; and causing, by the first catalyst, a first chemiluminogenic molecule to emit a photon. Under another aspect, a method of sequencing a first polynucleotide includes providing the first polynucleotide to be sequenced and coupled to a substrate; b) hybridizing a second polynucleotide to the first polynucleotide; and contacting the second polynucleotide with a polymerase and a plurality of nucleotides. A first subset of the plurality of nucleotides includes a first moiety, a second subset of the plurality of nucleotides includes a second moiety, a third subset of the plurality of nucleotides includes a third moiety, and a fourth subset of the plurality of nucleotides includes a fourth moiety or no moiety. The method further can include adding a nucleotide of the plurality of nucleotides to the second polynucleotide based on a sequence of the first polynucleotide. The method further can include exposing the nucleotide to a catalyst coupled to a fifth moiety; exposing the nucleotide to chemiluminogenic molecules; and detecting emission of photons or an absence of photons from the chemiluminogenic molecules. The method further can include exposing the nucleotide to a catalyst coupled to a sixth moiety; exposing the nucleotide to chemiluminogenic molecules; and detecting emission of photons or an absence of photons from the chemiluminogenic molecules. The method further can include exposing the nucleotide to a cleaver molecule; exposing the nucleotide to chemiluminogenic molecules; and detecting emission of photons or an absence of photons from the chemiluminogenic molecules. The method further can include detecting the added nucleotide based on the detection of emission of photons or absence of photons from the chemiluminogenic molecules at one or more of the detection steps or a combination thereof. Under another aspect, a composition includes a catalyst operable to cause a chemiluminogenic molecule to emit a photon; a substrate; a first polynucleotide coupled to the substrate; a second polynucleotide hybridized to the first polynucleotide; and a quencher coupled to a first nucleotide of the second polynucleotide, the quencher operable to inhibit photon emission by the chemiluminogenic molecule. Under another aspect, a method includes providing a catalyst operable to cause a first chemiluminogenic molecule to emit a photon; providing a substrate; providing a first polynucleotide coupled to the substrate; hybridizing a second polynucleotide to the first

polynucleotide; coupling a first quencher to a first nucleotide of the second polynucleotide; and inhibiting, by the first quencher, photon emission by the first chemiluminogenic molecule. Under another aspect, a method of sequencing a first polynucleotide includes providing the first polynucleotide to be sequenced and coupled to a substrate; hybridizing a second polynucleotide to the first polynucleotide; and providing a catalyst coupled sufficiently close to the second polynucleotide that a quencher coupled to the second polynucleotide can inhibit photon emission from chemiluminescent molecules that interact with the catalyst. The method further can include contacting the second polynucleotide with a polymerase and a plurality of nucleotides. A first subset of the plurality of nucleotides includes a first moiety, a second subset of the plurality of nucleotides includes a second moiety, a third subset of the plurality of nucleotides includes a third moiety, and a fourth subset of the plurality of nucleotides includes a fourth moiety or no moiety.

[517] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0137876, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method that may be used to substantially reduce or eliminate high quality errors that may be generated during first extension. In another embodiment, the methods may also be used to reduce errors caused by mis-incorporation of nucleotides during the first few cycles of amplification. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing with improved accuracy comprising; providing a nucleic acid template; producing, by linear amplification directly from the template nucleic acid, a population comprising a plurality of complementary strands retained in close proximity to each other or identifiable as being obtained from the same template nucleic acid; and performing a sequencing reaction on said proximity retained (e.g. surface bound) oligonucleotides. In some embodiments, the method further comprises the step of carrying out further (exponential) amplification of the population of complementary strands after the rounds of linear amplification and prior to performing the sequencing reaction. Optionally the linear amplification (directly from the nucleic acid template) includes the steps of; hybridising said nucleic acid template to a first primer; extending the first primer to produce a complementary strand to the template; denaturing to

release the complementary strand which remains in close proximity (e.g. it remains bound to the surface and thus does not travel at all or does not diffuse far before re-hybridising nearby); and repeating the hybridisation and amplification steps to produce a population of surface bound complementary strands obtained directly from the template nucleic acid.

[518] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0101676, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include techniques for enrichment of target sequences in a nucleic acid library and reducing the capture of off-target sequences by a set of target hybridization probes. Because target hybridization probes have imperfect specificity for their nucleic acid targets, a sequencing run using a set of target hybridization probes may also include a certain percentage of reads that represent sequences that are off-target. For example, in an exome sequencing reaction, certain hybridization probes may pull down intronic or intergenic sequences from a nucleic acid library along with target sequences. These off-target fragments, once pulled down, are then present in the pool of nucleic acid fragments that are sequenced. While the sequencing information representative of the off-target reads is typically discarded, the present techniques use acquired sequencing information of these off-target reads to design hybridization probes that are specific for the off-target sequences and that are used to separate and/or remove fragments that include these sequences from the pool of fragments captured by the target-specific hybridization probes. The off-target hybridization probes are designed based on analysis of the off-target reads of a hybrid capture sequencing run that is performed with a set of target hybridization probes. In certain embodiments, the on-target probe design may also be based on systematic off-target analysis across samples to improve the specificity of the target hybridization probes for their desired targets. Additionally or alternatively, detection of a genetic biomarker can include a method of reducing off-target capture in a targeted sequencing reaction. The method includes the steps of providing a set of off-target hybridization probes that specifically bind to a plurality of off-target sequences present in a nucleic acid library generated from a sample, the nucleic acid library comprising a plurality of nucleic acid fragments and providing a set of target-specific hybridization probes that specifically bind to a plurality of target sequences present in the nucleic acid library. The

method also includes the steps of contacting the off-target hybridization probes with the nucleic acid library under conditions whereby the off-target hybridization probes hybridize to the off-target sequences and contacting the target-specific hybridization probes with the nucleic acid library under conditions whereby the target-specific hybridization probes hybridize to the target sequences. The method also includes the steps of selecting a group of nucleic acid fragments from the nucleic acid library bound to the target-specific hybridization probes; and sequencing the group of nucleic acid fragments bound to the target-specific hybridization probes. Additionally or alternatively, detection of a genetic biomarker can include a method of providing probes for off-target sequence capture in a targeted sequencing reaction. The method includes the steps of receiving a request for a set of target-specific hybridization probes. The method also includes the steps of contacting the target-specific hybridization probes with a reference nucleic acid library generated from a reference sample, the nucleic acid library comprising a plurality of nucleic acid fragments, to generate a reference group of target-specific and off-target nucleic acid fragments bound to the target-specific hybridization probes and separating the reference group of nucleic acid fragments bound to the target-specific hybridization probes from unbound nucleic acid fragments. The method also includes the steps of sequencing the reference group of nucleic acid fragments to generate reference sequencing data; identifying off-target sequences in the reference sequencing data; and providing a set of off-target hybridization probes based on the identified off-target sequences. Additionally or alternatively, detection of a genetic biomarker can include a sequencing kit for reducing off-target capture in a targeted sequencing reaction that includes a set of off-target hybridization probes that specifically bind to a plurality of off-target sequences present in a nucleic acid library generated from a sample, the nucleic acid library comprising a plurality of nucleic acid fragments and a set of target-specific hybridization probes that specifically bind to a plurality of target sequences present in the nucleic acid library.

[519] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2016/0319345, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, apparatus, systems, and computer program products for determining nucleic acid fragment sequences using unique

molecular indices (UMIs). In various implementations, sequencing methods determine the sequences of nucleic acid fragments from both strands of the nucleic acid fragments. In some implementations, the methods employ physical UMIs located on one or both strands of sequencing adapters. In some implementations, the methods also employ virtual UMIs located on both strands of the nucleic acid fragments. One aspect relates to a method for sequencing nucleic acid molecules from a sample using unique molecular indices (UMIs). Each unique molecular index (UMI) is an oligonucleotide sequence that can be used to identify an individual molecule of a double-stranded DNA fragment in the sample. The method include: (a) applying adapters to both ends of double-stranded DNA fragments in the sample, wherein the adapters each include a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a physical UMI on one strand or each strand of the adapters, thereby obtaining DNA-adapter products; (b) amplifying both strands of the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads each associated with a physical UMI; (d) identifying a plurality of physical UMIs associated with the plurality of reads; (e) identifying a plurality of virtual UMIs associated with the plurality of reads, wherein each virtual UMI is a sequence found in a DNA fragment in the sample; and (f) determining sequences of the double-stranded DNA fragments in the sample using the plurality of reads obtained in (c), the plurality of physical UMIs identified in (d), and the plurality of virtual UMIs identified in (e). In some implementations, the method include operation (f) includes: (i) combining, for each of one or more of the double-stranded DNA fragments in the sample, (1) reads having a first physical UMI and at least one virtual UMI in the 5′ to 3′ direction and (2) reads having a second physical UMI and the at least one virtual UMI in the 5′ to 3′ direction to determine a consensus nucleotide sequence; and (ii) determining, for each of the one or more of the double-stranded DNA fragments in the sample, a sequence using the consensus nucleotide sequence. In some implementations, the adapters each include a physical UMI on only one strand of the adapters on the single-stranded 5′ arm or the single-stranded 3′ arm. In some of these implementation, (f) includes: (i) collapsing reads having a same first physical UMI into a first group to obtain a first consensus nucleotide sequence; (ii) collapsing reads having a same second physical UMI into a second group to obtain a second consensus

nucleotide sequence; and (iii) determining, using the first and second consensus nucleotide sequences, a sequence of one of the double-stranded DNA fragments in the sample. In some implementations, (iii) includes: (1) obtaining, using localization information and sequence information of the first and second consensus nucleotide sequences, a third consensus nucleotide sequence, and (2) determining, using the third consensus nucleotide sequence, the sequence of one of the double-stranded DNA fragments. In some implementations, operation (e) includes identifying the plurality of virtual UMIs, while the adapters each include the physical UMI on only one strand of the adapters in the single-stranded 5′ arm region or the single-stranded 3′ arm region. In some implementations, (f) includes: (i) combining reads having a first physical UMI and at least one virtual UMI in the 5′ to 3′ direction and reads having a second physical UMI and the at least one virtual UMI in the 5′ to 3′ direction to determine a consensus nucleotide sequence; and (ii) determining a sequence of one of the double-stranded DNA fragments in the sample using the consensus nucleotide sequence. In some implementations of the methods above, obtaining the plurality of reads in operation (c) includes: obtaining two pair-end reads from each of the amplified polynucleotides, where in the two pair-end reads include a long read and a short read, the long read being longer than the short read. In some of these implementations, operation (f) includes: combining read pairs associated with a first physical UMI into a first group and combining read pairs associated with a second physical UMI into a second group, wherein the first and the second physical UMIs are uniquely associated with a double-stranded fragment in the sample; and determining the sequence of the double-stranded fragment in the sample using sequence information of long reads in the first group and sequence information of long reads in the second group. Another aspect adapters to both ends of double-stranded DNA fragments in the sample, wherein the adapters each include a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a physical unique molecular index (UMI) on the single-stranded 5′ arm or the single-stranded 3′ arm; (b) amplifying both strands of ligation products from (a), thereby obtaining a plurality of single-stranded, amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads each associated with a physical UMI; (d) identifying a plurality of physical UMIs associated with the plurality of reads; and (e) determining sequences of the double-stranded DNA fragments in the sample

using the plurality of sequences obtained in (c) and the plurality of physical UMIs identified in (d). An additional aspect relates to a method for sequencing nucleic acid molecules from a sample. The method includes: (a) attaching adapters to both ends of double-stranded DNA fragments in the sample, wherein the adapters each include a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a physical unique molecular index (UMI) shorter than 12 nucleotides on one strand or each strand of the adapters; (b) amplifying both strands of ligation products from (a), thereby obtaining a plurality of single-stranded, amplified polynucleotides each including a physical UMI; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads each associated with a physical UMI; (d) identifying a plurality of physical UMIs associated with the plurality of reads; and (e) determining sequences of the double-stranded DNA fragments in the sample using the plurality of reads obtained in (c) and the plurality of physical UMIs identified in (d). Another aspect relates a method for making a duplex sequencing adapter having a physical UMI on each strand. The method includes: providing a preliminary sequencing adapter including a double-stranded hybridized region, two single-stranded arms, and an overhang including 5′-CCANNNNANNNNTGG-3′ at an end of the double-stranded hybridized region that is further away from the two single stranded arms; extending one strand of the double-stranded hybridized region using the overhang as a template, thereby producing an extension product; and applying restriction enzyme Xcm1 to digest a double-stranded end of the extension product, thereby producing the duplex sequencing adapter having a physical UMI on each strand. In some implementations, the preliminary sequencing adapter includes a read primer sequence on each strand. A further aspect relates to a computer program product including a non-transitory machine readable medium storing program code that, when executed by one or more processors of a computer system, causes the computer system to implement a method for determining sequence information of a sequence of interest in a sample using unique molecular indices (UMIs). The program code includes: (a) code for obtaining reads of a plurality of amplified polynucleotides, wherein the plurality of amplified polynucleotides are obtained by amplifying double-stranded DNA fragments in the sample including the sequence of interest and attaching adapters to the double-stranded DNA fragments; (b) code for identifying a plurality of physical UMIs in the reads of the plurality of

amplified polynucleotides, wherein each physical UMI is found in an adapter attached to one of the double-stranded DNA fragments; (c) code for identifying a plurality of virtual UMIs in the received reads of the plurality of amplified polynucleotides, wherein each virtual UMI is found in an individual molecule of one of the double-stranded DNA fragments; and (c) code for determining sequences of the double-stranded DNA fragments using the reads of the plurality of amplified polynucleotides, the plurality of physical UMIs, and the plurality of virtual UMIs, thereby reducing errors in the determined sequences of the double-stranded DNA fragments. In some implementations, the adapters each include a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a physical unique molecular index (UMI) on one strand or each strand of the adapters. An additional aspect relates to a computer system, including: one or more processors; system memory; and one or more computer-readable storage media. The media has stored thereon computer-executable instructions that causes the computer system to implement a method to determine sequence information of a sequence of interest in a sample using unique molecular indices (UMIs), which are oligonucleotide sequences that can be used to identify individual molecules of double-stranded DNA fragments in the sample. The instructions includes: (a) receiving reads of a plurality of amplified polynucleotides, wherein the plurality of amplified polynucleotides are obtained by amplifying double-stranded DNA fragments in the sample including the sequence of interest and attaching adapters to the double-stranded DNA fragments; (b) identifying a plurality of physical UMIs in the received reads of the plurality of amplified polynucleotides, wherein each physical UMI is found in an adapter attached to one of the double-stranded DNA fragments; (c) identifying a plurality of virtual UMIs in the received reads of the plurality of amplified polynucleotides, wherein each virtual UMI is found in an individual molecule of one of the double-stranded DNA fragments; and (d) determining sequences of the double-stranded DNA fragments using the sequences of the plurality of amplified polynucleotides, the plurality of physical UMIs, and the plurality of virtual UMIs, thereby reducing errors in the determined sequences of the double-stranded DNA fragments. One aspect provides methods for sequencing nucleic acid molecules from a sample using nonrandom unique molecular indices (UMIs). The methods involve: (a) applying adapters to both ends of DNA fragments in the sample, wherein the adapters each include a double-

stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a nonrandom unique molecular index (UMI) on one strand or each strand of the adapters, thereby obtaining DNA-adapter products; (b) amplifying the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads associated with a plurality of nonrandom UMIs; (d) from the plurality of reads, identifying reads sharing a common nonrandom UMI; and (e) from the identified reads sharing the common nonrandom UMI, determining the sequence of at least a portion of a DNA fragment, from the sample, having an applied adaptor with the common non-random UMI. Another aspect relates to methods for sequencing nucleic acid molecules from a sample using nonrandom unique molecular indices (UMIs). In some implementations, a method involves: (a) applying adapters to both ends of double-stranded DNA fragments in the sample, wherein the adapters each include a double-stranded hybridized region, a single-stranded 5′ arm, a single-stranded 3′ arm, and a nonrandom unique molecular index (UMI) on one strand or each strand of the adapters, thereby obtaining DNA-adapter products, wherein the nonrandom UMI can be combined with other information to uniquely identify an individual molecule of the double-stranded DNA fragments; (b) amplifying both strands of the DNA-adapter products to obtain a plurality of amplified polynucleotides; (c) sequencing the plurality of amplified polynucleotides, thereby obtaining a plurality of reads each associated with a nonrandom UMI; (d) identifying a plurality of nonrandom UMIs associated with the plurality of reads; and (e) using the plurality of reads and the plurality of nonrandom UMIs to determine sequences of the double-stranded DNA fragments in the sample. Additionally or alternatively, detection of a genetic biomarker can include a system, apparatus, and computer program products for determining DNA fragment sequences implementing the methods disclosed. One aspect provides a computer program product including a non-transitory machine readable medium storing program code that, when executed by one or more processors of a computer system, causes the computer system to implement a method to determine sequence information of a sequence of interest in a sample using unique molecular indices (UMIs). The program code includes instructions to perform the methods above.

[520] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0360193, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, compositions and kits for the amplification of nucleic acid samples to generate nucleic acid libraries. Additionally or alternatively, detection of a genetic biomarker can include a method of creating a nucleic acid library from a nucleic acid sample, the method comprising: a) providing a set of amplification primers to a nucleic acid sample, the set of amplification primers comprising a plurality of random primers and a plurality of locus specific primers, wherein the locus specific primers are configured to amplify a plurality of predetermined regions of the nucleic acid library, and wherein the random primers are in greater abundance compared to the locus specific primers; and b) amplifying the nucleic acid library using the set of amplification primers, thereby creating a nucleic acid library. Also presented is a kit for amplifying a nucleic acid sample, wherein the kit comprises a plurality of random primers and a plurality of locus specific primers configured to amplify a plurality of predetermined regions of a nucleic acid library. In certain aspects, the kit further comprises a set of instructions for using the random primers and the locus specific primers in an amplification reaction set, wherein the random primers are in greater abundance compared to the locus specific primers. In certain aspects, the kit further comprises a set of instructions for combining the set of amplification primers with a nucleic acid library and amplifying the nucleic acid library. In addition to the foregoing method, also presented is a method of creating a nucleic acid library from a nucleic acid sample, the method comprising: a) amplifying a nucleic acid sample with an AT-rich set of random amplification primers. In certain aspects, the AT-rich set of random amplification primers is a mixture of primers. Also presented is a kit for amplifying a nucleic acid sample, wherein the kit comprises an AT-rich set of random amplification primers. In certain aspects, the kit further comprises a set of instructions for combining the set of amplification primers with a nucleic acid library and amplifying the nucleic acid library. In certain other aspects, the kit further comprises a DNA polymerase. In still other aspects, the AT-rich set of random amplification primers is a mixture of primers. Additionally or alternatively, detection of a genetic biomarker can include a method of creating a nucleic acid library from a nucleic acid sample, the method comprising:

a) amplifying a nucleic acid sample with a set of random amplification primers, the random amplification primers comprising AT-rich 5′ tails. In certain aspects, the set of random amplification primers is a mixture of primers. Also presented is a method of creating a nucleic acid library from a nucleic acid sample, the method comprising: amplifying a nucleic acid sample with a set of variable-length random amplification primers, wherein each variable-length random amplification primer comprises a random 3′ portion and a degenerate 5′ tail, the degenerate 5′ tail being proportional in length to the A/T content of the random 3′ portion of the primer. In certain aspects, the set of variable-length random amplification primers is a mixture of primers. Also presented is a method of creating a nucleic acid library from a nucleic acid sample, the method comprising: a) amplifying a nucleic acid sample with a set of random amplification primers, wherein each primer comprises a random 3′ portion and a constant 5′ priming portion, thereby producing amplification products, wherein each amplification product comprises the constant 5′ priming portion; b) circularizing the amplification products; and c) amplifying the circularized amplification products using primers which hybridize to the constant 5′ priming portion. In certain aspects, the amplifying in step (c) comprises performing multiple displacement amplification. In certain aspects, the set of random amplification primers is a mixture of primers.

[521] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0176071, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include determining proximity of sequence fragments with respect to a larger target nucleic acid from which the fragments were derived. For example, the methods can be used to determine phasing and to identify haplotypes for a relatively long target nucleic acid sequence when individual sequence reads are shorter than the length of the target nucleic acid under evaluation. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing a target nucleic acid polymer. The method can include the steps of (a) modifying a target nucleic acid polymer to produce a modified nucleic acid polymer, wherein the modified nucleic acid polymer includes a plurality of sequence regions from the target nucleic acid polymer; (b) producing fragments of the modified nucleic acid polymer in a vessel having a solid support surface, each fragment

comprising one of the sequence regions; (c) capturing the fragments randomly at locations in a region of the solid support surface; (d) determining nucleotide sequences of the sequence regions by detecting the fragments at the locations; and (e) producing a representation of the nucleotide sequence for the target nucleic acid polymer based on the nucleotide sequences from the fragments and the relative distances between the locations on the solid support surface. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing a target nucleic acid polymer that includes the steps of (a) adding inserts into a target nucleic acid polymer to form a modified nucleic acid polymer including a plurality of internal inserts; (b) producing fragments of the modified nucleic acid polymer in a fluid that is in contact with a solid support surface, thereby releasing fragments that each include at least a portion of the inserts; (c) capturing the fragments from the fluid randomly at locations on a solid support surface; (d) determining nucleotide sequences from the fragments by detecting the fragments at the locations; and (e) producing a representation of the nucleotide sequence for the target nucleic acid polymer based on the nucleotide sequences from the fragments and the relative distances between the locations on the solid support surface. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing a target nucleic acid polymer, that includes the steps of (a) modifying a target nucleic acid polymer to produce a modified nucleic acid polymer, wherein the modified nucleic acid polymer includes a plurality of sequence regions from the target nucleic acid polymer; (b) attaching the modified nucleic acid polymer to a region on a solid support surface; (c) producing fragments of the modified nucleic acid polymer that is attached to the solid support surface, wherein the fragments are attached to locations at the region of the solid support surface; (d) determining nucleotide sequences from the fragments by detecting the fragments at the locations; and (e) producing a representation of the nucleotide sequence for the target nucleic acid polymers based on the nucleotide sequences from the fragments and the relative distances between the locations on the solid support surface. Additionally or alternatively, detection of a genetic biomarker can include a method of determining the source for individual sequences in a mixture of sequences from different sources. The method can include the steps of (a) providing a mixture of target nucleic acid polymers from a plurality of different sources; (b) modifying the mixture of target nucleic acid polymers to produce a mixture of modified nucleic acid

polymers, wherein the mixture of modified nucleic acid polymers includes a plurality of sequence regions from the different sources; (c) producing fragments of the modified nucleic acid polymers in a vessel having a solid support surface, each fragment comprising a sequence region from a single one of the different sources; (d) capturing the fragments randomly at locations of the solid support surface, under conditions wherein fragments from a common target nucleic acid polymer preferentially localize to proximal locations on the solid support surface; (e) determining nucleotide sequences of the fragments at the locations; and (f) identifying the nucleotide sequences that are derived from a common source in the plurality of different sources based on the nucleotide sequences from the fragments and the relative distances between the locations on the solid support surface.

[522] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2014/0364323, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for determining the presence of a plurality of nucleotide sequences of interest in a plurality of samples, while preserving the identity of each sample. The method can be used in many applications, including genotyping, expression analysis, and identification of individual species in complex samples. In one embodiment, each sample is contacted with a plurality of probe sets. A first probe has a first identification sequence and a first hybridization sequence complementary to a first portion of the sequence of interest. A second probe has a second hybridization sequence complementary to a second portion of the same sequence of interest and a second identification sequence. If the first hybridization sequence is hybridized to the first portion of the sequence of interest, and the second hybridization sequence is hybridized to the second portion of the same sequence of interest, then the first and second probes are joined. This can also be performed using ligation and/or extension methods, such as with a GoldenGate® assay design. The presence of the sequence of interest and the identity of the sample containing the sequence of interest are determined, based on identification sequence codes present in the joined probes.

[523] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2013/0059741, which is hereby incorporated by reference in its entirety. For

example, detection of a genetic biomarker can include compositions and methods for assaying the presence of a target analyte in a sample using a solid support. Additionally or alternatively, detection of a genetic biomarker can include a solid support having a binding protein, such as an antibody, antibody fragment or protein receptor, immobilized to the solid support and at least two separate nucleic acid primers immobilized near the binding protein. Additionally or alternatively, detection of a genetic biomarker can include a solid support wherein a binding complex is formed between the binding protein immobilized to the solid support, a target analyte and a second binding protein. In some embodiments, a solid support is provided wherein such a binding complex further forms a hybridization complex between one nucleic acid primer immobilized on the solid support and an oligonucleotide tag linked to the second binding protein. Additionally or alternatively, detection of a genetic biomarker can include an array that in includes a plurality of these solid supports. In some embodiments, solid supports can be used in a method for detecting numerous target analytes. In one embodiment, the method for detecting a target analyte includes providing a solid support having a binding protein immobilized to the solid support and a second binding protein provided in solution, wherein the first binding protein recognizes and is capable of binding a target analyte in the presence of the second binding protein, which also recognizes and binds the same target analyte, contacting the solid support with target analyte and the second binding protein under sufficient conditions to allow formation of a binding complex between the target analyte and both the first and second binding proteins, hybridizing the oligonucleotide tag linked to the second binding protein to a first nucleic acid primer immobilized on the solid support, extending this first primer whereby a complement of the oligonucleotide tag is generated, amplifying the newly generated complement using a second nucleic acid primer immobilized to the solid support and detecting the presence of the amplicon, wherein the presence of the amplicon indicates the presence of the target analyte. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a target analyte, wherein the method described above alternatively proceeds following the extension step by hybridizing the complement of the oligonucleotide tag that is generated, to a second nucleic acid primer immobilized on the solid support forming a second hybridization complex, then extending the second nucleic acid primer with at least one labeled nucleic acid residue, using methods such

as single base extension or sequencing by synthesis, wherein the nucleic acid residue added to the primer is dependent on the nucleic acid sequence of the oligonucleotide tag, followed by detecting the presence of the labeled nucleic acid residue on the solid surface, wherein the presence of the labeled nucleic acid residue indicates the presence of the target analyte.

[524] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2012/0156753, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for 5′ ligation tagging of uncapped RNA in a sample that has a 5′ polyphosphate group, comprising: (A) providing: (i) a sample that contains uncapped RNA that has a 5′ polyphosphate group, including wherein the sample additionally contains RNA that has a 5′ monophosphate group and/or capped RNA and/or RNA that has a 5′ hydroxyl group; (ii) RNA 5′ polyphosphatase; (iii) an acceptor oligonucleotide that exhibits a tag; and (iv) RNA ligase; (B) contacting the sample with the RNA 5′ polyphosphatase under conditions and for sufficient time wherein the uncapped RNA that has a 5′ polyphosphate group is converted to RNA that has a 5′ monophosphate group; and (C) contacting the sample from step (B) with the acceptor oligonucleotide and the RNA ligase under conditions and for sufficient time wherein the 3′ end of the acceptor oligonucleotide is ligated to RNA that has a 5′ monophosphate group but not to the capped RNA and 5′-ligation-tagged RNA is generated. In other embodiments, the sample provided in step (A) additionally contains RNA that has a 5′ monophosphate group but the acceptor oligonucleotide is only ligated to the RNA that has a 5′ monophosphate group which was converted from the uncapped RNA that has a 5′ polyphosphate group in step (B) and is not ligated to the RNA that has a 5′ monophosphate group already in the sample provided in step (A), wherein the method additionally comprises the substeps of: providing an RNA 5′ monophosphatase; and, prior to step (B), contacting the sample with the RNA 5′ monophosphatase under conditions and for sufficient time wherein RNA in the sample that has a 5′ monophosphate group is converted to RNA that has a 5′ hydroxyl group; and inactivating or removing the RNA 5′ monophosphatase. In other embodiments, the method additionally comprises 5′ ligation tagging of the capped RNA in the sample, wherein the method additionally comprises the substeps of: providing a nucleic acid pyrophosphatase or decapping enzyme; and, prior to step (C), contacting the

sample from step (B) with the nucleic acid pyrophosphatase or the decapping enzyme under conditions and for sufficient time wherein capped RNA in the sample is converted to RNA that has a 5′ monophosphate group, whereby the capped RNA contained in the sample provided in step (A) is also 5′-ligation tagged in step (C).

[525] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2012/0010091, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for preparing a cDNA library from a plurality of single cells. In one aspect, the method includes the steps of releasing mRNA from each single cell to provide a plurality of individual mRNA samples, synthesizing a first strand of cDNA from the mRNA in each individual mRNA sample and incorporating a tag into the cDNA to provide a plurality of tagged cDNA samples, pooling the tagged cDNA samples and amplifying the pooled cDNA samples to generate a cDNA library having double-stranded cDNA. In some embodiments, a cDNA library can be produced by the above methods. Additionally or alternatively, detection of a genetic biomarker can include methods for analyzing gene expression in a plurality of cells by preparing a cDNA library as described above and sequencing the library.

[526] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2011/0152111, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting a target nucleic acid sequence in an archived tissue sample comprising providing a nucleic acid sample prepared from an archived tissue sample, hybridizing a first set of ligation probes to said target sequence to form a ligation structure, ligating said probes using a ligase to form a ligated probe, amplifying said ligated probe to form amplicons, and detecting said amplicons. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a plurality of target nucleic acid sequences in an archived tissue sample comprising providing a nucleic acid sample prepared from an archived tissue sample, said sample comprising a plurality of target nucleic acid sequences, adding a plurality of detection probes, each substantially complementary to one of said target nucleic acid sequences, providing an enzyme to form

modified detection probes, amplifying said modified detection probes to form amplicons and detecting said amplicons. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a plurality of target nucleic acid sequences in an archived tissue sample comprising providing a nucleic acid sample prepared from an archived tissue sample, said sample comprising a plurality of target nucleic acid sequences, hybridizing a plurality of sets of ligation probes to said target sequence to form a plurality of ligation structures, ligating each of said plurality of ligation structures using a ligase to form a plurality of ligated probes, amplifying said ligated probes to form a plurality of amplicons and detecting said amplicons as an indication of the presence of said plurality of target nucleic acid sequences.

[527] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/019456, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions that facilitate the characterization of transcriptomes and/or genomic variation in tissues while preserving spatial information related to the origin of target nucleic acids in the tissue. For example, the methods can enable the identification of the location of a cell or a cell cluster in a tissue biopsy that carries an aberrant mutation. The methods can therefore be useful for diagnostic purposes, e.g., for the diagnosis of cancer, and possibly aid in the selection of targeted therapies. Additionally or alternatively, detection of a genetic biomarker can include a capture array for spatial detection and analysis of nucleic acids in a tissue sample, comprising a capture site comprising a pair of capture probes immobilized on a surface, wherein a first capture probe of the pair of capture probes comprises a first primer binding region and a spatial address region, and wherein a second capture probe of the pair of capture probes comprises a second primer binding region and a capture region. Additionally or alternatively, detection of a genetic biomarker can include a method for spatial detection and analysis of nucleic acids in a tissue sample that includes (a) providing a capture array, comprising a capture site comprising a pair of capture probes immobilized on a surface, wherein a first capture probe of the pair of capture probes comprises a first primer binding region and a spatial address region, and wherein a second capture probe of the pair of capture probes comprises a second primer binding region and a capture region. Additionally or alternatively, detection of a genetic biomarker can include

a method for spatial detection and analysis of nucleic acids in a tissue sample that includes providing a magnetic nanoparticle comprising an immobilized capture probe comprising a capture region. Additionally or alternatively, detection of a genetic biomarker can include a capture array for spatial detection and analysis of nucleic acids in a tissue sample, comprising a capture site comprising a capture probe comprising a spatial address region, and a transposon end (TE) region.

[528] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2016/130704, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include to methods and compositions relating to evaluating components of a single cell preserved or embedded or contained within a contiguity preserving elements(CE). In one aspect are methods for analyzing plurality of analyte types from a single cell. In some embodiments, a plurality of contiguity preserving elements (CE) are provided, each CE comprises a single cell. The cells are lysed within the CE such that the plurality of analytes within the single cell are released within the CE. In some embodiments, plurality of types of reporter moieties are provided such that each type of reporter moiety is specific for each type of analyte. In some embodiments, the reporter moiety identify a single cell. The plurality of analytes are modified such that each type of analyte comprise a reporter moiety specific for the analyte type. In some embodiments, the CE comprising the analytes comprising said reporter moieties are combined. In some embodiments, the combined CE comprising the analytes comprising said reporter moieties are compartmentalized. In some embodiments, additional reporter moieties are provided and combined with the analytes comprising analytes such that the analytes comprise two or more different reporter moieties. The analytes comprising the reporter moieties are analyzed such that the identity of the analyte is detected and the reporter moiety identifies the source of the analyte from a single cell. In some embodiments, the exemplary plurality of analytes include but are not limited to DNA, RNA, cDNA, protein, lipids, carbohydrates, cellular organelles, (e.g., nucleus, Golgi apparatus, ribosomes, mitochondria, endoplasmic reticulum, chloroplast, cell membrane, etc.), cellular metabolites, tissue sections, cells, single cell, contents from cells or from a single cell, nucleic acid isolated from cells or from a single cell, or nucleic acid isolated from cells or from a single

cell and further modified, or cell free DNA (e.g., from placental fluid or plasma). In some embodiments, the plurality of analytes include genomic DNA and mRNA. In some embodiments, the mRNA have poly A tail. In some embodiments, the genomic DNA and the mRNA are immobilized on a solid support within the CE simultaneously. In some embodiments, the immobilization of the genomic DNA is sequential to the immobilization of the mRNA to the solid support. In some embodiments, the genomic DNA is combined with transposome complexes and the transposon ends are immobilized on a solid support and the mRNA are immobilized to the solid by hybridization of oligo (dT) probes immobilized on a solid support. In some embodiments, the genomic DNA is combined with transposome complexes and, optionally, the transposon ends hybridize to complementary sequences immobilized on a solid support such that the mRNA are immobilized to the solid by hybridization of oligo (dT) probes immobilized on a solid support. Other methods can be used to immobilize the mRNA as well. In some embodiments, the solid support is a bead. In some embodiments, the solid support is a flow cell surface. In some embodiments, the solid surface is the wall of a reaction vessel. In some embodiments, the methods include sequencing nucleic acids preserved or embedded or contained within CE. Some embodiments relate to preparing DNA within CE to obtain phasing and sequence assembly information from a target nucleic acid, and obtaining phasing and sequence assembly sequence information from such templates. Particular embodiments relate to the use of integrases, for example transposases, to maintain physical proximity of associated ends of fragmented nucleic acids; and to the use of combinatoric indexing to create individual libraries from each CE. Obtaining haplotype information from CE includes distinguishing between different alleles (e.g., SNPs, genetic anomalies, etc.) in a target nucleic acid. Such methods are useful to characterize different alleles in a target nucleic acid, and to reduce the error rate in sequence information.

[529] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2002/012897, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include array compositions comprising a substrate with a surface comprising discrete sites, at least one fiducial, and a population of microspheres comprising at least a first and a second subpopulation. Each subpopulation comprises a bioactive agent, and

the microspheres are distributed on said surface. Each subpopulation may optionally comprise a unique optical signature, an identifier binding ligand that will bind a decoder binding ligand such that the identification of the bioactive agent can be elucidated, or both. In an additional aspect, compositions comprising a computer readable memory to direct a computer to function in a specified manner are provided. The computer readable memory comprises an acquisition module for receiving a data image of a random array comprising a plurality of discrete sites, a registration module for registering a data image, and a comparison module for comparing registered data images. Each module comprises computer code for carrying out its function. The registration module may utilize any number of fiducials, including a fiducial,fiber when the substrate comprises a fiber optic bundle, a fiducial microsphere, or a fiducial template generated from the random array. In some embodiments, methods of making the array compositions comprise forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, and incorporating at least one fiducial onto the surface are provided. When the array has complete rotational freedom, at least two fiducials are preferred in the array to allow for correction of rotation. Additionally or alternatively, detection of a genetic biomarker can include methods for comparing separate data images of a random array. The methods comprise using a computer system to register a first data image of the random array to produce a registered first data image, using the computer system to register a second data image of the random array to produce a registered second data image, and comparing the first and the second registered data images to determine any differences between them. Some embodiments provide methods of decoding a random array composition comprising providing a random array composition. A first plurality of decoding binding ligands is added to the array composition and a first data image is created. A fiducial is used to generate a first registered data image. A second plurality of decoding binding ligands is added to the array composition and a second data image is created. The fiducial is used to generate a second registered data image. A computer system is used to compare the first and the second registered data image to identify the location of at least two bioactive agents. Some embodiments provide methods of determining the presence of a target analyte in a sample. The methods comprise acquiring a first data image of a random array composition, and registering the first data image to create a

registered first data image. The sample is then added to the random array and a second data image is acquired from the array. The second data image is registered to create a registered second data image. Then the first and the second registered data images are compared to determine the presence or absence of the target analyte. Optionally, the data acquisition may be at different wavelengths. Some embodiments provide methods for preprocessing or prefiltering signal data comprising acquiring a data image from an array, and determining the similarity of a first signal from at least one array site to a reference signal to determine whether the site comprises a candidate bead.

[530] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/136416, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for identifying splice variants. In one implementation, a method comprises: determining one or more sample splice junctions from a plurality of RNA sequence reads from a single biological sample; retrieving, a set of baseline splice junctions determined from a plurality of healthy RNA samples; comparing the one or more sample splice junctions to the set of baseline splice junctions; and identifying one or more filtered sample splice junctions, the filtered sample splice junctions comprising sample splice junctions that do not overlap with the baseline splice junctions, wherein the one or more filtered sample splice junctions are candidate oncogenic events. Some embodiments further comprise outputting the list of candidate oncogenic events. In some embodiments, the plurality of healthy RNA samples comprises healthy RNA samples taken from a cross section of one or more of: geographical regions, ages, genders, ethnic groups, tissue types, or sample preservation qualities type. In some embodiments, the plurality of healthy RNA samples comprises samples from one or more tissue types selected from the group consisting of: lung, adrenal gland, bladder, breast, ovary, liver, prostate, skin, and spleen. In some embodiments, the plurality of healthy RNA samples comprises samples from donors across a range of ages. In some embodiments, the baseline splice junctions from the plurality of healthy RNA samples are determined prior to the determining the sample junctions from the single sample. In some embodiments, the plurality of healthy RNA samples for the base line splice junctions are not obtained from the same biological object as the single biological sample. In some

embodiments, the baseline junctions are from a same genomic region as the sample junctions. In some embodiments, the single biological sample is from a tumor sample. In some embodiments, the sample splice junctions and the baseline splice junctions are both determined using a common assay. In some embodiments, determining the one or more sample junctions comprises: determining the plurality of RNA sequence reads from the single biological sample; retrieving, a DNA reference sequence aligned with the RNA sequence reads from the single biological sample; and determining one or more sample junctions as missing contiguous locations in the RNA read compared with the DNA reference. In some embodiments, the filtered sample splice junctions do not overlap with third party junctions, the third party junctions determined from a splice graph that captures multiple alternate combinations of exons for a given gene. In some embodiments, the set of baseline splice junctions are determined without determining a splice graph that captures multiple alternate combinations of exons for a given gene. Some embodiments provide a system for identifying splice variants. The system includes a memory, at least one processor; and at least one non-transitory computer- readable medium containing instructions that, when executed by the at least one processor, cause the at least one processor to perform operations comprising determining one or more sample splice junctions from a plurality of RNA sequence reads from a single biological sample; retrieving, a set of baseline splice junctions determined from a plurality of healthy RNA samples; comparing the one or more sample splice junctions to the set of baseline splice junctions; and identifying one or more filtered sample splice junctions, the filtered sample splice junctions comprising sample splice junctions that do not overlap with the set of baseline splice junctions, wherein the filtered sample splice junctions are candidate oncogenic events.

[531] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/093780, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a computer implemented method for validating variant calls. The method operates under control of one or more processors executing program instructions for, receiving sequencing data including a sample read that has a corresponding sequence of nucleotides along the genomic sequence of interest, receiving an indication of a

potential variant call at a designated position within the sequence of nucleotides along the genomic sequence of interest, and obtaining baseline variant frequencies at the designated position within one or more baseline genomic sequences. The method obtains a sample variant frequency at the designated position for the genomic sequence of interest. The method analyzes the baseline and sample variant frequencies at the designated position to obtain a quality score; and validates the potential variant call for the genomic sequence of interest based on the quality score. Optionally, the analyzing operation includes obtaining a relation between the sample variant frequency and a distribution of the baseline variant frequencies, the quality score based on the relation. Optionally, the analyzing operation comprises indexing the sample variant frequency with respect to a distribution of the baseline variant frequencies. The relation may be based on a non-parametric Wilcoxon rank sum test. The baseline variant frequencies indicate a degree of background noise at corresponding positions along the baseline genomic sequence. Optionally, the validating further comprises comparing the quality score to a threshold; and declaring the potential variant call to be a valid variant call when the quality score exceeds the threshold. The baseline variant frequencies may be derived from multiple baseline genomic sequences that are associated with more than one type of allele. Optionally, the method further comprises receiving sequencing data that includes a plurality of reference reads of a sequence of nucleotides along the baseline genomic sequence, and determining the baseline variant frequencies for the reference reads at the designated positions. The determining of the baseline variant frequencies may further comprise receiving the sequencing data from the reference reads for a set of positions within a current base pair window; identifying a candidate variant frequency for one or more positions in the set of positions within the current base pair window; selecting one of the candidate variant frequencies as the baseline variant frequency for a designated position within the reference read; and shifting the base pair window along the baseline genomic sequence and repeating the operations. In accordance with the above embodiments, systems and methods are described to reduce false positive variant calling from systematic errors. Systematic errors may arise due to various factors such as FFPE artifacts, sequencing errors, library preparation errors, PCR errors and the like. Variant calls are statically subjected to a locus specific background error distribution that may be compiled from a panel of FFPE normal samples with varied DNA quality from various tissues sequenced

by the NGS-based assay. The same sequencing data of the FFPE normal samples may also be utilized to normalize systematic bias in read coverage caused by PCR, DNA quality, probe pull-down efficiency, or sequence GC content to reveal the true copy number alterations in a test sample. To further enlarge the signal to noise ratio in CNV calling, additional enhancer probes may be added in the hybrid capture to provide robust estimation of gene amplification. Additionally or alternatively, detection of a genetic biomarker can include methods and systems that address noise problems and prevent systematic errors from contributing to false positive variant calls. In connection there with, a set of normal samples is used to identify systematic bias in order for the system to increase the calling stringency in tumor samples in regions with high background noise. For FFPE samples, normal FFPE samples may be used to construct the baseline. For ctDNA samples, normal genomic DNA data may be used to construct the baseline.

[532] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/068014, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include systems and methods for sequencing polynucleotides. In one embodiment, the system comprises: a memory comprising a reference nucleotide sequence; a processor configured to execute instructions that perform a method comprising: receiving a first nucleotide subsequence of a read from a sequencing system; processing the first nucleotide subsequence using a first alignment path to determine a first plurality of candidate locations of the read on the reference sequence; determining whether the first nucleotide subsequence aligns to the reference sequence based on the determined candidate locations; receiving a second nucleotide subsequence from the sequencing system; processing the second nucleotide subsequence to determine a second plurality of candidate locations of the read that align to the reference sequence using: a second alignment path if the read is aligned to the reference sequence, and the first alignment path if otherwise, wherein the second alignment path is more computationally efficient than the first alignment path to determine the second plurality of candidate locations of the read. In one embodiment, the method comprises: receiving a first nucleotide subsequence from a sequencing system during a sequencing run; and performing a secondary analysis of the first nucleotide subsequence of a read based on a

reference sequence using a first analysis path or a second analysis path, wherein the second analysis path is more computationally efficient than the first processing path in performing the secondary analysis.

[533] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/057770, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include detection of copy number variations in a biological sample. In one embodiment, copy number variants may be at least a single gene in size. In another embodiment, copy number variants may be at least 140bp, 140-280bp, or at least 500bp. In one embodiment, a "copy number variant" refers to the sequence of nucleic acid in which copy-number differences are found by comparison of a sequence of interest in test sample with an expected level of the sequence of interest. In some embodiments, a reference sample is derived from a set of sequencing data of unmatched samples to generate normalization information that permits an individual test sample to be normalized such that deviations from expected copy numbers may be determined on normalized sequencing data. The normalization data is generated using the techniques provided and permits normalization to a hypothetical most representative sample matched to the test sample. By normalizing the test sample, noise introduced by sequencing or other bias is removed. In certain embodiments, the raw sequencing data coverage from a targeted sequencing run is normalized to reduce technical and biological noise to improve CNV detection. In one embodiment, samples of interest (e.g., fixed formalin paraffin embedded samples) are sequenced according to a desired sequencing technique, such as a targeted sequencing technique that uses a sequencing panel of probes to target regions of interest. Once the sequencing data is collected, the sequencing data is normalized to remove noise, and the normalized data is subsequently analyzed to detect CNVs. In some embodiments, a method of normalizing copy number is provided that includes the steps of receiving a sequencing request from a user to sequence one or more regions of interest in a biological sample; acquiring baseline sequencing data from the one or more regions of interest from a plurality of baseline biological samples that are not matched to the biological sample; determining copy number normalization information using the baseline sequencing data, wherein the copy number normalization information comprises at least one copy number

baseline for a region of interest of the one or more regions of interest; and providing the copy number normalization information to the user. In another embodiment, a method of detecting copy number variation is provided that includes the steps of acquiring sequencing data from a biological sample, wherein the sequencing data comprises a plurality of raw sequencing read counts for a respective plurality of regions of interest; and normalizing the sequencing data to remove region- dependent coverage. The normalizing comprises: for each region of interest, comparing a raw sequencing read count of one or bins in a region of interest of the biological sample to a baseline median sequencing read count to generate a baseline-corrected sequencing read count for the one or more bins in the region of interest, wherein the baseline median sequencing read count for one or more bins in the region of interest is derived from a plurality of baseline samples that are not matched to the biological sample and is determined from only the most representative portions of the baseline sequencing data for each region of interest; and removing GC bias from the baseline-corrected sequencing read count to generate a normalized sequencing read count for each region of interest. The method also includes determining copy number variation in each region of interest based on the normalized sequencing read count of the one or more bins in each region of interest. In another embodiment, a method of assessing a targeted sequencing panel is provided that includes the steps of identifying a first plurality of targets in a genome for a targeted sequencing panel, wherein the first plurality of targets corresponds to portions of a respective plurality of genes; determining a GC content of each of the first plurality of targets; eliminating targets of the first plurality of targets with GC content outside of a predetermined range to yield a second plurality of targets smaller than the first plurality of targets; when, after the eliminating, the an individual gene has fewer than a predetermined number of targets corresponding portions to the individual gene, identifying additional targets in the individual gene; adding the additional targets to the second plurality to yield a third plurality of targets; and providing a sequencing panel comprising probes specific for the third plurality of targets.

[534] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/197027, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for enriching or amplifying polynucleotides, and

more specifically to methods for enriching or amplifying a target DNA sequence using endonuclease systems, e.g., CRISPR-Cas systems or Argonaute systems, and applications thereof. Additionally or alternatively, detection of a genetic biomarker can include methods for amplifying a target double-stranded nucleic acid using CRISPR-Cas systems. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a target double- stranded nucleic acid including: (a) providing a system having: a clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA) or a derivative thereof, and a CRISPR- associated (Cas) protein or a variant thereof, wherein the crRNA or the derivative thereof contains a target-specific nucleotide region complementary to a region of a first strand of the target double-stranded nucleic acid; (b) contacting the target double-stranded nucleic acid with the system to form a complex; (c) hybridizing a primer to a second strand of the target double- stranded nucleic acid, the primer containing a sequence complementary to a region of the second strand of the target double-stranded nucleic acid, and (d) extending a nucleic acid complementary to the second strand of the target double-stranded nucleic acid from the primer using a polymerase. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a target double- stranded nucleic acid comprising: (a) providing a first system having: a first clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA) or a derivative thereof, and a first CRISPR-associated (Cas) protein or a variant thereof, wherein the first crRNA or the derivative thereof contains a target-specific nucleotide region complementary to a region of a first strand of the target double-stranded nucleic acid; (b) providing second system having: a second clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA) or a derivative thereof, and a second CRISPR-associated (Cas) protein or a variant thereof, wherein the second crRNA or the derivative thereof contains a target-specific nucleotide region complementary to a region of a second strand of the target double-stranded nucleic acid; (c) contacting the target double-stranded nucleic acid with the first system and the second system; (d) hybridizing a first primer to a second strand of the target double-stranded nucleic acid, the first primer containing a sequence complementary to a region of the second strand of the target double-stranded nucleic acid, and hybridizing a second primer to a first strand of the target double-stranded nucleic acid, the second primer containing a sequence complementary to a region of

the first strand of the target double-stranded nucleic acid, and (e) extending the 3' end of the first primer and the second primer with one or more polymerases to generate a first and a second double stranded target nucleic acid. In some embodiments, the method further includes repeating step (a) and step (e) for one or more times, e.g., until a desired degree of amplification is reached. Additionally or alternatively, detection of a genetic biomarker can include a method for amplifying a target double- stranded nucleic acid including: (a) providing a system having: a 5' phosphorylated single- stranded nucleic acid or a derivative thereof, and an Argonaute protein or a variant thereof, wherein the 5' phosphorylated single-stranded nucleic acid or the derivative thereof contains a target-specific nucleotide region complementary to a region of a first strand of the target double- stranded nucleic acid; (b) contacting the target double-stranded nucleic acid with the system to form a complex; (c) hybridizing a primer to a second strand of the target double-stranded nucleic acid, the primer containing a sequence complementary to a region of the second strand of the target double-stranded nucleic acid, and (d) extending a nucleic acid complementary to the second strand of the target double-stranded nucleic acid from the primer using a polymerase. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching a target nucleic acid including: obtaining a population of cell free DNA (cfDNA) from a subject's plasma or serum, the population of cell free DNA containing the target nucleic acid; providing a system having: a 5' phosphorylated single-stranded nucleic acid or a derivative thereof, and an Argonaute protein or a variant thereof, wherein the 5' phosphorylated single-stranded nucleic acid or the derivative thereof contains a target-specific nucleotide region complementary to a region of the target nucleic acid; contacting the target nucleic acid with the endonuclease system to form a complex, and separating the complex and thereby enriching for the target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting single nucleotide variant (SNV) including: obtaining a population of cell free DNA from a subject's plasma or serum; providing a first system having: a first 5' phosphorylated single-stranded nucleic acid or a derivative thereof, and a first Argonaute protein or a variant thereof, wherein the first 5' phosphorylated single-stranded nucleic acid or the derivative thereof contains a first target- specific nucleotide region complementary to a region of a first target nucleic acid, and wherein the first Argonaute protein has nuclease activity; cleaving the first target nucleic acid

using the first endonuclease system, and amplifying a second target nucleic acid using Polymerase Chain Reaction (PCR), wherein the second target nucleic acid contains a single nucleotide variant version of the first target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for labeling a target nucleic including providing a first system having: a 5' phosphorylated single-stranded nucleic acid or a derivative thereof, and a first Argonaute protein or a variant thereof, wherein the first 5' phosphorylated single-stranded nucleic acid or the derivative thereof contains a first target- specific nucleotide region complementary to a first region of the target nucleic acid, and wherein the first Argonaute protein is capable of generating a single-stranded nick; contacting a double-stranded nucleic acid containing the target nucleic acid with the first nuclease system to generate a first single-stranded nick at the first region of the target nucleic acid, and labeling the target nucleic acid. In some embodiments, the method further includes separating the target nucleic acid through the labeling and thereby enriching the target nucleic acid. In some embodiments, the method further includes amplifying the target nucleic acid. In some embodiments, the method further includes providing a second system having: a second 5' phosphorylated single-stranded nucleic acid or a derivative thereof, and a second Argonaute protein or a variant thereof, wherein the second 5' phosphorylated single-stranded nucleic acid or the derivative thereof contains a second target- specific nucleotide region complementary to a second region of the target nucleic acid, and wherein the second Argonaute protein is capable of generating a single-stranded nick, and contacting the double-stranded nucleic acid containing the target nucleic acid with the second nuclease system to generate a second single-stranded nick at the second region of the target nucleic acid, wherein the first region of the target nucleic acid is different from the second region of the target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for enriching a target nucleic acid including: providing a population of Argonaute proteins programmed with a set of 5' phosphorylated single-stranded nucleic acids, wherein the set of 5' phosphorylated single-stranded nucleic acids contains 5' phosphorylated single-stranded nucleic acids complementary to a series of different regions of the target nucleic acid; contacting the target nucleic acid with the population of Argonaute proteins programmed with the set of 5' phosphorylated single-stranded nucleic acids to generate a series of nucleic acid fragments, and ligating adaptors to

at least one of nucleic acid fragments, wherein the Argonaute proteins are capable of generating double-stranded DNA breaks. Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing a target nucleic acid including: providing a population of Argonaute proteins programmed with a set of 5' phosphorylated single-stranded nucleic acids, wherein the set of 5' phosphorylated single- stranded nucleic acids contains 5' phosphorylated single-stranded nucleic acids complementary to a series of different regions across the target nucleic acid; contacting the target nucleic acid with the population of Argonaute proteins programmed with the set of 5' phosphorylated single- stranded nucleic acids to generate a series of nucleic acid fragments, and sequencing the series of nucleic acid fragments. Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing a target nucleic acids including: providing a plurality of populations of Argonaute proteins, each population of Argonaute proteins being programmed with a different set of 5' phosphorylated single-stranded nucleic acids, wherein each set of 5' phosphorylated single-stranded nucleic acids contains 5' phosphorylated single-stranded nucleic acids complementary to a different series of regions across the target nucleic acid, contacting the target nucleic acid with each of the plurality of populations of Argonaute proteins in a separate reaction to generate a different series of nucleic acid fragments, and sequencing the nucleic acid fragments.

[535] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2015/198074, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, apparatus, systems and computer program products for presenting sequence information. In some embodiments, this includes obtaining a first sequence and a second sequence, determining a similarity between the first sequence and the second sequence, wherein the similarity is based upon distance between the first sequence and the second sequence, and displaying a block at an intersection point on a matrix plot based on the similarity between the first sequence and the second sequence.

[536] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2002/099982, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a composition that includes a substrate with a surface

comprising discrete sites, a reflective coating on the surface, and a population of microspheres distributed on the substrate. The microspheres comprise at least a first and a second subpopulation. Generally, at least one subpopulation comprises a bioactive agent. Additionally or alternatively, detection of a genetic biomarker can include a composition wherein the substrate comprises a first and a second surface, wherein the first surface comprises the discrete sites, and the reflective coating is on the second surface. The population of microspheres are distributed on the first surface. Additionally or alternatively, detection of a genetic biomarker can include a method of making a reflective array. The method includes providing a substrate with a surface comprising discrete sites, applying to the surface a coating of reflective material and distributing microspheres on the surface. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a non-labeled target analyte in a sample comprising providing a substrate with a plurality of discrete sites, distributing on the sites a population of microspheres comprising a bioactive agent and a signal transducer element, contacting the substrate with the sample, whereby upon binding of the target analyte to the bioactive agent, a signal from the signal transducer element is altered as an indication of the presence of the target analyte.

[537] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2002/016649, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence of the target nucleic acid. In addition, the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined.

[538] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,914,973, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, compositions, and kits for detecting gene dysregulations such as those arising from gene fusions and chromosomal translocations. The methods, compositions and kits are useful for detecting mutations that cause the differential expression of a 5′ region of a target gene relative to the 3′ region of the target gene. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence or absence of a dysregulation in a target gene in a test sample. In one embodiment, the method includes: (a) amplifying portions of a 5′ region of a transcript of the target gene or a cDNA derived therefrom, if present in a test sample, with two or more different 5′ target primer pairs that are directed to the portions of the 5′ region of the target gene; (b) amplifying portions of a 3′ region of a transcript of the target gene or a cDNA derived therefrom, if present in the test sample, with two or more different 3′ target primer pairs that are directed to the portions of 3′ region of the target gene; (c) detecting the amplification products produced by the two or more 5′ target primer pairs and the two or more 3′ target primer pairs; (d) determining the average cycle threshold (Ct) among the two or more 5′ target primer pairs and the average Ct among the two or more 3′ target primer pairs, (e) calculating an IDE Score as the difference between the average cycle threshold among the 5′ target primer pairs and the average cycle threshold among the 3′ target primer pairs, and (f) identifying the test sample as (i) having a target gene dysregulation if the IDE Score is significantly different than a cutoff value and the difference indicates the presence of a target gene dysregulation, or (ii) not having a target gene dysregulation if the IDE Score in the test sample does not differ significantly from the cutoff value. Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosing the presence or absence of cancer or a susceptibility to cancer in a subject. In one embodiment, the method includes: (a) obtaining a test sample that comprises nucleic acid from the subject; (b) amplifying portions of a 5′ region of a transcript of a target gene or a cDNA derived therefrom, if present in the test sample, with two or more different 5′ target primer pairs that are directed to the portions of the 5′ region of the target gene; (c) amplifying portions of a 3′ region of a transcript of the target gene or a cDNA derived therefrom, if present in the

test sample, with two or more different 3′ target primer pairs that are directed to the portions of the 3′ region of the target gene; (d) detecting the amplification products produced by the two or more 5′ target primer pairs and the two or more 3′ target primer pairs; (e) determining the average cycle threshold (Ct) among the two or more 5′ target primer pairs and the average Ct among the two or more 3′ target primer pairs; (f) calculating an IDE Score as the difference between the average cycle threshold among the 5′ target primer pairs and the average cycle threshold among the 3′ target primer pairs, and (g) diagnosing the subject as (i) having cancer or a susceptibility to cancer when the IDE Score is significantly different than a cutoff value and the difference indicates the presence of cancer or a susceptibility to cancer, or (ii) not having cancer or a susceptibility to cancer resulting from dysregulation of the target gene if the IDE Score in the test sample does not differ significantly from the cutoff value. In some embodiments, the expression level of the 5′ region of a target gene is determined by amplification using two, three, four, five or six different primer pairs directed to various portions of the 5′ region of the target gene. Similarly, two, three, four, five or six different primer pairs directed to various portions of the 3′ region of the target gene may be used to determine the expression level of the 3′ region of the target gene. The amounts of amplification products each may be normalized to the amount of an endogenous control gene transcript ("Control") such as, for example, ABL. In some embodiments, the expression level or relative amount of transcript can be determined using real-time PCR and comparing the threshold cycle (Ct) for each amplicon. The average Ct values for each of the 3′ (avgCt3′) and 5′ (avgCt5′) regions of a target gene are used to calculate an IDE Score, which may be calculated as IDE=(avgCt5′−avgCt3′), or IDE=(avgCt5′)/(Ctcontrol)−(avgCt3′)/(Ctcontrol), or IDE=[Ln((avgCt5′)/Ctcontrol)]−[Ln((avgCt3′)/Ctcontrol)]. In some embodiments, the Ct values are normalized to a reference sample.

[539] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,783,854, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions for detecting target nucleic acids at very low levels and in the presence of large amounts of non-target nucleic acids. Generally, a target and non-target nucleic acid are distinguished by the presence or absence of a fragmentation site,

such as a restriction enzyme recognition site. By differentiating the target and non-target by a fragmentation site, the methods and compositions can be used with various nucleic acid detection methods known in the art, such as PCR. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence or absence of a target nucleic acid by testing a sample that potentially contains the target nucleic acid in the presence of non-target nucleic acid, the method includes: a) fragmenting the sample nucleic acid under conditions such that a subsequent amplification directed to the target nucleic acid results in an increased detection of the target nucleic acid over the non-target nucleic acid as compared to amplification without fragmentation; b) amplifying the target nucleic acid with a pair of primers, where a first primer is specific for the target nucleic acid; and c) detecting the presence or absence of an amplification product, which indicates the presence or absence of the target nucleic acid in the sample. Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosing a cancer or detecting the presence of a tumor cell by determining if an individual has a mutant sequence associated with the cancer or tumor cell type, the method includes: a) obtaining a sample including nucleic acid from the individual; b) fragmenting the sample nucleic acid under conditions such that a subsequent amplification directed to the target nucleic acid results in an increased detection of the target nucleic acid over the non-target nucleic acid as compared to amplification without fragmentation; c) amplifying the target nucleic acid with a pair of primers, where a first primer is specific for the target nucleic acid; and d) detecting the presence or absence of an amplification product containing the mutant sequence, where diagnosis of cancer is determined by the presence absence or amount of amplification product containing the mutant sequence. Additionally or alternatively, detection of a genetic biomarker can include a method for determining prognosis with cancer by determining if an individual has a mutant sequence associated with the cancer, the method includes: a) obtaining a sample containing nucleic acid from the individual; b) fragmenting the mutant nucleic acid under conditions such that a subsequent amplification directed to the mutant nucleic acid results in an increased detection of the mutant nucleic acid over the non-mutant nucleic acid as compared to amplification without fragmentation; c) amplifying the mutant nucleic acid with a pair of primers, where a first primer is specific for the mutant nucleic acid; and d) detecting the presence, absence and/or amount of an

amplification product containing the mutant sequence, where the likelihood of an outcome in the individual is associated with the presence and or amount of mutant nucleic acid sequence. Additionally or alternatively, detection of a genetic biomarker can include a method for determining drug sensitivity of an individual diagnosed with cancer, the method includes: a) obtaining a sample comprising nucleic acid from the individual; b) fragmenting the mutant nucleic acid under conditions such that a subsequent amplification directed to the mutant nucleic acid results in an increased detection of the mutant nucleic acid over the non-mutant nucleic acid as compared to amplification without fragmentation; c) amplifying the mutant nucleic acid with a pair of primers, where a first primer is specific for the mutant nucleic acid; d) detecting the presence, absence and/or amount of an amplification product containing the mutant sequence; and e) relating the presence, absence and/or amount of an amplification product containing the mutant sequence to cancer drug sensitivity. In some embodiments, the mutated nucleic acid sequence is due to a deletion, insertion, substitution and/or translocation or combinations thereof. In preferred embodiments, fragmentation of nucleic acid sequence in which cleavage of wild-type sequence is with a restriction enzyme, Such pre-amplification digestion treatment allows for fragmentation to destroy or substantially decrease the number of wild-type sequences that might be amplified. In yet more preferred embodiments, the fragmentation using a restriction enzyme is combined with the use of a mutation specific primer (or mutated sequence primer). In preferred embodiments, a mutated sequence destroys or disrupts a restriction enzyme recognition site present in the corresponding wild-type sequence and that a mutation specific primer can be designed to bind to the mutated version of the sequence and not its wild-type counterpart. For example, a mutation specific primer can overlap a border region, which is a region that contains portions of both a wild-type sequence adjacent to a portion of the mutated sequence. In one approach, a sample is assayed for the presence or absence of a mutated sequence by amplification and detection of the resulting amplification products. In a preferred embodiment, amplification of target nucleic acids is accomplished by polymerase chain reaction (PCR). Single or multiple mutant sequences can be assayed. Amplification of multiple mutant sequences can be performed simultaneously in a single reaction vessel, e.g., multiplex PCR. In this case, probes may be distinguishably labeled and/or amplicons may be distinguishable by size differentiation. Alternatively, the assay could

be performed in parallel in separate reaction vessels. In such later case, the probes could have the same label. In some embodiments, the methods further comprise a nucleic acid extraction step. In some embodiments, at least one primer of each primer pair in the amplification reaction is labeled with a detectable moiety. Thus, following amplification, the various target segments can be identified by size and color. The detectable moiety is preferably a fluorescent dye. In some embodiments, different pairs of primers in a multiplex PCR may be labeled with different distinguishable detectable moieties. Thus, for example, HEX and FAM fluorescent dyes may be present on different primers in multiplex PCR and associated with the resulting amplicons. In other embodiments, the forward primer is be labeled with one detectable moiety, while the reverse primer is labeled with a different detectable moiety, e.g. FAM dye for a forward primer and HEX dye for a reverse primer. Use of different detectable moieties is useful for discriminating between amplified products which are of the same length or are very similar in length. Thus, in certain embodiments, at least two different fluorescent dyes are used to label different primers used in a single amplification. In still another embodiment, control primers can be labeled with one moiety, while the patient (or test sample) primers can be labeled with a different moiety, to allow for mixing of both samples (post PCR) and the simultaneous detection and comparison of signals of normal and test sample. In a modification of this embodiment, the primers used for control samples and patient samples can be switched to allow for further confirmation of results.

[540] Analysis of amplified products from amplification reactions, such as multiplex PCR, can be performed using an automated DNA analyzer such as an automated DNA sequencer (e.g., ABI PRISM 3100 Genetic Analyzer) which can evaluate the amplified products based on size (determined by electrophoretic mobility) and/or respective fluorescent label.

[541] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,546,404, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, compositions, and kits directed to the detection of gene dysregulations such as those arising from gene fusions and chromosomal abnormalities, e.g., translocations, insertions, inversions and deletions. In some embodiments, the methods, compositions and kits are useful for detecting mutations that cause the differential expression

of a 5′ region of a target gene relative to the 3′ region of the target gene. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a dysregulation in a target gene. The method may include: (a) amplifying a 5′ region of the target gene transcript, if present, in a biological sample with one or more 5′ target primer pairs which are complementary to the 5′ region of the target gene; (b) amplifying a 3′ region of the target gene transcript, if present, in the biological sample with one or more 3′ target primer pairs which are complementary to the 3′ region of the target gene; and (c) detecting the amounts of amplification product produced by the one or more 5′ target primer pairs and the one or more 3′ target primer pairs. The method may also provide that a difference in the amounts of amplification products produced by steps (a) and (b) indicates that the target gene is dysregulated. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence or absence of a dysregulation in a target gene in a sample. The method may include: (a) measuring the amount of transcription of a 5′ region of the target gene and a 3′ region of the target gene in the test sample; and (b) comparing the relative expression of the 5′ region to the 3′ region of the target gene in the test sample to the relative expression of the 5′ region to the 3′ region of the target gene in a reference sample. The method may also provide that a difference in the relative expression in the test sample compared to the reference sample is indicative of the presence of a gene dysregulation. In an embodiment, the relative amount of transcript can be determined using real-time PCR and comparing the threshold cycle, or Ct, value, for each amplicon. The Ct value can be normalized to a reference sample. Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosing cancer or a susceptibility to cancer in a subject. The method may include: (a) amplifying a 5′ region of the target gene transcript, if present, in a biological sample with one or more 5′ target primer pairs which are complementary to the 5′ region of the target gene; (b) amplifying a 3′ region of the target gene transcript, if present, in the biological sample with one or more 3′ target primer pairs which are complementary to the 3′ region of the target gene; and (c) detecting the amounts of amplification product produced by the one or more 5′ target primer pairs and the one or more 3′ target primer pairs. The method may also provide that a difference in the amounts of amplification products produced by steps (a) and (b) indicates that the subject has cancer or is susceptible to cancer resulting from a gene dysregulation.

Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosing prostate cancer or a susceptibility to prostate cancer in a subject. The method may include: (a) amplifying a 5′ region of the target gene transcript, if present, in a biological sample with one or more 5′ target primer pairs which are complementary to the 5′ region of the target gene; (b) amplifying a 3′ region of the target gene transcript, if present, in the biological sample with one or more 3′ target primer pairs which are complementary to the 3′ region of the target gene; and (c) detecting the amounts of amplification product produced by the one or more 5′ target primer pairs and the one or more 3′ target primer pairs. The method may also provide that a difference in the amounts of amplification products produced by steps (a) and (b) indicates that the target gene is dysregulated. Optionally, the nucleic acid sample containing the target gene of interest may be subjected to another analysis to determine the nature of the gene dysregulation. Suitable analyses include, for example, comparative hybridization (e.g., comparative genomic hybridization). Comparative hybridization techniques such as comparative genomic hybridization (CGH) is limited by the fact that this technique is only able to detect unbalanced rearrangements (rearrangements that lead to gain or loss of genetic material). Comparative hybridization cannot adequately detect chromosomal abnormalities such as balanced translocations. Thus, any of the methods may be used in combination with a comparative hybridization technique. The combination of the methods with comparative hybridization (e.g., CGH) will be able to detect both balanced and unbalanced rearrangements and provide a more accurate diagnosis than if the comparative hybridization technique was used alone. In the case of unbalanced rearrangements, the comparative hybridization technique may be used as a confirmatory assay. In some embodiments, target gene dysregulations may arise from gene fusions and chromosomal abnormalities including, for example, translocations, deletions, inversions, and insertions. In some embodiments, the biological sample is contacted with the one or more 5′ target primer pairs and the one or more 3′ target primer in a multiplex amplification reaction. In one embodiment, the detecting is accomplished using a labeled oligonucleotide probe complementary to each amplification product. For example, each oligonucleotide probe may include a different detectable label, such as a donor fluorophore and quencher moiety. In another embodiment, at least one of the primers for the 5′ region and/or at least one of the primers for the 3′ region is detectably labeled, preferably with

different detectable labels. In illustrative embodiments, the amplifying is performed using quantitative RT-PCR, e.g., real-time RT-PCR. In some embodiments, the chromosomal abnormality is selected from the group consisting of: a translocation, a deletion, an inversion, and an insertion. In one embodiment, the biological sample is a sample from a subject to be tested for a chromosomal abnormality. In some embodiments, the methods further include amplifying a region of an endogenous control gene transcript present in the biological sample with a primer pair complementary to the endogenous control gene and detecting the amplification of the region of the endogenous control gene. In some embodiments, the amount of amplified target gene transcripts (i.e., the 5′ region and the 3′ region) may be normalized to the amount of amplified endogenous control gene transcript. In some embodiments, the method further includes: (a) measuring the amount of transcription of a 5′ region of a second target gene and a 3′ region of the second target gene in the test sample; and (b) comparing the relative expression of the 5′ region to the 3′ region of the second target gene in the test sample to the relative expression of the 5′ region to the 3′ region of the second target gene in a reference sample. The method may also provide that a difference in the relative expression of both the target gene and the second target gene in the test sample compared to the reference sample is indicative of the presence of a target gene:second target gene translocation. Suitable biological samples include, for example, whole blood, isolated blood cells, plasma, serum, and urine.

[542] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,911,942, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of performing comparative hybridization by comparing the amount of test and reference nucleic acids hybridized to a nucleic acid array, the amounts determined by detecting a signal from the hybridized nucleic acids which are labeled with the same detectable label. This method is applicable to comparative hybridization methods in general and to comparative genomic hybridization (CGH) in particular. Accordingly, reference to CGH where the test and reference nucleic acid is genomic nucleic acid should be understood to encompass methods where the test and reference nucleic acids are other than genomic nucleic acids. In a preferred embodiment, CGH is performed using two samples of genomic nucleic acids; a test sample containing genomic nucleic acids, and a reference or control sample

containing genomic nucleic acids with no known chromosomal or genetic abnormalities. The test sample and the reference sample are co-hybridized to a nucleic acid array that contains a plurality of nucleic acids or nucleic acid segments spotted onto a surface (such as a glass slide) at discrete locations. The array may contain target nucleic acid markers for certain known genetic mutations or disease states, or may represent (in aggregate) an entire chromosome, or the full chromosomal complement to obtain a genetic profile similar to karyotyping. In these approaches, the detectable label may be attached to the test and reference nucleic acids before hybridization or after hybridization. In another approach, the detectable label may be attached to one of the test or reference nucleic acids before hybridization while the label is attached to the other of the test or reference nucleic acid after hybridization. The detectable label may be attached covalently or non-covalently such as by a ligand-receptor interaction or by hybridization between complementary nucleotide sequences. In some embodiments, the comparative hybridization can be done using the same detectable label by another approach that may be referred to as an "additive" approach. In accordance with this approach, the test sample nucleic acids comprise a first tag; and the reference sample nucleic acids comprise a second tag. Following hybridization, the surface is contacted with a first complex containing a detectable label and a first entity, such that the first complex selectively binds with the first tag. The next step comprises determining the location and amount of the detectable label bound to the array surface (i.e., to "read" the array). Once the array is read to determine the amount of detectable label associated with nucleic acid that comprises the first tag, the surface is then contacted with a second complex containing the same detectable label as present in the first complex and containing a second entity, such that the second complex selectively binds with the second tag. The array is then read a second time to determine the location and amount of the total detectable label representing both nucleic acids hybridized to the surface. The last step comprises using the results of the two reads to determine the amount of the hybridized nucleic acid that is associated with the second tag. In a preferred approach, the first read is subtracted from the second read to obtain the signal representing the nucleic acid that is linked to the second tag. The signal from the two samples thus determined can be used to identify differences between the test sample genomic nucleic acids and the reference sample genomic nucleic acids so as to detect any chromosomal or genetic abnormalities associated with the test

sample nucleic acid. In some embodiments, the amount of the hybridized nucleic acid that is associated with the second tag can be determined using a duplicate of the hybridized array but which has not been contacted with the first complex. Thus, the duplicate array is contacted with the second complex and not the first complex. The signal from this second array directly represents the amount of hybridized nucleic acid with the second tag, which can be compared to the amount of signal from the first array that was contacted only with the first complex and represents the amount of hybridized nucleic acid associated with the first tag. Because the two analyses are independent of each other, each array may be processed in any order or simultaneously. In some embodiments, one may first hybridize the array with the test and reference nucleic acids wherein one of the test and reference nucleic acids has already been labeled (e.g. by random priming). The array is then read after hybridization to determine signal corresponding with the particular labeled nucleic acid sample. The array is then contacted with a complex comprising a detectable label and an entity, wherein the complex selectively reacts with the other of the test or reference nucleic acid via a tag attached to said other of the test or reference nucleic acid. The assay is read again to measure the total signal for both hybridized nucleic acids. The next step comprises using the results of the two reads to determine the amount of the hybridized nucleic acid that is associated with the tag. In a preferred approach, the first read is subtracted from the second read to obtain the signal representing the nucleic acid that was linked to the tag. The signal from the two samples thus determined can be used to identify differences between the test sample genomic nucleic acids and the reference sample genomic nucleic acids so as to detect any chromosomal or genetic abnormalities associated with the test sample nucleic acid. In some embodiments, the hybridized nucleic acid that is associated with the second tag can be determined using a duplicate of the hybridized array except that the duplicate is prepared by hybridizing to test and reference nucleic acids that do not contain a detectable label. In this case, the duplicate array is contacted with a complex comprising a detectable label and an entity, wherein the complex selectively reacts with the other of the test or reference nucleic acid via a tag attached to said other of the test or reference nucleic acid. The signal from this second array directly represents the amount of hybridized nucleic acid with the second tag, which can be compared to the amount of signal from the first array that was contacted only with the first complex and represents the amount of hybridized

nucleic acid associated with the first tag. Because the two analyses are independent of each other, each array may be processed in any order or simultaneously. Additionally or alternatively, detection of a genetic biomarker can include a method of comparing the expression of genes in a test sample versus that of reference sample. The first step of the method includes contacting under hybridization conditions cDNA prepared from mRNA of a test sample and cDNA prepared from mRNA of a reference sample to a surface containing a plurality of nucleic acid segments each immobilized at discrete locations on the surface. In this case, the test sample cDNA and the reference sample cDNA are labeled before or after hybridization with the same detectable label which is linked to the cDNA of the test sample via a first linkage, and to the cDNA of the reference sample via a second linkage. Either the first linkage or the second linkage is susceptible to selective removal and the detectable label linked to nucleic acids hybridized to the surface determined. The location and amount of detectable label linked to nucleic acids hybridized the surface of the support is determined. The label is then selectively removed from either the hybridized test sample cDNA or the hybridized reference sample cDNA. The location and amount of the detectable label remaining on the support is then determined and represents one of the samples. The difference between the location and amount remaining after removal compared and the location and amount prior to removal represents the other of the samples. The relative amount of each sample nucleic acid hybridized to the array reflects the expression of genes in the test sample compared to the reference sample.

[543] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,871,687, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for determining a sequence of contiguous bases within a polynucleotide, the method relying on single-base primer extension using labeled dideoxynucleotide terminators. The primers are immobilized to solid supports (e.g. microspheres or two-dimensional arrays), allowing for the identification of the labeled terminator incorporated into each primer. Data on the incorporated terminators is used to determine the base identity of a contiguous sequence of nucleotides in a target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for

determining a contiguous sequence comprising at least four bases of a target nucleic acid comprising: (a) preparing one or more reaction mixtures containing the target nucleic acid and four or more primers complementary to a portion of the target nucleic acid such that the primers each have a 3′ end located 5′ to each nucleotide position of the sequence to be determined, wherein each reaction contains from one to all of said primers in any combination and is under conditions where the primers anneal to the target nucleic acid; (b) extending the one or more primers from step (a) with a polymerase in the presence of one or more labeled dideoxynucleotides; (c) immobilizing said primers to a solid support; and (d) detecting the label of the dideoxynucleotide incorporated into each primer and utilizing this information to determine said contiguous sequence of at least four bases of the target nucleic acid. The primers may extended before immobilization to the solid support, i.e. step (b) occurs before step (c) or extended after immobilization on the solid support, i.e. step (c) occurs before step (a). In one embodiment, at least two differently-labeled dideoxynucleotides are provided in the same reaction mixture. In another embodiment, four differently-labeled dideoxynucleotides are provided in the same reaction mixture. Additionally or alternatively, detection of a genetic biomarker can include methods for determining a contiguous sequence of four or more bases of a target nucleic acid by performing singleplex single-base primer extension reactions or multiplex single-base primer extension reactions. In one embodiment, the four or more primers corresponding to the entire portion of the target nucleic acid to be sequenced are combined in a single reaction mixture. In another embodiment, two or more primers are combined in one reaction mixture, and two or more primers are combined in an additional reaction mixture or mixtures. Alternatively, the four or more primers are each added to a separate reaction mixture. In one embodiment, the primers comprise a tag sequence and are immobilized to the solid support via hybridization to a complementary capture oligonucleotide conjugated to the solid support. In another embodiment, the primers are immobilized to the solid support via a covalent attachment. In one embodiment, the solid support is a labeled microsphere. For example, the microspheres may be made of polystyrene. In one embodiment, the label of each microsphere is optically-detected, based upon varying concentrations of at least two dyes. In certain embodiments, the labeled microspheres and the labeled dideoxynucleotide are detected by flow cytometry. In another embodiment, the solid support is a two-dimensional array and

the immobilized primers are positionally defined on the array. The primers may be immobilized to the array via a covalent attachment or via a linker sequence. In certain embodiments, the extended primers with labeled dideoxynucleotides are detected by scanning the array.

[544] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,492,089, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of performing comparative hybridization by comparing the amount of test and reference nucleic acids hybridized to a nucleic acid array, the amounts determined by detecting a signal from the hybridized nucleic acids which are labeled with the same detectable label. This method is applicable to comparative hybridization methods in general and to CGH in particular. Accordingly, reference to CGH where the test and reference nucleic acid is genomic nucleic acid should be understood to encompass methods where the test and reference nucleic acids are other than genomic nucleic acids. In a preferred embodiment, CGH is performed using two samples of genomic nucleic acids: a test sample containing genomic nucleic acids, and a reference or control sample containing genomic nucleic acids with no known chromosomal or genetic abnormalities. The test sample and the reference sample are co-hybridized to a nucleic acid array that contains a plurality of nucleic acids or nucleic acid segments spotted onto a surface (such as a glass slide) at discrete locations. The array may contain target nucleic acid markers for certain known genetic mutations or disease states, or may represent (in aggregate) an entire chromosome, or the full chromosomal complement to obtain a genetic profile similar to karyotyping. In these approaches, the detectable label may be attached to the test and reference nucleic acids before hybridization or after hybridization. In another approach, the detectable label may be attached to one of the test or reference nucleic acids before hybridization while the label is attached to the other of the test or reference nucleic acid after hybridization. The detectable label may be attached covalently or non-covalently such as by a ligand-receptor interaction or by hybridization between complementary nucleotide sequences. In some embodiments, the test and reference samples are labeled with a detectable label; preferably the test and reference samples are labeled with the same detectable label; preferably the detectable label is a

flourochrome; preferably the detectable label is dCTP-Cy3. In certain aspects, methods are provided that allow for the use of a single label to determine the relative amount of test and reference nucleic acids hybridized to the array. Additionally or alternatively, detection of a genetic biomarker can include a method of determining differences between nucleic acid in a test sample and a reference sample, wherein the method involves amplifying nucleic acid sequence from the test sample nucleic acid and amplifying nucleic acid sequence from the reference sample nucleic acid, where one of the amplification reactions is conducted using dUTP and not dTTP and the other is conducted using dTTP and not dUTP; hybridizing to a nucleic acid array a solution comprising the amplified test sample and amplified reference sample; and determining the relative amount of hybridized test and reference nucleic acids bound to the array. In certain embodiments, determining the relative amount of hybridized test and reference nucleic acids includes a) determining a signal for the detectable label hybridized to the array representing the total of hybridized test and reference nucleic acid; b) treating the hybridized nucleic acids with an enzyme that selectively degrades DNA having uracil residues; and c) determining a signal for the detectable label hybridized to the array following step b), which signal represents one of the hybridized test or reference nucleic acid. In particularly preferred embodiments, the enzyme that selectively degrades DNA having uracil residues is uracil-DNA N-glycosylase (UNG). Additionally or alternatively, detection of a genetic biomarker can include a method of determining differences between nucleic acid in a test sample and a reference sample is provided, where the method involves: (a) contacting under hybridization conditions a test sample containing nucleic acids and a reference sample containing nucleic acids to a surface containing a plurality of nucleic acid segments each immobilized at discrete locations on the surface, where the test sample and the reference sample are labeled before or after hybridization with the same detectable label; (b) determining the location and amount of the detectable label linked to nucleic acids hybridized to the surface; (c) selectively removing either the hybridized test sample nucleic acids or the hybridized reference sample nucleic acids; (d) determining the location and amount of the detectable label linked to nucleic acids hybridized to the surface following step (c); and (e) comparing the results of step (b) to the results of step (d) to detect differences in the nucleic acids of the test sample and reference sample. In some preferred embodiments, the step of selectively removing

hybridized test nucleic acids or reference nucleic acids is performed by subjecting the nucleic acids to an enzyme that selectively degrades DNA having certain properties; preferably an enzyme that degrades DNA having uracil residues; more preferably the enzyme that selectively degrades DNA having uracil residues is uracil-DNA N-glycosylase (UNG). In some embodiments, the step of selectively removing hybridized test nucleic acids or reference nucleic acids by subjecting nucleic acids to an enzyme that selectively degrades DNA having uracil residues is achieved by (1) amplifying sequence from a test sample and amplifying sequence from a reference sample nucleic acid, where one of the amplification reactions is conducted using dUTP and not dTTP and the other is conducted using dTTP and not dUTP; (2) hybridizing the amplified nucleic acids; and (3) treating the hybridized nucleic acids with an enzyme that selectively degrades DNA having uracil residues. In some embodiments, the methods may be used to detect any differences between nucleic acids in a test sample and a reference sample, including differences in the amount of nucleic acids having a particular sequence or differences in nucleic acid sequences. In particularly preferred embodiments, the methods are used to detect genetic abnormalities in the test sample. The methods may be applied to CGH using a chromosomal spread or array-based CGH. In some preferred embodiments, the methods provided may be used to compare the expression of genes in a test sample versus that of a reference sample. Additionally or alternatively, detection of a genetic biomarker can include a method of performing comparative hybridization. The method includes comparing the amount of test and reference nucleic acids hybridized to a nucleic acid array, wherein the amount of hybridized test and reference nucleic acids is determined by detecting a signal from the hybridized nucleic acids which are labeled with the same detectable label. In one embodiment, the amount of hybridized test and reference nucleic acids are determined by: a) determining a signal for the detectable label hybridized to the array representing the total of hybridized test and reference nucleic acid; b) treating the hybridized nucleic acids to selectively remove one of the test or reference nucleic acids; c) determining a signal for the detectable label hybridized to the array following step b), which represents one of the hybridized test or reference nucleic acid; and d) determining a signal for the other of the hybridized test or reference by using the signal from c) and b). In certain preferred embodiments, the step of amplifying sequence from a test sample and amplifying sequence

from a reference sample involves amplifying genomic DNA in the samples is conducted using random priming such as is well known in the art. Alternatively, the step of amplifying sequence from a test sample and amplifying sequence from a reference sample may involve using RNA to generate cDNA and amplifying the cDNA using random priming and or amplifying specific sequences using particular primers. In certain preferred embodiments, the amplification reaction may be performed using one or more labeled nucleotides as a means to label the amplified nucleic acids with a detectable label; preferably both test and reference sample nucleic acids are amplified with the same labeled nucleotide; preferably the labeled nucleotide is dCTP-Cy3. Additionally or alternatively, detection of a genetic biomarker can include a method of comparing the expression of genes in a test sample versus that of a reference sample is provided. The method includes comparing the amount of cDNA prepared from mRNA of a test sample and cDNA prepared from mRNA of a reference sample hybridized to a nucleic acid array, the amount of hybridized test and reference cDNA determined by detecting a signal from the hybridized cDNA which is labeled with the same detectable label. The method involves amplifying nucleic acid sequence from cDNA prepared from RNA of the test sample and amplifying nucleic acid sequence from cDNA prepared from RNA of the reference sample, where one of the amplification reactions is conducted using dUTP and not dTTP and the other is conducted using dTTP and not dUTP; hybridizing to the nucleic acid array a solution comprising the amplified test sample and amplified reference sample; and determining the relative amount of hybridized test and reference nucleic acids bound to the array. In certain embodiments, determining the relative amount of hybridized test and reference nucleic acids includes a) determining a signal for the detectable label hybridized to the array representing the total of hybridized test and reference nucleic acid; b) treating the hybridized nucleic acids with an enzyme that selectively degrades DNA having uracil residues; and c) determining a signal for the detectable label hybridized to the array following step b), which signal represents one of the hybridized test or reference nucleic acid.

[545] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,093,063, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can methods for detecting a genomic nucleic acid of interest in a test

sample without amplification and without the need for intact cells or nuclei. Generally, a genomic nucleic acid is hybridized to a labeled probe and anchored to a solid support through means other than nucleic acid hybridization. The genomic nucleic acid is detected by detecting the label in the hybridized complex on the solid support. The method may be used to detect a genetic abnormality e.g., point mutation, gene duplication or deletion, and chromosomal translocation. The method may also be used for diagnosis or prognosis of a disease. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a target sequence in genomic nucleic acid, by: a. contacting a sample of genomic nucleic acid containing the target sequence with a probe specific for the target sequence and forming on a solid support a complex consisting of the genomic nucleic acid and the probe hybridized to the target sequence, wherein the probe contains a detectable label, the genomic nucleic acid is anchored to the solid support through means other than nucleic acid hybridization and the target sequence of the genomic nucleic acid has not been amplified; and b. detecting the presence of the target sequence in the genomic nucleic acid by detecting association of the label with the solid support. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence or absence of a genetic abnormality in genomic nucleic acid, by: a. contacting a sample of genomic nucleic acid with a probe specific for the genetic abnormality and forming on a solid support a complex consisting of the genomic nucleic acid and the probe if the genetic abnormality is present in the genomic nucleic acid, the genomic nucleic acid is anchored to the solid support through means other than nucleic acid hybridization and the target sequence of the genomic nucleic acid has not been amplified; b. detecting the presence of the genetic abnormality by detecting association of the label with the solid support. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting genetic abnormality in a genomic nucleic acid, by: a. contacting a sample of genomic nucleic acid containing the genetic abnormality with a first probe specific for the genetic abnormality and forming a first complex on a solid support consisting of the genomic nucleic acid and the first probe, wherein the probe contains a detectable label, the genomic nucleic acid is anchored to the solid support through means other than nucleic acid hybridization and the target sequence of the genomic nucleic acid has not been amplified; b. contacting a sample of genomic nucleic acid with a second probe specific

for the reference nucleic acid and forming a second complex on a solid support consisting of the reference nucleic acid and the second probe, wherein the second probe contains a detectable label; and c. measuring the amount of the first complex formed by detecting the detectable label of the first probe associated with the complex and measuring the amount of second complex formed by detecting the detectable label of the second probe associated with the complex; and d. comparing the amount of the first complex to the amount of the second complex, wherein a difference in the amount of two complexes is an indicative of genetic abnormality. In some embodiments, the genomic nucleic acid and reference nucleic acid are from the same sample. In another embodiment of any of the foregoing aspects, the genomic nucleic acid and the reference nucleic acid are from a different sample, which may be from the same or different individuals. In another embodiment, the amount of first complex and the second complex are determined using the same solid support, and the detectable labels of the first probe and the second probe are different. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting genetic abnormality in a genomic nucleic acid, by: a. contacting a sample of genomic nucleic acid containing the genetic abnormality with a first probe specific for the genetic abnormality and forming a first complex on a solid support consisting of the genomic nucleic acid and the first probe, wherein the probe contains a detectable label, the genomic nucleic acid is anchored to the solid support through means other than nucleic acid hybridization and the target sequence of the genomic nucleic acid has not been amplified; b. contacting a sample of genomic nucleic acid with a second probe specific for the reference nucleic acid and forming a second complex on a solid support consisting of the reference nucleic acid and the second probe, wherein the second probe contains a detectable label; and c. measuring the amount of the first complex formed by detecting the detectable label of the first probe associated with the complex and measuring the amount of second complex formed by detecting the detectable label of the second probe associated with the complex; and d. obtaining a ratio of the amount of the first and the second complex; and e. comparing the ratio obtained to a ratio similarly obtained using genomic nucleic acid from a reference sample, wherein a difference in the ratios is indicative of genetic abnormality. In preferred embodiments, the genomic nucleic acid and the reference nucleic acid are anchored to the solid support through interaction of biotin and avidin. In another preferred embodiment,

the solid support is a bead. In another preferred embodiment, the first and second complexes are detected by flow cytometry. Additionally or alternatively, detection of a genetic biomarker can include a method for diagnosis in an individual by: a. contacting a sample of genomic nucleic acid from the individual with a probe complementary to nucleic acid sequence specific for the disease and forming on a solid support a complex consisting of the genomic nucleic acid and the probe if the genomic nucleic acid contains the nucleic acid sequence specific for the disease, wherein the probe contains a detectable label, the genomic nucleic acid is anchored to the solid support through means other than nucleic acid hybridization and the target sequence of the genomic nucleic acid has not been amplified; and b. measuring the amount of the complex formed on the solid support by detecting the amount of detectable label associated with the support; and c. comparing the amount of complex formed to the amount of complex formed using genomic nucleic acid from a reference sample assayed under similar conditions, wherein a difference in amount of complex formed from the individual as compared to the reference sample is diagnostic for the disease. In one embodiment, the reference sample may be obtained from an individual assumed to be free of the disease. In another embodiment, the reference sample may be obtained from an individual known to have the disease. In another embodiment, the reference sample is obtained from the same individual after obtaining the first sample. In one embodiment, the method may be used for measuring tumor burden in an individual suspected of having cancer. In another embodiment, the method may be used for prognosis of a disease. The genomic nucleic acid may be anchored covalently or non-covalently to the solid support. In some embodiments, the genomic nucleic acid may be anchored non-covalently to the solid support via a "binding pair," which refers to two molecules which form a complex through a specific interaction. Thus, the genomic nucleic acid can be captured on the solid support through an interaction between one member of the binding pair linked to the genomic nucleic acid and the other member of the binding pair coupled to the solid support. In a preferred embodiment, the binding pair is biotin and avidin, or variants of avidin e.g. streptavidin, and NeutrAvidin™. In other embodiments, the binding pair may be a ligand-receptor, a hormone-receptor, an antigen-antibody. In some embodiments, the genomic nucleic acid may be anchored to the solid support through covalent linking. In one embodiment, the covalent linking of the genomic nucleic acid to the solid support is

achieved through photoactive groups e.g. azido, azidophenacyl, 4-nitrophenyl 3-diazopyruvate, psolarens, psolaren derivatives. In another embodiment, the genomic nucleic acid can be cross-linked to variety of solid surfaces by UV cross linking. In another embodiment, the genomic nucleic acid may be anchored to the solid support though chemical coupling using chemical linkers. In another preferred embodiment, the genomic nucleic acid is genomic DNA. In another embodiment, the reference nucleic acid is a house keeping gene or a single copy sequence in a chromosome. In some embodiments. the test sample or the reference sample containing genomic nucleic acid and reference nucleic acid, respectively, can be obtained from or accessed within cells, tissues, body fluids, plasma, serum, urine, central nervous system fluid, stool, bile duct, paraffin-embedded tissue, cell lysates, tissue lysates and the like. The test and reference nucleic acid may be obtained from any number of sources and by any method.

[546] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,076,074, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for detecting chromosomal abnormalities including balanced translocations, wherein the method involves performing array-based CGH in conjunction with probes for detecting the translocations. In one aspect, the methods involve hybridizing to a genomic nucleic acid array a test sample of genomic nucleic acid, a reference sample of nucleic acid, and at least one probe for detecting a balanced translocation; and determining the relative amount of hybridized test and reference nucleic acids hybridized to the array as well as determining hybridization to the array of the probe or probes for detecting the translocation. In a preferred embodiment, the methods are performed using two samples of genomic nucleic acid; a test sample containing genomic nucleic acid, and a reference or a control sample containing genomic nucleic acid the latter with no known chromosomal or genetic abnormalities. The test and reference samples are co-hybridized to a nucleic acid array containing a plurality of nucleic acids or nucleic acid segments spotted onto a surface (such as a glass side) at discrete locations. The array may contain target nucleic acid markers for certain known genetic mutations or disease states, or may represent (in aggregate) an entire chromosome, or the full chromosomal complement to obtain a genetic profile. In these

approaches, the detectable label may be attached to the test and reference nucleic acids before or after hybridization and in any order. The detectable label may be attached covalently or non-covalently such as by a ligand-receptor interaction or by hybridization between complementary nucleotide sequences. In addition, a probe for detecting translocations is hybridized to the genomic DNA. In one approach, the probe is complementary to a moving segment of the genome which is translocated. The moving segment may be upstream or 5′ of the translocation break point or downstream or 3′ of the translocation breakpoint. If the test sample does not contain the balanced translocation, then the probe will hybridize to the array where the moving segment is located in the wildtype. If the test sample does contain the balanced translocation, then the probe will again hybridize to the array where the moving segment is located in the wildtype and to the area of array which contains the nucleic acid which now contains the moving segment. Additionally, multiple probes all complementary to the moving segment being translocated can be used in a single hybridization.

[547] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,021,888, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for performing a rapid hybridization assay. The method can be used to reduce the time to complete nucleic acid hybridization between nucleic acids in solution and nucleic acid immobilized to a solid support. The method applies acoustic surface waves during any of prehybridization to non-specific nucleic acid, hybridization to target nucleic acid or during any washing steps following hybridization. In one approach, nucleic acid hybridization to immobilized nucleic acid includes the following steps: a) contacting a solid support comprising one or more immobilized nucleic acid probe molecules under hybridization conditions with a non-specific blocking nucleic acid wherein the one or more immobilized nucleic acid probe molecules are capable of hybridizing with a sequence complementary thereto; b) contacting the solid support under hybridization conditions with a test sample containing nucleic acid target molecules; c) applying acoustic surface waves to the hybridization of step a) or step b) or both; and d) determining whether the one or more nucleic acid probes of the solid support have hybridized to test sample nucleic acid target molecules. In another approach, nucleic acid hybridization to immobilized nucleic acid includes the

following steps: a) contacting a solid support containing one or more immobilized nucleic acid probe molecules under hybridization conditions with a nucleic acid test sample containing one or more nucleic acid target molecules, the one or more immobilized nucleic acid probe molecules capable of hybridizing with a sequence complementary thereto; b) applying acoustic surface waves to the hybridization of step a); and c) determining whether the one or more nucleic acid probes of the solid support has hybridized to test sample nucleic acid target molecules. This method also may include a prehybridization step with non-specific nucleic acid such as described for the method further above. One or more washing steps may be applied after the prehybridization step or the hybridization step. One or more washing steps may include application of acoustic surface waves. With the application of acoustic waves, the prehybridization step may be limited to less than about 7 hours, more preferably less than about 5 hours and even more preferably less than about 3 hours. The hybridization step to target nucleic acid may be less than about 3 hours, more preferably less than about 2 hours and even more preferably less than about 1 hours. The washing steps are performed for less than about 1 hour, more preferably less than about 30 minutes. In a preferred embodiment, the method is performed in less than about 9 hours, more preferably less than about 7 hours and even more preferably less than about 5 hours. The method of hybridization to a test nucleic acid target molecule may further include one or more reference nucleic acid target molecules. The test and/or reference nucleic acid target molecules may be labeled with a detectable agent. In some embodiments, the solid support may contain an array of immobilized nucleic acid probe molecules. In some embodiments, the immobilized nucleic acid probe molecules may include the sequence of a bacterial artificial chromosome.

[548] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0142304, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions for the detection of mutations that are predictive of the responsiveness of a subject diagnosed with breast cancer, colorectal cancer, melanoma, or lung cancer to a particular therapeutic regimen. In some embodiments, the methods allow for rapid and sensitive detection of mutations in the target nucleic acid sequences of AKT1, ERBB2, FOXL2, IDH2, NRAS, RET, ALK, ERBB4,

GNA11, KIT, PDGFRA, SMO, BRAF, FBXW7, GNAQ, KRAS, PIK3CA, STK11, CTNNB1, FGFR2, GNAS, MAP2K1, PIK3R1, TP53, DDR2, FGFR3, HRAS, MET, PTCH1, EGFR, FGFR4, IDH1, NOTCH1, and PTEN. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting at least one mutation in a plurality of cancer-related genes in a subject comprising (a) extracting genomic DNA from a formalin fixed paraffin-embedded tumor sample obtained from the subject; (b) generating a library comprising amplicons corresponding to each of the plurality of cancer-related genes, said plurality of cancer-related genes comprising AKT1, ERBB2, FOXL2, IDH2, NRAS, RET, ALK, ERBB4, GNA11, KIT, PDGFRA, SMO, BRAF, FBXW7, GNAQ, KRAS, PIK3CA, STK11, CTNNB1, FGFR2, GNAS, MAP2K1, PIK3R1, TP53, DDR2, FGFR3, HRAS, MET, PTCH1, EGFR, FGFR4, IDH1, NOTCH1, and PTEN, wherein (i) generating said library occurs without the use of a bait set comprising nucleic acid sequences that are complementary to at least one of the plurality of amplicons; and (ii) the quality of the genomic DNA extracted from the formalin fixed paraffin-embedded tumor sample is not assessed using quantitative PCR prior to generating the library; (c) ligating an adapter sequence to the ends of the plurality of amplicons; and (d) detecting at least one mutation in at least one of the plurality of amplicons using high throughput massive parallel sequencing. In some embodiments of the method, the at least one mutation detected is a mutation in EGFR, KRAS, BRAF, NRAS, ERBB2 or PIK3CA. In one embodiment, the at least one mutation detected is selected from the group consisting of BRAF V600E, BRAF V600K, BRAF K483Q, BRAF G466V, BRAF G464V, BRAF E501V, BRAF E501K, EGFR ΔE746_A750, EGFR R680Q, EGFR G598E, KRAS A146T, KRAS R68M, KRAS L19F, KRAS G12V, KRAS G12D, KRAS G12C, KRAS G13D, KRAS G13C, KRAS G12A, KRAS G12S, KRAS Q22K, NRAS Q61K, NRAS Q61R, NRAS G12R, NRAS G12D, PIK3CA C420R, PIK3CA G106R, PIK3CA R38H, PIK3CA E453K, PIK3CA H1044R, PIK3CA N1044K, PIK3CA E545K, PIK3CA Q546H, PIK3CA H1047R, PIK3CA H1043L, PIK3CA M1043V, PIK3CA E542K, PIK3CA E542Q, PIK3CA T1053A, PIK3CA I121V, PIK3CA H1047L, ERBB2 L755S, ERBB2 S310Y, ERBB2 D769Y, ERBB2 S255R, DDR2 H92Y, DDR2 R31L, DDR2 L34P, DDR2 P381R and DDR2 K392N. In some embodiments of the method, the library comprising amplicons corresponding to each of the plurality of cancer-related genes is generated using no more than 10 ng of extracted genomic

DNA from the formalin fixed paraffin-embedded tumor sample. In some embodiments of the method, the library comprising amplicons corresponding to each of the plurality of cancer-related genes is generated using 11-25 ng of extracted genomic DNA from the formalin fixed paraffin-embedded tumor sample. In certain embodiments, the high throughput massive parallel sequencing is performed using pyrosequencing, reversible dye-terminator sequencing, SOLiD sequencing, Ion semiconductor sequencing, Helioscope single molecule sequencing, sequencing by synthesis, sequencing by ligation, or SMRT™ sequencing. In some embodiments of the method, the adapter sequence is a P5 adapter, P7 adapter, P1 adapter, A adapter, or Ion Xpress™ barcode adapter. Additionally or alternatively, in some embodiments, the plurality of amplicons further comprises a unique index sequence. In some embodiments, the formalin fixed paraffin-embedded tumor sample is a heterogeneous tumor. In certain embodiments, 5% of the cells of the heterogeneous tumor harbor at least one mutation in at least one of the plurality of amplicons.

[549] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0051329, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can methods for determining the presence of a variant in one or more genes in a subject comprising: (a) providing raw sequencing data generated from a nucleic acid sequencing reaction on a nucleic acid sample from the subject using a nucleic acid sequencer; (b) removing low quality reads from the raw sequencing data that fail a quality filter; (c) trimming adapter and/or molecular identification (MID) sequences from the filtered raw sequencing data; (d) mapping the filtered raw sequencing data to a genomic reference sequence to generate mapped reads; (e) sorting and indexing the mapped reads; (f) adding read groups to a data file to generate a processed sequence file; (g) creating realigner targets; (h) performing local realignment of the processed sequence file to generate a re-aligned sequence file; (i) removing of duplicate reads from the re-aligned sequence file; (j) analyzing coding regions of interest; and (k) generating a report that identifies whether the variant is present based on the analysis in step (j), wherein steps (g) and (j) are performed using a modified genomic alignment utility limited to nucleic acid regions containing the one or more genes of interest. In some embodiments, the method comprises performing the nucleic acid

sequencing reaction on the nucleic acid sample from the subject using a nucleic acid sequencer to generate the raw sequencing data of step (a). In some embodiments, analyzing coding regions of interest comprises calling variants at every position in the regions of interest. In some embodiments, the regions of interest are padded by an additional 150 bases. In some embodiments, variant calling is performed with a modified GATK variant caller. In some embodiments, mapping the reads to a genomic reference sequence is performed with a Burrows Wheeler Aligner (BWA). In some embodiments, mapping the reads to a genomic reference sequence does not comprise soft clipping. In some embodiments, the genomic reference sequence is GRCh37.1 human genome reference. In some embodiments, the sequencing method comprises emulsion PCR (emPCR), rolling circle amplification, or solid-phase amplification. In some embodiments, the solid-phase amplification is clonal bridge amplification. In some embodiments, the nucleic acid for sequence analysis is extracted from a biological sample from a subject. In some embodiments, the biological sample is a fluid or tissue sample. In some embodiments, the biological sample is a blood sample. In some embodiments, the nucleic acid is genomic DNA. In some embodiments, the nucleic acid is cDNA reversed transcribed from mRNA. In some embodiments, wherein the nucleic acid samples is prepared prior to sequencing by performing one or more of the following methods: (a) shearing the nucleic acid; (b) concentrating the nucleic acid sample; (c) size selecting the nucleic acid molecule in a sheared nucleic acid sample; (d) repairing ends of the nucleic acid molecules in the sample using a DNA polymerase; (e) attaching one or more adapter sequences; (f) amplifying nucleic acids to increase the proportion of nucleic acids having an attached adapter sequence; (g) enriching the nucleic acid sample for one or more genes of interest; and/or (h) quantification of the nucleic acid sample primer immediately prior to sequencing. In some embodiments, the one or more adapter sequences comprises nucleic acid sequences for priming the sequencing reaction and/or a nucleic acid amplification reaction. In some embodiments, the one or more adapter sequences comprises a molecular identification (MID) tag. In some embodiments, enriching the nucleic acid sample for one or more genes of interest comprises exon capture using one or more biotinylated RNA baits. In some embodiments, the nucleic acid for sequence analysis is obtained from a subject that is a mammal. In some embodiments, the subject is a human patient. In some embodiments, the

subject is a human suspected of having cancer or suspected of being at risk of developing a cancer. In some embodiments, the methods provided further comprise confirming the presence of the one or more variants by sequencing. Additionally or alternatively, detection of a genetic biomarker can include systems comprising one or more electronic processors configured to: (a) remove low quality reads from the raw sequencing data that fail a quality filter; (b) trim adapter and/or molecular identification (MID) sequences from the filtered raw sequencing data; (c) map the filtered raw sequencing data to a genomic reference sequence to generate mapped reads; (d) sort and index the mapped reads; (e) add read groups to a data file to generate a processed sequence file; (f) create realigner targets; (g) perform local realignment of the processed sequence file to generate a re-aligned sequence file; (h) remove of duplicate reads from the re-aligned sequence file; and (i) analyze coding regions of interest. In some embodiments, analyzing coding regions of interest comprises calling variants at every position in the regions of interest. In some embodiments, the regions of interest are padded by an additional 150 bases. In some embodiments, variant calling is performed with a modified GATK variant caller. In some embodiments, mapping the reads to a genomic reference sequence is performed with a Burrows Wheeler Aligner (BWA). In some embodiments, mapping the reads to a genomic reference sequence does not comprise soft clipping. In some embodiments, the genomic reference sequence is GRCh37.1 human genome reference. Additionally or alternatively, detection of a genetic biomarker can include non-transitory computer-readable media having instructions stored thereon, the instructions comprising: (a) instructions to remove low quality reads that fail a quality filter; (b) instructions to trim adapter and MID sequences from the filtered raw sequencing data; (c) instructions to map the filtered raw sequencing data to a genomic reference sequence to generate mapped reads; (d) instructions to sort and index the mapped reads; (e) instructions to add read groups to a data file to generate a processed sequence file; (f) instructions to create realigner targets; (g) instructions to perform local realignment of the processed sequence file to generate a re-aligned sequence file; (h) instructions to remove duplicate reads from the re-aligned sequence file; and (i) instructions to analyze coding regions of interest. In some embodiments, analyzing coding regions of interest comprises calling variants at every position in the regions of interest. In some embodiments, the regions of interest are padded by an additional 150 bases. In some

embodiments, variant calling is performed with a modified GATK variant caller. In some embodiments, mapping the reads to a genomic reference sequence is performed with a Burrows Wheeler Aligner (BWA). In some embodiments, mapping the reads to a genomic reference sequence does not comprise soft clipping. In some embodiments, the genomic reference sequence is GRCh37.1 human genome reference.

[550] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0316149, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include apparatus, systems, and methods for classifying genetic variants. In some embodiments, a standardized, rules-based process may provide a variant pathogenicity risk score based on clinical grade information in a CLIA-certified laboratory. Such a standardized system may provide reliable pathogenicity scores for DNA variants encountered in a clinical laboratory setting. In some embodiments, a sample of DNA may be obtained from a patient, who may or may not have been diagnosed with a disease or other medical condition. From the sample, the patient's genome may be sequenced in whole or in part. The result of sequencing may then be compared, e.g., to one or more reference genomes to identify variants in the patient's genome. One or more of the variants may be compared to databases of known variants. The result of that comparison may be identification of one or more previously unknown variants, one or more variants that are known but unclassified, or both. In some embodiments, an unclassified variant may be evaluated against one or more objective criteria. For example, in an embodiment, an embodiment may be assigned a starting score. Application of one or more objective criteria may cause additions and subtractions from the score, leading to a final score that may be used to classify the variant. In some embodiments, classification of one or more previously-classified variants may be revisited, e.g., periodically, to reevaluate the variants in light of new information gained since the previous evaluation. Additionally or alternatively, detection of a genetic biomarker can include a method of assigning a score to a genetic variant is based on multiple scoring criteria and reflects an estimate of pathogenicity of the variant. The method comprises identifying the variant in sequenced DNA obtained from a patient and assigning a starting score to the variant, where the starting score is a single numeric value that is associated with variants of unknown

significance. In some embodiments, the method also comprises: calculating a first score adjustment that is based on objective evaluation of minor evidence and splicing predictions; calculating a second score adjustment that is based on objective evidence of the frequency with which the variant occurs in a general population; calculating a third score adjustment that is based on objective evidence of the frequency with which the variant occurs in clinically characterized patients; calculating a fourth score adjustment that is based on objective evidence of the frequency with which the variant has been observed to co-occur with one or more other variants that are known to be pathogenic; calculating a fifth score adjustment that is based on objective evidence of a degree to which the variant exhibits segregation within one or more families; calculating a sixth score adjustment that is based on objective evidence of association between the variant and one or more disease phenotypes within data describing one or more families; and calculating a seventh score adjustment based on objective evidence regarding whether the variant affects functions of one or more proteins that are known to be associated with disease. In some embodiments, the method also comprises calculating a variant score based on the starting value, the first score adjustment, the second score adjustment, the third score adjustment, the fourth score adjustment, the fifth score adjustment, the sixth score adjustment, and the seventh score adjustment, the variant score being a single numeric value. And the method comprises assigning the variant to an assigned classification based solely on the variant score, where the assigned classification is one of a group that consists of a plurality of classifications, each classification in the plurality being associated with a respective different evaluation of variant pathogenicity.

[551] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0009287, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include apparatus, systems, and methods of detecting variations in the number of copies of genetic subsequences within the genome of an organism. According to some embodiments, samples of genetic material, including DNA, may be taken from several patients. Sections of the patients' DNA may then be sequenced, e.g., through a process that includes, for each patient, purifying, concentrating, and fragmenting that patient's DNA. Each fragment may receive a molecular label that identifies the patient from

whom the DNA was received and the DNA may otherwise be modified in preparation for sequencing (e.g., through one or more steps that may include one or more of: filtration, amplification, and modification such as to attach primers to the fragments). The fragments from several patients may be pooled, and the pool may include, e.g., one or more controls that comprise known genetic material. The fragments in the pool may then be sequenced, and the results of the sequencing may be stored, e.g., as one or more computer files. The results may then be processed, e.g., by one or more computer systems, to identify possible copy number variations in the patients from whom the samples were taken. For example, in some embodiments, the sequences may be demultiplexed to identify the respective patients whose DNA each sequence represents. Each patient's samples may then be aligned to a reference genome, and coverage for each base pair in each region of interest on the patient's genome may then determined. From the base pair coverage, the coverage of one or more subunits of the patient's genome may then be determined. For example, in some embodiments, the coverage of multiple exons may be determined. In some embodiments, the measurements of the coverage may then go through one or more steps of normalization. For example, the mean coverage of one or more amplicons known to be on autosomes may be compared to the mean coverage of one or more amplicons known to be on the X chromosome to provide a rough estimate of the number of X chromosomes (viz., one or two) in the patient's karyotype. If the patient is determined to have only one X chromosome, normalization may include doubling the coverage of all amplicons known to come from the X chromosome. Following normalization, reference values may be calculated for each amplicon, and CNV may be detected by comparing actual coverage values for each patient's amplicons with the calculated reference values. Additionally or alternatively, detection of a genetic biomarker can include a method is provided of detecting copy number variation (CNV) in the DNA of a plurality of patients. The method comprises receiving a plurality of samples, each sample containing DNA from a single patient, and from each sample, generating a plurality of fragments of DNA. The method also comprises barcoding each of the fragments with an identifier that uniquely identifies the respective patient from whom the DNA was received, pooling the plurality of samples into a DNA library, and subjecting the DNA library to one or more stages of filtering to increase the relative concentration of fragments within a plurality of selected regions of

interest. In some embodiments, the method further comprises producing sequencing data for the plurality of patients by sequencing the filtered DNA library, demultiplexing the sequencing data, and, for each patient, generating coverage data by identifying, for each of the regions of interest, coverage of each region of interest in the sequencing data. In some embodiments, the method comprises generating normalized coverage data from the coverage data and generating reference coverage, common to all samples, for each region of interest, the generation of the reference coverage being based upon the normalized coverage data. In some embodiments, the method also comprises automatically detecting CNV for at least one subsequence of at least one of the regions of interest of at least one of the patients based upon comparing the reference coverage to the normalized coverage data and providing output that identifies the patient, the subsequence, and the CNV. In some embodiments, generating normalized coverage data from the coverage data comprises generating raw coverage data for each patient by at least generating an estimate of the number of the patient's X chromosomes based on the coverage data and scaling the patient's coverage of at least one region of interest that is known to be X-linked and further comprises generating normalized coverage data from the raw coverage data. In some embodiments, generating the estimate of the number of each patient's X chromosomes occurs without reference to any demographic information about the respective patient and without reference to any information about the respective patient's phenotype. Alternatively, in some embodiments, the method comprises, for each patient, generating a second estimate of the number of the patient's X chromosomes based on the normalized coverage data and also comprises revising the normalized coverage data based on the second estimates. In some embodiments, generating the second estimate of the number of each patient's X chromosomes occurs without reference to any demographic information about the respective patient and without reference to any information about the respective patient's phenotype. In some embodiments, the coverage data comprises per-base coverage for each region of interest within the sequencing data; generating raw coverage data comprises scaling the patient's per-base coverage of the at least one region of interest that is known to be X-linked; the normalized coverage data comprises per-base coverage; the reference coverage comprises per-base coverage for each position within each region of interest; and automatically detecting CNV is based upon the per-base reference coverage and the normalized coverage data. In some

embodiments, each region of interest corresponds respectively to exactly one exon and contains that exon. In some embodiments, the method comprises automatically detecting CNV for a plurality of adjacent exons within a gene of a patient, each of the adjacent exons having the same CNV and automatically rolling up the CNV of the adjacent exons. Further, in an embodiment, the method comprises automatically detecting CNV for all exons within a gene of a patient, each of the exons within the gene having the same CNV, and automatically rolling up the CNV of the exons within the gene into a single CNV for the gene. In some embodiments, the method comprises subjecting the DNA library to one or more stages of amplification, such that each region of interest is an amplicon. In some embodiments, the coverage data comprises per-base coverage for each region of interest within the sequencing data; the normalized coverage data comprises per-base coverage; the reference coverage comprises per-base coverage for each position within each region of interest; and automatically detecting CNV is based upon the per-base reference coverage and the normalized coverage data.

[552] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2009/0088328, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of determining the printing quality of nucleic acid arrays and to provide methods to determine the efficiency of procedures to block non-specific binding on nucleic acid arrays. Additionally or alternatively, detection of a genetic biomarker can include utilizing fluorescence detection to evaluate the quality of a printed nucleic acid array without the need to add or otherwise link a fluorescent compound or dye to the nucleic acid. Nucleic acid arrays suitable for this analysis are those where the spots of the array are formed by printing a solution that contains the nucleic acid and one or more ions. Thus, the array is formed from nucleic acid in an ionic solution and the printing quality is evaluated by the fluorescence associated with each printed spot. Printing quality may be evaluated by measuring the intensity of fluorescence at the location of each printed sample, and/or by measuring the "morphology" (i.e. shape) of the printed sample. Printed spots can be "imaged" by measuring fluorescence across a spotted sample in two dimensions. The resulting image of a printed spot can be compared with a reference printed image expected for the printing equipment and solid phase used. The methods can be used to determine the quality the

quality of specific spots on an array, to determine the quality of specific regions of an array, or to determine the quality of an array as a whole. Spot quality and/or array quality can be detected immediately following array printing or after the array is subject to processing steps prior to hybridization. Such steps may include exposing the array to heat, humidity, UV irradiation, a blocking procedure, and/or washing. In the case where the quality of a blocking step for non-specific binding is performed, the quality of blocking can be determined by measuring fluorescence at each loaded sample prior to and following a blocking procedure. A decrease in the fluorescence after the washing and/or blocking procedure indicates the efficiency of the blocking and/or washing step. Additionally or alternatively, detection of a genetic biomarker can include a method for determining the printing quality of a nucleic acid array prior to hybridization, said method comprising: (a) printing an array of nucleic acid samples onto a solid support, each sample comprising nucleic acid in an ionic solution; and (b) detecting fluorescence of printed samples to determine the quality of printing.

[553] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2006/0292576, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of detecting and analyzing chromosomal abnormalities of interest in a test sample. In preferred embodiments, nucleic acids from a test sample are hybridized to two probes complementary to different segments of a gene of interest or different segments to a chromosomal fragment of interest. One probe is anchored to the solid support while the second probe comprises a detectable label which is used for detection. This method provides for the capture and detection of target nucleic acids hybridizing to both probes simultaneously. Hybridization of both the first and second probes to the same target nucleic acid indicates detection of a chromosomal abnormality in the target nucleic acid, while hybridization of only one of the probes to the same target nucleic acid indicates the absence of a genetic abnormality in the target nucleic acid. The anchored probe may be anchored covalently or non-covalently to the support. If non-covalent attachment is used, a preferred method is via a "binding pair," which refers to two molecules which form a complex through a specific interaction. Thus, the nucleic acid probe can be captured on the solid support through an interaction between one member of the binding pair linked to the

probe and the other member of the binding pair coupled to the solid support. A binding pair member also can be used to link the detectable label to the other nucleic acid probe. In a preferred embodiment, the binding pair is biotin and avidin or streptavidin. In other embodiments, the binding pair is comprised of a ligand-receptor, a hormone-receptor, an antigen-antibody, or an oligonucleotide-complement. In some embodiments, the two probes may be hybridized to the target nucleic acid in a liquid and then the complex can be captured by a solid support. The anchored probe in this approach is preferably anchored non-covalently and preferably via a binding pair. In other variants, the solid support may first comprise the anchored probe, which is then contacted for hybridization with the target nucleic acid, alone or together with the labeled probe. Additionally or alternatively, detection of a genetic biomarker can include methods of detecting the presence or absence of a genetic abnormality in a target nucleic acid in a test sample. The method includes forming on a solid support a complex comprising the target nucleic acid, a first nucleic acid probe hybridizing to a first segment of the target nucleic acid, the first nucleic acid probe labeled with a detectable label, and a second nucleic acid probe hybridizing to a second segment of the target nucleic acid, the second nucleic acid probe anchored to the solid support. The complex is detected by detecting incorporated detectable label, wherein hybridization of both the first and second probes to the same target nucleic acid indicates the presence of genetic abnormality in the target nucleic acid, while hybridization of only one of the probes to the same target nucleic acid indicates the absence of a genetic abnormality in the target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include methods of detecting a chromosomal translocation in the nucleic acid of a test sample. The method includes the hybridization of two nucleic acid probes, one complementary to a sequence of the donor chromosome segment and the other complementary to a sequence of the recipient chromosome which adjoins or is near to the inserted donor chromosome segment. One probe is anchored to the support and the other probe is labeled with a detectable label. A test sample of genomic DNA hybridizing to both probes will form a complex on the support or such a complex is preformed and then captured on a solid support and detected via the detectable label. The quantity of captured, labeled complex from the test sample represents the test value. If the test value shows that label is associated with captured hybridization complexes, the test sample is determined to contain the

chromosomal translocation. In one embodiment, one can compare the test value for the test sample with a test value from a reference sample which contains the target gene but lacking the translocation. Additionally or alternatively, detection of a genetic biomarker can include methods of detecting a duplication or deletion in a particular target chromosomal region or gene in an individual. The method includes forming on a solid support a complex comprising the nucleic acid associated with the particular chromosomal region or gene which is obtained from the sample, a labeled nucleic acid probe hybridizing to a first segment of the particular chromosomal region or gene, and a second nucleic acid probe hybridizing to a second segment of the particular chromosomal region or gene, wherein the second nucleic acid probe is anchored to the solid support. In a preferred embodiment, the target nucleic acid is genomic DNA which has been fragmented. The quantity of captured, labeled complex from the test sample represents the test value. The test value may be compared to a control value which may be obtained from the quantity of complex obtained from a different target gene or chromosomal region preferably from the same sample. A higher test value as compared to the control value is indicative of duplication or amplification, whereas a lower test value as compared to control value is indicative of a chromosomal or gene deletion. In another approach, one can determine a ratio of the test value of the test sample to the control value in that sample and compare to a similar ratio representing the test value and control value of a reference sample which contains nucleic acid that does not contain a deletion, duplication, or amplification in the chromosomal region or gene of interest. Additionally or alternatively, detection of a genetic biomarker can include methods of determining the diagnosis, predicting response to therapy, detecting minimal residual disease or prognosis of a disease in an individual. In this method, a complex is formed between a target nucleic acid from a test sample, a probe comprising a detectable label and hybridizing to one segment of a target nucleic acid and a second probe anchored to the support and hybridizing to a second segment of the target nucleic acid. The amount of complex on the solid support is measured through detection of incorporated detectable label of the first probe. The amount of complex formed is compared to the amount of complex formed in a similar manner from a sample obtained from a reference sample. The reference sample may be obtained from a normal individual, wherein a difference between the measurements from the test and reference samples is correlated with diagnosis or prognosis of a disease.

Additionally or alternatively, detection of a genetic biomarker can include methods of monitoring treatment or progression of a disease. In this method samples are obtained from a patient at different points in time (e.g., before and after a regimen of treatment of the disease). A complex is formed between a target nucleic acid from the first sample, a probe comprising a detectable label and hybridizing to one segment of a target nucleic acid and a second probe anchored to the support and hybridizing to a second segment of a target nucleic acid. The amount of complex on the support from the first sample is compared to the amount of complex formed using the same probes and target nucleic acid from the second sample. A difference in amount of complex formed can be correlated to progression of the disease or success of the treatment regimen. Additionally or alternatively, detection of a genetic biomarker can include methods of measuring tumor burden in an individual. In this method, a complex is formed on a solid support between a target nucleic acid from a test sample, a probe comprising a detectable label and hybridizing to one segment of a target nucleic acid and a second probe anchored to the support and hybridizing to a second segment of the target nucleic acid. The amount of complex on the solid support is measured through detection of incorporated detectable label of the first probe. The amount of complex formed is compared to a reference value or set of values of the amount of complex formed in a similar manner from a sample obtained from a reference sample, from a patient whose tumor burden is known, to determine tumor burden of the test sample. In some embodiments, methods of determining tumor burden include the formation of two complexes on solid support. The first complex comprises a first target nucleic acid from a test sample from the individual and two nucleic acid probes; one containing a detectable label and the other anchored to the support. The second complex comprises a second or control target nucleic acid from the test sample and two different nucleic acid probes, one containing a detectable label, distinguishable from the label of the first complex, and the other probe anchored to the solid support. The amount of each of the two complexes is measured and a test ratio determined. This ratio is then compared to a reference ratio or set of ratios that correlate the test ratio to tumor burden.

[554] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2006/0127918, which is hereby incorporated by reference in its entirety. For

example, detection of a genetic biomarker can include a nucleic-containing substrate that includes: (a) an organosilane-pretreated surface; (b) a polymer film cross-linked to the organosilane-pretreated surface; and (c) a nucleic acid molecule bound to one or more of the polymer film and the organosilane-pretreated surface. In preferred embodiments, the polymer film is formed from a polymer comprising reactive groups, and the nucleic acid molecule has not been covalently modified to facilitate covalent attachment at the reactive groups. The nucleic acid molecule may be associated with or bound to one or more of the polymer film and the organosilane-pretreated surface through covalent and/or noncovalent interactions. In preferred embodiments, the nucleic acid molecule is at least about 250 nucleotides in length, and more preferably at least about 500 nucleotides in length. In one embodiment, the nucleic acid molecule is a DNA molecule present in the form of a bacterial artificial chromosome (BAC) or another suitable cloning vector (e.g., an E. coli P1 based artificial chromosome, a plasmid, a cosmid, and the like). In some embodiments, the bound nucleic acid molecule is present on the surface of the substrate at a concentration sufficient to detect a nucleic acid target molecule by nucleic acid hybridization methodology. For example, the nucleic acid molecule may be present at a concentration of at least about 500 copies/cm2 on the surface of the substrate. More suitably the nucleic molecule is present on the surface of the substrate at a concentration of at least about 1000 copies/cm2 and/or at least about 5000 copies/cm2. The nucleic acid molecule preferably remains substantially attached to the substrate when subjected to washing under high stringency conditions (e.g., when the slide is washed with a low salt buffer optionally including a non-ionic detergent at a relatively high temperature). In some embodiments, the organosilane is a modified silane molecule that includes alkyl groups. In one embodiment, the organosilane includes alkyl groups with six or more carbon atoms and preferably ten or more carbon atoms. The organosilane may include alkoxy groups. The organosilane may also include halide groups. In some embodiments, the polymer comprises reactive groups. Suitable reactive groups include electrophilic groups that react with nucleophilic groups under suitable conditions. For example, reactive groups may include amino-reactive groups (i.e., groups that react with the nitrogen atom of an amino group), thiol-reactive groups (i.e., groups that react with the sulfur atom of a thiol-group), hydroxyl-reactive groups (i.e., groups that react with the oxygen atom of a hydroxyl-group), and combinations

thereof. In some embodiments, the polymer may include activated esters, epoxides, azlactones, activated hydroxyls, aldehydes, isocyanates, thioisocyanates, carboxylic acid chlorides, alkyl halides, maleimide, α-iodoacetamides, or combinations thereof. In one embodiment, the reactive group is an activated ester, and in particular, the activated ester may include an N-hydroxylsuccinimide ester. In some embodiments, the nucleic acid-containing substrate is configured as a nucleic acid microarray. The nucleic acid microarray may be suitable for performing comparative genomic hybridization analysis. In one embodiment, the nucleic acid microarray comprises genomic DNA cloned in bacterial artificial chromosomes (BACs). Additionally or alternatively, detection of a genetic biomarker can include a method for preparing a nucleic acid-containing substrate as described above. The method typically includes: (a) pretreating a surface of the substrate with a composition that includes an organosilane; (b) coupling a polymer to the organo-silane pretreated surface to form a polymer film; and (c) binding a nucleic acid molecule to one or both of the organosilane-pretreated surface and the polymer film. In preferred embodiments, the polymer film is formed from a polymer comprising reactive groups, and the nucleic acid has not been covalently modified to facilitate covalent attachment at the reactive groups. The nucleic acid molecule may be associated with and/or bound to one or more of the polymer film and the organosilane-pretreated surface through covalent and/or noncovalent interactions. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence and/or amount of a target nucleic acid molecule in a sample that includes: a) contacting the target molecule with a nucleic acid-containing substrate, which is prepared as described above, under suitable conditions for hybridizing the target to the nucleic acid of the substrate; and b) detecting the presence of the target molecule bound to the substrate. In preferred embodiments, the nucleic acid-containing substrate is a nucleic acid microarray, and detection of the presence and/or amount of the nucleic acid target is performed using comparative genomic hybridization analysis.

[555] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/125892, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and polynucleotide adapter compositions related

to the detection of mutations in ctDNA present in samples derived from a subject diagnosed as having, or suspected of having cancer. In some embodiments, the methods allow for rapid and sensitive detection and profiling of ctDNA mutations in various target nucleic acid sequences in the exons and/or introns of one or more cancer-related genes including, but not limited to ALK, BRAF, EGFR, ERBB2, KIT, KRAS, MET, NRAS, NTRK1, PIK3CA, ROS1, and RET The methods provide for a framework for ultrasensitive ctDNA profiling achieved using accurate analytical models of detection limits. These qualities improve detection limits over previous methods for samples with limited DNA content. Additionally or alternatively, detection of a genetic biomarker can include a nucleic acid adapter comprising a first oligonucleotide strand and a second oligonucleotide strand, wherein (a) the first oligonucleotide strand (i) comprises a first proximal region and a first distal region, wherein the first proximal region comprises a first unique molecular identifier sequence and a first spacer sequence having the sequence 5' TGACT 3' (SEQ ID NO:), wherein the first spacer sequence is located 3' to the first unique molecular identifier sequence; and (ii) does not comprise a degenerate or semi-degenerate sequence; (b) the second oligonucleotide strand (i) comprises a second proximal region and a second distal region, wherein the second proximal region comprises a second unique molecular identifier sequence and a second spacer sequence having the sequence 5' GTCA 3' (SEQ ID NO:), wherein the spacer sequence is located 5' to the second unique molecular identifier; and (ii) does not comprise a degenerate or semi-degenerate sequence; (c) the first proximal region of the first oligonucleotide strand hybridizes with the second proximal region of the second oligonucleotide strand; and (d) the first distal region of the first oligonucleotide strand does not hybridize with the second distal region of the second oligonucleotide strand. In some embodiments of the nucleic acid adapter, the "T" nucleotide located at the 3' end of the first spacer sequence contains a phosphorothioate bond. In some embodiments of the nucleic acid adapter, the 5' end of the first oligonucleotide strand is labelled with biotin. In other embodiments of the nucleic acid adapter, the 3' end of the second oligonucleotide strand is labelled with biotin. In some embodiments, the nucleic acid adapter is used to sequence a double-stranded target nucleic acid molecule selected from the group consisting of double-stranded DNA or double-stranded RNA. The double-stranded DNA may be sheared genomic DNA, or cell-free DNA. In some embodiments, the nucleic

acid adapter of the present technology further comprises at least two PCR primer binding sites, at least two sequencing primer binding sites, or any combination thereof. Additionally or alternatively, in some embodiments, the nucleic acid adapter of the present technology further comprises a sample- specific barcode sequence, wherein the sample-specific barcode sequence comprises 2-20 nucleotides. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting at least one mutation in a double-stranded circulating tumor DNA (ctDNA) molecule present in a sample obtained from a patient comprising (a) ligating a plurality of Y-shaped adapters to both ends of the double-stranded ctDNA molecule to form a double-stranded adapter-ctDNA complex, each Y-shaped adapter comprising a first oligonucleotide strand and a second oligonucleotide strand; (b) amplifying both strands of the adapter-ctDNA complex to produce first amplicons and second amplicons, wherein the first amplicons are derived from the first oligonucleotide strand, and the second amplicons are derived from the second oligonucleotide strand; (c) sequencing the first and second amplicons; (d) detecting at least one mutation in the double-stranded ctDNA molecule, when a mutation detected in the first amplicons is consistent with a mutation detected in the second amplicons. In some embodiments of the method, the patient is diagnosed with ovarian cancer, breast cancer, colon cancer, lung cancer, prostate cancer, gastric cancer, pancreatic cancer, cervical cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, head and neck cancer, or brain cancer. In some embodiments, the method further comprises enriching the first amplicons and second amplicons with a plurality of bait sequences, wherein the plurality of bait sequences comprises at least one gene region that corresponds to each of a plurality of cancer-related genes. The plurality of cancer-related genes may comprise ALK, BRAF, EGFR, ERBB2, KIT, KRAS, MET, NRAS, NTRK1, PIK3CA, ROS1, and RET. Additionally or alternatively, in some embodiments of the method, the plurality of bait sequences are RNA baits, DNA baits, or a mixture of RNA baits and DNA baits. In certain embodiments, the plurality of bait sequences comprises a 1 : 1 mixture of RNA baits and DNA baits. In other embodiments, the plurality of bait sequences comprises a mixture of RNA baits and DNA baits having a ratio of 2: 1, 1.5: 1, 0.75: 1 or 0.5: 1 . In certain embodiments of the method, both of the 3' ends of the double-stranded ctDNA molecule further comprise an "A"-overhang. In any of the above embodiments, each Y-shaped adapter further

comprises at least two sequencing primer binding sites. Additionally or alternatively, in some embodiments, each Y-shaped adapter further comprises a patient-specific barcode sequence, wherein the patient-specific barcode sequence comprises 2-20 nucleotides. Each Y-shaped adapter of the present technology may be labelled with biotin. In some embodiments of the method, the sample comprises no more than 5 ng of cell-free DNA. In other embodiments, the sample comprises at least 6-30 ng of cell-free DNA. In certain embodiments, the sample is whole blood, serum, plasma, synovial fluid, lymphatic fluid, ascites fluid, or interstitial fluid.

[556] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,389,234, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and system for molecular profiling and using the results from molecular profiling to identify treatments for individuals. In some embodiments, the treatments were not identified initially as a treatment for the disease. Additionally or alternatively, detection of a genetic biomarker can include a method of identifying a candidate treatment for a subject in need thereof, comprising: performing an immunohistochemistry (IHC) analysis on a sample from the subject to determine an IHC expression profile on at least five proteins; performing a microarray analysis on the sample to determine a microarray expression profile on at least ten genes; performing a fluorescent in-situ hybridization (FISH) analysis on the sample to determine a FISH mutation profile on at least one gene; performing DNA sequencing on the sample to determine a sequencing mutation profile on at least one gene; and comparing the IHC expression profile, microarray expression profile, FISH mutation profile and sequencing mutation profile against a rules database. The rules database comprises a mapping of treatments whose biological activity is known against cancer cells that: i. overexpress or underexpress one or more proteins included in the IHC expression profile; ii. overexpress or underexpress one or more genes included in the microarray expression profile; iii. have no mutations, or one or more mutations in one or more genes included in the FISH mutation profile; and/or iv. have no mutations, or one or more mutations in one or more genes included in the sequencing mutation profile. The candidate treatment is identified if: i. the comparison step indicates that the treatment should have biological activity against the cancer; and ii. the comparison step does not contraindicate the treatment for treating the cancer. In some

embodiments, the IHC expression profiling comprises assaying one or more of SPARC, PGP, Her2/neu, ER, PR, c-kit, AR, CD52, PDGFR, TOP2A, TS, ERCC1, RRM1, BCRP, TOPO1, PTEN, MGMT, and MRP1. In some embodiments, the microarray expression profiling comprise assaying one or more of ABCC1, ABCG2, ADA, AR, ASNS, BCL2, BIRC5, BRCA1, BRCA2, CD33, CD52, CDA, CES2, DCK, DHFR, DNMT1, DNMT3A, DNMT3B, ECGF1, EGFR, EPHA2, ERBB2, ERCC1, ERCC3, ESR1, FLT1, FOLR2, FYN, GART, GNRH1, GSTP1, HCK, HDAC1, HIF1A, HSP90AA1, IL2RA, HSP90AA1, KDR, KIT, LCK, LYN, MGMT, MLH1, MS4A1, MSH2, NFKB1, NFKB2, OGFR, PDGFC, PDGFRA, PDGFRB, PGR, POLA1, PTEN, PTGS2, RAF1, RARA, RRM1, RRM2, RRM2B, RXRB, RXRG, SPARC, SRC, SSTR1, SSTR2, SSTR3, SSTR4, SSTR5, TK1, TNF, TOP1, TOP2A, TOP2B, TXNRD1, TYMS, VDR, VEGFA, VHL, YES1, and ZAP70. In some embodiments, the FISH mutation profiling comprises assaying EGFR and/or HER2. In some embodiments, the sequencing mutation profiling comprises assaying one or more of KRAS, BRAF, c-KIT and EGFR. Additionally or alternatively, detection of a genetic biomarker can include a method of identifying a candidate treatment for a subject in need thereof, comprising: performing an immunohistochemistry (IHC) analysis on a sample from the subject to determine an IHC expression profile on at least five of: SPARC, PGP, Her2/neu, ER, PR, c-kit, AR, CD52, PDGFR, TOP2A, TS, ERCC1, RRM1, BCRP, TOPO1, PTEN, MGMT, and MRP1; performing a microarray analysis on the sample to determine a microarray expression profile on at least five of: ABCC1, ABCG2, ADA, AR, ASNS, BCL2, BIRC5, BRCA1, BRCA2, CD33, CD52, CDA, CES2, DCK, DHFR, DNMT1, DNMT3A, DNMT3B, ECGF1, EGFR, EPHA2, ERBB2, ERCC1, ERCC3, ESR1, FLT1, FOLR2, FYN, GART, GNRH1, GSTP1, HCK, HDAC1, HIF1A, HSP90AA1, IL2RA, HSP90AA1, KDR, KIT, LCK, LYN, MGMT, MLH1, MS4A1, MSH2, NFKB1, NFKB2, OGFR, PDGFC, PDGFRA, PDGFRB, PGR, POLA1, PTEN, PTGS2, RAF1, RARA, RRM1, RRM2, RRM2B, RXRB, RXRG, SPARC, SRC, SSTR1, SSTR2, SSTR3, SSTR4, SSTR5, TK1, TNF, TOP1, TOP2A, TOP2B, TXNRD1, TYMS, VDR, VEGFA, VHL, YES1, and ZAP70; performing a fluorescent in-situ hybridization (FISH) analysis on the sample to determine a FISH mutation profile on EGFR and/or HER2; performing DNA sequencing on the sample to determine a sequencing mutation profile on at least one of KRAS, BRAF, c-KIT and EGFR; and comparing the IHC expression

profile, microarray expression profile, FISH mutation profile and sequencing mutation profile against a rules database. The rules database comprises a mapping of treatments whose biological activity is known against cancer cells that: i. overexpress or underexpress one or more proteins included in the IHC expression profile; ii. overexpress or underexpress one or more genes included in the microarray expression profile; iii. have no mutations, or one or more mutations in one or more genes included in the FISH mutation profile; and/or iv. have no mutations, or one or more mutations in one or more genes included in the sequencing mutation profile. The candidate treatment is identified if: i. the comparison step indicates that the treatment should have biological activity against the cancer; and ii. the comparison step does not contraindicate the treatment for treating the cancer. In some embodiments, the IHC expression profiling is performed on at least 50%, 60%, 70%, 80% or 90% of the biomarkers listed. In some embodiments, the microarray expression profiling is performed on at least 50%, 60%, 70%, 80% or 90% of the biomarkers listed. Additionally or alternatively, detection of a genetic biomarker can include a method of identifying a candidate treatment for a cancer in a subject in need thereof, comprising: performing an immunohistochemistry (IHC) analysis on a sample from the subject to determine an IHC expression profile on at least the group of proteins consisting of: SPARC, PGP, Her2/neu, ER, PR, c-kit, AR, CD52, PDGFR, TOP2A, TS, ERCC1, RRM1, BCRP, TOPO1, PTEN, MGMT, and MRP1; performing a microarray analysis on the sample to determine a microarray expression profile on at least the group of genes consisting of ABCC1, ABCG2, ADA, AR, ASNS, BCL2, BIRC5, BRCA1, BRCA2, CD33, CD52, CDA, CES2, DCK, DHFR, DNMT1, DNMT3A, DNMT3B, ECGF1, EGFR, EPHA2, ERBB2, ERCC1, ERCC3, ESR1, FLT1, FOLR2, FYN, GART, GNRH1, GSTP1, HCK, HDAC1, HIF1A, HSP90AA1, IL2RA, HSP90AA1, KDR, KIT, LCK, LYN, MGMT, MLH1, MS4A1, MSH2, NFKB1, NFKB2, OGFR, PDGFC, PDGFRA, PDGFRB, PGR, POLA1, PTEN, PTGS2, RAF1, RARA, RRM1, RRM2, RRM2B, RXRB, RXRG, SPARC, SRC, SSTR1, SSTR2, SSTR3, SSTR4, SSTR5, TK1, TNF, TOP1, TOP2A, TOP2B, TXNRD1, TYMS, VDR, VEGFA, VHL, YES1, and ZAP70; performing a fluorescent in-situ hybridization (FISH) analysis on the sample to determine a FISH mutation profile on at least the group of genes consisting of EGFR and HER2; performing DNA sequencing on the sample to determine a sequencing mutation profile on at least the group of genes consisting of KRAS,

BRAF, c-KIT and EGFR; and comparing the IHC expression profile, microarray expression profile, FISH mutation profile and sequencing mutation profile against a rules database. The rules database comprises a mapping of treatments whose biological activity is known against cancer cells that: i. overexpress or underexpress one or more proteins included in the IHC expression profile; ii. overexpress or underexpress one or more genes included in the microarray expression profile; iii. have zero or more mutations in one or more genes included in the FISH mutation profile; and/or iv. have zero or more mutations in one or more genes included in the sequencing mutation profile. The candidate treatment is identified if: i. the comparison step indicates that the treatment should have biological activity against the cancer; and ii. the comparison step does not contraindicate the treatment for treating the cancer. In some embodiments, the microarray expression profiling is performed using a low density microarray, an expression microarray, a comparative genomic hybridization (CGH) microarray, a single nucleotide polymorphism (SNP) microarray, a proteomic array or an antibody array.

[557] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0171337, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method, comprising: a) determining a molecular profile for at least one sample from the subject by assessing a plurality of genes and/or gene products; and b) identifying, based on the molecular profile, at least one of: i) at least one treatment that is associated with benefit for treatment of the cancer; ii) at least one treatment that is associated with lack of benefit for treatment of the cancer; and iii) at least one treatment associated with a clinical trial. The plurality of genes and/or gene products can be chosen from amongst genes and or gene products (e.g., transcripts and proteins) with efficacy known to be related to various chemotherapeutic agents. Additionally or alternatively, detection of a genetic biomarker can include mutational analysis performed on any desired panel of genes. In an embodiment, assessing the plurality of genes and/or gene products further comprises mutational analysis of at least one, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45 or 46, of ABL1, AKT1, ALK, APC, ATM, BRAF, BRCA1,

BRCA2, CDH1, CSF1R, CTNNB1, EGFR, ERBB2 (HER2), ERBB4 (HER4), FBXW7, FGFR1, FGFR2, FLT3, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, JAK2, JAK3, KDR (VEGFR2), KIT (cKIT), KRAS, MET (cMET), MPL, NOTCH1, NPM1, NRAS, PDGFRA, PIK3CA, PTEN, PTPN11, RB1, RET, SMAD4, SMARCB1, SMO, STK11, TP53 and VHL. The mutational analysis may comprise any useful combination of these genes. The mutational analysis can be used to assess at least one, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 of a mutation, a polymorphism, a deletion, an insertion, a substitution, a translocation, a fusion, a break, a duplication, an amplification, a repeat, a copy number variation, a transcript variant, and a splice variant. The mutational analysis can be performed using any useful laboratory method or combination of methods. For example, the mutational analysis can be performed using at least one of ISH, amplification, PCR, RT-PCR, hybridization, microarray, sequencing, pyrosequencing, Sanger sequencing, high throughput or Next Generation sequencing (NGS), fragment analysis or RFLP. In some embodiments, the mutational analysis comprises Next Generation Sequencing.

[558] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication Nos. 2017/0175197, 2017/0039328, and 2015/0307947 and P.C.T. Publication No. WO 2012/092336, which are hereby incorporated by reference in its entirety.

[559] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/053915, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include systems, methods, apparatuses, and computer program products for providing a user interface for an application for analyzing biological data. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing biological data, the method comprising: receiving, at a computing device comprising a processor and memory, patient data for a plurality of patients, the patient data corresponding to at least one of a biological sampling event, a biological processing event, at least one therapeutic regime, at least one biomarker status, and a patient status; determining at least one interrelationship between any one of the biological sampling event, the biological processing event, the at least one therapeutic regime, the at least one biomarker status, and the patient

status; performing a therapeutic regime analysis to determine an interrelationship status for the interrelationship between at least one therapeutic regime and at least one of the patient status and the at least one biomarker status; and displaying at least one graphical interface on a user interface in communication with the computing device, the graphical interface including a plurality of visual elements, each visual element of the plurality of visual elements being associated with the patient data, at least one visual element being associated with the at least one interrelationship, at least one visual element including an indicium corresponding to at least one of the interrelationship status and the biomarker status. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing biological data associated with a biological sample from a target patient, the method comprising: receiving, at a computing device comprising a processor and memory, patient data associated with the target patient, the patient data corresponding to a biological sampling event, a biological processing event, a therapeutic regime, a marker status, and a patient status; receiving reference data associated with a plurality of patients, the reference data corresponding to a plurality of biological sampling events, biological processing events, therapeutic regimes, marker statuses, and patient statuses; determining at least one interrelationship between any one of the biological sampling events, the biological processing events, the therapeutic regimes, the marker statuses, and the patient statuses; performing a therapeutic regime analysis to determine the interrelationship between at least one therapeutic regime and at least one of the at least one patient status and the at least one marker status; displaying at least one graphical user interface, the graphical user interface configured to: i) display a plurality of graphical user interface objects associated with the reference data, ii) display a plurality of graphical user interface objects associated with the patient data, iii) display, on at least one graphical interface on a user interface in communication with the computing device, a primary graphical user interface object configured to, upon receiving an indication of a user input defining a selection of the primary graphical user interface object, cause the graphical user interface to display a secondary graphical user interface object; and assisting in providing patient care based on the one or more interrelationships displayed on the user interface. In some embodiments, the method may further comprise manipulating a primary visual element to display a secondary visual element including additional information corresponding to the patient data upon

selection thereof. The method may further comprise displaying the secondary visual element such that the secondary visual element overlays the primary visual element or the primary visual element is resized such that the secondary visual element is displayed adjacent to the primary visual element. In some embodiments, the method may further comprise assisting in providing patient care based on the one or more interrelationships displayed on the user interface. In some embodiments, assisting in providing the patient care comprises assisting in at least one of providing a diagnosis, providing a prognosis, selecting a recommended therapeutic regime, generating a hypothesis, and evaluating an efficiency of the therapeutic regime, based on the one or more interrelationships. In some embodiments, assisting in providing the patient care comprises selectively manipulating the graphical interface and one or more of the plurality of visual elements displayed thereon to visually compare a target patient against a set of reference patients. Visually comparing the target patient against the set of reference patients can be based on various desired attributes, including without limitation shared patient attributes, the at least one therapeutic regime, and / or the at least one biomarker status. Additionally or alternatively, detection of a genetic biomarker can include a computer-readable storage medium that is non-transitory and has computer-readable program code portions stored therein that, in response to execution by a processor, cause an apparatus to at least: receive, at a computing device comprising the processor and memory, patient data for a plurality of patients, the patient data corresponding to at least one of a biological sampling event, a biological processing event, at least one therapeutic regime, at least one biomarker status, and a patient status; determine at least one interrelationship between any one of the biological sampling event, the biological processing event, the at least one therapeutic regime, the at least one biomarker status, and the patient status; perform a therapeutic regime analysis to determine an interrelationship status for the interrelationship between at least one therapeutic regime and at least one of the patient status and the at least one biomarker status; and display at least one graphical interface on a user interface in communication with the computing device, the graphical interface including a plurality of visual elements, each visual element of the plurality of visual elements being associated with the patient data, at least one visual element being associated with the at least one interrelationship, at least one visual element including an indicium corresponding to at least one of the interrelationship status and

the biomarker status. Additionally or alternatively, detection of a genetic biomarker can include an apparatus for analyzing biological data, the apparatus including a user interface, and a computing device in communication with the user interface, the computing device comprising a processor and memory including computer- readable program code stored therein, the computer-readable code configured, upon the execution thereof by the processor, to cause the apparatus to: receive patient data for a plurality of patients, the patient data corresponding to at least one of a biological sampling event, a biological processing event, at least one therapeutic regime, at least one biomarker status, and a patient status; determine at least one interrelationship between any one of the biological sampling event, the biological processing event, the at least one therapeutic regime, the at least one biomarker status, and the patient status; perform a therapeutic regime analysis to determine an interrelationship status for the interrelationship between at least one therapeutic regime and at least one of the patient status and the at least one biomarker status; and display at least one graphical interface on the user interface, the graphical interface including a plurality of visual elements, each visual element of the plurality of visual elements being associated with the patient data, at least one visual element being associated with the at least one interrelationship, at least one visual element including an indicium corresponding to at least one of the interrelationship status and the biomarker status.

[560] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/064229, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include aptamers that bind biomarkers of interest. In some embodiments, oligonucleotide probes are used to detect the presence or levels of biomarkers or other biological entity in a biological sample.

[561] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/205686, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include oligonucleotide probes that recognize tissues having phenotypes of interest. In various embodiments, the oligonucleotide probes are used in diagnostic, prognostic or theranostic processes to characterize a phenotype of that sample. The

diagnosis may be related to a cancer. Additionally or alternatively, detection of a genetic biomarker can include a method of enriching an oligonucleotide library comprising a plurality of oligonucleotides, comprising: (a) providing a support arrayed with a plurality of samples; (b) contacting the support with the plurality of oligonucleotides; and (c) recovering members of the oligonucleotide probe library that bound to members of the plurality of samples, thereby enriching the oligonucleotide probe library. Additionally or alternatively, detection of a genetic biomarker can include a method of enriching an oligonucleotide library comprising a plurality of oligonucleotides, the method comprising: (a) performing at least one round of positive selection, wherein the positive selection comprises: (i) simultaneously contacting a plurality of samples with the plurality of oligonucleotides; and (ii) recovering members of the plurality of oligonucleotides that associated with the plurality of samples; (iii) optionally performing at least one round of negative selection, wherein the negative selection comprises: (i) simultaneously contacting a plurality of control samples with the plurality of oligonucleotides; (ii) recovering members of the plurality of oligonucleotides that did not associate with the plurality of control samples. In embodiments of the methods of enrichment, the plurality of samples is chosen to be representative of a phenotype of interest. Additionally or alternatively, detection of a genetic biomarker can include a method of characterizing a phenotype in a sample comprising: (a) arraying at least one sample on a substrate; (b) contacting the substrate with a plurality of oligonucleotides; and (b) measuring a presence or level of a complex formed between members of the plurality of oligonucleotides and the samples arrayed on the substrate, wherein the presence or level is used to characterize the phenotype. Additionally or alternatively, detection of a genetic biomarker can include a kit comprising at least one reagent for carrying out the methods, including methods of enrichment and characterizing. Additionally or alternatively, detection of a genetic biomarker can include use of at least one reagent for carrying out the methods. The at least one reagent can be any useful reagent, including without limitation at least one of a support, a plurality of nucleotides, a filtration unit, and PEG.

[562] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 10,011,826, which is hereby incorporated by reference in its entirety. For example, detection of a genetic

biomarker can include a method of isolating/extracting in parallel various biomolecules, in particular nucleic acids and proteins, from the same fixed biological samples. In some embodiments, the methods also comprise quantifying and analyzing the biomolecules isolated by the method, a kit for isolating/extracting in parallel various biomolecules from a fixed sample, and using said kit for diagnosing, prognosing, deciding the therapy of and monitoring the therapy of a disease. In some embodiments, a method of parallel purification of various kinds of biomolecules from the same biological starting material fixed by crosslinking, comprises: a) a step of dissolving said crosslinking of the starting material, b) a step of separating the different biomolecules present in the starting material into at least one fraction (A) and at least one fraction (B), and c) isolating or detecting, or isolating and detecting different biomolecules from at least one of said fractions (A) and (B) of step b), and a kit for performing said method.

[563] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,797,000, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting the presence of a target RNA, the method comprising: a) providing at least one DNA capture probe, wherein the at least one DNA capture probe is bound to a support; b) hybridizing the target RNA to said at least one DNA capture probe, yielding a target RNA:DNA capture probe complex; c) isolating the target RNA:DNA capture probe complex; d) providing at least one DNA amplification probe, and hybridizing said at least one DNA amplification probe to said target RNA:DNA capture probe complex, yielding a target RNA:DNA capture/amplification probe complex; e) providing an anti-RNA:DNA hybrid antibody, and incubating said target RNA:DNA capture/amplification probe complex with said antibody, yielding a target RNA:DNA:antibody complex; f) detecting said antibody, wherein said detecting indicates the presence of said target RNA. In some embodiments, the antibody is conjugated to a detectable marker, and the step of detecting comprises detecting the marker. In one aspect, the detectable marker is selected from the group consisting of alkaline phosphatase and horseradish peroxidase. In some embodiments, the step of detecting comprises providing a second antibody that binds to said anti-RNA:DNA hybrid antibody, wherein said second antibody is conjugated to a detectable marker, and wherein said

detecting further comprises detecting the marker. In some embodiments, the support comprises a magnetic bead. In one aspect, the magnetic bead is conjugated to at least one streptavidin molecule, and the at least one DNA capture probe is conjugated to a biotin molecule. Additionally or alternatively, detection of a genetic biomarker can include a method of providing target RNA for detection, the method comprising: incubating a biological sample containing the target RNA with carboxyl beads; isolating the beads; lysing the biological sample attached to the isolated beads; and isolating the beads from the lysed biological sample, wherein the resulting supernatant contains the target RNA for detection.

[564] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,689,047, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting a target nucleic acid in a sample comprising non-target nucleic acids is provided, said method comprising: (a) purifying the target nucleic acid from the sample by a method comprising: (i) contacting the sample with at least one purification probe, wherein at least a portion of the nucleic acid probe hybridizes to the at least one target nucleic acid to form a DNA:RNA hybrid; (ii) immobilizing the DNA:RNA hybrid to a first solid support by a method comprising contacting the DNA:RNA hybrid with at least a first antibody capable of binding to the DNA:RNA hybrid, wherein the antibody is bound to or adapted to be bound to the first solid support; and (iii) separating the first solid support from the sample to generate at least one purified target nucleic acid; b. genotyping the purified target nucleic acid by a method comprising: (i) amplifying at least a portion of the purified target nucleic acid to generate an amplicon, such as by an isothermal amplification, such as whole genome amplification; (ii) immobilizing the amplicon to a second solid support by a method comprising contacting the amplicon with at least one immobilization probe, wherein: (α) the immobilization probe is bound to or adapted to be bound to the second solid support; and (β) at least a portion of the immobilization probe hybridizes the at least one target nucleic acid; (iii) contacting the immobilized amplicon with at least one detection probe, wherein the at least a portion of the detection probe hybridizes to the at least one target nucleic acid to generate a detection complex; and (iv) detecting at least a first detectable signal generated by the detection complex, wherein the detectable signal indicates the genotype of the target nucleic acid. In

some embodiments, the plurality of purified target nucleic acids is contacted with a plurality of immobilization probes, wherein each of the plurality of immobilization probes is specific for a distinct purified target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method is provided comprising: a. a purifying step comprising: generating a double-stranded nucleic acid hybrid of the at least one target nucleic acid by hybridizing the at least one target nucleic acid to a hybrid probe set comprising at least a first nucleic acid probe specific for the at least one target nucleic acid; immobilizing the double-stranded nucleic acid hybrid to a first solid support through by contacting the double-stranded nucleic acid hybrid with at least a first antibody capable of binding to the double-stranded nucleic acid hybrid and binding the at least a first antibody to the first solid support; and separating the double-stranded nucleic acid hybrid from the sample to generate at least one purified nucleic acid; b. an amplifying step, wherein at least a portion of the at least one purified nucleic acid is amplified to generate amplified nucleic acids; and c. a genotyping step comprising: immobilizing the amplified nucleic acids to at least a second solid support by hybridizing the amplified nucleic acids to an immobilization probe set comprising at least one polynucleotide probe specific for the at least one target nucleic acid; and detecting the presence of the at least one target nucleic acid with a detection probe set comprising at least one polynucleotide probe specific for the at least one target nucleic acid.

[565] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,422,593, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting at least one target nucleic acid comprising: (1) sequence-specific isolation of a target nucleic acid from a sample; (2) amplifying the isolated target nucleic acid; and (3) detecting the target nucleic acid using a plurality of detectably labeled nucleic acid detection probes, wherein each (a) bears a different detectable label from the other detection probes, and/or (b) has a different melting temperature from probes bearing the same detectable label. In some embodiments, the method comprises: A. purifying the at least one target nucleic acid by a method comprising: A1. generating a double-stranded nucleic acid hybrid of the at least one target nucleic acid by hybridizing the at least one target nucleic acid to a hybrid probe set comprising at least a first nucleic acid probe specific for the at least

one target nucleic acid; A2. separating the double-stranded nucleic acid hybrid from the sample to generate at least one purified nucleic acid; B. amplifying at least a portion of the at least one purified nucleic acid; and C. detecting the target nucleic acid by a method comprising: C1. contacting the amplified nucleic acid with at least one detection probe set, wherein: C1(a). each of the detection probes of the detection probe set bears a detectable label; C1(b). at least two of the detection probes of the detection probe set carry the same detectable label; and C1(c). each of the probes carrying the same detectable label has a melting temperature (Tm) which differs from the other probes with the same label; C2. detecting the amplified nucleic acid by determining whether the labeled probe has hybridized to its nucleic acid sequence; and C3. detecting the temperature at which each detection probe dissociates from the nucleic acid sequence to which it has bound. In some embodiments, the double-stranded nucleic acid hybrid is separated from the sample by a method comprising contacting the double stranded nucleic acid hybrid with a molecule that binds specifically to double-stranded nucleic acid hybrids, preferably an anti-DNA:RNA hybrid antibody.

[566] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,593,366, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of randomly amplifying a target nucleic acid sequence, the method comprising, bringing into contact a set of primers, DNA polymerase, and a target sample, wherein the primers are random G-deficient primers, and incubating the target sample under conditions that promote replication of the target sequence, wherein replication of the target sequence results in replicated strands. Additionally or alternatively, detection of a genetic biomarker can include a method of randomly amplifying a target nucleic acid sequence, the method comprising, bringing into contact a set of primers, DNA polymerase, and a target sample, wherein the primers are random G-deficient primers, and incubating the target sample under conditions that promote replication of the target sequence, wherein nucleic acids in the target sample are not separated from other material in the target sample. Additionally or alternatively, detection of a genetic biomarker can include a method of randomly amplifying messenger RNA, the method comprising, reverse transcribing messenger RNA to produce a first strand cDNA, bringing into contact a set of random G-deficient primers, DNA

polymerase, and the first strand cDNA, and incubating under conditions that promote replication of the first strand cDNA, wherein replication of the first strand cDNA results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the first strand cDNA by strand displacement replication of another replicated strand. Additionally or alternatively, detection of a genetic biomarker can include a method of randomly amplifying a target nucleic acid sequence, the method comprising: (a) mixing a set of random G-deficient primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the random G-deficient primers and the target sequence in the primer-target sample mixture, and (b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence, wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand, wherein the target sequence is a nucleic acid sample of substantial complexity. Additionally or alternatively, detection of a genetic biomarker can include a method of randomly amplifying a whole genome, the method comprising, bringing into contact a set of random G-deficient primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence.

[567] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,487,823, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions and a method for amplification of nucleic acid sequences of interest. In some embodiments, the method is based on strand displacement replication of the nucleic acid sequences by primers. In some embodiments, the method is a form of multiple displacement amplification (MDA) useful for amplifying genomic nucleic acid samples and other nucleic acid samples of high complexity. The method can be used to amplify such highly complex nucleic acid samples using only one or a limited number of primers. It has been discovered that one or a small number of primers can effectively amplify whole genomes and other nucleic acid samples of high sequence complexity. The primers are specially selected or

designed to be able to prime and efficiently amplify the broad range of sequences present in highly complex nucleic acid samples despite the limited amount of primer sequence represented in the primers. The method generally involves bringing into contact one, a few, or more primers having specific nucleic acid sequences, DNA polymerase, and a nucleic acid sample, and incubating the nucleic acid sample under conditions that promote replication of nucleic acid molecules in the nucleic acid sample. Replication of the nucleic acid molecules results in replicated strands such that, during replication, the replicated strands are displaced from the nucleic acid molecules by strand displacement replication of another replicated strand. The replication can result in amplification of all or a substantial fraction of the nucleic acid molecules in the nucleic acid sample. In some embodiments, the method, which uses a form of whole genome strand displacement amplification (WGSDA), one, a few, or more primers are used to prime a sample of genomic nucleic acid (or another sample of nucleic acid of high complexity). Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying human genomes, the method comprising: bringing in to contact a single DNA primer of at least 6 nucleotides in length which is non-degenerate and non-random, a non-human, strand displacement DNA polymerase, and a human genomic nucleic acid sample to form a mixture, and incubating the mixture under conditions that promote replication of nucleic acid molecules in the human genomic nucleic acid sample; wherein the primer hybridizes to nucleic acid molecules in the genomic nucleic acid sample, and wherein the primer has a specific nucleotide sequence, wherein the genomic nucleic acid sample comprises all or a substantial portion of a human genome; and replicating the nucleic acid molecules in the human genomic nucleic acid sample under isothermal conditions, wherein replication of nucleic acid molecules in the genomic nucleic acid sample proceeds by strand displacement replication, wherein replication of the nucleic acid molecules in the genomic nucleic acid sample results in replication of all or a substantial fraction of the nucleic acid molecules in the genomic nucleic acid sample.

[568] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,115,410, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a nucleic acid detection method, referred to as target-specific HYBRID

CAPTURE ("TSHC"). Additionally or alternatively, detection of a genetic biomarker can include a method of detecting and/or quantifying one or more target nucleic acids, comprising the steps of target enrichment, amplification, and detection for the rapid and sensitive detection of the target nucleic acid sequences. In some embodiments, one or more target nucleic acids are detected by: capturing the target nucleic acids to a solid support by mixing the target nucleic acids, nucleic acid probes complementary to the target nucleic acids, wherein one is RNA and the other is DNA, and a solid support; removing unbound target nucleic acids and nucleic acid probes; amplifying the captured target nucleic acids or nucleic acid probes, forming a plurality of amplicons, where the presence of the amplicons is indicative of the presence of the target nucleic acids; and detecting the target nucleic acids by mixing the target nucleic acids with selectable and distinguishable oligonucleotides which hybridize to a portion of the target nucleic acids, (i.e., capture sequence probes; CSPs) and nucleic acid probes complementary to a different portion of the target nucleic acids (i.e., signal sequence probes; SSPs), wherein either the probe or target is an RNA and the other is DNA, where DNA:RNA hybrids are detected by DNA:RNA hybrid-specific binding agents, which are directly or indirectly labeled, thereby detecting the target nucleic acids. The SSPs are not limited to serving as only a means for producing a signal for detection; but may be used in the target enrichment step by hybridizing to the target nucleic acid, enabling capture with a DNA:RNA hybrid-specific binding agent. In some embodiments, a plurality of target nucleic acids are detected by: hybridizing a plurality of target nucleic acids to nucleic acid probes which are complementary to the target nucleic acids, forming DNA:RNA hybrids; capturing the DNA:RNA hybrids with DNA:RNA hybrid-specific antibodies conjugated to solid supports; removing unbound target nucleic acids and nucleic acid probes; amplifying the captured target nucleic acids or nucleic acid probes, forming a plurality of amplicons, using random primers and DNA polymerase, where the presence of the plurality of amplicons is indicative of the presence of the target nucleic acids; hybridizing nucleic acid probes complementary to a portion of the target nucleic acid sequences, forming DNA:RNA hybrids between targets and probes; hybridizing oligonucleotides conjugated to a solid support to a different portion of the target nucleic acids, wherein the solid support is selectable; selecting the oligonucleotide complexes; and detecting the plurality of target nucleic acids by binding DNA:RNA hybrid-specific binding agents to

the DNA:RNA hybrids. In some embodiments, one or more target DNAs are detected by a multiplex method having the steps of: hybridizing a plurality of target DNAs to RNA probes which are complementary to the target DNAs, forming DNA:RNA hybrids; capturing the DNA:RNA hybrids with DNA:RNA hybrid-specific antibodies which are conjugated to beads; removing unbound nucleic acids and nucleic acid probes by washing excess nucleic acids and probes; isothermally amplifying the target DNAs using random primers and DNA polymerase, forming a plurality of amplicons; hybridizing RNA probes complementary to a portion of the target DNAs (i.e., SSPs), forming DNA:RNA hybrids; hybridizing specific DNA oligonucleotides to a different portion of the target DNAs, wherein the DNA oligonucleotides are conjugated to selectable beads; and detecting the plurality of target DNAs by binding detectably labeled DNA:RNA hybrid-specific antibodies to the DNA:RNA hybrids and selecting target DNA using selectable oligonucleotide-conjugated beads (i.e., CSPs), wherein the DNA:RNA hybrid-specific antibodies are detectably and distinguishably labeled. The presence of each target is detected by the labeled DNA:RNA antibody through SSPs which form DNA:RNA hybrids with the target, while the various targets are separated or selected based on the oligonucleotide-conjugated bead (i.e., CSP). The presence of amplicon and DNA:RNA hybrids is indicative of the presence of the target DNAs.

[569] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,051,606, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for making and using multicomponent Nucleic Acid Enzymes (MNAzymes). Additionally or alternatively, detection of a genetic biomarker can include a composition comprising at least two or more oligonucleotide components wherein at least a first oligonucleotide component and a second oligonucleotide component self-assemble in the presence of an MNAzyme assembly facilitator to form a catalytically active multi-component nucleic acid enzyme (MNAzyme), wherein each of said at least first and said second oligonucleotide components comprise a substrate arm portion, a catalytic core portion, and a sensor arm portion; wherein upon self-assembly, the sensor arm portion of said first and second oligonucleotide components act as sensor arms of the MNAzyme, the substrate arm portion of the first and second oligonucleotide components act as substrate arms of the MNAzyme, and

the catalytic core portion of the first and second oligonucleotide components act as a catalytic core of the MNAzyme; and wherein the sensor arms of the MNAzyme interact with said MNAzyme assembly facilitator so as to maintain the first and second oligonucleotide components in proximity for association of their respective catalytic core portions to form the catalytic core of the MNAzyme, said catalytic core capable of modifying at least one substrate, and wherein said substrate arms of said MNAzyme engage a substrate so that said catalytic core of said MNAzyme can modify said substrate. In some embodiments, the composition may further comprise at least a third oligonucleotide component which acts to stabilize at least one of said substrate arm portions or sensor arm portions. In some embodiments, the method may further comprise at least a third oligonucleotide component and a fourth oligonucleotide component that self-assemble in the presence of at least one additional assembly facilitator to form at least one additional catalytically active MNAzyme, wherein each of said at least third and fourth oligonucleotide components comprise a substrate arm portion, a catalytic core portion, and a sensor arm portion; wherein upon self-assembly of said at least a third oligonucleotide component and a fourth oligonucleotide component, the sensor arm portion of said at least third and said at least fourth oligonucleotide components form sensor arms of said at least one additional catalytically active MNAzyme, the substrate arm portion of said at least third and said at least fourth oligonucleotide components form substrate arms of said at least one additional catalytically active MNAzyme, and the catalytic core portion of said at least third and said at least fourth oligonucleotide components form a catalytic core of said at least one additional catalytically active MNAzyme; and wherein the sensor arms of said at least one additional MNAzyme interact with said at least one additional assembly facilitator so as to maintain said at least third and said at least fourth oligonucleotide components in proximity for association of their respective catalytic core portions to form the catalytic core of said at least one additional MNAzyme, said catalytic core capable of acting on at least one additional substrate, and wherein the substrate arms of said at least one additional MNAzyme engage at least one additional substrate so that the catalytic core of said at least one additional MNAzyme can act on said at least one additional substrate. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence of at least one assembly facilitator comprising: (a) providing two or more oligonucleotide components, wherein at least

a first oligonucleotide component and a second oligonucleotide component self-assemble in the presence of an assembly facilitator to form at least one catalytically active multi-component nucleic acid enzyme (MNAzyme); (b) contacting the two or more oligonucleotide components with a sample putatively containing the assembly facilitator under conditions permitting: (1) the self-assembly of said at least one catalytically active MNAzyme, and (2) the catalytic activity of said MNAzyme; and (c) determining the presence of the catalytic activity of said at least one MNAzyme, wherein the presence of the catalytic activity is indicative of the presence of said at least one assembly facilitator. In some embodiments, the method may further comprise a step of amplifying the assembly facilitator. The step of amplifying may comprise one or more of: polymerase chain reaction (PCR), strand displacement amplification (SDA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), or reverse transcription polymerase chain reaction (RT-PCR). Additionally or alternatively, detection of a genetic biomarker can include a method for detecting the presence of at least one assembly facilitator comprising: (a) providing two or more oligonucleotide components, wherein at least a first oligonucleotide component and a second oligonucleotide component self-assemble in the presence of at least a first assembly facilitator to form at least a first catalytically active multi-component nucleic acid enzyme (MNAzyme); (b) providing at least a first substrate, said first substrate capable of being modified by said first MNAzyme, wherein said modification of said substrate by said MNAzyme provides a detectable effect; (c) contacting said two or more oligonucleotide components with a sample putatively containing said at least first assembly facilitator under conditions permitting: (1) the self-assembly of said at least first MNAzyme, and (2) the catalytic activity of said at least first MNAzyme; and (d) detecting said detectable effect. In some embodiments, the method may further comprise the step of amplifying the nucleic acid. The step of amplifying may comprise one or more of: polymerase chain reaction (PCR), strand displacement amplification (SDA), loop-mediated isothermal amplification (LAMP), rolling circle amplification (RCA), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence based amplification (NASBA), or reverse transcription polymerase chain reaction (RT-PCR). Additionally or alternatively, detection of

a genetic biomarker can include a method for detecting the presence of at least one target comprising: (a) providing two or more oligonucleotide components wherein at least a first oligonucleotide component and at least a second oligonucleotide component are capable of self-assembly in the presence of said target to form a catalytically active multi-component nucleic acid enzyme (MNAzyme); and wherein at least one of said first and said second oligonucleotide components further comprises at least one aptamer portion; (b) contacting said oligonucleotide components with a sample putatively containing said at least one target under conditions permitting: (1) binding of said target to said aptamer portions and (2) catalytic activity of the MNAzyme; and (c) determining the presence of the catalytic activity of the MNAzyme, wherein the presence of the catalytic activity is indicative of the presence of said target. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a target using an MNAzyme mediated signal amplification cascade comprising: (a) providing a first oligonucleotide component and a second oligonucleotide component that self assemble in the presence of said target to form a first catalytically active multi-component nucleic acid enzyme (MNAzyme); (b) providing an insoluble support having a first and a second substrate attached thereto, said first and second substrates are capable of being modified by said first MNAzyme, wherein said first and second substrates comprise at least a third and a fourth oligonucleotide component respectively, capable of forming a second catalytically active MNAzyme, wherein said third and fourth oligonucleotide components are released upon modification of said first and second substrates by said first MNAzyme; (c) providing said insoluble support having a third and a fourth substrate attached thereto, said third and fourth substrates are capable of being modified by said second MNAzyme, wherein said third and fourth substrates comprise at least a fifth and a sixth oligonucleotide component respectively, capable of forming a third catalytically active MNAzyme, wherein said fifth and said sixth oligonucleotide components are released upon modification of said third and fourth substrates by said second MNAzyme, and; (d) providing an assembly facilitator capable of facilitating the assembly of said second and said third MNAzyme, and; (e) providing a fifth substrate which is capable of being modified by said second MNAzyme to provide a detectable effect; (f) contacting said first and second oligonucleotide components with a sample putatively containing said target, in the presence of said assembly facilitator, and in the presence of said

insoluble support having said first, second, third and fourth substrates attached thereto under conditions permitting: (1) self-assembly of said first, second and third, MNAzymes, and (2) catalytic activity of said first, second and third, MNAzymes; and (g) wherein said third MNAzyme modifies said first and second substrates thereby further providing said second MNAzyme wherein said second MNAzyme further modifies at least one of said third, fourth and fifth substrates thereby further providing said third MNAzyme thereby further providing said detectable effect, and; (h) wherein detection of said detectable effect is indicative of the presence of said target.

[570] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,012,149, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for synthesis of a cDNA that contains the sequence of an miRNA or other small RNA that can be amplified using standard nucleic acid amplification methods such as the Polymerase Chain Reaction. The method can provide higher specificity of cDNA synthesis from small RNAs, while simultaneously permitting experimenters to carry out the two key enzymatic reactions necessary for this synthesis under substantially the same reaction conditions, conditions that include the presence of divalent cations at concentrations from 10 millimolar and 80 millimolar. When these reactions conditions are used as part of an assay for a small RNA, especially for an miRNA, greater specificity and sensitivity results. In some embodiments, the method for preparing a cDNA copy of a small RNA molecule, comprises: (a) providing a small RNA from a biological sample, wherein said RNA is from 18 to 28 nucleotides in length; (b) incubating the small RNA with an enzyme capable of catalyzing the addition of nucleotides at the 3′ end of the small RNA in the presence of a single ribonucleotide triphosphate selected from the group consisting of ATP, GTP, UTP, and CTP and at a final concentration of divalent magnesium cation between 20 millimolar and 80 millimolar in a reaction to add nucleotides to the small RNA to generate a tailed small RNA; (c) annealing a DNA primer to the tailed small RNA whereby the DNA template extends from the 3′ end of the tailed small RNA, thereby providing a single stranded region of DNA that may be used to direct polymerization of deoxyribonucleotide triphosphates; and (d) incubating the annealed tailed small RNA and DNA primer in the presence of reverse transcriptase and

deoxyribonucleotide triphosphates and at a final concentration of divalent magnesium cation between 20 millimolar and 80 millimolar under conditions allowing reverse transcription into cDNA and amplification of the annealed tailed small RNA to produce an amplification product.

[571] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,962,250, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of nucleic acid amplification and quantification such as a method of amplifying a plurality of selected nucleic acid molecules from a pool of nucleic acid molecules comprising: (a) amplifying a plurality of selected nucleic acid molecules in a first round multiplex amplification reaction including a plurality of outer primer pairs each pair being specific for a selected nucleic acid sequence wherein the amplification reaction is allowed to proceed to a point prior to that at which significant competition between amplicons for reaction components has occurred; and (b) further amplifying the selected nucleic acid molecules in a plurality of second round amplification reactions, each including a portion of the completed multiplex reaction as a template and at least one pair of inner primers each pair being specific for one of the selected nucleic acid sequences such that each second round reaction further amplifies a subset of the plurality of selected nucleic acid molecules respectively. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying a plurality of selected nucleic acid molecules from a pool of nucleic acid molecules comprising: (a) amplifying a plurality of selected nucleic acid molecules in a first round multiplex amplification reaction including a plurality of outer primer pairs each pair being specific for a selected nucleic acid sequence wherein the amplification reaction is allowed to proceed to a point prior to that at which significant competition between amplicons for reaction components has occurred; and (b) further amplifying the selected nucleic acid molecules in a plurality of second round amplification reactions, each including a portion of the completed multiplex reaction as a template and at least one pair of primers each pair comprising an inner primer and one of the outer primers and being specific for one of the selected nucleic acid sequences such that each second round reaction further amplifies a subset of the plurality of selected nucleic acid molecules respectively. Additionally or alternatively,

detection of a genetic biomarker can include a method of estimating the number of selected nucleic acid molecules from a pool of nucleic acid molecules comprising: (a) amplifying a plurality of selected nucleic acid molecules in a first round multiplex amplification reaction including a plurality of outer primer pairs each pair being specific for a selected nucleic acid sequence wherein the amplification reaction is allowed to proceed to a point prior to that at which significant competition between amplicons for reaction components has occurred; (b) further amplifying the selected nucleic acid molecules in a plurality of second round amplification reactions, each including a detectible reporter, a portion of the completed multiplex reaction as a template and at least one pair of inner primers each pair being specific for one of the selected nucleic acid sequences whereby each second round reaction further amplifies a subset of the plurality of selected nucleic acid molecules respectively; and (c) monitoring each second round amplification reaction by means of the detectible reporter such that the number of selected nucleic acid molecules of each selected sequence is estimated. Additionally or alternatively, detection of a genetic biomarker can include a method of estimating the number of selected nucleic acid molecules from a pool of nucleic acid molecules comprising: (a) amplifying a plurality of selected nucleic acid molecules in a first round multiplex amplification reaction including a plurality of outer primer pairs each pair being specific for a selected nucleic acid sequence wherein the amplification reaction is allowed to proceed to a point prior to that at which significant competition between amplicons for reaction components has occurred; and (b) further amplifying the selected nucleic acid molecules in a plurality of second round amplification reactions, each including a detectible reporter, a portion of the completed multiplex reaction as a template and at least one pair of primers each pair comprising an inner primer and one of the outer primers and being specific for one of the selected nucleic acid sequences such that each second round reaction further amplifies a subset of the plurality of selected nucleic acid molecules respectively; and (c) monitoring each second round amplification reaction by means of the detectible reporter such that the number of selected nucleic acid molecules of each selected sequence is estimated. In some embodiments, the fully nested form of the Multiplex Tandem-Polymerase Chain Reaction (MT-PCR) method is used according to the first and third aspects, whereby each selected nucleic acid molecule is amplified using a pair of outer primers in the first round of amplification and two inner primers

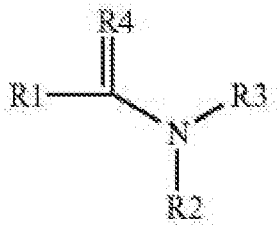
in the second round of amplification. In some embodiments, the hemi-nested MT-PCR method is used according to the second and fourth aspects, whereby each selected nucleic acid molecule is amplified using a pair of outer primers in the first round of amplification and the selected nucleic acid sequence is amplified further in the second round of amplification using a pair of primers comprising one of the outer primers used in the first round of amplification paired with one inner primer. In some embodiments, the second round amplification reaction includes a plurality of primer pairs and a plurality of fluorescent probes such that a plurality of selected nucleic acid molecules of each selected sequence are amplified and quantified by means of the fluorescent probes each being specific for a selected nucleic acid sequence. In some embodiments, at least one of the outer primers includes UTP nucleotides whereby the primer is amenable to digestion by a UNG enzyme and the outer primers are removed at the end of the first round of amplification by digestion with a UNG enzyme thereby substantially preventing contamination of the second round amplification reaction by the first round primers. In some embodiments, the methods are used in a method of detecting polymorphisms, mutations, insertions and deletions. Additionally or alternatively, detection of a genetic biomarker can include a method of identifying and/or quantifying at least one selected nucleic acid sequence including the steps of: (i) mixing one or more selected nucleic acid sequences with one or more detectible reporters; (ii) generating a melting curve by measuring the signal generated by said one or more detectible reporters; (iii) identifying and/or quantifying said one or more selected nucleic acid sequences from said melting curve.

[572] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,877,436, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for determining the presence of a target nucleic acid molecule in a sample containing biological material. In some embodiments, the method for determining the presence of a target nucleic acid molecule in a sample comprises: a) suspending the sample in a collection medium; b) releasing target nucleic acid molecules from the sample into the collection medium; c) converting double-stranded target nucleic acid molecules to single-stranded target nucleic acid molecules; d) contacting one or more probes with the single-stranded target nucleic acid molecules under conditions that allow the probes and target single-

stranded target nucleic acid molecules to hybridize forming double-stranded nucleic acid hybrids; e) capturing the double-stranded nucleic acid hybrids; f) separating the double-stranded nucleic acid hybrids from un-bound single-stranded target nucleic acid molecules; and g) detecting the double-stranded nucleic acid hybrids, thereby indicating the presence of the target nucleic acid. In some embodiments, the detection method may be automated, either fully automated, or partially automated—in other words requiring some human input. In some embodiments, the detection of target nucleic acid molecules in multiple samples at the same time or within a very short period of time, for example in a machine or a series of machines. Additionally or alternatively, detection of a genetic biomarker can include a collection medium into which a sample containing a target nucleic acid molecule are collected. The target nucleic acid molecule can be kept in the collection medium with minimal degradation of the target nucleic acid molecule over a time period of weeks or months. In some embodiments, DNA-based target sample material can be kept in the collection medium with minimal degradation of the target nucleic acid molecule over a time period of weeks or months. In some embodiments, the detergent-based collection medium allows for the rapid analysis and processing of a sample. In some embodiments, the collection medium comprises about 0.5% to about 2.0% NP-40, about 0.10% to about 0.40% sodium deoxycholate, about 25 mM to about 75 mM Tris-HCl, about 10 mM to about 50 mM EDTA, about 50 mM to about 200 mM NaC1, and about 0.01% to about 0.10% sodium azide.

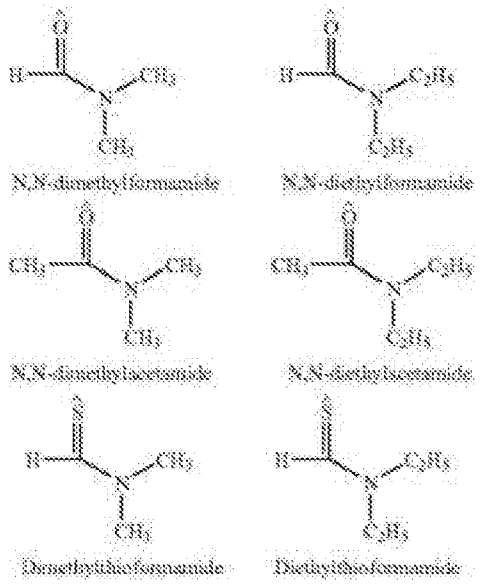
[573] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,372,637, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of stabilizing a biological sample that has the following steps:

[574] a) preparation of a biological sample, and b) contacting the biological sample with a composition having a substance according to the following structural formula:



[575] in which R1 is a hydrogen residue or a methyl residue, R2 and R3 are identical or different hydrocarbon residues with a length of the carbon chain of 1-20, and R4 is an oxygen, sulfur or selenium residue. The hydrocarbon residues R2 and/or R3 can be selected independently of one another from the group comprising alkyl, long-chain alkyl, alkenyl, alkoxy, long-chain alkoxy, cycloalkyl, aryl, haloalkyl, alkylsilyl, alkylsilyloxy, alkylene, alkenediyl, arylene, carboxylates and carbonyl. In some embodiments, the chain length n on R2 and/or R3 can have the values 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 and 20. In some embodiments, R2 and R3 have lengths of the carbon chain of 1-10. In some embodiments, R2 and R3 have lengths of the carbon chain of 1-5. In this case the chain length n can in particular have the values 1, 2, 3, 4 and 5. In some embodiments, methyl and ethyl residues are used on R2 and/or R3. The chain length n then has values of 1 and 2. In some embodiments, the substance used in the composition can be used as the sole agent for preservation. In some embodiments, the substance can also be used in conjunction with other preserving substances or even only as an additive to other preserving substances in the composition. In some embodiments, the volume ratio or weight ratio between the substance and one or more other preserving substances in the composition can be in the range from 0.01:100 to 100:0. Preferably it is in the range from 0.1:100 to 100:0 and especially preferably it is in the range from 1:100 to 100:0 and particularly preferably it is in the range from 5:100 to 100:0. In some embodiments, the class of substances used is for example dialkylacetamides (if R1 is a methyl residue) or dialkylformamides (if R1 is a hydrogen residue). In some embodiments, the biological sample is a material selected from the group comprising sample material, plasma, body fluids, blood, serum, cells, leukocyte fractions, crusta phlogistica, sputum, saliva, urine, semen, feces, forensic samples, smears, aspirates, biopsies, tissue samples, tissue parts and organs, food samples, environmental samples, plants and plant parts, bacteria, viruses, viroids, prions, yeasts and fungi, and fragments or constituents of the aforementioned materials, and/or isolated, synthetic or modified proteins, nucleic acids, lipids, carbohydrates, metabolic products and/or metabolites. In some embodiments, the substance is a substance selected from the group comprising N,N-dimethylacetamide, N,N-diethylacetamide, N,N-dimethylformamide, N,N-diethylformamide, N,N-

dimethylthioformamide and N,N-diethylthioformamide. Their structural formulas are as follows:



[576] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,043,834, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions and methods useful for labeling and detection of analytes. In some embodiments, the compositions are associations of three components: reporter binding agents, amplification target circles, and DNA polymerase. The compositions are assembled prior to their use in a rolling circle amplification reaction and can be stored and transported prior to use without substantial loss of activity. In some embodiments, the composition comprises a reporter binding agent, an amplification target circle, and DNA polymerase, wherein the reporter binding agent comprises a specific binding molecule and a rolling circle replication primer, wherein the specific binding molecule is specific for a target molecule, wherein the specific binding molecule is not bound to the target molecule, wherein the composition does not comprise tandem sequence DNA, wherein the reporter binding agent, the amplification target circle, and the DNA polymerase are directly associated with each other and form a complex, and wherein the composition is not in an assay or reaction. In some embodiments, the composition can be used as universal reagents of rolling circle amplification.

For this purpose, the compositions can have specific binding molecules that can interact with particular moieties or molecules that are present on, or are used to label any target molecule of interest. For example, the specific binding molecule in the reagent composition can be streptavidin or another biotin-specific molecule (such as an anti-biotin antibody). Any target molecule labeled with biotin can then be associated with the reagent composition and labeled and/or detected via rolling circle amplification mediated by the composition. This reagent composition can be used with any biotinylated target molecule. Similarly, use of an antibody specific to a class of antibodies (for example, and anti-mouse antibody) as the specific binding molecule in reagent compositions. Such reagent compositions can be used to label and detect a class of antibodies in an assay. For example, the reagent composition can be used to label and detect all mouse antibodies bound to antigen in immunoassays regardless of the specificity of the individual mouse antibodies. This is analogous to the use of antibodies specific to a class of antibodies in sandwich immunoassays. The reagents compositions provide greater signal amplification and tighter localization of the signal than in traditional immunoassays.

[577] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,682,790, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions for the isolation and/or stabilisation of nucleic acids in materials of biological origin. The compositions contain as an essential ingredient a cationic compound of general formula

[578] $Y^+R1R2R3R4X^-$

[579] wherein

[580] Y may denote nitrogen or phosphorus;

[581] R1, R2, R3 and R4 independently of one another may denote a branched or unbranched C1-C20-alkyl group and/or a C6-C20-aryl group as well as a C6-C26-aralkyl group; and

[582] X^- may represent an anion of an inorganic or organic, mono- or polybasic acid and at least one proton donor as additive. In some embodiments, the cationic compounds consist of an ammonium salt wherein R1 denotes a higher alkyl group, preferably with 12, 14 or 16 carbon atoms, and R2, R3 and R4 in each case denote a methyl group. In some embodiments, R1 denotes an aralkyl group, preferably a benzyl group, R2 denotes a higher alkyl group—

preferably with 12, 14 or 16 carbon atoms—and R3 and R4 denote a methyl group. In some embodiments, the anion is bromide, chloride, phosphate, sulphate, formate, acetate, propionate, oxalate or succinate. In some embodiments, aliphatic hydroxy-di- and -tricarboxylic acids, e.g., tartronic acid, D-(+), L-(−) or DL-malic acid, (2R, 3R)-(+)-tartaric acid, (2S,3S)-(−)-tartaric acid, meso-tartaric acid and citric acid, are used. In some embodiments, aliphatic ketodicarboxylic acids may also be used as additives, such as e.g. mesoxalic acid and oxaloacetic acid, of which oxaloacetic acid is most particularly preferred. In some embodiments, amino acids may be used, of which α-amino acids—such as e.g. aminoacetic acid (glycine), α-aminopropionic acid (alanine), α-amino-iso-valeric acid (valine), α-amino-iso-caproic acid (leucine) and α-amino-β-methylvaleric acid (isoleucine) are preferred. As further additives, mineral acids and their salts may also be used. Preferably, the salts of mineral acids—such as phosphoric acid or sulphuric acid—with alkali metals or the ammonium salts thereof are used. Phosphoric acid and ammonium sulphate are most preferably used. Additionally or alternatively, detection of a genetic biomarker can include a method of stabilizing nucleic acids in a biological sample, the method comprising: mixing a storage stabilization composition with a solution containing the nucleic acids, wherein the composition comprises a cationic compound of the general formula

[583] $Y^+R1R2R3R4X^-$

[584] wherein Y represents nitrogen or phosphorus;

[585] R1, R2, R3 and R4, independently, represent a branched or unbranched C1-C20-alkyl group and/or a C6-C20-aryl group as well as a C6-C26-aralkyl group;

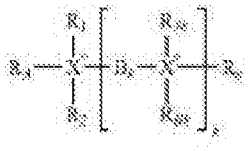
[586] X^- represents an anion of an inorganic or organic, mono- or polybasic acid; and

[587] at least one proton donor

[588] wherein the proton donor is present in the composition in a concentration of above 50 mM to saturation and wherein the proton donor is selected from the group consisting of saturated aliphatic monocarboxylic acids, unsaturated alkenyl-carboxylic acids, saturated and/or unsaturated aliphatic C2-C6-dicarboxylic acids, aliphatic hydroxyl-di- and tricarboxylic acids, aliphatic ketocarboxylic acids, amino acids or the inorganic acids or the salts thereof, on their own or in combination; stabilizing the nucleic acids, wherein the nucleic acids are stabilized by forming an ionic complex with the cationic compound; optionally separating the

insoluble ionic complex from the solution; and optionally releasing the nucleic acids from the insoluble ionic complex.

[589] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,683,035, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include (1) a method of stabilizing and/or isolating nucleic acids from a biological sample, comprising the following step: contacting the biological sample with at least one cationic compound of formula (I):



[590] wherein conjugated bases of strong and/or weak inorganic and/or organic acids are used as anion (A), and wherein the substance consisting of (I) and the anion is neutral in charge on the whole, and wherein

[591] X represents nitrogen (N) or phosphorus (P),

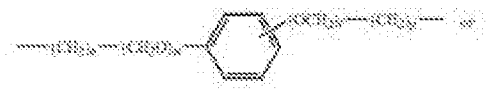
[592] k represents the integer 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24,

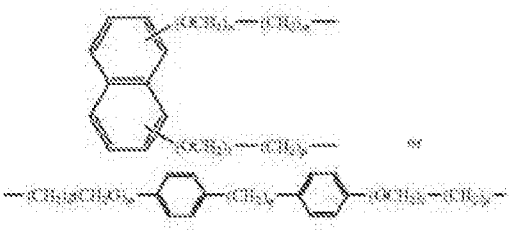
[593] Bk represents aliphatic alkanediyl bridges, which may be substituted on none, on one or more carbon atoms, and wherein one or more non-adjacent carbon atoms may be replaced by oxygen, and which have the structure

[594] —(CH2)n—(OCH2)m—

[595] wherein n and m independently represent the integer 0, 1, 2, 3, 4, 5, or 6, with n+m>0; alternatively,

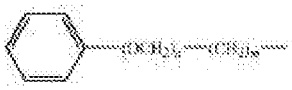
[596] Bk represents a substituted phenyl, naphthyl or biphenyl bridge, which, in addition, may be substituted on one or more carbon atoms and has the structure





[597] wherein n, m, l, p, q independently represent the integer 0, 1, 2, 3, 4, 5, or 6;

[598] R1, R2, R3k, which may be identical or different and which may be unsubstituted or substituted on one or more carbon atoms, represent hydrogen, linear or branched C1-C6 alkyl, linear or branched C1-C6 alkenyl, linear or branched C1-C6 alkynyl, phenyl, benzyl, and phenoxyethyl having the structure



[599] wherein n, m independently represent the integer 0, 1, 2, 3, 4, 5, or 6, and

[600] Z represents one of the structures —O—, —CO—, —CO2—, —OCO—, —CO—N—, —N—CO—, —O—CO—N—, —N—CO—O—, —S—, or —S—S—;

[601] or R1, R2, R3k represent phenyl, benzyl, phenoxyethyl having the structure

[602] wherein n, m independently represent the integer 0, 1, 2, 3, 4, 5, or 6;

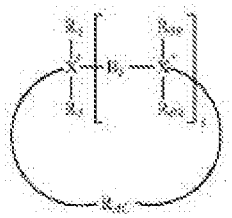
[603] RA, RBk, RC, which may be identical or different and which may be unsubstituted or substituted on one or more carbon atoms, represent hydrogen, linear or branched C1-C21 alkyl, linear or branched C1-C21 alkenyl, linear or branched C1-C21 alkynyl, and a structure

[604] CH3—(CH2)n—Z—(CH2)m—

[605] wherein n, m independently represent the integer 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24, and

[606] Z represents —O—, —CO—, —CO2—, —OCO—, —CO—N—, —N—CO—, —O—CO—N—, —N—CO—O—, —S—, or —S—S—;

[607] alternatively, RA and RC together form a residue RAC having a cyclic structure



[608] wherein the residue RAC, which may be unsubstituted or substituted on one or more carbon atoms, represents linear or branched C1-C8 alkyl, linear or branched C1-C8 alkenyl, or linear or branched C1-C8 alkynyl, and

[609] if k>1, the bridging groups Bk and the groups RBk and R3k are the same or different;

[610] (2) A kit for stabilizing and/or isolating nucleic acids, comprising at least one cationic compound as defined above by formula (I); (3) A complex, comprising a nucleic acid and at least one cationic compound, formed as the result of the method in (1); (4) A composition of matter, comprising at least one cationic compound as defined above by formula (I); (5) A pharmaceutical composition, comprising the composition of matter in (4); (6) A diagnostic composition, comprising the composition of matter in (4); and (7) A composition for research, comprising the composition of matter in (4).

[611] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,323,310, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include an amplification reaction mixture for selectively amplifying RNA from a target RNA template comprising: a cellular RNA-dependent RNA-polymerase and at least two primers complementary to said target RNA template. In some embodiments, the RNA-dependent RNA-polymerase (RdRp) is a tomato or other cellular RdRp. In some embodiments, the RdRp is a cellular RdRp, and in a particularly preferred embodiment, the RdRp is selected from the group consisting of tomato RdRp, Tobacco RdRp, cucumber RdRp, and wheat RdRp. In some embodiments, the amplification reaction mixture comprises a cellular RdRp and at least two primers complementary to a target RNA template. In a preferred embodiment, the reaction mixtures further comprise an RNA helicase, an energy source and optionally a divalent cation such as, e.g., Mg2+, Mn2+ or Co2+. The amplification reaction mixtures may further include RNase inhibitors, RNA stabilizing agents, single-stranded

binding proteins, rNTPs and analogs of rNTPs, for the amplification of target RNA into product RNA. An amplification buffer is also provided which is supportive of both RdRp and RNA helicase activity. Additionally or alternatively, detection of a genetic biomarker can include a method for selectively amplifying RNA from an RNA template, comprising: contacting the template RNA with an amplification reaction mixture according to claim 1; and incubating said amplification reaction mixture to produce amplified RNA product, wherein said incubation step comprises at least one denaturation condition.

[612] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,977,153, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method involving synthesizing first strand cDNA molecules from RNA molecules, circularizing the first strand cDNA molecules and replicating the circularized first strand cDNA molecules using rolling circle replication. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying RNA sequences, the method comprising: incubating a cDNA primer and an RNA sample comprising RNA molecules under conditions that promote synthesis of first strand cDNA molecules from the RNA molecules; incubating a circularization probe and the first strand cDNA molecules under conditions that promote circularization of the first strand cDNA molecules; and incubating the circularized first strand cDNA molecules under conditions that promote rolling circle replication of the circularized first strand cDNA molecules, thereby amplifying RNA sequences. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying RNA sequences, the method comprising: incubating a cDNA primer and an RNA sample comprising RNA molecules under conditions that promote synthesis of first strand cDNA molecules from the RNA molecules, wherein the conditions that promote synthesis of first strand cDNA molecules comprise incubating the cDNA primer and the RNA sample in the presence of a reverse transcriptase; incubating the first strand cDNA molecules in the presence of an RNAse H activity; incubating the first strand cDNA molecules under alkaline conditions; neutralizing the first strand cDNA molecules; purifying the first strand cDNA molecules; incubating a circularization probe and the first strand cDNA molecules under conditions that promote circularization of the first strand cDNA molecules, wherein the

conditions that promote circularization of the first strand cDNA molecules comprise incubating the circularization probe and the first strand cDNA molecules in the presence of ligase; incubating the circularized first strand cDNA molecules under conditions that promote rolling circle replication of the circularized first strand cDNA molecules, thereby amplifying RNA sequences, wherein the conditions that promote rolling circle replication of the circularized first cDNA molecules comprise incubating the circularized first strand cDNA molecules in the presence of a DNA polymerase. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying RNA sequences, the method comprising: incubating a cDNA primer and an RNA sample comprising RNA molecules under conditions that promote synthesis of first strand cDNA molecules from the RNA molecules; incubating a circularization probe and the first strand cDNA molecules under conditions that promote ligation of the first strand cDNA molecules to each other to form first strand cDNA concatemers; and incubating the first strand cDNA concatemers under conditions that promote strand displacement replication of the first strand cDNA concatemers, thereby amplifying RNA sequences.

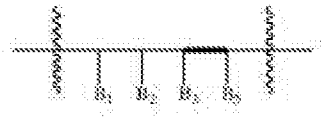
[613] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,815,212, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods provided for detecting the binding of a first member to a second member of a ligand pair, comprising the steps of (a) combining a set of first tagged members with a biological sample which may contain one or more second members, under conditions, and for a time sufficient to permit binding of a first member to a second member, wherein said tag is correlative with a particular first member and detectable by non-fluorescent spectrometry, or potentiometry, (b) separating bound first and second members from unbound members, (c) cleaving the tag from the tagged first member, and (d) detecting the tag by non-fluorescent spectrometry, or potentiometry, and therefrom detecting the binding of the first member to the second member. A wide variety of first and second member pairs may be utilized, including for example, nucleic acid molecules (e.g., DNA, RNA, nucleic acid analogues such as PNA, or any combination of these), proteins or polypeptides (e.g., an antibody or antibody fragment (e.g., monoclonal antibody, polyclonal antibody, or a binding

partner such as a CDR), oligosaccharides, hormones, organic molecules and other substrates (e.g., xenobiotics such as glucuronidase--drug molecule), or any other ligand pair. In some embodiments, the first and second members may be the same type of molecule or of different types. For example, representative first member second member ligand pairs include: nucleic acid molecule/nucleic acid molecule; antibody/nucleic acid molecule; antibody/hormone; antibody/xenobiotic; and antibody/protein. Additionally or alternatively, detection of a genetic biomarker can include methods for analyzing the pattern of gene expression from a selected biological sample, comprising the steps of (a) exposing nucleic acids from a biological sample, (b) combining the exposed nucleic acids with one or more selected tagged nucleic acid probes, under conditions and for a time sufficient for said probes to hybridize to said nucleic acids, wherein the tag is correlative with a particular nucleic acid probe and detectable by non-fluorescent spectrometry, or potentiometry, (c) separating hybridized probes from unhybridized probes, (d) cleaving the tag from the tagged fragment, and (e) detecting the tag by non-fluorescent spectrometry, or potentiometry, and therefrom determining the patter of gene expression of the biological sample. Within one embodiment, the biological sample may be stimulated with a selected molecule prior to the step of exposing the nucleic acids. Representative examples of "stimulants" include nucleic acid molecules, recombinant gene delivery vehicles, organic molecules, hormones, proteins, inflammatory factors, cytokines, drugs, drug candidates, paracrine and autocrine factors, and the like. Within further embodiments, the tag(s) may be detected by fluorometry, mass spectrometry, infrared spectrometry, ultraviolet spectrometry, or, potentiostatic amperometry (e.g., utilizing coulometric or amperometric detectors). Representative examples of suitable spectrometric techniques include time-of-flight mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry and electric sector mass spectrometry. Specific embodiments of such techniques include ion-trap mass spectrometry, electrospray ionization mass spectrometry, ion-spray mass spectrometry, liquid ionization mass spectrometry, atmospheric pressure ionization mass spectrometry, electron ionization mass spectrometry, fast atom bombard ionization mass spectrometry, MALDI mass spectrometry, photo-ionization time-of-flight mass spectrometry, laser droplet mass spectrometry, MALDI-TOF mass spectrometry, APCI mass spectrometry, nano-spray mass spectrometry, nebulised spray ionization mass

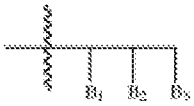
spectrometry, chemical ionization mass spectrometry, resonance ionization mass spectrometry, secondary ionization mass spectrometry and thermospray mass spectrometry.

[614] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,361,940, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include compositions and methods to increase the specificity of hybridization of nucleic acids and priming of nucleic acids in PCR. In some embodiments, the composition comprises a nucleic acid and a salt, the salt comprising an anion and a cation, the anion selected from halogenated acetate, propionate and halogenated propionate, the cation selected from primary, secondary and tertiary ammonium comprising 1-36 carbon atoms, and quaternary ammonium comprising 4-48 carbon atoms. In some embodiments, the composition is non-flowing and comprises an oligonucleotide of 6-100 nucleotides and a salt, the salt comprising an anion and a cation, the anion selected from acetate, halogenated acetate, propionate, and halogenated propionate, the cation selected from primary, secondary and tertiary ammonium comprising 1-36 carbon atoms, and quaternary ammonium comprising 4-48 carbon atoms. In some embodiments, the composition is free from organic solvent and comprises an oligonucleotide of 6-100 nucleotides and a salt, the salt comprising an anion and a cation, the anion selected from acetate, halogenated acetate, propionate, and halogenated propionate, the cation selected from primary, secondary and tertiary ammonium comprising 1-36 carbon atoms, and quaternary ammonium comprising 4-48 carbon atoms. In some embodiments, the composition comprises a nucleic acid and a salt, the nucleic acid immobilized on a solid support, the salt .comprising an anion and a cation, the anion selected from acetate, halogenated acetate, propionate and halogenated propionate, the cation selected from primary, secondary and tertiary ammonium comprising 1-36 carbons, and quaternary ammonium comprising 4-48 carbons. Additionally or alternatively, detection of a genetic biomarker can include a salt selected from the group: (a) an acetate salt of a cation of the formula HN(CH3)2Ra wherein Ra is a C4-C7 hydrocarbyl; (b) a halogenated acetate salt of a cation of the formula HN(CH3)2Rb wherein Rb is a C7-C12 hydrocarbyl; (c) acetate and halogenated acetate salts of a cation of the formula H2N(C5-C7cycloalkyl)Rc where R c is a C 1-C 12 hydrocarbyl; and (d) acetate and halogenated acetate salts of N-substituted piperdine, wherein the nitrogen of

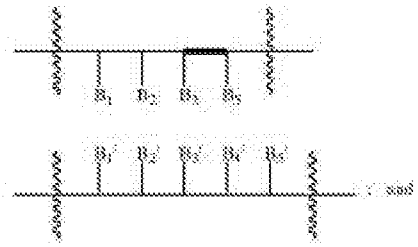
piperidine is substituted with C1-C12 hydrocarbyl. Additionally or alternatively, detection of a genetic biomarker can include an oligonucleotide in solution, where the oligonucleotide is formed from constituents including a plurality of fragments, each fragment shown schematically by structure (1)



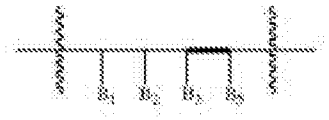
[615] wherein,



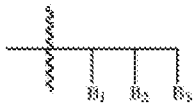
[616] represents a sequence of at least three nucleotides as found in wild-type DNA, where "B" represents a base independently selected at each location; — represents a series of covalent chemical bonds termed a "specificity spacer," which separates and connects two bases B 3 and B 5; the specificity spacer having steric and chemical properties such that (a) it does not prevent hybridization between a fragment of structure (1) and an oligonucleotide fragment having a complementary base sequence, as shown schematically as structure (2)



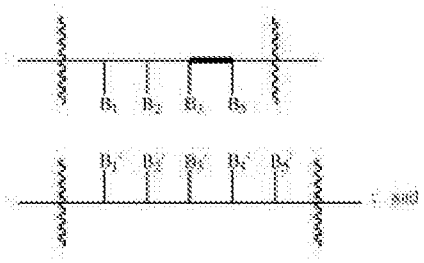
[617] and (b) it cannot enter into hydrogen bonding with a base positioned opposite itself in a hybridized complementary base sequence of structure (2). Additionally or alternatively, detection of a genetic biomarker can include an array which includes a plurality of oligonucleotides immobilized in an array format to a solid support, each oligonucleotide of the plurality formed from components which include a plurality of fragments, each fragment shown schematically by structure (1)



[618] wherein,



[619] represents a sequence of at least three nucleotides as found in wild-type DNA, where "B" represents a base independently selected at each location; — represents a series of covalent chemical bonds termed a "specificity spacer," which separates and connects two bases B 3 and B 5; the specificity spacer having steric and chemical properties such that (a) it does not prevent hybridization between a fragment of structure (1) and an oligonucleotide fragment having a complementary base sequence, as shown schematically as structure (2)



[620] and (b) it cannot enter into hydrogen bonding with a base positioned opposite itself in a hybridized complementary base sequence of structure (2). Additionally or alternatively, detection of a genetic biomarker can include a method of distinguishing between hybridization of a complementary nucleic acid target and a nucleic acid probe in which the probe and target are perfectly complementary and in which the probe and target have one or more base mismatches, comprising: (a) mixing the nucleic acid target with the nucleic acid probe in a solution comprising a hybotrope; (b) hybridizing at a discriminating temperature; and (c) detecting probe hybridized to target, thereby determining whether the nucleic acid probe and target are perfectly complementary or mismatched. In a preferred embodiment, the nucleic acid probe is labeled with a radioactive molecule, fluorescent molecule, mass-spectrometry tag or enzyme. In preferred embodiments, the nucleic acid probe and/or the target nucleic acid is from 6 to 40 bases. Preferably, the hybotrope is an ammonium salt. Specific preferred ammonium

salt hybotropes include, without limitation, bis(2-methoxyethyl)amine acetate, 1-ethylpiperidine acetate, 1-ethylpiperidine trichloroacetate, 1-ethylpiperidine trifluoroacetate, 1-methylimidizole acetate, 1-methylpiperidine acetate, 1-methylpiperidine trichloroacetate, 1-methylpyrrolidine acetate, 1-methylpyrrolidine trichloroacetate, 1-methylpyrrolidine trifluoroacetate, 2-methoxyethylamine acetate, N,N-dimethylcyclohexylamine acetate, N,N-dimethylcyclohexylamine trifluoroacetate, N,N-dimethylcyclohexylamine, N,N-dimethylheptylamine acetate, N,N-dimethylheptylamine acetate, N,N-dimethylhexylamine acetate, N,N-dimethylhexylamine acetate, N,N-dimethylisopropylamine acetate, N-ethylbutylamine acetate, N-ethylbutylamine trifluoroacetate, N,N-dimethylaminobutane trichloroacetate, N,N-dimethylisopropylamine trichloroacetate, triethanolamine acetate, triethylamine acetate, triethylamine trichloroacetate, tripropylamine acetate, and tetraethylammonium acetate. Other suitable hybotropes include LiTCA, RbTCA, GuSCN, NaSCN, NaClO 4, KI, TMATCA TEATCA, TMATBA, TMTCA, TMTBA, TBATCA and TBATBA. Preferably, the hybotrope is present at a molarity of from about 0.005 M to about 6 M. Preferably, the probe nucleic acid is DNA or RNA, and the target nucleic acid is DNA or RNA. Preferably, the target nucleic acid is affixed to a solid substrate. Preferably, the method further comprises polymerase chain reaction. Additionally or alternatively, detection of a genetic biomarker can include a method of distinguishing between hybridization of a complementary nucleic acid target and a nucleic acid probe in which the probe and target are perfectly complementary and in which the probe and target have one or more base mismatches, comprising: (a) mixing a nucleic acid target with a nucleic acid probe containing at least one abasic or deoxyNebularine substitution; (b) hybridizing at a discriminating temperature; and (c) detecting probe bound to the target, thereby determining whether the nucleic acid probe and target are perfectly complementary or mismatched. Additionally or alternatively, detection of a genetic biomarker can include a method of increasing discrimination in a nucleic acid synthesis procedure, comprising: (a) mixing a single-stranded nucleic acid target with an oligonucleotide primer in a solution comprising a hybotrope and a polymerase; (b) annealing the primer to the target at a discriminating temperature; and (c) synthesizing a complementary strand to the target to form a duplex. Additionally or alternatively, detection of a genetic biomarker can include a method of distinguishing a single base change in a nucleic acid

molecule from a wild-type sequence, comprising: (a) mixing a single-stranded nucleic acid target with an oligonucleotide primer in a solution comprising an amine-based salt and a polymerase, wherein the oligonucleotide primer has a 3'-most base complementary to the wild-type sequence or the single base change; (b) annealing the primer to the target at a discriminating temperature; (c) extending the primer, wherein a complementary strand to the target is synthesized when the 3'-most base of the primer is complementary to the target; and (d) detecting the extension of the primer.

[621] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,248,521, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of amplifying nucleic acid molecules from a template comprising (a) mixing single-stranded nucleic acid templates on a solid substrate with a solution comprising an oligonucleotide primer that hybridizes to the templates and a DNA polymerase, wherein the mixing occurs in discrete areas on the substrate, and wherein the solution remains in the discrete areas; (b) synthesizing a complementary strand to the template to form a duplex; (c) denaturing the duplex; and (d) synthesizing complementary strands to the template, therefrom amplifying nucleic acid molecules; wherein mixing, synthesizing, and denaturing are conducted at dew point. The solid substrate may be a silicon wafer or glass slide. The templates may be covalently attached to the solid substrate or deposited on the surface of the substrate. The template may be uniformly applied to the entire array prior to mixing or applied individually to each discrete area on the substrate. When applied individually, preferably the applying is performed using spring probes. In a most preferred embodiment, an apparatus is used to control the dew point. Additionally or alternatively, detection of a genetic biomarker can include a method of performing single nucleotide extension assay is provided, comprising (a) mixing oligonucleotides on a solid substrate with a solution comprising single-stranded nucleic acid molecules that hybridize to the oligonucleotides, a single nucleotide, and a DNA polymerase, wherein the mixing occurs in discrete areas of the substrate, and wherein the solution remains in discrete areas; and (b) detecting an extension product of the oligonucleotide; wherein the oligonucleotide will be

extended only when the single nucleotide is complementary to the nucleotide adjacent to the hybridized oligonucleotide, wherein mixing is performed at dew point.

[622] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0155705, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for isolating extracellular nucleic acids from a biological sample, comprising (a) preparing from the sample a binding mixture comprising: i) extracellular nucleic acids; ii) particles providing an anion exchange surface; iii) at least one non-ionic detergent which is a polyoxyalkylene fatty alcohol ether; iv) optionally at least one salt, wherein the binding mixture has a pH so that extracellular nucleic acids bind to the particles, (b) separating the particles with the bound extracellular nucleic acids from the remaining binding mixture; (c) optionally washing the bound extracellular nucleic acids; and (d) optionally eluting bound extracellular nucleic acids. In some embodiments, the binding mixture is prepared by forming a suspension by contacting the particles with a lysis and/or binding composition which comprises the at least one polyoxyalkylene fatty alcohol ether and which optionally comprises a salt and/or a buffer; contacting the suspension with the sample comprising extracellular nucleic acids; and optionally adding a proteolytic enzyme prior to, at the same time or after the sample was contacted with the suspension. Additionally or alternatively, detection of a genetic biomarker can include a kit for performing the method, which comprises (a) a lysis and/or binding composition comprising: i) at least one non-ionic detergent which is a polyoxyalkylene fatty alcohol ether; ii) optionally at least one salt; iii) at least one buffer; wherein said composition has an acidic pH; (b) particles providing an anion exchange surface; (c) optionally a proteolytic enzyme; (d) optionally one or more wash solutions and (e) optionally one or more elution solutions.

[623] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0148716, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of generating a circular double-stranded DNA (dsDNA) or a sequencing library, wherein the method comprises circulating a dsDNA or ligating a first and a second dsDNA in the presence of a DNA ligase and a single-

stranded DNA binding protein or a double-stranded DNA-binding protein. In some embodiments, the method of generating a sequencing library comprises further steps, preceding the ligation, of: (i) providing DNA fragments; (ii) end-repairing the DNA fragments by a polynucleotide kinase enzyme and an enzyme with polymerase and exonuclease activities; and (iii) optionally adding a terminal adenine to the end of the end-repaired DNA fragments by a deoxynucleotidyl transferase enzyme. In some embodiments, said method further comprises the subsequent steps of purification and size-selection of the ligated fragments for sequencing. In some embodiments, the adapter-ligated fragments are amplified prior to sequencing. Additionally or alternatively, detection of a genetic biomarker can include a kit comprising: (i) a DNA ligase; and (ii) a single-stranded DNA (ssDNA) binding protein or a double-stranded DNA (dsDNA)-binding protein. In some embodiments, the kit comprises: (i) a polynucleotide kinase and an enzyme with polymerase and exonuclease activities; (ii) optionally a deoxynucleotidyl transferase; (iii) a DNA ligase; (iv) a single-stranded or a double-stranded DNA binding protein; and (v) optionally a reaction buffer. In preferred embodiments, any of the kits comprises a mixture of a ligase, a single-stranded DNA (ssDNA) binding protein or a double-stranded DNA (dsDNA) binding protein, and optionally a reaction buffer. In a preferred embodiment, the enzyme with polymerase and exonuclease activities is a DNA polymerase. In the methods or kits referenced above, the polynucleotide kinase enzyme is the T4 Polynucleotide Kinase (PNK), the enzyme with polymerase and exonuclease activities is T4 DNA Polymerase, and/or the deoxynucleotidyl transferase enzyme is a Taq polymerase or a Klenow Fragment exo-. In some embodiments, ligation methods are referred to, wherein both the first and the second dsDNAs comprise two ssDNA ends, whereby each of the ssDNA ends of the first dsDNA ligates with each of the complementary ss ends of the second dsDNA to provide ligated circular dsDNA. In some embodiments, the first or the second DNA is capable of conferring the ability to auto-replicate within competent cells. In the methods or kits referenced above, the DNA binding protein is a viral, bacterial, archaeal, or eukaryotic single-stranded DNA binding protein or double-stranded DNA binding protein. In some embodiments, the DNA ligase in any of the above methods or kits is a T3 DNA ligase or a T4 DNA ligase. In other embodiments, the ligase is a T7 DNA ligase or an Ampligase®. In some embodiments of the above methods, each of the first and the second dsDNA have one

or two single stranded DNA (ssDNA) end(s). This/these ssDNA end(s) is/are less than 20 nucleotides (nt) in length.

[624] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0002738, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for amplifying target nucleic acids in a nucleic acid sample and kits useful in such methods. In some embodiments, the method for amplifying target nucleic acids in a nucleic acid sample, comprises: (a) extending each of a plurality of barcode primers (BC primers) to obtain extension products using the target nucleic acids as templates, wherein (i) each barcode primer comprises, from 5′ to 3′, a 1st universal primer sequence (US1), a molecular tag sequence (MT), and a 1st target-specific sequence (TS1), (ii) a plurality of barcode primers comprise at least 20 different barcode primers, and (iii) among the plurality of barcode primers (BC primers), the 1st universal primer sequences (US1) are the same, but the 1st target-specific sequences (TS1) are different; (b) separating the plurality of barcode primers that have not been extended in step (a) from the extension products; and (c) amplifying the extension products of step (b) in the presence of a plurality of limited amplification primers (LA primers) to obtain a plurality of 1st amplification products, wherein (i) each limited amplification primer comprises, from 5′ to 3′, a 2nd universal primer sequence (US2) and a 2nd target-specific sequence (TS2), and (ii) among the plurality of limited amplification primers, the 2nd universal primer sequences (US2) are the same, but the 2nd target-specific sequences (TS2) are different. Additionally or alternatively, detection of a genetic biomarker can include a kit comprising: (1) a plurality of barcode primers (BC primers), wherein (i) each barcode primer comprises, from 5′ to 3′, a 1st universal primer sequence (US1), a molecular tag sequence (MT), and a 1st target-specific sequence (TS1), (ii) a plurality of barcode primers comprise at least 20 different barcode primers, and (iii) among the plurality of barcode primers, the 1st universal primer sequence (US1) are the same, the molecular tag sequences (MT) are different, and the 1st target-specific sequence (TS1) are different; and (2) a plurality of limited amplification primers (LA primers), wherein (i) each limited amplification primer comprises, from 5′ to 3′, a 2nd universal primer sequence (US2) and a 2nd target-specific sequence (TS2), and (ii) among the plurality of limited amplification

primers, the 2nd universal primer sequences (US2) are the same, but the 2nd target-specific sequence (TS2) are different.

[625] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2016/0374330, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method suitable for stabilizing an extracellular nucleic acid population comprised in a cell-containing biological sample is provided, comprising contacting the cell-containing sample with at least one poly(oxyethylene) polymer as stabilizing agent or with mono-ethylene glycol as stabilizing agent. Additionally or alternatively, detection of a genetic biomarker can include a method for isolating extracellular nucleic acids from a cell-containing biological sample is provided, wherein said method comprises: a) stabilizing the cell-containing biological sample according to the method defined above; and b) isolating extracellular nucleic acids from the stabilized sample. Additionally or alternatively, detection of a genetic biomarker can include a composition suitable for stabilizing a cell-containing biological sample is provided comprising: i) a poly(oxyethylene) polymer as stabilizing agent or ii) mono-ethylene glycol as stabilizing agent and one or more, preferably two or more further additives selected from the group consisting of: one or more primary, secondary or tertiary amides; a caspase inhibitor; an anticoagulant and/or a chelating agent. Preferably, the composition comprises a poly(oxyethylene) polymer, which preferably is a high molecular weight poly(oxyethylene) polymer having a molecular weight of at least 1500, as stabilizing agent and furthermore comprises one or more, preferably two or more further additives selected from the group consisting of at least one further poly(oxyethylene) polymer having a molecular weight that is at least 100, preferably at least 200, at least 300 or at least 400 below the molecular weight of the first poly(oxyethylene) polymer, which preferably is a high molecular weight poly(oxyethylene) polymer, wherein said further poly(oxyethylene) polymer preferably is a low molecular weight poly(oxyethylene) polymer having a molecular weight of 1000 or less; one or more primary, secondary or tertiary amides; a caspase inhibitor; an anticoagulant and/or a chelating agent. Additionally or alternatively, detection of a genetic biomarker can include a collection device for collecting a cell-containing biological sample is provided, wherein the

collection device comprises i) a poly(oxyethylene) polymer as stabilizing agent or ii) mono-ethylene glycol as stabilizing agent and one or more further additives selected from the group consisting of: one or more primary, secondary or tertiary amides; a caspase inhibitor; an anticoagulant and/or a chelating agent. Preferably, the collection device according to the fifth aspect comprises a poly(oxyethylene) polymer, which preferably is a high molecular weight poly(oxyethylene) polymer having a molecular weight of at least 1500, as stabilizing agent and furthermore comprises one or more, preferably two or more further additives selected from the group consisting of at least one further poly(oxyethylene) polymer having a molecular weight that is at least 100, preferably at least 200, at least 300 or at least 400 below the molecular weight of the first poly(oxyethylene) polymer which preferably is a high molecular weight poly(oxyethylene) polymer, wherein said further poly(oxyethylene) polymer preferably is a low molecular weight poly(oxyethylene) polymer having a molecular weight of 1000 or less; one or more primary, secondary or tertiary amides; a caspase inhibitor; an anticoagulant and/or a chelating agent.

[626] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2016/0048564, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for building a community database of variant observations, comprising: receiving human variant datasets derived from samples generated by a plurality of distinct users, wherein the users consented to share pooled variant observations with other users; storing the received human variant datasets in a knowledge base of genomic information; searching the knowledge base to identify a plurality of variant observations that meet inclusion criteria for a pool; adding each identified variant observation to the pool; and calculating one or more anonymized allele statistics from the pool, wherein at least one of the receiving, storing, searching, adding, or calculating are performed by one or more computers. Additionally or alternatively, detection of a genetic biomarker can include a method for determining a candidate for a clinical trial, comprising: receiving clinical trial enrollment criteria from a user including genetic targeting criteria; searching a knowledge base of patient test information received from a plurality of independent entities for patients that match the clinical trial enrollment criteria; and providing to the user search results for

consented patients that match the clinical trial enrollment criteria; wherein at least one of the receiving, searching, or providing are performed by one or more computers.

[627] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2016/0017320, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for reducing errors in sequencing and thus improving accuracy in mutation detection and transcriptome profiling including methods that use semi-random barcodes to tag sequencing fragments before amplification to reduce bias and sequencing errors. Additionally or alternatively, detection of a genetic biomarker can include oligonucleotides that comprise semi-random barcode sequences, including sequencing adapters, reverse transcription primers and PCR primers. The term "semi-random barcode sequences," "semi-random sequences," or "semi-random barcodes" refers to a population of semi-random nucleotide sequences each consisting of (Xmer)n, wherein Xmer is 3-mer (i.e., a 3-nucleotide oligonucleotide, also referred to as "trimer"), 4-mer (i.e., a 4-nucleotide oligonucleotide, also refers to as "tetramer")), 5-mer (i.e., a 5-nucleotide oligonucleotide, also refers to as "pentamer"), or 6-mer (i.e., a 6-nucleotide oligonucleotide, also refers to as "hexamer"), and n is an integer from 2 to 10. Each nucleotide sequence in the population is referred to as "semi-random barcode sequence," "semi-random barcode," or "semi-random sequence." In certain embodiments, the semi-random sequence consist of (Xmer)n, wherein Xmer is 3-mer, and n is 2, 3, 4, 5, 6, 7, 8, 9, or 10, preferably 4, 5, 6, 7, 8 or 9. In certain embodiments, Xmer is 4-mer, and n is 2, 3, 4, 5, 6, 7, 8, or 9, preferably 2, 3, 4, 5, 6, or 7. In certain embodiments, Xmer is 5-mer, and n is 2, 3, 4, 5, 6, 7, or 8, preferably 2, 3, 4, 5, or 6. In certain embodiments, Xmer is 6-mer, and n is 2, 3, 4, 5, 6, or 7 preferably 2, 3, 4, or 5. The semi-random barcode sequences may be synthesized from a mixture of Xmers with defined sequences. For example, in certain embodiments, the semi-random barcodes consist of (Xmer)n, wherein Xmer is 3-mer and n is 7. In other words, the semi-random barcodes are a population of 21 bp oligonucleotides that consist of 7 trimers. Such semi-random barcodes may be synthesized with 7 successive steps during each of which steps, a random trimer from a defined trimer mixture may be incorporated. A defined Xmer mixture for synthesizing semi-random barcodes may have 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,

16, 17, 18, 19, 20, 21, 22, 23, 24, or 25, or at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25, different Xmers. The number of different semi-random barcode sequences synthesized from a defined Xmer mixture may be at least 100, 200, 300, 400, 500, 1,000, 2,000, 3,000, 4,000, 5,000, 10,000, 50,000, 100,000, 50,000, 100,000, 500,000, or 1,000,000. Preferably, each Xmer (e.g., trimer, tetramer, pentamer, and hexamer) has at least 2 bases different from another Xmer in a defined Xmer mixture so that any single-base variant within each Xmer block in sequencing reads can be identified as errors, not a different barcode. In certain embodiments, each Xmer (e.g., tetramer, pentamer, and hexamer) has at least 3 bases different from another Xmer in a defined Xmer mixture so that any single- or 2-base variant within each Xmer block in sequencing reads can be identified as errors, not a different barcode. In certain embodiments, each Xmer (e.g., pentamer and hexamer) has at least 4 bases different from another Xmer in a defined Xmer mixture so that any 1-, 2-, or 3-base variant within each Xmer block in sequencing reads can be identified as errors, not a different barcode. Additionally or alternatively, detection of a genetic biomarker can include a plurality of single-stranded (ss) oligonucleotides, wherein each oligonucleotide comprises from the 5′ to 3′ direction a 1st sequence and a 2nd sequence; (a) the 1st sequence is a semi-random sequence consisting of (Xmer)n, wherein Xmer is 3-mer, 4-mer, 5-mer, or 6-mer, and n is an integer from 2 to 8, and (b) the 2nd sequence is (i) at least 10 nucleotides in length, (ii) fully or substantially complementary to a target sequence, and (iii) the same among the plurality of oligonucleotides. Additionally or alternatively, detection of a genetic biomarker can include a plurality of double-stranded (ds) sequencing adapters, wherein each sequencing adapter comprises: (a) an oligonucleotide ("1st oligonucleotide") from above, and (b) a 2nd ss oligonucleotide that comprises from the 3′ to 5′ direction (i) a sequence ("Sequence A") that is fully complementary to the 1st sequence of the 1st oligonucleotide of the sequencing adapter, and (ii) the target sequence ("Sequence B"), and wherein the 1st oligonucleotide anneals to the 2nd ss oligonucleotide. Additionally or alternatively, detection of a genetic biomarker can include a plurality of sets of double-stranded (ds) sequencing adapters, wherein (A) each set comprises a plurality of single-stranded (ss) sequencing adapters, wherein each sequencing adapter in each set comprises: (a) an oligonucleotide ("1st oligonucleotide") of the plurality of ss oligonucleotides from above, and (b) a 2nd ss oligonucleotide that comprises: (i) a sequence

("Sequence A") that is fully complementary to the 1st sequence of the 1st oligonucleotide of the sequence adapter, and (ii) the target sequence ("Sequence B") located 5′ to Sequence A, and (iii) a sequence ("Sequence C") that is located 3′ to Sequence B and is fully complementary to the 3rd sequence of the 1st oligonucleotide, and wherein the 1st oligonucleotide anneals to the 2nd oligonucleotide; and (B) wherein the plurality of ds sequencing adapters in different sets are identical to each other except in the 3rd sequence of the 1st oligonucleotide and in Sequence C of the 2nd oligonucleotide. Additionally or alternatively, detection of a genetic biomarker can include a method for preparing a sequencing library that comprises (1) ligating the plurality of ds sequencing adapters that comprise a semi-random barcode sequence (i.e., the 1st sequence of the 1st oligonucleotide) to dsDNA molecules or fragments of a sample.

[628] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0275267, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method is provided for preparing a target RNA depleted composition from an initial RNA containing composition, comprising: a) contacting the initial RNA containing composition with one or more groups of probe molecules, wherein a group of probe molecules has the following characteristics: i) the group comprises two or more different probe molecules having a length of 100 nt or less; ii) the probe molecules comprised in said group are complementary to a target region present in a target RNA; iii) when hybridized to said target region, the two or more different probe molecules are located adjacent to each other in the formed double-stranded hybrid; and generating a double-stranded hybrid between the target RNA and the probe molecules; b) capturing the double-stranded hybrid by using a binding agent which binds the double-stranded hybrid, thereby forming a hybrid/binding agent complex; c) separating the hybrid/binding agent complexes from the composition, thereby providing a target RNA depleted composition. Additionally or alternatively, detection of a genetic biomarker can include specifically designed groups of probe molecules which hybridize to and thus mark unwanted target RNA, such as e.g. different rRNA species, for depletion. Each group of probe molecules targets a specific region in a target RNA, also referred to as target region, and comprises two or more different short probe molecules which hybridize to said target region. When hybridized to their target region, the

short probe molecules of one group are located adjacent to each other in the formed double-stranded hybrid and thus are located in close proximity. The formed double-stranded hybrid spans and thus covers the target region. The formed double-stranded hybrid which comprises the short probe molecules of one group is then bound by an anti-hybrid binding agent, whereby a hybrid/binding agent complex is formed. Said complexes can be easily separated from the remaining composition, thereby removing unwanted target RNA and thus providing a target RNA depleted composition. Additionally or alternatively, detection of a genetic biomarker can include a method for sequencing RNA molecules of interest comprised in a sample, comprising: a) obtaining a RNA containing composition, preferably by isolating total RNA from the sample; b) depleting unwanted target RNA from the RNA containing composition, which preferably is total RNA, using the method according to the first aspect, thereby providing a target RNA depleted composition; c) optionally removing unbound probe molecules; d) sequencing RNA molecules comprised in the target RNA depleted composition.

[629] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0225775, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for performing polymerase chain reaction (PCR), comprising: a) amplifying one or more different target nucleic acids in the presence of one or more different primer pairs specific to the one or more different target nucleic acids in a single reaction mixture via PCR, wherein each primer of the one or more different primer pairs contains one or more cleavable bases, and wherein in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 4 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 5 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 6 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or

more cleavable bases is at least 7 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 8 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. Step a) may comprise amplifying a single target nucleic acid in the presence of a primer pair specific to the single target nucleic acid in the single reaction mixture. Alternatively, step a) may comprise amplifying a plurality of different primer pairs specific to the plurality of different target nucleic acids in the single reaction mixture. In certain embodiments, in all of the primers of the one or more different primer pairs, each of one or more cleavable bases is at least 4 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in all of the primers of the one or more different primer pairs, each of one or more cleavable bases is at least 5 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in all of the primers of the one or more different primer pairs, each of one or more cleavable bases is at least 6 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in all of the primers of the one or more different primer pairs, each of one or more cleavable bases is at least 7 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in all of the primers of the one or more different primer pairs, each of one or more cleavable bases is at least 8 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. Preferably, the cleavable base is uracil. Alternatively, the cleavable base is inosine, an oxidized pyrimidine, an oxidized purine, 5-hydroxyuracil, 5-hydroxylmethyluracil, or 5-formyluracil. The one or more different primer pairs may comprise at least 100 different primer pairs. In some embodiments, the method may further comprise one or more: b) cleaving the one or more cleavable bases in the amplification product(s) of step a) to produce single-stranded DNA overhangs in the amplification product(s), c) digesting the single stranded DNA overhangs obtained in step b) to generate trimmed amplification product(s), d) ligating adapters to the trimmed amplification product(s) to produce adapter-linked trimmed amplification product(s), and e) sequencing the adapter-linked trimmed amplification product(s) of step d). Additionally

or alternatively, detection of a genetic biomarker can include a primer pair set, comprising: one or more of different primer pairs specific for one or more different target nucleic acids, wherein each primer of the one or more different primer pairs contains one or more cleavable bases, and wherein in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 4 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 5 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 6 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 7 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. In certain other embodiments, in substantially all of the primers of the one or more different primer pairs, each of the one or more cleavable bases is at least 8 nucleotides away from the 3′ terminus of the primer that comprises the one or more cleavable bases. Additionally or alternatively, detection of a genetic biomarker can include a PCR reaction mixture, comprising: the primer pair set, a DNA polymerase, dNTPs, and a PCR reaction buffer.

[630] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0197787, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method is provided for enriching target sequences from a sequencing library to provide a target enriched sequencing library, wherein the sequencing library is suitable for massive parallel sequencing and comprises a plurality of double-stranded nucleic acid molecules, wherein the method comprises: a) providing nucleoprotein filaments comprising (i) a single stranded invasion probe, wherein the invasion probe has a region of substantial complementarity to one strand of a double-stranded target sequence, (ii) a recombinase; b) forming a complex between the invasion probe and a complementary portion of the target sequence wherein complex formation is mediated by the

recombinase; c) separating the complexes from the remaining sequencing library, thereby enriching the target sequences. Additionally or alternatively, detection of a genetic biomarker can include a method is provided for sequencing a target region of interest, comprising: a) providing a sequencing library suitable for massive parallel sequencing and comprising a plurality of double stranded nucleic acid molecules, wherein a portion of the double stranded nucleic acid molecules comprised in the sequencing library, the target sequences, comprise a sequence which lies in the target region of interest; b) enriching target sequences corresponding to the target region of interest according to the method above, thereby providing a target enriched sequencing library; c) sequencing the enriched target sequences in parallel. Additionally or alternatively, detection of a genetic biomarker can include use of the method for sequencing for exome sequencing, exon sequencing, targeted genomic resequencing, gene panel orientated targeted genomic resequencing, transcriptome sequencing and/or molecular diagnostics. Additionally or alternatively, detection of a genetic biomarker can include a kit for performing a method according to first aspect, which comprises a) adaptors for creating a sequencing library suitable for massive parallel sequencing; b) optionally one or more ligation reagents for coupling the adaptors to a nucleic acid fragment; c) a recombinase, preferably a RecA like recombinase; d) a non-hydrolyzable co-factor for the recombinase, preferably adenosine 5′-(gamma-thio)triphosphate; e) a plurality of different invasion probes wherein the invasion probes differ in their region of complementarity to a target region of interest; f) a plurality of different stabilization probes being at least partially complementary to the plurality of invasion probes; and g) a solid support suitable for capturing synaptic complexes formed between the invasion probes and target sequences.

[631] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0093756, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of amplifying a target nucleic acid in a helicase-dependent reaction. Additionally or alternatively, detection of a genetic biomarker can include methods of amplifying and detecting a target nucleic acid in a helicase-dependent reaction as well as modified detection labels to assist in the detection. In some embodiments, the method for amplifying a target nucleic acid in a helicase-dependent reaction,

the method comprises: (a) providing target nucleic acid to be amplified; wherein the target nucleic acid is double stranded and is denatured by heating at 65° C. for 10 minutes in the presence of 50 mM NaOH prior to step (b); (b) adding oligonucleotide primers for hybridizing to the target nucleic acid of step (a); (c) synthesizing an extension product of the oligonucleotide primers which are complementary to the templates, by means of a DNA polymerase to form a duplex; (d) contacting the duplex of step (c) with a helicase preparation for unwinding the duplex such that the helicase preparation comprises a helicase and a single strand binding protein (SSB) unless the helicase preparation comprises a thermostable helicase wherein the single strand binding protein is optional; and (e) repeating steps (b) (d) to exponentially and selectively amplify the target nucleic acid in a helicase-dependent reaction. Additionally or alternatively, detection of a genetic biomarker can include a method amplifying a target nucleic acid in a helicase-dependent reaction where the target nucleic acid is subjected to a "pre" step involving RNA probes and RNA-DNA hybrid capture antibodies. This method comprises: (a) providing target nucleic acid to be amplified; wherein the target nucleic acid is single stranded DNA and wherein an RNA probes that is complementary is added to the single stranded DNA to bind to the DNA to form a target nucleic acid RNA-DNA hybrid; and wherein a hybrid capture antibodies that recognizes RNA-DNA hybrids bound to a magnetic bead is added to the RNA-DNA hybrid to be used in step (b) (b) adding oligonucleotide primers for hybridizing to the target nucleic acid RNA-DNA hybrid of step (a); (c) synthesizing an extension product of the oligonucleotide primers which are complementary to the templates, by means of a DNA polymerase to form a duplex; (d) contacting the duplex of step (c) with a helicase preparation for unwinding the duplex such that the helicase preparation comprises a helicase and a single strand binding protein (SSB) unless the helicase preparation comprises a thermostable helicase wherein the single strand binding protein is optional; and (e) repeating steps (b)-(d) to exponentially and selectively amplify the target nucleic acid in a helicase-dependent reaction. Additionally or alternatively, detection of a genetic biomarker can include a modified TaqMan probe (and method using this probe). The probe has a short tail at the 3′- or 5′-end complementary to the 5′- or 3′-end, and wherein the TaqMan probe is complementary to the target nucleic acid except for this short tail, and wherein the short tail sequence forms a stem loop structure.

[632] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0011416, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for determining the presence of one or more target polynucleotides, the method comprising; performing a PCR amplification regimen comprising cycles of strand separation, primer annealing, and primer extension on a reaction mixture comprising a nucleic acid sample and a set of oligonucleotide primers specific for each target polynucleotide; wherein each set of oligonucleotide primers comprises a first subset of at least one truncated dual domain forward primer and a second subset of at least one reverse primer; wherein each truncated dual domain primer of a set comprises a 5′ tail region that differs from the 5′ tail region on other truncated dual domain primers in the set and a 3′ core region complementary to a sequence on one strand of a double-stranded nucleic acid comprising the target; wherein for each truncated dual domain primer, the 3′ core substantially anneals to its complementary target site sequence at a first annealing temperature, and the sequence comprised by the 5′ tail and 3′ core region substantially anneals to its complement at a second annealing temperature, the second annealing temperature being higher than the first annealing temperature, such that at the second annealing temperature the 3′ core of the truncated dual domain primer cannot substantially anneal to a template molecule that does not also have the complement of the truncated dual domain primer's 5′ tail sequence; wherein for each truncated dual domain primer of a primer set: the 5′ tail sequence does not have any homology to the target sequence; and the 5′ tail sequence has 6 or fewer contiguous homologous bases relative to any other 5′ tail sequence of the truncated dual domain primer set; wherein the PCR amplification regimen comprises first and second phases, the first phase comprising annealing at the first annealing temperature for a first set of cycles, and; the second phase comprising annealing at the second annealing temperature for a second set of cycles; and detecting an amplified product for each target polynucleotide, wherein the detecting indicates the presence of the target polynucleotide. In some embodiments, a reverse primer comprises a dual domain primer. In some embodiments, a reverse primer comprises a truncated dual domain primer. In some embodiments, a reverse primer comprises an amplifying primer. In some embodiments, the set of primers comprises at least one dual domain forward primer;

wherein each dual domain primer of a set comprises a 5′ tail region that differs from the 5′ tail region of other dual domain primers in the set, a 3′ core region complementary to a sequence on one strand of a double-stranded nucleic acid comprising said target, and a terminal nucleotide complementary to one of the variant nucleotides occurring at said target site; wherein for each dual domain primer, the 3′ core substantially anneals to its complementary target site sequence at a first annealing temperature, and the sequence comprised by the 5′ tail and 3′ core region substantially anneals to its complement at a second annealing temperature, the second annealing temperature being higher than the first annealing temperature, such that at said second annealing temperature said 3′ core of said dual domain primer cannot substantially anneal to a template molecule that does not also have the complement of the dual domain primer's 5′ tail sequence; and wherein for each truncated dual domain primer of a primer set: the 5′ tail sequence does not have any homology to the target sequence; and the 5′ tail sequence has 6 or fewer contiguous homologous bases relative to any other 5′ tail sequence of the dual domain or truncated dual domain primer set. Additionally or alternatively, detection of a genetic biomarker can include a composition for determining the presence of one or more target polynucleotides, comprising; at least one set of oligonucleotide primers specific for each target polynucleotide; wherein each set of oligonucleotide primers comprises a first subset of at least one truncated dual domain forward primer and a second subset of at least one reverse primer; wherein each truncated dual domain primer of a set comprises a 5′ tail region that differs from the 5′ tail region on other truncated dual domain primers in the set and a 3′ core region complementary to a sequence on one strand of a double-stranded nucleic acid comprising the target; wherein for each truncated dual domain primer, the 3′ core substantially anneals to its complementary target site sequence at a first annealing temperature, and the sequence comprised by the 5′ tail and 3′core region substantially anneals to its complement at a second annealing temperature, the second annealing temperature being higher than the first annealing temperature, such that at the second annealing temperature the 3′ core of the truncated dual domain primer cannot substantially anneal to a template molecule that does not also have the complement of the primer's 5′ tail sequence; wherein for each member of the truncated dual domain primer set: the 5′ tail sequence does not have any homology to the target sequence; and the 5′ tail sequence has 6 or fewer contiguous homologous bases relative to the

other 5′ tail sequences of the truncated dual domain primer set. In some embodiments, the composition can further comprise a nucleic acid sample. Additionally or alternatively, detection of a genetic biomarker can a method for determining the presence of one or more target polynucleotides, the method comprising; performing a PCR amplification regimen comprising cycles of strand separation, primer annealing, and primer extension on a reaction mixture comprising a nucleic acid sample and a set of oligonucleotide primers specific for each target polynucleotide; wherein each set of oligonucleotide primers comprises a first subset of at least one truncated dual domain forward primer and a second subset of at least one reverse primer; wherein each truncated dual domain primer of a set comprises a 5′ tail region that differs from the 5′ tail region on other truncated dual domain primers in the set and a 3′ core region complementary to a sequence on one strand of a double-stranded nucleic acid comprising the target; wherein for each truncated dual domain primer, the 3′ core substantially anneals to its complementary target site sequence at a first annealing temperature, and the sequence comprised by the 5′ tail and 3′ core region substantially anneals to its complement at a second annealing temperature, the second annealing temperature being higher than the first annealing temperature, such that at the second annealing temperature the 3′ core of the truncated dual domain primer cannot substantially anneal to a template molecule that does not also have the complement of the truncated dual domain primer's 5′ tail sequence; wherein for each truncated dual domain primer of a primer set: the 5′ tail sequence does not have any homology to the target sequence; and the 5′ tail sequence has 6 or fewer contiguous homologous bases relative to any other 5′ tail sequence of the truncated dual domain primer set; wherein the PCR amplification regimen comprises first and second phases, the first phase comprising annealing at the first annealing temperature for a first set of cycles, and; the second phase comprising annealing at the second annealing temperature for a second set of cycles; and detecting an amplified product for each target polynucleotide, wherein the detecting indicates the presence of the target polynucleotide. Additionally or alternatively, detection of a genetic biomarker can include a composition for determining the presence of one or more target polynucleotides, comprising; at least one set of oligonucleotide primers specific for each target polynucleotide; wherein each set of oligonucleotide primers comprises a first subset of at least one truncated dual domain forward primer and a second subset of at least one reverse

primer; wherein each truncated dual domain primer of a set comprises a 5′ tail region that differs from the 5′ tail region on other truncated dual domain primers in the set and a 3′ core region complementary to a sequence on one strand of a double-stranded nucleic acid comprising the target; wherein for each truncated dual domain primer, the 3′ core substantially anneals to its complementary target site sequence at a first annealing temperature, and the sequence comprised by the 5′ tail and 3′ core region substantially anneals to its complement at a second annealing temperature, the second annealing temperature being higher than the first annealing temperature, such that at the second annealing temperature the 3′ core of the truncated dual domain primer cannot substantially anneal to a template molecule that does not also have the complement of the primer's 5′ tail sequence; wherein for each member of the truncated dual domain primer set: the 5′ tail sequence does not have any homology to the target sequence; and the 5′ tail sequence has 6 or fewer contiguous homologous bases relative to the other 5′ tail sequences of the truncated dual domain primer set.

[633] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2010/0113758, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a process for the purification of biomolecules from a sample which comprises the following steps: a) arrangement of a reaction vessel with a binding matrix in a centrifuge, wherein a solution or suspension of a sample containing biomolecules is prepared in the reaction vessel or introduced into the reaction vessel before or after this step; and b) inclusion of at least one multi-stage centrifugation step comprising at least a first centrifugation step at a first acceleration value and at least a second centrifugation step at a second acceleration value which is higher than the first acceleration value; wherein c) step b) can be a binding step, a washing step and/or an elution step. Preferably, the multi-stage step b) is a binding step in which the biomolecules are bound to the binding matrix by centrifugation. Particularly preferably, it is envisaged that the biomolecules are substances chosen from the group containing nucleic acids, amino acids, oligopeptides, polypeptides, monosaccharides, oligosaccharides, polysaccharides, fats, fatty acids and/or lipids. In some embodiments, the binding matrix comprises a silicate substrate, and that furthermore the sample containing biomolecules is mixed with at least one chaotropic salt

before the centrifugation. The embodiment is suitable in particular for nucleic acids. Preferably, the following steps are envisaged in this embodiment: a) arrangement of a column-like reaction vessel with a binding matrix comprising a silicate substrate in a centrifuge, wherein a solution or suspension of a nucleic acid-containing sample and at least one chaotropic salt is prepared in the reaction vessel or introduced into the reaction vessel before or after this step; b) inclusion of a first centrifugation step at a first acceleration value; c) inclusion of a second centrifugation step at a second acceleration value which is higher than the first acceleration value; d) optionally inclusion of further centrifugation steps between step c) and step d) or after step d); e) optionally inclusion of one or more washing steps; and f) elution of the nucleic acids bound to the silicate substrate with an elution solution. In this embodiment, the multi-step centrifugation step is a binding step in which the nucleic acids are bound to the silicate matrix.

[634] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2009/0298187, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for determining the presence of a target nucleic acid in a sample. The method comprises: a) contacting one or more polynucleotide probes with the sample under a hybridization condition sufficient for the one or more polynucleotide probes to hybridize to the target nucleic acid in the sample to form double-stranded nucleic acid hybrids, wherein the one or more polynucleotide probes does not hybridize to a variant of the target nucleic acid; and b) detecting the double-stranded nucleic acid hybrids, wherein detecting comprises contacting the double-stranded nucleic acid hybrids with a first anti-hybrid antibody that is immunospecific to double-stranded nucleic acid hybrids, whereby detection of the double-stranded nucleic acid hybrids determines the target nucleic acid in the sample. In some embodiments, the hybridization of the nucleic acids and detection of the double-stranded nucleic acid hybrids are performed at the same time. In some embodiments, after the double-stranded nucleic acid hybrids are contacted with a first anti-hybrid antibody that is immunospecific to double-stranded nucleic acid hybrids, a second anti-hybrid antibody is added to detect the double-stranded nucleic acid hybrids whereby detection

of the double-stranded nucleic acid hybrids by these second anti-hybrid antibodies determines the presence of target nucleic acid in the sample.

[635] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,686,157, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method and compositions for the sensitive detection of the amount and location of specific nucleic acid sequences. In some embodiments, the method makes use of a branched oligomer, referred to as a lollipop oligomer, that has a tail portion, a right arm portion, and a left arm portion. These three components are joined at a common junction making a three-tailed structure. The two arms each end with sequences complementary to adjacent sequences in a target sequence. This allows the right and left arms to be ligated together when the oligomer is hybridized to the target sequence, thus topologically linking the oligomer to the target sequence. The tail portion can then be detected at the location of the target sequence. By using the tail of the oligomer to prime rolling circle replication of a DNA circle, a long tandem repeat DNA is associated with the target sequence. Rolling circle replication does not disturb association of the arms and the target sequence, thus maintaining close association of the tandem repeat DNA and the target sequence. Additionally or alternatively, detection of a genetic biomarker can include a method of amplifying nucleic acid sequences, the method comprising: (a) mixing one or more different lollipop oligomers with one or more target samples each comprising one or more target sequences, and incubating under conditions that promote hybridization between the oligomers and the target sequences, wherein the lollipop oligomers each comprise a branched oligomer comprising a tail portion, wherein the tail portion comprises a rolling circle replication primer, wherein the rolling circle replication primer comprises a complementary portion that is complementary to a primer complement portion of an amplification target circle, (b) prior to, simultaneous with, or following step (a), mixing one or more amplification target circles with the oligomers, and incubating under conditions that promote hybridization between the amplification target circles and the rolling circle replication primer portions of the oligomers, and (c) mixing DNA polymerase with the oligomers and amplification target circles, and incubating under

conditions that promote replication of the amplification target circles, wherein replication of the amplification target circles results in the formation of tandem sequence DNA.

[636] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,090,935, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for isolating nucleic acid from a sample, said method comprising boiling said sample, cooling the boiled sample, allowing the nucleic acid in the liquid phase of the cooled sample to directly bind to a solid support comprising magnetic particles, and separating the solid support with the nucleic acid bound thereto from the remainder of said liquid phase. Additionally or alternatively, detection of a genetic biomarker can include a method for isolating nucleic acid from a sample that is fixed or aged, said method comprising boiling the fixed or aged sample, cooling the boiled sample allowing the nucleic acid in the cooled sample to directly bind to a solid support having a high surface area comprising magnetic particles, and separating the solid support with the nucleic acid bound thereto from the remainder of the cooled sample.

[637] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/032808, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of RNA sequencing, whereby said method comprises: (i) providing RNA; (ii) generating (a) single-stranded first DNA strand(s) (cDNA), which is/are complementary to the RNA, by subjecting the RNA to reverse transcription by using a reverse transcriptase, a first set of oligonucleotide primers, and the RNA of step (i), and (iii) generating a second DNA strand by using a DNA polymerase, a second set of oligonucleotide primers, and the single-stranded cDNA of (ii), wherein a) the first set of oligonucleotide primers comprises a covalently coupled moiety at its/their 5' terminal nucleotide, which blocks ligation at the 5' terminus of the generated first DNA strand; or b) the second set of oligonucleotide primers comprises a covalently coupled moiety at its/their 5' terminal nucleotide, which blocks ligation at the 5' terminus of the generated second DNA strand. In some embodiments, the method further comprises the subsequent steps of: (iv) optionally end-repairing the double-stranded DNA strands using a polynucleotide kinase and

an enzyme with polymerase and exonuclease activities to obtain end- repaired DNA strands; (v) optionally adding a terminal adenine to the 3' termini of the DNA strands using a deoxynucleotidyl transferase enzyme; and (vi) ligation of adapters, which optionally comprise terminal thymines, to the DNA strands, which optionally comprise 3' terminal adenines. Said methods may further comprise sequence analysis of the generated DNA. In some embodiments, said method comprises: (i) providing RNA; (ii) generating (a) single-stranded first DNA strand(s) (cDNA), which is/are complementary to the RNA, by subjecting the RNA to reverse transcription by using a reverse transcriptase, a first set of oligonucleotide primers, and the RNA of step (i); (iii) generating a second DNA strand by using a DNA polymerase, a second set of oligonucleotide primers, and the single-stranded cDNA of (ii); (iv) ligating adapters to the double-stranded DNA; of step (iii) and (v) sequencing the generated DNA, wherein a) the first set of oligonucleotide primers comprises a covalently coupled moiety at its/their 5' terminal nucleotide, which blocks ligation at the 5' terminus of the generated first DNA strand; or b) the second set of oligonucleotide primers comprises a covalently coupled moiety at its/their 5' terminal nucleotide, which blocks ligation at the 5' terminus of the generated second DNA strand. By generating the second DNA strand, a double-stranded DNA is generated. In some embodiments of the above-mentioned method, prior to step (iv), the method comprises the step of: (iii)(a) end-repairing the double-stranded DNA strands using a polynucleotide kinase and an enzyme with polymerase and exonuclease activities to obtain end-repaired DNA strands. In some embodiments, step (iii)(a) is followed by step (iii)(b) comprising adding a terminal adenine to the 3' termini of the DNA strands by using a deoxynucleotidyl transferase enzyme, wherein the adapters comprise 3' terminal thymines, which in step (iv) ligate to the DNA strands comprising 3' terminal adenines. In some embodiments, the oligonucleotide primers, which are covalently coupled to a blocking moiety and/or unmodified oligonucleotide primers, are random oligonucleotide primers. In some embodiments, said methods comprise the initial step of extracting and optionally enriching the RNA of interest. In some embodiments, the extracted RNA is fragmented to an average size of 19-510 bp. In some embodiments of the above methods, the molecules may be attached to a solid support for paired-end sequencing. In some embodiments a "moiety, which blocks ligation", or a "blocking moiety" refers to a specific part of a larger molecule, which is more

than one atom, herein the part of a modified oligonucleotide, which is covalently coupled to the 5' nucleotide of a modified primer oligonucleotide. Said moiety preferably blocks any ligation at the site, where the moiety is located, preferably at the 5' terminal nucleotide of the 5' terminus of an oligonucleotide. In some embodiments of the above methods, the oligonucleotide primer comprising a blocking moiety is characterized in that (i) the oligonucleotide comprises at the 5' terminal nucleotide a 5' phosphate that is not free, wherein optionally a 5' OH group or a 5' phosphate group at the 5' terminal nucleotide is covalently coupled to the moiety, which blocks ligation; (ii) the base of the 5' terminal nucleotide is not any one of thymine, adenine, cytosine, guanine and uracil; (iii) one or both 2' hydrogen(s) of the deoxyribose of the 5' terminal nucleotide is/are replaced by another atom or a blocking moiety; and/or (iv) the oligonucleotide comprises a 5' terminal nucleotide having a pentose in a sterical conformation, which is not the sterical conformation of ribose or deoxyribose in RNA or DNA. In some embodiments of the above methods, the oligonucleotide primers comprising a covalently coupled moiety, which blocks ligation, comprise a 5' OH or a free 5' phosphate group at the 5' terminal nucleotide before being covalently coupled to a moiety, which confers the property of ligation-blocking.

[638] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2016/193490, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a poly(alkylene oxide) polymer based size selective DNA isolation method for isolating DNA molecules having a size above a certain cut-off value from a DNA containing sample is provided, comprising (a) preparing a binding mixture comprising the DNA containing sample, at least one poly(alkylene oxide) polymer and at least one divalent cation, wherein said binding mixture has a pH that lies in the range of 8 to 10 and binding precipitated DNA molecules to a solid phase having an unmodified silicon containing surface, thereby providing a solid phase having bound thereto DNA molecules having a size above the cut-off value, wherein under the used binding conditions DNA molecules having a size which is less than the cut-off value substantially do not bind to the solid phase; (b) separating the bound DNA molecules from the remaining sample; optionally washing the bound DNA molecules; and optionally eluting the bound DNA molecules from the solid phase. In some

embodiments, DNA molecules having a size above the desired cut-off value efficiently bind to the solid phase with high yield while DNA molecules having a size below said cut-off value are predominantly not bound and thus are not recovered in step (a). The cut-off value can be adjusted by modifying the concentration of the poly(alkylene oxide) polymer in the binding mixture as it is known from the prior art and also demonstrated by the examples. The presence of the divalent cation and the alkaline pH value as specified ensures efficient binding of the DNA molecules having a size above the cut-off value, even though a solid phase having an unmodified silicon containing surface is used. The method is particularly suitable for isolating adapter ligated DNA molecules as target DNA molecules from an adapter ligation sample and for removing adapter monomers and adapter-adapter ligation products.

[639] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,811,759, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for creating a signature ncRNA profile for a disease state or condition, said method comprising: a. determining a first ncRNA profile from a first source, said first source being characterized as being free from said disease state or condition; b. determining a second ncRNA profile from a second source, said second source characterized as being positive for said disease state or condition, said first and second ncRNA profile being obtained according to a method for determining a profile of a plurality of target ncRNA molecules in a RNA sample, said method comprising the steps of: i. providing said RNA sample from a subject, said sample containing said plurality of target ncRNAs; ii. contacting said sample with a first oligonucleotide specific for each of said target ncRNAs to be detected under conditions appropriate to faun a complex between said first oligonucleotides and said target ncRNAs, each of said first oligonucleotides comprising a first signal generator to generate a first detectable signal and each of said first oligonucleotides having a first Tm for binding each of said target ncRNAs that is substantially the same; iii. contacting said sample with a second oligonucleotide capable of binding each of said target ncRNAs to be detected under conditions appropriate to form a complex between said second oligonucleotides and said target ncRNAs, said second oligonucleotide comprising a second signal generator to generate a second detectable signal and each of said second oligonucleotides having a second Tm for

binding each of said target ncRNAs that is substantially the same; iv. determining the presence of said plurality of target ncRNA in said sample by measuring the first and second detectable signals; and v. generating a profile of the sample based on the target ncRNAs detected c. comparing said first and second ncRNA profiles and identifying those ncRNA molecules that are altered in said second ncRNA profile to create a signature ncRNA profile for said disease state or condition.

[640] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2005/0244847, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for amplifying a circular nucleic acid template, comprising contacting the template with a reaction mixture comprising a thermostable polymerase, individual nucleotides and forward and reverse primers complementary to a common region within the template, wherein the common region is preferably from about 80 to 150 base pairs in length. In one embodiment, the 5' ends of the primers hybridize to opposite strands of the template about 10 to 50 base pairs apart, still more preferably from zero to twenty-five base pairs apart. In some embodiments, the 5' end of the forward primer will generally be proximal to the 5' end of the reverse primer and distal to the 3' end of the reverse primer when the primers are hybridized to the template. In a particularly preferred embodiment, the common region is a conserved region, e.g., an origin of replication, within an extrachromosomal nucleic acid. The reaction mixture may further include a reaction buffer comprising a weak organic base and a weak organic acid. Additionally or alternatively, detection of a genetic biomarker can include reagents for performing in vitro amplification of extrachromosomal DNA, including solutions supporting amplification and subsequent ligation reactions and solutions supporting a combined amplification and ligation reaction, i.e., which provide the appropriate environment for simultaneous polymerase and ligase enzyme activity.

[641] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/137826, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for enriching template nucleic acids and to methods for generating a sequencing library. In some embodiments, the method for enriching

template nucleic acids or for generating a sequencing library comprises: a) hybridizing template nucleic acids to oligonucleotides bound to a solid surface and initially comprising at least two functional sequence elements; b) extending the surface bound oligonucleotides hybridized to the template nucleic acids to form a double strand; c) optionally modifying the double-stranded nucleic acids generated in step b); d) 3' truncation of the surface bound oligonucleotides that have not been used in the template nucleic acid hybridization of step a); and e) optionally modifying the single-stranded surface bound oligonucleotides generated in step d). In some embodiments, the further comprises the additional step of: f) hybridizing further template nucleic acids to the surface bound oligonucleotides or using functional sequence elements within surface bound oligonucleotides for a downstream application. In some embodiments, the downstream application is nucleic acid amplification on the solid surface, de-coupling from solid surface, in-vitro transcription by the use of an RNA polymerase promotor within the oligonucleotide, labeling of immobilized nucleic acid by the use of a primer binding site or a molecular barcode region for identification within the oligonucleotide, sequencing, or a combination thereof. In some embodiments, at least one of the functional sequence elements is a hybridization site or preferably a sequence useful for a downstream application. In another embodiment, the functional sequence elements are consecutive or overlapping. In certain embodiments, the functional sequence elements are separated by predefined cleavage sites or generated by hybridization of protecting oligonucleotides to the surface bound oligonucleotides. In some embodiments, steps a) to c) are repeated at least once with template nucleic acids from different samples. In other embodiments, steps a) to e) are repeated at least once with template nucleic acids from the same sample or from different samples, optionally wherein the repetition(s) is (are) performed in parallel. In some embodiments, the density of the surface bound oligonucleotides is between 500 - 500000 oligonucleotides / μη2, more preferably 750 - 200000 oligonucleotides / μη2, most preferably 1000 - 100000 oligonucleotides / μηη2. In other embodiments, the surface bound oligonucleotides comprise 2 to 20 functional sequence elements, more preferably 2 to 10, most preferably 2 to 5. In certain embodiments, the length of the surface bound oligonucleotides is within the range of 4-200 nt, preferably 10-200 nt, more preferably 6-180 nt, more preferably 8-160 nt, more preferably 10-140 nt, most preferably 20-100 nt. In some embodiments, the

length of the surface bound oligonucleotides is 10 nt, preferably 20 nt. In some embodiments, all functional sequence elements of the same position within a surface bound oligonucleotide have a unique sequence or comprise 2-100000, preferably 2-50000, more preferably 2-25000, more preferably 2-10000, more preferably 2-5000, more preferably 2-2500, most preferably 2-1000 different sequences. In certain embodiments, the 3' truncation is achieved enzymatically or chemically. In some embodiments, the double-stranded nucleic acids bound to the surface are modified by introducing barcode sequences, adding sequencing adaptors, adding a fluorophore at the terminus, incorporation of modified bases, or other modifications. In other embodiments, the single-stranded oligonucleotides bound to the surface are modified by adding biotin, labeling moieties, blocking moieties, or other modifications.

[642] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/013598, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, adapters and kits for performing single end duplex DNA sequencing. In some embodiments, the method for performing DNA sequencing, comprises: (a) performing a ligation reaction in the presence of a plurality of double-stranded target nucleic acids and a first set of substantially complementary double-stranded adapters to generate ligation products, wherein each adapter of the first set comprises a first strand and a second strand, the first strand comprises, from 5' to 3', a 5' region that is 10 or more nucleotides in length, a molecular tag sequence, and an optional 3' region, the second strand comprises, from 3' to 5', a 3' region that comprises a sequence fully complementary to a 10-nucleotide or longer portion of the 5' region of the first strand, a fully complementary sequence of the molecular tag sequence of the first strand, and an optional 5' region, at least one mismatch between the first and second strands is located in the 3' region of the first strand if the 3' region is present, and/or in the 5' region that is 3' to the 10-nucleotide or longer portion of the 5' region of the first strand, and different adapters of the first set comprise different molecular tag sequences in their first strands and corresponding fully complementary sequences of the different molecular tag sequences in their second strands, but are otherwise identical to each other, (b) performing an amplification reaction using the ligation products of step (a) as templates to generate amplification products, wherein the amplification products comprise one

or more locations that do not form complementary base pairs in the first and second strands of the substantially complementary double-stranded adapters, and (c) performing sequencing reactions using amplification products of step (b) or their further amplification products as templates to obtain sequence reads that comprise the one or more locations where a complementary base pair is not formed in the first and second strands of the double-stranded adapters. Additionally or alternatively, detection of a genetic biomarker can include a set of substantially complementary double-stranded adapters, comprising at least 16 different adapters, wherein each adapter of the set comprises a first strand and a second strand, the first strand comprises, from 5' to 3', a 5' region, a molecular tag sequence, and an optional 3' region, the second strand comprises, from 3' to 5', a 3' region that comprises a sequence fully complementary to a 10-nucleotide or longer portion of the 5' region of the first strand, a fully complementary sequence of the molecular tag sequence of the first strand, and an optional 5' region, at least one mismatch between the first and second strands is located in the 3' region of the first strand if the 3' region is present, and/or in the 5' region that is 3' to the 10-nucleotide or longer portion of the 5' region of the first strand, and different adapters comprise different molecular tag sequences in their first strands and corresponding fully complementary sequences of the different molecular tag sequences in their second strands, but are otherwise identical to each other. Additionally or alternatively, detection of a genetic biomarker can include a kit, comprising: (1) a set of substantially complementary double-stranded adapters, and (2) a ligase.

[643] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/165289, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include primers, primer sets, kits and methods for multiple displacement amplification (MDA). In some embodiments, the method for amplifying nucleic acids by multiple displacement amplification, comprises: performing one or more separate multiple displacement amplification reactions, wherein each reaction is performed in the presence of: (1) a primer set, wherein each primer of the primer set comprises a self-complementary sequence at its 5' terminus and a random sequence or a semi-random sequence at its 3' terminus, and wherein the self- complementary sequences in each primer set

are the same, but different from the self-complementary sequences in another primer set, (2) a DNA polymerase having a strand displacement activity, and (3) target nucleic acids. In certain embodiments, the self-complementary sequences in one or more primer sets are each 6 to 20 nucleotides in length. In certain embodiments, the random sequences or the semi- random sequences in one or more primer sets are 4 to 20 nucleotides in length. Preferably, the primers are resistant to 3'- 5' exonuclease proofreading activity. In certain embodiments, the DNA polymerase having a strand displacement activity is Phi29 polymerase. In certain embodiments, at least 2 separate multiple displacement amplification reactions are performed. In certain embodiments, the target nucleic acids used in one or more separate multiple displacement amplification reactions are genomic DNA from one or more different single cells, such as human cells. In certain embodiments, the multiple displacement amplification is performed at a temperature from about 20°C to about 40°C, such as cycling between two temperatures within the above-noted range or under an isothermal condition. In certain embodiments where a plurality of separate multiple displacement amplification reactions are performed, the method further comprises: pooling the nucleic acids amplified from the plurality of multiple displacement amplification reactions together, generating a sequencing library using the pooled amplified nucleic acids, and sequencing the pooled amplified nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include a primer set, wherein each primer in the primer set comprises a self-complementary sequence at its 5' terminus and a random sequence or a semi-random sequence at its 3' terminus, and wherein the self-complementary sequences of the primers are identical to each other. Additionally or alternatively, detection of a genetic biomarker can include a plurality of primer sets, wherein each primer comprises a self-complementary sequence at its 5' terminus and a random sequence or a semi-random sequence at its 3' terminus, wherein the self-complementary sequences of primers in each primer set are the same, but different from the self-complementary sequences of primers in another primer set. In certain embodiments, the plurality of primer sets comprises at least 3 different primer sets.

[644] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/085321, which is hereby incorporated by reference in its entirety. For example, detection

of a genetic biomarker can include a method for producing a sterilized composition suitable for stabilizing an extracellular nucleic acid population of a biological sample, the method comprising: a) providing a composition comprising: i. at least one caspase inhibitor, and ii. at least one compound selected from a thioalcohol (preferably N-acetyl- cysteine or glutathione), a water-soluble vitamin, and vitamin E or a derivative thereof; and b) irradiating the composition for sterilization. Additionally or alternatively, detection of a genetic biomarker can include a method for stabilizing an extracellular nucleic acid population comprised in a cell-containing biological sample comprising: a) obtaining i) a sterilized composition suitable for stabilizing an extracellular nucleic acid population of a biological sample, or ii) a composition above in sterilized form; and b) contacting the cell-containing biological sample with the sterilized composition for stabilization. Additionally or alternatively, detection of a genetic biomarker can include a method for isolating extracellular nucleic acids from a stabilized cell-containing biological sample comprising: a) stabilizing the cell-containing biological sample according to the method; and b) isolating extracellular nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include a method for processing and/or analyzing extracellular nucleic acids comprising: a) isolating extracellular nucleic acids from a stabilized cell-containing biological sample according to the method; and b) processing and/or analyzing the isolated extracellular nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include a method for producing a sterilizable composition, wherein the composition in sterilized form is suitable for stabilizing an extracellular nucleic acid population of a biological sample, the method comprising: a) preparing a composition comprising: i. at least one caspase inhibitor, and ii. at least one compound selected from a thioalcohol (preferably N-acetyl- cysteine or glutathione), a water-soluble vitamin, and vitamin E or a derivative thereof, and optionally b) sterilizing the composition. Additionally or alternatively, detection of a genetic biomarker can include a sterilizable composition, wherein the composition in sterilized form is suitable for stabilizing an extracellular nucleic acid population of a biological sample, wherein the composition is a composition as provided in step a) of the method. It comprises i. at least one caspase inhibitor, and ii. at least one compound selected from a thioalcohol (preferably N-acetyl-cysteine or glutathione), a water-soluble vitamin, and vitamin E or a derivative thereof. The sterilizable

composition according to the sixth aspect, which can be a composition as provided in step a) of the method, in embodiments can be sterilized to provide a sterilized composition. Additionally or alternatively, detection of a genetic biomarker can include a sample collection device such as a container, preferably a sample collection tube, comprising the sterilizable composition above. Additionally or alternatively, detection of a genetic biomarker can include the use of at least one compound selected from the group consisting of a thioalcohol (preferably N-acetyl-cysteine or glutathione), a water-soluble vitamin, and vitamin E or a derivative thereof, for protecting a composition suitable for stabilizing an extracellular nucleic acid population of a biological sample or components thereof during sterilization by irradiation.

[645] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2016/170147, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of generating dsDNA, wherein the method comprises ligating a first and a second dsDNA, both optionally having one or two single-stranded end(s), in the presence of a DNA ligase and an agent, which modulates the melting temperature of dsDNA. Additionally or alternatively, detection of a genetic biomarker can include a method for ligating a first and a second dsDNA, wherein both the first and the second dsDNAs comprise two ssDNA regions, whereby each of the ssDNA region ends of the first dsDNA ligates with each of the complementary ss region ends of the second dsDNA to provide ligated circular dsDNA in the presence of a an agent, which modifies the melting temperature of dsDNA. In some embodiments, the first or the second DNA is capable of conferring the ability to auto-replicate within competent cells. Additionally or alternatively, detection of a genetic biomarker can include a method for generation of a sequencing library, wherein the method comprises the steps of: (i) providing DNA fragments; (ii) end-repairing the DNA fragments by a polynucleotide kinase enzyme and an enzyme with polymerase and exonuclease activities to obtain blunt-ended, 5' phosphorylated DNA fragments; (iii) optionally adding a terminal adenine to the end of the end-repaired DNA fragments by a deoxynucleotidyl transferase enzyme; and (iv) ligating the DNA fragments, optionally having the terminal adenine, with sequencing adapters wherein preferably the adapters have a terminal thymidine if the fragments have a terminal adenine. In some embodiments, said method further

comprises step (v), wherein the ligated fragments of step (iv) are purified and size-selected for sequencing. In some embodiments, said method further comprises step (vi), wherein the adapter- ligated fragments are amplified and the amplification product is optionally purified prior to sequencing. In another embodiment, the fragments of step (v) or (vi) are subjected to sequencing. Additionally or alternatively, detection of a genetic biomarker can include a kit comprising: (i) a DNA ligase; and (ii) an agent, which modulates the melting temperature of dsDNA. In another embodiment, the agent which modulates the melting temperature of dsDNA is selected from any one of tetramethylammonium chloride (TMAC), piperazinium chloride, tetramethylpiperazinium chloride, tetraethylammonium chloride (TEAC), trimethylamine N-oxide (TMANO), 2-methyl-4-carboxy-5-hydroxy-3,4,5,6-tetrahydropyrimidine THP(A), 2-methyl-4-carboxy-3,4,5,6-tetrahydropyrimidine THP(B), non-ionic detergents, such as NP-40, and Triton®X-100, and mixtures thereof. In a preferred embodiment, the agent which modulates the melting temperature of dsDNA is selected from any one of tetramethylammonium chloride (TMAC), piperazinium chloride, tetramethylpiperazinium chloride, tetraethylammonium chloride (TEAC), trimethylamine N-oxide (TMANO), 2-methyl-4-carboxy-5-hydroxy-3, 4,5,6- tetrahydropyrimidine THP(A), 2-methyl-4-carboxy-3,4,5,6-tetrahydropyrimidine THP(B), and mixtures thereof. In some embodiments, the agent which modulates the melting temperature of dsDNA is in a ligation buffer. In some embodiments, the ligase and the agent which modulates the melting temperature of dsDNA are in separate containers.

[646] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2016/135300, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and kits for specific inhibition of enzymes involved in the DNA preparation for NGS library construction protocols. Additionally or alternatively, detection of a genetic biomarker can include a method of generating a sequencing library, wherein the method comprises the steps of: (i) providing DNA fragments; (ii) end-repairing the DNA fragments by a polynucleotide kinase enzyme and an enzyme with polymerase and exonuclease activities to obtain blunt-ended, 5' phosphorylated DNA fragments; (iii) optionally adding a terminal adenine to the end of the end-repaired DNA

fragments by a deoxynucleotidyl transferase enzyme; and (iv) ligating the DNA fragments, optionally having the terminal adenine base, with sequencing adaptors by a DNA ligase; whereby after completion of step (ii) and/or the optional step (iii) the enzyme or enzymes used in that/those step/s is/are inactivated by the addition of (a) specific inhibitor(s). None of the inhibitors of the above method inhibits the enzyme activity of a/the subsequent step(s). In some embodiments, the steps of the above method, which comprise enzyme inactivation by a specific inhibitor, do not comprise heat-inactivation of said enzyme(s). In some embodiments, the steps of the above method, which comprise enzyme inactivation by a specific inhibitor, do not comprise a subsequent purification step from said enzyme(s). In some alternative embodiments, the steps of the above method, which comprise addition of (a) specific inhibitor(s), comprise an upstream heat-inactivation of said enzyme(s), but do not comprise a purification step from said enzyme(s). In some embodiments, the above method may further comprise step (v), wherein the ligated fragments of step (iv) are purified and size-selected for sequencing.

[647] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2001/023618, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a composition comprising an oligonucleotide and an annealing promoting compound (APC). The composition may be used, for example, to reduce the specificity of a hybridization reaction involving the oligonucleotide. The oligonucleotide may optionally be immobilized on a solid surface, where suitable solid surfaces include a nylon tip, a nylon bead, and a nylon membrane. In a preferred embodiment, the APC is an aminoalcohol, where the aminoalcohol comprises at least one amine group and at least one hydroxyl group. The composition may further comprise an acid and/or a buffer, so that the aminoalcohol may be present in the composition, either entirely or in part, as a salt of the aminoalcohol. The composition is preferably aqueous, and has a pH of between 4 and 10. Exemplary aminoalcohol APCs are 4-hydroxypiperidine, l-methyl-3- piperidinemethanol, 4,4'-trimethylenebis(l-piperidineethanol), 3-piperidinemethanol, l-ethyl-4-hydroxy-piperidine, 2-piperidineethanol, 3-hydroxy-l-methylpiperidine, 1- ethyl-3-hydoxy-piperidine, 4-hydroxy-1 -methylpiperidine, 1 -methyl -2- piperidinemethanol, 2-piperidine-methanol, 2,2,6,6-

tetramethyl-4-piperidinol, 1,4-bis(2- hydroxyethyl)piperazine and 1 -(2-hydroxyethyl)piperazine. Additionally or alternatively, detection of a genetic biomarker can include a method of decreasing the specificity of a hybridization reaction between two oligonucleotides. The method comprises adding an annealing promoting compound (APC) to a hybridization reaction between two oligonucleotides. Additionally or alternatively, detection of a genetic biomarker can include a method of decreasing the specificity of a hybridization reaction between two oligonucleotides. The method comprises mixing a first oligonucleotide, a second oligonucleotide, and an annealing promoting compound (APC) under conditions suitable for the formation of an oligonucleotide duplex. Additionally or alternatively, detection of a genetic biomarker can include a method of identifying a target oligonucleotide. The method comprises: (a) mixing a first oligonucleotide having a sequence complementary to the target oligonucleotide, a second oligonucleotide having a sequence complementary to the complement of the target oligonucleotide, an annealing promoting compound (APC), a polymerase, a buffer compatible with polymerase activity, and a target oligonucleotide; (b) heating the mixture of (a) to a temperature above the melting temperature of the first oligonucleotide and the second oligonucleotide and their respective complementary sequences; (c) reducing the temperature of the mixture of (b) to below the melting temperature, to thereby allow hybridization between the first oligonucleotide, the second oligonucleotide, and the target oligonucleotide; (d) raising the temperature of the mixture of (c) to a temperature compatible with polymerase activity; and (e) detecting a product of polymerization.

[648] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,792,403, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a system for generating a characterization model (including, e.g., variant type and/or zygosity) for a variant (e.g., a mutation) in a tissue or sample, e.g., a tumor, or tumor sample, from a subject, e.g., a human subject, e.g., a cancer patient. The system comprises: at least one processor operatively connected to a memory, the at least one processor when executing is configured to: a) acquire: i) a sequence coverage input (SCI), which comprises, for each of a plurality of selected subgenomic intervals (e.g., exons) a value for sequence coverage at the selected subgenomic intervals (including, e.g., a normalized sequence

coverage value); ii) an SNP allele frequency input (SAFI), which comprises, for each of a plurality of selected germline SNPs, a value for the allele frequency, in the tissue or sample, e.g., tumor sample; iii) a variant allele frequency input (VAFI), which comprises the allele frequency for said variant, e.g., mutation, in the tissue or sample, e.g., tumor sample; b) acquire values, determined as a function of SCI and SAFI, for: a genomic segment total copy number (C), for each of a plurality of genomic segments; a genomic segment minor allele copy number (M), for each of a plurality of genomic segments; and sample purity (p); and c) calculate one or both, of: i) a value for variant type, e.g., mutation type, e.g., g, which is indicative of the variant being somatic, germline, subclonal somatic, or not-distinguishable, wherein the at least one processor when executing is configured calculate the value for variant type, e.g., mutation type, as a function of VAFI, p, C, and M; ii) an indication of the zygosity (e.g., homozygous, heterozygous, and absent) of the variant, e.g., mutation, in the tissue or sample, e.g., tumor sample, as function of C and M. In an embodiment, the system is configured such that the analysis can be performed without the need for analyzing non-tumor tissue from the subject. In an embodiment, the system is configured to determine for at least one of the tumor sample, the selected subgenomic intervals, and the selected germline SNPs that the variant type, e.g., mutation type, cannot be determined for analyzed values. In an embodiment, at least one processor when executing acquires the SCI calculated as a function (e.g., the log of the ratio) of the number of reads for a subgenomic interval and the number or reads for a control (e.g., a process-matched control). In an embodiment, at least one processor when executing is configured to calculate SCI as a function (e.g., the log of the ratio) of the number of reads for a subgenomic interval and the number or reads for a control (e.g., a process-matched control). In an embodiment, the at least one processor when executing is configured to validate a minimum number of subgenomic intervals have been selected or analyzed. In an embodiment, at least one processor when executing is configured to validate a minimum number of a plurality of germline SNPs have been selected or analyzed. In an embodiment, the minimum number of germline SNPs comprises at least 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 1,000, 2,000, 3,000, 4,000, 5000, 6000, 7000, 8000, 9000, 10,000, or 15,000 germline SNPs. In an embodiment, the SAFI is based, at least in part, on a minor allele frequency in the tumor sample. In an embodiment, the at least one processor when executing

is configured to calculate, or acquire, SAFI based, at least in part, on a minor allele frequency in the tumor sample. In an embodiment, the SAFI is based, at least in part, on an alternative allele frequency (e.g., an allele frequency other than a standard allele in a human genome reference database). In an embodiment, the at least one processor when executing is configured to calculate, or acquire, SAFI based, at least in part, on an alternative allele frequency (e.g., an allele frequency other than a standard allele in a human genome reference database). In an embodiment, the at least one processor when executing is configured to access values of C, M, and p calculated from fitting a genome-wide copy number model to the SCI and the SAFI. In an embodiment, the at least one processor when executing is configured to calculate C, M, and p. In an embodiment, the at least one processor when executing generates a best fit between the genome-wide copy number model and the SCI and the SAFI to calculate C, M, and p. In an embodiment, values of C, M, and p fit a plurality of genome-wide copy number model inputs of the SCI and the SAFI. In an embodiment, the at least one processor when executing is configured to generate a user interface. In an embodiment, the user interface is configured to accept as input any one or more of: a sequence coverage input (SCI), which comprises, for each of a plurality of selected subgenomic intervals, e.g., exons, a value for sequence coverage at the selected subgenomic intervals (including, e.g., a normalized sequence coverage value); an SNP allele frequency input (SAFI), which comprises, for each of a plurality of selected germline SNPs, a value for the allele frequency, in the tumor sample; a variant allele frequency input (VAFI), which comprises the allele frequency for said variant, e.g., mutation, in the tumor sample; a genomic segment total copy number (C), for each of a plurality of genomic segments; a genomic segment minor allele copy number (M), for each of a plurality of genomic segments; and sample purity (p). In an embodiment, responsive to the user interface input, e.g., for one or more (e.g., 2, 3, 4, 5 or all) of SCI, SAFI, VAFI, C, M, or p, the system generates a characterization model, e.g., a characterization model for a variant. Additionally or alternatively, detection of a genetic biomarker can include a method of characterizing a variant, e.g., a mutation, in a tissue or sample, e.g., a tumor, or tumor sample, from a subject, e.g., a human, e.g., a cancer patient, comprising: a) acquiring: i) a sequence coverage input (SCI), which comprises, for each of a plurality of selected subgenomic intervals, e.g., exons, a value for normalized sequence coverage at the selected subgenomic intervals; ii) an SNP allele

frequency input (SAFI), which comprises, for each of a plurality of selected germline SNPs, a value for the allele frequency, in the tumor or sample, e.g., tumor sample; iii) a variant allele frequency input (VAFI), which comprises the allele frequency for said variant, e.g., mutation, in the tumor or sample, e.g., tumor sample; b) acquiring values, as a function of SCI and SAFI, for: C, for each of a plurality of genomic segments, wherein C is a genomic segment total copy number; M, for each of a plurality of genomic segments, wherein M is a genomic segment minor allele copy number; and p, wherein p is sample purity; and c) acquiring one or both of: i) a value for variant type, e.g. mutation type, e.g., g, which is indicative of the variant, e.g., a mutation, being somatic, a subclonal somatic variant, germline, or not-distinguishable, and is a function of VAFI, p, C, and M; ii) an indication of the zygosity of the variant, e.g., mutation, in the tumor or sample, e.g., tumor sample, as function of C and M. In an embodiment, the analysis can be performed without the need for analyzing non-tumor tissue from the subject. In an embodiment, the analysis is performed without analyzing non-tumor tissue from the subject, e.g., non-tumor tissue from the same subject is not sequenced. In an embodiment, the SCI comprises values that are a function, e.g., the log of the ratio, of the number of reads for a subgenomic interval, e.g., from the sample, and the number or reads for a control, e.g., a process-matched control. In an embodiment, the SCI comprises values, e.g., log r values, for at least 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 1,000, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, or 10,000, subgenomic intervals, e.g., exons. In an embodiment, the SCI comprises values, e.g., log r values, for at least 100 subgenomic intervals, e.g., exons. In an embodiment, the SCI comprises values, e.g., log r values, for 1,000 to 10,000, 2,000 to 9,000, 3,000 to 8,000, 3,000 to 7,000, 3,000 to 6,000, or 4,000 to 5,000, subgenomic intervals, e.g., exons. In an embodiment, the SCI comprises values, e.g., log r values, for subgenomic intervals, e.g., exons, from at least 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 1,000, 2,000, 3,000, or 4,000, genes. In an embodiment, at least one, a plurality, or substantially all of the values comprised in the SCI are corrected for correlation with GC content. In an embodiment, a subgenomic interval, e.g., an exon, from the sample has at least 10, 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, or 1,000 reads. In an embodiment, a plurality, e.g., at least 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 1,000, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, or 10,000,

subgenomic intervals, e.g., exons, from the sample has a predetermined number of reads. In an embodiment, the predetermined number of reads is at least 10, 20, 30, 40, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, or 1,000. In an embodiment, the plurality of germline SNPs comprise at least 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 1,000, 2,000, 3,000, 4,000, 5000, 6000, 7000, 8000, 9000, 10,000, or 15,000 germline SNPs. In an embodiment, the plurality of germline SNPs comprise at least 100 germline SNPs. In an embodiment, the plurality of germline SNPs comprises 500 to 5,000, 1,000 to 4,000, or 2,000 to 3,000 germline SNPs. In an embodiment, the allele frequency is a minor allele frequency. In an embodiment, the allele frequency is an alternative allele, e.g., an allele other than a standard allele in a human genome reference database. In an embodiment, the method comprises characterizing a plurality of variants, e.g., mutants, in the tumor sample. In an embodiment, the method comprises characterizing at least 2, 3, 4, 5, 6, 7, 8 9, 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 variants, e.g., mutants. In an embodiment, the method comprises characterizing variants, e.g., mutants, in at least 2, 3, 4, 5, 6, 7, 8 9, 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 different genes. In an embodiment, the method comprises acquiring a VAFI for at least 2, 3, 4, 5, 6, 7, 8 9, 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 variants, e.g., mutants. In an embodiment, the method comprises performing one, two or all, of steps a), b), and c) for at least 2, 3, 4, 5, 6, 7, 8 9, 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, or 500 variants, e.g., mutants. In an embodiment, values of C, M, and p are, have, or can be obtained by, fitting a genome-wide copy number model to one or both of the SCI and the SAFI. In an embodiment, values of C, M, and p fit a plurality of genome-wide copy number model inputs of the SCI and the SAFI. In an embodiment, a genomic segment comprises a plurality of subgenomic intervals, e.g., exons, e.g., subgenomic intervals which have been assigned a SCI value. In an embodiment, a genomic segment comprises at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 275, 300, 400, or 500 subgenomic intervals, e.g., exons. In an embodiment, a genomic segment comprises 10 to 1,000, 20 to 900, 30 to 700, 40 to 600, 50 to 500, 60 to 400, 70 to 300, 80 to 200, 80 to 150, or 80 to 120, 90 to 110, or about 100, subgenomic intervals, e.g., exons. In an embodiment, a genomic segment comprises between 100 and 10,000, 100 and 5,000, 100 and 4,000, 100 and 3,000, 100 and 2,000, or 100 and 1,000, subgenomic intervals, e.g., exons. In

an embodiment, a genomic segment comprises 10 to 1,000, 20 to 900, 30 to 700, 40 to 600, 50 to 500, 60 to 400, 70 to 300, 80 to 200, 80 to 150, or 80 to 120, 90 to 110, or about 100 genomic SNPs, which have been assigned a SAFI value. In an embodiment, a genomic segment comprises between 100 and 10,000, 100 and 5,000, 100 and 4,000, 100 and 3,000, 100 and 2,000, or 100 and 1,000, genomic SNPs which have been assigned a SAFI value. In an embodiment, each of a plurality of genomic segments are characterized by having one or both of: a measure of normalized sequence coverage, e.g., log r, that differ by no more than a preselected amount, e.g., the values for log2 r for subgenomic intervals, e.g., exons, within the boundaries of the genomic segment differ by no more than a reference value, or are substantially constant; and SNP allele frequencies for germline SNPs that differ by no more than a preselected amount, e.g., the values for germline SNP allele frequencies for subgenomic intervals, e.g., exons, within the boundaries of the genomic segment differ by no more than a reference value, or are substantially constant. In an embodiment, the number of subgenomic intervals, e.g., exons, that are contained in, or are combined to form, a genomic segment is at least 2, 5, 10, 15, 20, 50, or 100 times the number of genomic segments. In an embodiment, the number of subgenomic intervals, e.g., exons, is at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 times the number of genomic segments. In an embodiment, a boundary for a genomic segment is provided. In an embodiment, the method comprises assembling sequences for subgenomic intervals, e.g., exons, into genetic segments. In an embodiment, the method comprises assembling sequences for subgenomic intervals, with a method, e.g., a method comprising a circular binary segmentation (CBS), an HMM based method, a Wavelet based method, or a Cluster along Chromosomes method. In an embodiment, fitting the genome-wide copy number model to the SCI comprises using the equation of:

$$\log Ratio_i = \log_2 \frac{pC_i + 2(1-p)}{p\psi + 2(1-p)},$$

[649] where ψ is tumor ploidy. In an embodiment, $\psi=(\Sigma iliCi)/\Sigma ili$, let li be the length of a genomic segment. In an embodiment, fitting the genome-wide copy number model to the SAFI comprises using the equation of:

$$AF = \frac{pM + 1(1-p)}{pC + 2(1-p)},$$

[650] where AF is allele frequency. In an embodiment, the fitting comprises using Gibbs sampling. In an embodiment, fitting comprises using e.g., Markov chain Monte Carlo (MCMC) algorithm, e.g., ASCAT (Allele-Specific Copy Number Analysis of Tumors), OncoSNP, or PICNIC (Predicting Integral Copy Numbers In Cancer). In an embodiment, fitting comprises using Metropolis-Hastings MCMC. In an embodiment, fitting comprises using a non-Bayesian approach, e.g., a frequentist approach, e.g., using least squares fitting. In an embodiment, g is determined by determining the fit of values for VAFI, p, C, and M to a model for somatic/germline status. In an embodiment, the method comprises acquiring an indication of heterozygosity for said variant, e.g., mutation. In an embodiment, sample purity (p) is global purity, e.g., is the same for all genomic segments. In an embodiment, the value of g is acquired by:

$$AF = \frac{pM + g(1-p)}{pC + 2(1-p)},$$

[651] where AF is allele frequency. In an embodiment, a value of g that is close to 0, e.g., does not differ significantly from 0, indicates the variant is a somatic variant. In an embodiment, a value of g that is 0, or close to 0, e.g., within a predetermined distance from 0, e.g., a value of g of less than 0.4, indicates the variant is a somatic variant. In an embodiment, a value of g that is close to 1, e.g., does not differ significantly from 1, indicates the variant is a germline variant. In an embodiment, a value of g that is 1, or close to 1, e.g., within a predetermined distance from 1, e.g., a value of g of more than 0.6, indicates the variant is a germline variant. In an embodiment, a value of g is less than 1 but more than 0, e.g., if it is less than 1 by a predetermined amount and more than 0 by a predetermined amount, e.g., if g is between 0.4 and 0.6, it indicates an indistinguishable result. In an embodiment, a value of g that is significantly less than 0, is indicative of a subclonal somatic variant. In an embodiment, the value of g is acquired by:

$$AF = \frac{pM' + g(1-p)}{pC + 2(1-p)},$$

[652] where AF is allele frequency, and M′=C−M (e.g., when M is a non-minor allele frequency), e.g., the variant is a germline polymorphism if g=1 and the variant is a somatic mutation if g=0.

[653] In an embodiment, the somatic/germline status is determined, e.g., when the sample purity is below about 40%, e.g., between about 10% and 30%, e.g., between about 10% and 20%, or between about 20% and 30%. In an embodiment, when: a value of M equal to 0 not equal to C is indicative of absence of the variant, e.g., mutation, e.g., not existent in the tumor;

[654] a non-zero value of M equal to C is indicative of homozygosity of the variant, e.g., mutation, e.g., with loss of heterozygosity (LOH); a value of M equal to 0 equal to C indicates a homozygous deletion of the variant, e.g., mutation, e.g., not existent in the tumor; and a non-zero value of M not equal to C is indicative of heterozygosity of the variant, e.g., mutation. In an embodiment, the method comprises acquiring an indication of zygosity for said variant, e.g., mutation. In an embodiment, the mutation status is determined as homozygous (e.g., LOH) if $M=C\neq 0$. In an embodiment, the mutation status is determined as homozygous deletion if $M=C=0$. In an embodiment, the mutation status is determined as heterozygous is $0<M<C$. In an embodiment, the mutation is absent from the tumor if $M=0$ and $C\neq 0$. In an embodiment, the zygosity is determined, e.g., when the sample purity is greater than about 80%, e.g., between about 90% and 100%, e.g., between about 90% and 95%, or between about 95% and 100%. In an embodiment, the control is a sample of euploid (e.g., diploid) tissue from a subject other than the subject from which the tumor sample is from, or a sample of mixed euploid (e.g., diploid) tissues from one or more (e.g., at least 2, 3, 4, or 5) subjects other than the subject from which the tumor sample is from. In an embodiment, the method comprises sequencing each of the selected subgenomic intervals and each of the selected germline SNPs, e.g., by next generation sequencing (NGS). In an embodiment, the sequence coverage prior to normalization is at least about 10×, 20×, 30×, 50×, 100×, 250×, 500×, 750×, or 1000× the depth of the sequencing.

[655] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/0218113, which is hereby incorporated by reference in its entirety.

[656] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2017/0356053, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include the use of hybridization of sample

nucleic acid to a bait set to evaluate a region of interest, e.g., to evaluate the clonal profile of a region of interest, in the sample. Additionally or alternatively, detection of a genetic biomarker can include a method of evaluating or providing a clonal profile of a subject interval, e.g., a subgenomic interval, or an expressed subgenomic interval (or of a cell containing the same), in a subject, comprising: (a) acquiring a nucleic acid library comprising a plurality of members, each member of the plurality comprising a nucleic acid from the subject, e.g., a plurality of tumor members from a solid tumor or hematologic malignancy (or premalignancy) sample; (b) contacting the library with a bait set to provide a plurality of selected members, each of which comprises the subject interval, or a portion thereof (sometimes referred to herein as a library catch); optionally, (c) amplifying each member of the plurality of selected members, e.g., to provide an amplified sequence of the subject interval; (d) acquiring the sequence of one or more occurrences of the subject interval; thereby providing or evaluating the clonal profile of a subject interval. In an embodiment, the method comprises evaluating the clonal profile of a subgenomic interval and of an expressed subgenomic interval. In an embodiment, the method comprises comparing the sequence of a first allele or signature (e.g., a first V segment) at the subject interval with a comparison value, e.g., a preselected value, e.g., a value that is a function of the sequence of a second allele or signature (e.g., a second V segment). In an embodiment, the method further comprises: (e) acquiring: (i) a value for the distribution, expression (the occurrence or level of transcribed copies of a subgenomic signature), abundance, or identity, of a sequence, signature or allele at the subject interval, e.g., the relative abundance, of a sequence, a signature, or an allele, or the relative abundance of each of a plurality of sequences, signatures, or alleles, at the subject interval; or (ii) a value for variability, e.g., sequence variability arising from a somatic hypermutation, sequence variability arising from a VD, DJ, or VJ junction, e.g., by the formation of an indel at the junction, or a CDR, e.g., heavy chain CDR3, sequence variability, within a signature or subject interval, e.g., wherein a value for variability is a function of the number of different variants present for the subject interval in a subject or sample. In an embodiment, the method comprises providing the clonal profile of a sequence, allele or signature, e.g., a V segment, or VDJ or VJ rearrangement, at a first subject interval; and i) a phenotype, e.g., disease state, of the subject; or ii) the genotype at a second subject interval. In an embodiment, step (d): (i) comprises acquiring the sequence of each of a

plurality of occurrences of the subject interval, e.g., acquiring the sequence of first occurrence of a subject interval comprising a V segment and of a second occurrence of the interval comprising the V segment, wherein the first and second occurrences differ by the diversity at a VD, DJ, or VJ junction; or (ii) comprises acquiring the sequence of a first subject interval and of a second different subject interval, e.g., wherein the first subject interval comprises a sequence from a first gene and the second subject interval comprises sequence from a second gene. In an embodiment, step (d) comprises acquiring the sequence of each of a plurality of occurrences of the subject interval, e.g., a plurality of occurrences of a subject interval comprising a VDJ sequence, e.g., a plurality of occurrences of a subject interval comprising a VDJ sequence comprising a specific V segment, a specific D segment, and a specific J segment. In an embodiment, the method comprises acquiring a value for e(i). In an embodiment, the value of (e)(i) comprises a value for the abundance of a sequence, signature, or allele (e.g., a first V segment) in a subject interval relative to a comparison value, e.g., a preselected value, e.g., a value that is a function of the abundance of a second sequence, signature, or allele (e.g., a second V segment). In an embodiment, the value of (e)(i) comprises a value for the abundance of an event, e.g., a sequence, allele, or signature, e.g., a mutation or rearrangement, in a subject interval, relative to a comparison value, e.g., a preselected value, e.g., a value that is a function of the abundance of a sequence lacking the event, e.g., an unmutated or unrearranged sequence in the subject interval. In an embodiment, the value of (e)(i) comprises a value of relative abundance for each of X unique (i.e., different from one another) sequences, signatures, or alleles, at a subject interval. Additionally or alternatively, detection of a genetic biomarker can include a method of evaluating a subject for the occurrence of a whole arm or large rearrangement, e.g., a rearrangement, e.g., a translocation, duplication, insertion, or deletion, comprising, e.g., at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90%, or all of a chromosome arm, comprising: (a) acquiring a nucleic acid library comprising a plurality of members, each member of the plurality comprising nucleic acid from the subject; (b) contacting the library with a bait set, e.g., under conditions of solution hybridization, to provide a plurality of selected members, each of which comprises a subject interval, or a portion thereof (sometimes referred to herein as a library catch); (c) amplifying each member of the plurality, e.g., by a method that does not rely on a sequence specific interaction with target/subject

nucleic acid in the member, e.g., by amplifying each member of the plurality with a primer that does not bind to target/subject nucleic acid in the member; and (d) acquiring the sequence of a plurality of subject intervals, wherein said plurality of subject intervals is disposed on a chromosome such as to allow determination of a whole arm or large rearrangement. Additionally or alternatively, detection of a genetic biomarker can include a method of evaluating a subject, comprising: (a) acquiring a nucleic acid library comprising a plurality of members, each member of the plurality comprising nucleic acid from the subject, e.g., a plurality of tumor members from a hematological-cancer sample; (b) contacting the library with a bait set, e.g., under conditions of solution hybridization, to provide a plurality of selected members, each of which comprises the subject interval, or a portion thereof (sometimes referred to herein as a library catch); (c) amplifying each member of the plurality of selected members, e.g., by a method that does not rely on a sequence specific interaction with target/subject nucleic acid in the member, e.g., by amplifying each member of the plurality of selected members with a primer that does not bind to target/subject nucleic acid in the member; (d) acquiring the sequence of a subgenomic interval and an expressed subgenomic interval; thereby evaluating the subject, wherein: (i) the method comprises contacting the library with a bait set that provides both a subgenomic interval and an expressed subgenomic interval; (ii) the method comprises contacting the library with a first bait set that provides a subgenomic interval and a second bait set that provides an expressed subgenomic interval; (iii) wherein the library comprises genomic DNA and is contacted with a bait set that provides a subgenomic interval and the method further comprises a second library which comprises cDNA which is contacted with the bait set to provide an expressed subgenomic interval; (iv) wherein the library comprises genomic DNA and is contacted with a bait set that provides a subgenomic interval and the method further comprises a second library which comprises cDNA which is contacted with a second bait set to provide an expressed subgenomic interval; or (v) the method comprises performing one of steps (a), (b) and (c) in a first reaction mix to provide a first subject interval, e.g., a subgenomic interval, and on a second reaction mix to provide a second subject interval, e.g., an expressed subgenomic interval, e.g., that corresponds to the subgenomic interval. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample from a hematologic malignancy

(or premalignancy), e.g., a hematologic malignancy (or premalignancy). The method comprises: (a) acquiring one or a plurality of libraries comprising a plurality members from a sample, e.g., a plurality of tumor members from a tumor sample; (b) optionally, enriching the one or a plurality of libraries for preselected sequences, e.g., by contacting the one or a plurality of libraries with a bait set (or plurality of bait sets) to provide selected members (sometimes referred to herein as library catch); (c) acquiring a read for a subject interval, e.g., a subgenomic interval or an expressed subgenomic interal, from a member, e.g., a tumor member from a library or library catch, e.g., by a method comprising sequencing, e.g., with a next generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, optionally wherein: a read from each of X unique subject intervals (e.g., subgenomic intervals, expressed subgenomic intervals, or both) is aligned with a unique alignment method, wherein unique subject interval (e.g., subgenomic interval or expressed subgenomic interval) means different from the other X-1 subject intervals (e.g., subgenoimc intervals, expressed subgenomic intervals, or both), and wherein unique alignment method means different from the other X-1 alignment methods, and X is at least 2. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample from a hematologic malignancy (or premalignancy), e.g., a hematologic malignancy (or premalignancy). The method comprises: (a) acquiring one or a plurality of libraries comprising a plurality members from a sample, e.g., a plurality of tumor members from the sample, e.g., the tumor sample; (b) optionally, enriching the one or a plurality of libraries for preselected sequences, e.g., by contacting the library with a bait set (or plurality of bait sets) to provide selected members, e.g., a library catch; (c) acquiring a read for a subject interval (e.g., a subgenomic interval or an expressed subgenomic interval) from a member, e.g., a tumor member from said library or library catch, e.g., by a method comprising sequencing, e.g., with a next generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method or a calling method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample. optionally wherein a nucleotide value is assigned for a nucleotide position in each of

X unique subject intervals (subgenomic intervals, expressed subgenomic intervals, or both) is assigned by a unique calling method, wherein unique subject interval (e.g., subgenomic interval or expressed subgenomic interval) means different from the other X-1 subject intervals (e.g., subgenoimc intervals, expressed subgenomic intervals, or both), and wherein unique calling method means different from the other X-1 calling methods, and X is at least 2. The calling methods can differ, and thereby be unique, e.g., by relying on different Bayesian prior values.

[657] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0324519, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods, systems, and apparatuses for making more accurate variant calls based on sequencing reads of a sample, e.g., obtained from a targeted sequencing. For example, once sequence reads are received and aligned to a reference sequence, sequence reads having a variant at a location can be counted. A first variant frequency of a particular variant measured at one location of a sample can be compared to one or more second variant frequencies of the particular variant measured at other positions and/or from other samples. The second variant frequency can correspond to an expected value for sequencing errors for a sequencing run. In some embodiments, a probability value indicating the confidence level that a variant is a true positive at a location can be calculated based on variant counts and total read counts at a plurality of locations in the target region in one or more samples. The probability value can then be compared with a threshold level to determine whether the detected variant is a true positive. In other embodiments, a difference in variant counts and total reads counts at a same location in a test sample and a reference sample (e.g., assumed to only have sequencing errors at the location) can be used to determine whether a variant is a true positive in a test sample. According to one embodiment, a method can detect true positives for rare variants in a target region of a test sample. For each sample, variant frequencies for variants of a same variant class at locations where a reference allele exists on a reference sequence can be calculated using variant counts and total read counts. A distribution of the variant frequencies for variants of the same class can be used to determine the probability value of a variant at a location in the test sample with a determined variant

frequency. Based on the probability value, the variant at the location in the test sample is classified as either a true positive (mutation) or a false positive. In other embodiments, a method can detect true positives for rate variants in a target region of a test sample by using a comparison with one or more reference samples. A variant count and a wild type count for a specific variant at a specific location in the test sample can be determined from the aligned sequence reads, and compared with a variant count and a wild type count for the specific variant at the specific location in the one or more reference samples to determine a probability value. Based on the probability value, the specific variant at the specific location in the test sample is classified as either a true positive or false positive. In one embodiment, a computer-implemented method of detecting low frequency variants in a target region in a first sample is provided. In some embodiments, the method comprises (at a computer system) receiving a plurality of sequence reads obtained from sequencing DNA fragments from one or more samples, the one or more samples including the first sample, wherein the sequencing includes targeting the target region in the DNA fragments; aligning the plurality of sequence reads to the target region of a reference sequence; identifying a first candidate variant having a first allele at a first location of the target region based on sequence reads of the first sample differing from a reference allele at the first location of the reference sequence; determining a first variant frequency for the first allele at the first location based on sequence reads of the first sample that align to the first location of the reference sequence; identifying the first candidate variant as corresponding to a first variant class selected from a plurality of variant classes, each variant class of the plurality of variant classes corresponding to a different type of variant; identifying a set of second locations in the target region of the reference sequence that have the reference allele, wherein at least 50% of the other locations in the one or more samples exhibit a false positive for the first allele, and wherein the set of second locations includes the first location; at each of the set of second locations and for each of the one or more samples: determining a second variant frequency of the first allele based on sequence reads of the sample that align to the second location of the reference sequence, the second variant frequencies forming a statistical distribution; comparing the first variant frequency to a statistical value of the statistical distribution to determine a probability value of the first variant frequency relative to the statistical value of the statistical distribution; and comparing the probability value to a

threshold value as part of determining whether the first candidate variant is a true positive in the first sample for the first allele, the threshold value differentiating between false positives and true positives for the first allele. In certain embodiments, the reference sequence corresponds to a consensus sequence as determined from normal cells. In some embodiments, the one or more samples are derived from cell-free DNA fragments. In some embodiments, the one or more samples are derived from RNA of a biological sample. In some embodiments, the plurality of samples are sequenced in a single sequencing run. In other embodiments, the statistical value of the statistical distribution includes a mean value. In other embodiments, the probability value is a z-score, modified z-score, cumulative probability, Phred quality score, or modified Phred quality score. In other embodiments, the statistical distribution is the statistical distribution of logarithmic transformations of the second variant frequencies. In other embodiments, the threshold is determined using support vector machines classifier based on training data obtained from one or more sequencing runs. In other embodiments, the threshold is a function of variant frequency. In another embodiment, a computer-implemented method of detecting a variant having a first allele at a first location in a target region in a first sample is provided. In some embodiments, the method comprises (at a computer system): receiving a plurality of sequence reads obtained from sequencing DNA fragments from at least two samples, the at least two samples including the first sample, wherein the sequencing includes targeting the target region in the DNA fragments; aligning the plurality of sequence reads to the target region of a reference sequence; identifying whether the first allele exists at the first location in each sample of the at least two samples based on aligned sequence reads of each sample at the first location differing from a reference allele at the first location of the reference sequence; determining a variant count of the first allele at the first location and a wild type count of the reference allele at the first location for each sample of the at least two samples; selecting, from the at least two samples, at least one sample as a reference sample; comparing a first variant count of the first allele at the first location and a first wild type count of the reference allele at the first location for the first sample to a second variant count of the first allele at the first location and a second wild type count of the reference allele at the first location for the reference sample to determine a probability value of the variant having the first allele at the first location for the first sample; and comparing the probability value to a threshold

value as part of determining whether the first allele at the first location in the first sample is a true positive for the first allele, the threshold value differentiating between false positives and true positives for the first allele at the first location. In certain embodiments, the reference sample comprises two samples with lowest variant frequencies for the first allele at the first location among the at least two samples other than the first sample. In some embodiments, the probability value is determined using chi-squared cumulative distribution function. In some embodiments, the probability value is determined using Pearson proportion test. In some embodiments, the probability value is one or more of z-score, modified z-score, p-value, chi-squared value, cumulative probability value, and quality score. In some embodiments, the quality score is determined using a look-up table. In some embodiments, the threshold is determined using support vector machines classifier based on training data obtained from one or more sequencing runs. In some embodiments, the threshold is a function of variant frequency. In another embodiment, a computer product comprising a non-transitory computer readable medium storing a plurality of instructions that when executed control a computer system to detect true variants in a target region of a first sample is provided. In some embodiments, the instructions comprise receiving a plurality of sequence reads obtained from sequencing DNA fragments from one or more samples, the one or more samples including the first sample, wherein the sequencing includes targeting the target region in the DNA fragments; aligning the plurality of sequence reads to the target region of a reference sequence; identifying a set of sequence locations in the target region of the reference sequence that have a reference allele of variants in a variant class, wherein at least 50% of the sequence locations in the one or more samples exhibit a false positive for the variants in the variant class in the sequence reads, and wherein the set of sequence locations includes a first location; at each location of the set of sequence locations and for each sample of the one or more samples: determining a read count at each location for each sample; identifying candidate variants having variant alleles for the variants in the variant class based on sequence reads of each sample differing from the reference allele at the same location of the reference sequence, a total number of the candidate variants at each location in each sample being the variant count in each location for each sample; determining a variant frequency of variants in the variant class based on the read count and the variant count, the variant frequency for each location in each sample forming a

statistical distribution, wherein the variant frequency at a first location in the set of sequence locations for the first sample is a first variant frequency; comparing the first variant frequency to a value of the statistical distribution to determine a probability value of the first variant frequency relative to the value of the statistical distribution; and comparing the probability value to a threshold value as part of determining whether candidate variants in the first sample are true positives, the threshold value differentiating between false positives and true positives for the variants in the variant class. In certain embodiments, the statistical distribution is the statistical distribution of a logarithmic transformation of the variant frequency at each location for each sample.

[658] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,340,830, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of analyzing a tumor sample. The method comprises: (a) acquiring a library comprising a plurality of target members, e.g., tumor members, from a sample, e.g., a tumor sample; (b) optionally, contacting the library with a bait set (or plurality of bait sets) to provide selected members (sometimes referred to herein as "library catch"); (c) acquiring a read for a subgenomic interval from a tumor member from said library or library catch, e.g., by sequencing, e.g., with a next generation sequencing method; (d) aligning said read; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayeisan method) from said read for a preselected nucleotide position, e.g., for a preselected nucleotide position in each of a plurality of subgenomic intervals, e.g., each of a plurality genes, thereby analyzing said sample, wherein: (i) each of X nucleotide positions is analyzed under a unique set of conditions for one or a combination of steps (b), (c), (d), or (e) (wherein unique means different from the other X−1 sets of conditions and wherein X is at least 2, 5, 10, 20, 30, 40, 50, 100, 200, 300 or 500). E.g., a first set of conditions, is used for a first nucleotide position, e.g., in a first subgenomic interval or gene, and a second set of conditions, e.g., a second set of conditions, is used for a second nucleotide position, e.g., in a second subgenomic interval or gene; (ii) for each of X nucleotide positions, responsive to a characteristic of a preselected alteration, e.g., mutation, that can occur at the nucleotide position, the nucleotide position is analyzed under a unique set of conditions (wherein unique means different from the other X−1

sets of conditions and wherein X is at least 2, 5, 10, 20, 30, 40, 50, 100, 200, 300 or 500). E.g., responsive to a characteristic, e.g., a characteristic, of a preselected alteration, e.g., mutation, that can occur at a nucleotide position in a first subgenomic interval, the nucleotide position is analyzed under a first set of conditions, and responsive to a characteristic, e.g., a characteristic, of a preselected alteration, e.g., mutation, that can occur at a nucleotide position in a second subgenomic interval, the nucleotide position is analyzed under second set of conditions; (iii) wherein said method is performed on a sample, e.g., a preserved tumor sample, under conditions that allow for 95, 98, or 99% sensitivity or specificity for nucleotide positions in at least 2, 5, 10, 20, 50 or 100 subgenomic intervals, e.g., genes; or (iv) wherein the method comprises one or more or all of: a) sequencing a first subgenomic interval to provide for about 500× or higher sequencing depth, e.g., to sequence a mutation present in no more than 5% of the cells from the sample; b) sequencing a second subgenomic interval to provide for about 200× or higher, e.g., about 200×—about 500×, sequencing depth, e.g., to sequence a mutation present in no more than 10% of the cells from the sample; c) sequencing a third subgenomic interval to provide for about 10-100× sequencing depth, e.g., to sequence one or more subgenomic intervals (e.g., exons) that are chosen from: a) a pharmacogenomic (PGx) single nucleotide polymorphism (SNP) that may explain the ability of patient to metabolize different drugs, or b) a genomic SNPs that may be used to uniquely identify (e.g., fingerprint) a patient; d) sequencing a fourth subgenomic interval to provide for about 5-50× sequencing depth, e.g., to detect a structural breakpoint, such as a genomic translocation or an indel. For example, detection of an intronic breakpoint requires 5-50× sequence-pair spanning depth to ensure high detection reliability. Such bait sets can be used to detect, for example, translocation/indel-prone cancer genes; or e) sequencing a fifth subgenomic interval to provide for about 0.1-300× sequencing depth, e.g., to detect copy number changes. In one embodiment, the sequencing depth ranges from about 0.1-10× sequencing depth to detect copy number changes. In other embodiments, the sequencing depth ranges from about 100-300× to detect a genomic SNPs/loci that is used to assess copy number gains/losses of genomic DNA or loss-of-heterozygosity (LOH). Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample. The method comprises: (a) acquiring a library comprising a plurality members from a sample, e.g., a plurality of tumor

members from a tumor sample; (b) optionally, enriching the library for preselected sequences, e.g., by contacting the library with a bait set (or plurality of bait sets) to provide selected members (sometimes referred to herein as library catch); (c) acquiring a read for a subgenomic interval from a member, e.g., a tumor member from said library or library catch, e.g., by a method comprising sequencing, e.g., with a next generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, wherein a read from each of X unique subgenomic intervals is aligned with a unique alignment method, wherein unique subgenomic interval means different from the other X−1 subgenoimc intervals, and wherein unique alignment method means different from the other X−1 alignment methods, and X is at least 2. In an embodiment, step (b) is present. In an embodiment step (b) is absent. In an embodiment, X is at least 3, 4, 5, 10, 15, 20, 30, 50, 100, 500, or 1,000. In an embodiment, a method (e.g., element (d) of the method recited above) comprises selecting or using an alignment method for analyzing, e.g., aligning, a read, wherein said alignment method is a function of, is selected responsive to, or is optimized for, one or more or all of: (i) tumor type, e.g., the tumor type in said sample; (ii) the gene, or type of gene, in which said subgenomic interval being sequenced is located, e.g., a gene or type of gene characterized by a preselected or variant or type of variant, e.g., a mutation, or by a mutation of a preselected frequency; (iii) the site (e.g., nucleotide position) being analyzed; (iv) the type of variant, e.g., a substitution, within the subgenomic interval being evaluated; (v) the type of sample, e.g., an FFPE sample; and (vi) sequence in or near said subgenomic interval being evaluated, e.g., the expected propensity for misalignment for said subgenomic interval, e.g., the presence of repeated sequences in or near said subgenomic interval. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample. The method comprises: (a) acquiring a library comprising a plurality members from a sample, e.g., a plurality of tumor members from the sample, e.g., the tumor sample; (b) optionally, enriching the library for preselected sequences, e.g., by contacting the library with a bait set (or plurality of bait sets) to provide selected members, e.g., a library catch; (c) acquiring a read for a subgenomic interval from a member, e.g., a tumor member from said library or library catch, e.g., by a method comprising sequencing, e.g., with a next

generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method or a calling method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, wherein a nucleotide value is assigned for a nucleotide position in each of X unique subgenomic intervals is assigned by a unique calling method, wherein unique subgenomic interval means different from the other X−1 subgenoimc intervals, and wherein unique calling method means different from the other X−1 calling methods, and X is at least 2. The calling methods can differ, and thereby be unique, e.g., by relying on different Bayesian prior values. In an embodiment, step (b) is present. In an embodiment, step (b) is absent. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample. The method comprises: (a) acquiring a library comprising a plurality of members (e.g., target members) from a sample, e.g., a plurality of tumor members from a tumor sample; (b) contacting the library with a bait set to provide selected members (e.g., a library catch); (c) acquiring a read for a subgenomic interval from a member, e.g., a tumor member from said library or library catch, e.g., by a method comprising sequencing, e.g., with a next generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method or a method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, wherein the method comprises contacting the library with a plurality, e.g., at least two, three, four, or five, of baits or bait sets, wherein each bait or bait set of said plurality has a unique (as opposed to the other bait sets in the plurality), preselected efficiency for selection. E.g., each unique bait or bait set provides for a unique depth of sequencing. In an embodiment, the efficiency of selection of a first bait set in the plurality differs from the efficiency of a second bait set in the plurality by at least 2 fold. In an embodiment, the first and second bait sets provide for a depth of sequencing that differs by at least 2 fold. In an embodiment, the method comprises contacting one, or a plurality of the following bait sets with the library: a) a bait set that selects sufficient members comprising a subgenomic interval to provide for about 500× or higher sequencing depth, e.g., to sequence a mutation present in no more than 5% of the cells from the sample; b) a bait set that selects sufficient members comprising a subgenomic interval to provide for about 200× or higher, e.g., about 200×—about 500×, sequencing depth,

e.g., to sequence a mutation present in no more than 10% of the cells from the sample; c) a bait set that selects sufficient members comprising a subgenomic interval to provide for about 10-100× sequencing depth, e.g., to sequence one or more subgenomic intervals (e.g., exons) that are chosen from: a) a pharmacogenomic (PGx) single nucleotide polymorphism (SNP) that may explain the ability of patient to metabolize different drugs, or b) a genomic SNPs that may be used to uniquely identify (e.g., fingerprint) a patient; d) a bait set that selects sufficient members comprising a subgenomic interval to provide for about 5-50× sequencing depth, e.g., to detect a structural breakpoint, such as a genomic translocation or an indel. For example, detection of an intronic breakpoint requires 5-50× sequence-pair spanning depth to ensure high detection reliability. Such bait sets can be used to detect, for example, translocation/indel-prone cancer genes; or e) a bait set that selects sufficient members comprising a subgenomic interval to provide for about 0.1-300× sequencing depth, e.g., to detect copy number changes. In one embodiment, the sequencing depth ranges from about 0.1-10× sequencing depth to detect copy number changes. In other embodiments, the sequencing depth ranges from about 100-300× to detect a genomic SNPs/loci that is used to assess copy number gains/losses of genomic DNA or loss-of-heterozygosity (LOH). Such bait sets can be used to detect, for example, amplification/deletion-prone cancer genes. Additionally or alternatively, detection of a genetic biomarker can include a sample, e.g., a tumor sample. The method comprises: (a) acquiring a library comprising a plurality members from a sample, e.g., a plurality of tumor members from a tumor sample; (b) optionally, enriching the library for preselected sequences, e.g., by contacting the library with a bait set (or plurality of bait sets) to provide selected members (e.g., a library catch); (c) acquiring a read for a subgenomic interval from a member, e.g., a tumor member from said library or library catch, e.g., by a method comprising sequencing, e.g., with a next generation sequencing method; (d) aligning said read by an alignment method; and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method or a method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, wherein the method comprises sequencing, e.g., by a next generation sequencing method, a subgenomic interval from at least five, six, seven, eight, nine, ten, fifteen, twenty, twenty-five, thirty or more genes or gene products from the sample, wherein the genes or gene products are chosen from: ABL1, AKT1, AKT2, AKT3, ALK, APC, AR, BRAF, CCND1,

CDK4, CDKN2A, CEBPA, CTNNB1, EGFR, ERBB2, ESR1, FGFR1, FGFR2, FGFR3, FLT3, HRAS, JAK2, KIT, KRAS, MAP2K1, MAP2K2, MET, MLL, MYC, NF1, NOTCH1, NPM1, NRAS, NTRK3, PDGFRA, PIK3CA, PIK3CG, PIK3R1, PTCH1, PTCH2, PTEN, RB1, RET, SMO, STK11, SUFU, or TP53. In an embodiment, step (b) is present. In an embodiment, step (b) is absent.

[659] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/151524, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of evaluating the mutation load in a sample, by providing a sequence of a set of subgenomic intervals from the sample; and determining a value for the mutational load, wherein the value is a function of the number of alterations in the set of subgenomic intervals. In certain embodiments, the set of subgenomic intervals are from a predetermined set of genes, for example, a predetermined set of genes that does not include the entire genome or exome. In certain embodiments, the set of subgenomic intervals is a set of coding subgenomic intervals. In other embodiments, the set of subgenomic intervals contains both a coding subgenomic interval and a non-coding subgenomic interval. In certain embodiments, the value for the mutation load is a function of the number of an alteration (e.g., a somatic alteration) in the set of subgenomic intervals. In certain embodiments, the number of an alteration excludes a functional alteration, a germline alteration, or both. In some embodiments, the sample is a tumor sample or a sample derived from a tumor. Additionally or alternatively, detection of a genetic biomarker can include methods comprising, e.g., one or more of: acquiring a library comprising a plurality of tumor members from the sample; contacting the library with a bait set to provide selected tumor members by hybridization, thereby providing a library catch; acquiring a read for a subgenomic interval comprising an alteration from the tumor member from the library catch; aligning the read by an alignment method; assigning a nucleotide value from the read for a preselected nucleotide position; and selecting a set of subgenomic intervals from a set of the assigned nucleotide positions, wherein the set of subgenomic intervals are from a predetermined set of genes. Additionally or alternatively, detection of a genetic biomarker can include a method of evaluating the mutation load in a sample, e.g., a tumor sample (e.g., a sample acquired from a tumor), the method

includes: a) providing a sequence, e.g., a nucleotide sequence, of a set of subgenomic intervals (e.g., coding subgenomic intervals) from the sample, wherein the set of subgenomic intervals are from a predetermined set of genes; and b) determining a value for the mutation load, wherein the value is a function of the number of an alteration (e.g., one or more alterations), e.g., a somatic alteration (e.g., one or more somatic alterations), in the set of subgenomic intervals. In certain embodiments, the number of an alteration excludes a functional alteration in a subgenomic interval. In other embodiments, the number of an alteration excludes a germline alteration in a subgenomic interval. In certain embodiments, the number of an alteration excludes a functional alteration in a subgenomic interval and a germline alteration in a subgenomic interval. In certain embodiments, the set of subgenomic intervals comprises coding subgenomic intervals. In other embodiments, the set of subgenomic intervals comprises non-coding subgenomic intervals. In certain embodiments, the set of subgenomic intervals comprises coding subgenomic intervals. In other embodiments, the set of subgenomic intervals comprises one or more coding subgenomic intervals and one or more non-coding subgenomic intervals. In certain embodiments, about 5% or more, about 10% or more, about 20% or more, about 30% or more, about 40% or more, about 50% or more, about 60% or more, about 70% or more, about 80% or more, about 90% or more, or about 95% or more, of the subgenomic intervals in the set of subgenomic intervals are coding subgenomic intervals. In other embodiments, about 90% or less, about 80% or less, about 70% or less, about 60% or less, about 50% or less, about 40% or less, about 30% or less, about 20% or less, about 10% or less, or about 5% or less, of the subgenomic intervals in the set of subgenomic intervals are non-coding subgenomic intervals. In other embodiments, the set of subgenomic intervals does not comprise the entire genome or the entire exome. In other embodiments, the set of coding subgenomic intervals does not comprise the entire exome. In certain embodiments, the mutation load is expressed as a percentile, e.g., among the mutation loads in samples from a reference population. In certain embodiments, the reference population includes patients having the same type of cancer as the subject. In other embodiments, the reference population includes patients who are receiving, or have received, the same type of therapy, as the subject. Additionally or alternatively, detection of a genetic biomarker can include a method of evaluating the mutation load in a sample, e.g., a tumor sample or a sample derived from a

tumor. The method includes: (i) acquiring a library comprising a plurality of tumor members from the sample; (ii) contacting the library with a bait set to provide selected tumor members, wherein said bait set hybridizes with the tumor member, thereby providing a library catch; (iii) acquiring a read for a subgenomic interval comprising an alteration (e.g., a somatic alteration) from a tumor member from said library catch, e.g., by a next-generation sequencing method; (iv) aligning said read by an alignment method; (v) assigning a nucleotide value from said read for a preselected nucleotide position; (vi) selecting a set of subgenomic intervals (e.g., coding subgenomic intervals) from a set of the assigned nucleotide positions, wherein the set of subgenomic intervals are from a predetermined set of genes; and (vii) determining a value for the mutational load, wherein the value is a function of the number of an alteration (e.g., one or more alterations), e.g., a somatic alteration (e.g., one or more somatic alterations), in the set of subgenomic intervals. In certain embodiments, the number of an alteration (e.g., a somatic alteration) excludes a functional alteration in a subgenomic interval. In other embodiments, the number of an alteration excludes a germline alteration in a subgenomic interval. In certain embodiments, the number of an alteration (e.g., a somatic alteration) excludes a functional alteration in a subgenomic interval and a germline alteration in a subgenomic interval. In certain embodiments, the predetermined set of genes comprises a plurality of genes, which in mutant form, are associated with an effect on cell division, growth or survival, or are associated with a cancer. In certain embodiments, the method further comprises acquiring a library comprising a plurality of tumor members from the sample. In certain embodiments, the method further comprises contacting a library with a bait set to provide selected tumor members, wherein said bait set hybridizes with a tumor member from the library, thereby providing a library catch. In certain embodiments, the method further comprises acquiring a read for a subgenomic interval comprising the alteration (e.g., somatic alteration) from a tumor member from a library or library catch, thereby acquiring a read for the subgenomic interval, e.g., by a next-generation sequencing method. In certain embodiments, the method further comprises aligning a read for the subgenomic interval by an alignment method. In certain embodiments, the method further comprises assigning a nucleotide value for a preselected nucleotide position from a read for the subgenomic interval, e.g., by a mutation calling method. In certain embodiments, the method further comprises one, two, three, four, or all of: (a) acquiring a

library comprising a plurality of tumor members from the sample; (b) contacting the library with a bait set to provide selected tumor members, wherein said bait set hybridizes with the tumor member, thereby providing a library catch; (c) acquiring a read for a subgenomic interval comprising the alteration (e.g., somatic alteration) from a tumor member from said library catch, thereby acquiring a read for the subgenomic interval, e.g., by a next-generation sequencing method; (d) aligning said read by an alignment method; or (e) assigning a nucleotide value from said read for a preselected nucleotide position, e.g., by a mutation calling method. In certain embodiments, the germline alteration is excluded by a method or system comprising the use of an SGZ algorithm. In certain embodiments, the method further comprises characterizing a variant, e.g., an alteration, in the tumor sample by: a) acquiring: i) a sequence coverage input (SCI), which comprises, for each of a plurality of selected subgenomic intervals, a value for normalized sequence coverage at the selected subgenomic intervals, wherein SCI is a function of the number of reads for a subgenomic interval and the number of reads for a process-matched control; ii) an SNP allele frequency input (SAFI), which comprises, for each of a plurality of selected germline SNPs, a value for the allele frequency in the tumor sample, wherein SAFI is based, at least in part, on a minor or alternative allele frequency in the tumor sample; and iii) a variant allele frequency input (VAFI), which comprises the allele frequency for said variant in the tumor sample; b) acquiring values, as a function of SCI and SAFI, for: i) a genomic segment total copy number (C) for each of a plurality of genomic segments; ii) a genomic segment minor allele copy number (M) for each of a plurality of genomic segments; and iii) sample purity (p), wherein the values of C, M, and p are obtained by fitting a genome-wide copy number model to SCI and SAFI; and c) acquiring: a value for mutation type, g, for which is indicative of the variant, being somatic, a subclonal somatic variant, germline, or not-distinguishable, and is a function of VAFI, p, C, and M. The SGZ algorithm is described in International Application Publication No. WO 2014/183078 and U.S. Application Publication No. 2014/0336996, the contents of which are incorporated by reference in their entirety. Additionally or alternatively, detection of a genetic biomarker can include a system for evaluating the mutation load in a sample (e.g., a tumor sample or a sample derived from a tumor). The system includes at least one processor operatively connected to a memory, the at least one processor when executing is configured to: a) acquire a sequence,

e.g., a nucleotide sequence, of a set of subgenomic intervals (e.g., coding subgenomic intervals) from the sample, wherein the set of coding subgenomic intervals are from a predetermined set of genes; and b) determine a value for the mutational load, wherein the value is a function of the number of an alteration (e.g., a somatic alteration) in the set of subgenomic intervals. Additionally or alternatively, detection of a genetic biomarker can include a method of analyzing a sample, e.g., a tumor sample from a hematologic malignancy (or premaligancy). The method comprises: (a) acquiring one or a plurality of libraries comprising a plurality members from a sample, e.g., a plurality of tumor members from a tumor sample; (b) optionally, enriching the one or a plurality of libraries for preselected sequences, e.g., by contacting the one or a plurality of libraries with a bait set (or plurality of bait sets) to provide selected members (sometimes referred to herein as library catch); (c) acquiring a read for a subject interval, e.g., a subgenomic interval or an expressed subgenomic interval, from a member, e.g., a tumor member from a library or library catch, e.g., by a method comprising sequencing, e.g., with a next-generation sequencing method; (d) aligning said read by an alignment method, and (e) assigning a nucleotide value (e.g., calling a mutation, e.g., with a Bayesian method) from said read for the preselected nucleotide position, thereby analyzing said tumor sample, optionally wherein: a read from each of X unique subject intervals (e.g., subgenomic intervals, expressed subgenomic intervals, or both) is aligned with a unique alignment method, wherein unique subject interval (e.g., subgenomic interval or expressed subgenomic interval) means different from the other X-1 subject intervals (e.g., subgenomic intervals, expressed subgenomic intervals, or both), and wherein unique alignment method means different from the other X-1 alignment methods, and X is at least 2. In an embodiment, a method (e.g., element (d) of the method recited above) comprises selecting or using an alignment method for analyzing, e.g., aligning, a read, wherein said alignment method is a function of, is selected responsive to, or is optimized for, one or more or all of: (i) tumor type, e.g., the tumor type in said sample; (ii) the gene, or type of gene, in which said subject interval (e.g., subgenomic interval or expressed subgenomic interval) being sequenced is located, e.g., a gene or type of gene characterized by a preselected or variant or type of variant, e.g., a mutation, or by a mutation of a preselected frequency; (iii) the site (e.g., nucleotide position) being analyzed; (iv) the type of variant, e.g., a substitution, within the subject interval (e.g.,

subgenomic interval or expressed subgenomic interval) being evaluated; (v) the type of sample, e.g., an FFPE sample, a blood sample, or a bone marrow aspirate sample; and (vi) sequence in or near said subgenomic interval being evaluated, e.g., the expected propensity for misalignment for said subject interval (e.g., subgenomic interval or expressed subgenomic interval), e.g., the presence of repeated sequences in or near said subject interval (e.g., subgenomic interval or expressed subgenomic interval). In some embodiments, the method can comprise using an alignment method that is appropriately tuned and that includes: selecting a rearrangement reference sequence for alignment with a read, wherein said rearrangement reference sequence is preselected to align with a preselected rearrangement (in embodiments the reference sequence is not identical to the genomic rearrangement); comparing, e.g., aligning, a read with said preselected rearrangement reference sequence. In embodiments, other methods are used to align troublesome reads. These methods are particularly effective when the alignment of reads for a relatively large number of diverse subgenomic intervals is optimized. By way of example, a method of analyzing a tumor sample can comprise: performing a comparison, e.g., an alignment comparison, of a read under a first set of parameters (e.g., a first mapping algorithm or with a first reference sequence), and determining if said read meets a first predetermined alignment criterion (e.g., the read can be aligned with said first reference sequence, e.g., with less than a preselected number of mismatches); if said read fails to meet the first predetermined alignment criterion, performing a second alignment comparison under a second set of parameters, (e.g., a second mapping algorithm or with a second reference sequence); and, optionally, determining if said read meets said second predetermined criterion (e.g., the read can be aligned with said second reference sequence with less than a preselected number of mismatches), wherein said second set of parameters comprises use of a set of parameters, e.g., said second reference sequence, which, compared with said first set of parameters, is more likely to result in an alignment with a read for a preselected variant, e.g., a rearrangement, e.g., an insertion, deletion, or translocation.

[660] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2013/0266938, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods of detecting the presence or

absence of a target nucleic acid sequence in a biological sample. In some embodiments, the method comprises: a. contacting a detectably-labeled probe comprising an anchor nucleic acid domain and a reporter nucleic acid domain with the sample; and b. detecting the presence or absence of binding of the probe to the target nucleic acid, wherein the anchor and reporter domains are linked by a non-nucleoside linker, and neither the anchor nor the reporter domain forms a stem loop in the absence of the target nucleic acid; and wherein (i) the probe is not extendible by a polymerase; (ii) the linker is linked to the anchor domain within 2 nucleotides of the 3′ end of the anchor domain and the linker is linked to the reporter domain within 2 nucleotides of the 5′ end of the reporter domain, wherein the anchor domain is not linked to a detectable label; and/or (iii) the anchor domain and the reporter domain each comprise a contiguous sequence of at least 6 nucleotides complementary to the same strand of the target nucleic acid. In some embodiments, the probe is not extendible by a polymerase In some embodiments, the linker is linked to the anchor domain within 2 nucleotides of the 3′ end of the anchor domain and the linker is linked to the reporter domain within 2 nucleotides of the 5′ end of the reporter domain, wherein the anchor domain is not linked to a detectable label. In some embodiments, the anchor domain and the reporter domain each comprise a contiguous sequence of at least 10 nucleotides complementary to one strand of the target nucleic acid. In some embodiments, the detecting step comprises measuring the melting temperature of a complex formed between the reporter domain and the target nucleic acid. In some embodiments, the length of the reporter domain is between 4 to 20 nucleotides. In some embodiments, the length of the reporter domain is between 6 to 12 nucleotides. Additionally or alternatively, detection of a genetic biomarker can include reaction mixtures for detecting the presence or absence of a target sequence. In some embodiments, the reaction mixture comprises: a. a target nucleic acid comprising an anchor binding region and a reporter binding region, and b. a detectably-labeled probe comprising an anchor nucleic acid domain and a reporter nucleic acid domain, wherein the anchor and reporter domains are linked by a non-nucleoside linker, and neither the anchor nor the reporter domain forms a stem loop in the absence of the target nucleic acid, and wherein (i) the probe is not extendible by a polymerase; (ii) the linker is linked to the anchor domain within 2 nucleotides of the 3′ end of the anchor domain and the linker is linked to the reporter domain within 2 nucleotides of the 5′ end of the

reporter domain, wherein the anchor domain is not linked to a detectable label; and/or (iii) the anchor domain and the reporter domain each comprise a contiguous sequence of at least 6 nucleotides complementary to the same strand of the target nucleic acid. In some embodiments, the reaction mixture further comprises nucleoside triphosphates, a DNA polymerase, and/or an oligonucleotide primer. In some embodiments, the probe is not extendible by a polymerase. Additionally or alternatively, detection of a genetic biomarker can include a detectably-labeled probe comprising an anchor nucleic acid domain and a reporter nucleic acid domain, wherein: the anchor and reporter domains are linked by a non-nucleoside linker; neither the anchor nor the reporter domain forms a stem loop in the absence of the target nucleic acid; and wherein: (i) the probe is not extendible by a polymerase; and/or (ii) the linker is linked to the anchor domain within 2 nucleotides of the 3′ end of the anchor domain and the linker is linked to the reporter domain within 2 nucleotides of the 5′ end of the reporter domain, wherein the anchor domain is not linked to a detectable label. In some embodiments, the probe is not extendible by a polymerase. In some embodiments, the linker is linked to the anchor domain within 2 nucleotides of the 3′ end of the anchor domain and the linker is linked to the reporter domain within 2 nucleotides of the 5′ end of the reporter domain, wherein the anchor domain is not linked to a detectable label. In some embodiments, the length of the reporter domain is between 4 to 20 nucleotides. In some embodiments, the length of the reporter domain is between 6 to 12 nucleotides. In some embodiments, the anchor domain is between 6-40 nucleotides. In some embodiments, the label is a fluorescent label. In some embodiments, the probe comprises at least one non-natural nucleotide, wherein the non-natural nucleotide increases the melting temperature of the reporter domain compared to a corresponding natural nucleotide in the place of the non-natural nucleotide. In some embodiments, the linker is polyethylene glycol. In some embodiments, the linker is hexa-ethylene glycol.

[661] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2012/0225428, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a set of probes comprising DNA and LNA nucleotides. In some embodiments, at the 5′ end of the probes, the nucleobases are determined, whereas at the 3′ end, there are one or more (for example, two or three) random

nucleotides (also referred to as "wobble" positions). An embodiment consists of a short nucleic acid strand that can be used universally for the detection of various target sequences. The short nucleic acid sequence is also allele specific and enables the detection of a specific mutation, such as a single nucleotide polymorphism (SNP). Some embodiments include a composition comprising a first probe and a second probe. According to such embodiments, the first probe has a 5′ end opposite a 3′ end and at least eight nucleotides, the at least eight nucleotides comprising at least one DNA nucleotide and at least five locked nucleic acid nucleotides and a first discriminating position; and a second probe having a 5′ end opposite a 3′ end and a same number of nucleotides as the first probe. The nucleotides of the second probe comprise a same number of DNA nucleotides and locked nucleic acid nucleotides as the first probe and a second discriminating position located at a position corresponding to the first discriminating position in the first probe. Also, according to such embodiments, the nucleotides of the first and second probes comprise one of an adenine nucleobase, a cytosine nucleobase, a guanine nucleobase, a thymine nucleobase, a uracil nucleobase, and a methyl cytosine nucleobase, and the first and second probes comprise differing nucleobases at the first and second discriminating positions. However, according to such embodiments, the first and second probes comprise the same nucleobases at all other nucleotide positions of the probes. Other embodiments comprise a composition including a first and second set of probes. Each probe of the first and second sets have a 5′ end opposite a 3′ end and eight nucleotides. The nucleotides of each probe of the first set have at least one DNA nucleotide, at least five locked nucleic acid nucleotides, and a first discriminatory position, at least one locked nucleic acid nucleotide being a random locked nucleic acid nucleotide, whereas each probe of the second set of probes have a corresponding number of DNA nucleotides, locked nucleic acid nucleotides, and random locked nucleic acid nucleotides as a probe in the first set, and each probe of the second set has a second discriminating position located at a same nucleotide location as a first discriminating position of a probe in the first set. Also, according to some such embodiments, all probes of the first and second sets have a same nucleobase sequences with the exception of (i) the nucleobase at the random locked nucleic acid nucleotides; and (ii) the nucleobase at the first and second discriminating positions. Also, the nucleobase of the second discriminating position differs from the nucleobase of the first discriminating position at the same nucleotide location, and

the at least one random locked nucleic acid nucleotide of each probe of the second set comprises a same nucleobase located at a same nucleotide location of the at least one random locked nucleic acid nucleotide of a probe of the first set. According to such embodiments, the nucleobase of the random locked nucleic acid nucleotide is selected from one of adenine, cytosine, guanine, and thymine, and any possible nucleobase sequence resulting from nucleobase variations at the one or more random locked nucleic acid nucleobase position(s) is represented by at least one probe in both the first and second set of probes. Additionally or alternatively, detection of a genetic biomarker can include a method of determining a genotype at a locus of interest in a sample comprising genetic material is provided. The method includes the steps of contacting the genetic material with a first probe and a second probe and detecting the binding of the first or second probe to the genetic material, thereby determining the genotype at the locus. According to such embodiments, the first and second probes each have a 5′ end opposite a 3′ end and eight nucleotides comprising at least one DNA nucleotide and at least five locked nucleic acid nucleotides. The nucleotides of the first probe comprise a first discriminating position and the nucleotides of the second probe comprise a second discriminating position at a same nucleotide location in the second probe as the first discriminating position in the first probe. Also, the first discriminating position comprises a different nucleobase than the second discriminating position, wherein the nucleobases at the other nucleotides of the first and second probes are the same. Additionally or alternatively, detection of a genetic biomarker can include a composition including a first set of probes and a second set of probes, each of the probes having eight nucleotides being composed of one to three DNA nucleotides and five to seven LNA (locked nucleic acid) nucleotides. According to such embodiments, all probes of the first and the second set of probes have identical nucleotide sequences with the exception of (i) the base(s) at one, two or three LNA random position(s); and (ii) the base at a discriminating position, wherein the one, two or three LNA random position(s) and the discriminating position are located at identical positions in all probes of the first and the second set. Further, according to such embodiments at each LNA random position the base is independently selected from adenine, cytosine, guanine and thymine and any possible sequence resulting from the base variation(s) at the one, two or three LNA random position(s) is represented by at least one probe in each set of probes. Additionally, according

to such embodiments, the base at the discriminating position is identical within each set of probes, but differs between the first and the second set of probes. Additionally or alternatively, detection of a genetic biomarker can include a library of at least two sets of probes. According to such embodiments the library comprises a plurality of sets of probes each of the probes having eight nucleotides with the general structure 5′-D-L-L-L-L-L-X-X-3′ or 5′-D-L-L-L-L-L-X-X-X-3′ (where D is a DNA nucleotide; each L is a LNA nucleotide; and each X is a LNA random nucleotide). Also, within one set of probes, all probes have identical nucleotide sequences with the exception of the two and/or three LNA random nucleotides (with each position of a LNA random nucleotide base being independently selected from adenine, cytosine, guanine and thymine). Also, according to such embodiments, any possible sequence resulting from the base variation(s) at the two positions is represented by a probe in each set of probes and one set of probes differing from the other set of probes in the sequence of at least the DNA nucleotide D or an LNA nucleotide L. Additionally or alternatively, detection of a genetic biomarker can include a method of determining the genotype at a locus of interest in a sample obtained from a subject is provided. The method includes the steps of contacting the sample comprising the genetic material with any of the compositions of the composition embodiments above, and detecting the binding of a probe of the first or the second set of probes to the genetic material, thereby determining the genotype at the locus.

[662] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2010/0248991, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a solid support comprising at least two sequence specific amplification primers wherein at least one primer is bound to said support with an inducible cleavable linker. Preferably, said cleavable linker is a photo-cleavable linker. In a first major embodiment, said solid support is a bead. Such a bead is composed of a material selected from the group consisting of silicon, titanium-dioxide, aluminum oxide, lanthanide oxide, glass, silicates, polystyrene, cellulose, sepharose and polyamide. A bead is either of one pure material or composed of two or more materials, whereas the two or more materials are mixed or assembled in a ordered manner like in core shell particles. The surface of a bead is functionalized in such a manner that oligonucleotides can be attached. Additionally or

alternatively, detection of a genetic biomarker can include a library of beads as disclosed above. Preferably, each member of the plurality of primers which are bound to the bead via a cleavable linker carries a different detectable label or a unique mixture of multiple labels. In some embodiments, the solid support is a microtiter or picotiter (PTP) plate comprising a plurality of wells, characterized in that a plurality of said wells comprises a surface with at least two sequence specific amplification primers wherein at least one primer is bound to said support with a cleavable linker. Additionally or alternatively, detection of a genetic biomarker can include a method for preparing a solid support and preferably a bead comprising at least two sequence specific primers, further characterized in that at least one of said primers is cleavable, said method comprising the steps of providing a solid support carrying at least one or more functional groups, and reacting said one or more functional groups with the reactive group or groups of two sequence specific primers, wherein a cleavable reactive moiety is present either within one of the spacers connecting said solid support with its functional group or one of its functional groups or said cleavable moiety is present within one of the spacers connecting one of said sequence specific primers with its reactive group. Additionally or alternatively, detection of a genetic biomarker can include a method comprising the steps of providing a solid support comprising two functional groups each carrying a different protecting group, deprotecting a first functional group and reacting said group with the reactive group of a first primer, and deprotecting the second functional group and reacting said group of said bead with the reactive group of a second primer. Said two functional groups are connected to the bead via two separate linkers, but in a particular embodiment, said two functional groups are connected to the bead via a two arm linker. In some embodiments, the method comprises the steps of providing a solid support carrying exactly one functional group, deprotecting said functional group, and reacting said group with a mixture of a first and a second sequence specific primer, said first and second primers comprising identical reactive groups, characterized in that at least one of said primers is connected to its reactive group via a cleavable moiety. In some embodiments, the method comprises the steps of providing a bead carrying exactly one functional group, and deprotecting said functional group and reacting said group with an oligonucleotide representing a first and a second amplification primer which are connected by a cleavable moiety. In some embodiments, the method comprises the steps of

providing a bead carrying protected OH groups, protected with two different orthogonal protecting groups, cleaving off one of said orthogonal protecting groups and synthesizing the first primer on the bead, and cleaving off the second of said orthogonal protecting group and synthesizing the second primer on the bead.

[663] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2009/0105081, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and systems for the capture and enrichment of target nucleic acids and analysis of the enriched target nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include the enrichment of targeted sequences in a solution based format. In some embodiments, solution based capture methods comprise probe derived amplicons wherein said probes for amplification are affixed to a solid support. The solid support comprises support-immobilized nucleic acid probes to capture specific nucleic acid sequences (e.g., target nucleic acids) from, for example, a genomic sample. Probe amplification provides probe amplicons in solution which are hybridized to target sequences. Following hybridization of probe amplicons to target sequences, target nucleic acid sequences present in the sample are enriched by capturing (e.g., via linker chemistry such as biotin, digoxigenin, etc.) and washing the probes and eluting the hybridized target nucleic acids from the captured probes (FIG. 1). The target nucleic acid sequence(s), may be further amplified using, for example, non-specific ligation-mediated PCR (LM-PCR), resulting in an amplified pool of PCR products of reduced complexity compared to the original target sample. In some embodiments, hybridization between the probes and target nucleic acids is performed under preferably stringent conditions sufficient to support hybridization between the solution based probe amplicons, wherein said probes comprise linker chemistry and complementary regions of the target nucleic acid sample to provide probe/target hybridization complexes. The complexes are subsequently captured via the linker chemistry and washed under conditions sufficient to remove non-specifically bound nucleic acids and the hybridized target nucleic acid sequences are eluted from the captured probe/target complexes. Additionally or alternatively, detection of a genetic biomarker can include methods of isolating and reducing the genetic complexity of a plurality of nucleic acid molecules, the

method comprising the steps of exposing fragmented, denatured nucleic acid molecules of said population to multiple, different oligonucleotide probes that are bound on a solid support under hybridizing conditions to capture nucleic acid molecules that specifically hybridize to said probes, or exposing fragmented, denatured nucleic acid molecules of said population to multiple, different oligonucleotide probes under hybridizing conditions followed by binding the complexes of hybridized molecules to a solid support to capture nucleic acid molecules that specifically hybridize to said probes, wherein in both cases said fragmented, denatured nucleic acid molecules have an average size of about 100 to about 1000 nucleotide residues, preferably about 250 to about 800 nucleotide residues and most preferably about 400 to about 600 nucleotide residues, separating unbound and non-specifically hybridized nucleic acids from the captured molecules, eluting the captured molecules, and optionally repeating the aforementioned processes for at least one further cycle with the eluted captured molecules. Additionally or alternatively, detection of a genetic biomarker can include an enrichment method for target nucleic acid sequences in a genomic sample, such as exons or variants, preferably SNP sites. This can be accomplished by synthesizing genomic probes specific for a region of the genome to capture complementary target nucleic acid sequences contained in a complex genomic sample. In some embodiments, the method further comprises determining the nucleic acid sequence of the captured and eluted target molecules, in particular by means of performing sequencing by synthesis reactions. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting coding region variation relative to a reference genome, in particular relative to a reference genome that comprises fragmented, denatured genomic nucleic acid molecules, the method as previously described further comprising determining the nucleic acid sequence of the captured and eluted target molecules, in particular by means of performing sequencing by synthesis reactions and comparing the determined sequence to a sequence in a database, in particular to a sequence in a database of polymorphisms in the reference genome to identify variants from the reference genome. In embodiments, nucleic acid (pre-selected) capture probes are immobilized onto a solid support (e.g., slide, chip, bead, etc.) using any number of recognized methods (e.g., spotting, photolithography, in situ synthesis, etc.). In preferred embodiments, the probes are synthesized in situ by maskless array synthesis on a substrate and subsequently amplified by, for example,

PCR resulting in probe derived amplicons in solution. In some embodiments, the probe sequences as synthesized comprise primer binding sites for amplification at one or both the 3′ and 5′ termini (e.g., at or near the ends) of the probes. In some embodiments, the sequence of the primer binding sites on the probes are the same at both the 3′ and 5′ prime ends or the probes, whereas in other embodiments the sequence of the primer binding sites is different at the 3′ prime end then the sequence at the 5′ prime end. In some embodiments, amplification primers for probe amplification further comprise a restriction endonuclease site, for example an MlyI site for easy removal of primer sequences from the final captured target, wherein one of the primers (e.g., forward or reverse primer) further comprises linker chemistry such as a binding moiety or sequence (e.g., biotin, digoxigenin, HIS tag, etc.) and are deposited onto the support with the immobilized probes along with reagents necessary for exponential PCR amplification (e.g., PCR procedures for exponential amplification of targets as known to a skilled artisan). PCR is performed thereby creating amplicons of probe capture sequences such that one of the strands comprises linker chemistry, such as a binding moiety or sequence. The amplicon containing solution is transferred to a vessel (e.g., tube, well of a 96 well plate, etc.) and, in some embodiments, purified from reaction components. An additional round of amplification is preferentially performed on the probe derived amplicons using asymmetric PCR, wherein the linker chemistry labeled primer is in abundance compared to the non-labeled primer to preferentially synthesize single stranded binding moiety/sequence labeled amplicons. The amplicons are purified away from reaction components and transferred to a vessel, denatured nucleic acid sample is added, and hybridization is allowed to occur. Following hybridization, labeled amplicon/target nucleic acid complexes are captured. For example, when biotin is the binding moiety a streptavidin (SA) coated substrate such as SA coated beads (e.g., paramagnetic beads/particles) are used to capture the biotin labeled amplicon/target complex. The SA bound complex is washed and the hybridized target nucleic acids are eluted from the complex and utilized in downstream applications, such as sequencing applications. Additionally or alternatively, detection of a genetic biomarker can include methods for isolating and reducing the complexity of a plurality of nucleic acid sequences comprising providing a solid support wherein said solid support comprises hybridization probes hybridizable to target nucleic acid sequences and providing a fragmented nucleic acid sample

comprising target nucleic acid sequences, amplifying the hybridization probes wherein the amplification products comprise a binding moiety and wherein the amplification products are in solution, hybridizing the nucleic acid sample to the amplification products in solution under conditions such that hybridization between the amplification products and target nucleic acid sequences is allowed to occur, separating the hybridized target nucleic acid sequences/amplification product complexes from non-specifically hybridized nucleic acids by said binding moiety, and eluting the hybridized target nucleic acid sequences from the complex thereby isolation and reducing the complexity of a plurality of nucleic acid sequences. In some embodiments, the solid support is a microarray slide. In some embodiments, the target nucleic acid sample is fragmented genomic DNA with or without adaptor molecules at one or both ends of the fragments. In some embodiments, the hybridization probes comprise a restriction endonuclease site, for example a MlyI site. In some embodiments, probe amplification comprises exponential polymerase chain reaction, and may further comprise asymmetric non-exponential amplification. In some embodiments, the binding moiety is biotin and the capture substrate, such as a bead for example a paramagnetic particle, is coated with streptavidin for separation of the target nucleic acid/amplification product complex from non-specifically hybridized target nucleic acids. In some embodiments, the captured target nucleic acid/amplification product complexes are washed prior to elution of the bound target nucleic acids. In some embodiments, the eluted target nucleic acids are sequenced. Additionally or alternatively, detection of a genetic biomarker can include methods for isolating and reducing the complexity of a plurality of nucleic acid sequences comprising providing a solid support wherein said solid support comprises hybridization probes hybridizable to target nucleic acid sequences and providing a fragmented nucleic acid sample comprising target nucleic acid sequences, amplifying the hybridization probes wherein the amplification products comprise a binding moiety and wherein the amplification products are in solution, hybridizing the nucleic acid sample to the amplification products in solution under conditions such that hybridization between the amplification products and target nucleic acid sequences is allowed to occur, separating the hybridized target nucleic acid sequences/amplification product complexes from non-specifically hybridized nucleic acids by said binding moiety, eluting the hybridized target nucleic acid sequences from the complex thereby isolation and reducing the complexity of a

plurality of nucleic acid sequences, and sequencing the eluted target nucleic acid sequences. In some embodiments, the solid support is a microarray slide. In some embodiments, the target nucleic acid sample is fragmented genomic DNA with or without adaptor molecules at one or both ends of the fragments. In some embodiments, the hybridization probes comprise a restriction endonuclease site, for example a MlyI site. In some embodiments, probe amplification comprises exponential polymerase chain reaction, and may further comprise asymmetric non-exponential amplification. In some embodiments, the binding moiety is biotin and the capture substrate, such as a bead for example a paramagnetic particle, is coated with streptavidin for separation of the target nucleic acid/amplification product complex from non-specifically hybridized target nucleic acids. In some embodiments, the captured target nucleic acid/amplification product complexes are washed prior to elution of the bound target nucleic acids.

[664] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2018/077847, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of making a library of target nucleic acid molecules from a sample comprising a plurality of target molecules, the method comprising for substantially each target molecule: ligating a single adaptor to a target molecule forming a circular molecule, wherein the adaptor comprises two barcodes, two primer binding sites situated between the two barcodes, wherein the primers annealing to the binding sites are facing away from each other, and at least one modified nucleotide effecting a strand synthesis termination by a nucleic acid polymerase situated between the two primer binding sites; annealing a forward primer complementary to the adaptor to one strand of the target molecule; extending the forward primer up to the modified nucleotide, thereby producing a first strand; annealing a reverse primer complementary to the adaptor to the first strand; extending the first primer, thereby producing the second strand and a double- stranded molecule comprising the first strand sand the second strand wherein the two barcodes are flanking the target sequence. In some embodiments, at least one of the forward and the reverse primer comprises a 5'-fiap sequence not complementary to the adaptor and comprising an additional primer binding site. Then the method further comprises a step of annealing an additional primer to the sequence

complementary to the flap sequence in the forward primer and extending the additional primer thereby producing a double-stranded molecule comprising two additional primer sites and the two barcodes flanking the target sequence. In some embodiments, the target molecule and the adaptor are single-stranded. In other embodiments, the target molecule and the adaptor are double-stranded and the circular molecule is at least partially denatured primer to annealing of the primer. In some embodiments the barcode is a nucleotide sequence 4-20 bases long. The modified nucleotide effecting a strand synthesis termination by a nucleic acid polymerase may be selected from abasic nucleotides, nucleotides with protein side groups, synthetic nucleotide AraC (cytarabine) or deoxyuracil, isoguanine, 5- methylisocytosine, ethylene glycol spacers, nucleotides with bulky analogues such as fiuorophores, or unnatural base pair (UBP) "d5SICS-dNaM" nucleic acid analogues. The ligation may be selected from overhang ligation, T-A ligation, blunt-end ligation and topoisomerase catalyzed ligation. In some embodiments, the adaptor has a photocleavable linker on one end. In these embodiments, the linker is ligated on one end and exposed to UV light to enable ligation on the other end. In some embodiments, the additional primers are sequencing primers. Additionally or alternatively, detection of a genetic biomarker can include a library of target nucleic acid molecules wherein each molecule is a circular molecule comprising a target sequence and an adaptor linking the ends of the target sequence, the adaptor comprising: two barcodes; two primer binding sites situated between the two barcodes, wherein the primers annealing to the binding sites are facing away from each other; at least one modified nucleotide effecting a strand synthesis termination by a nucleic acid polymerase situated between the two primer binding sites. In some embodiments, the barcode is a nucleotide sequence 4-20 bases long. The modified nucleotide effecting a strand synthesis termination by a nucleic acid polymerase may be selected from abasic nucleotides, nucleotides with protein side groups, synthetic nucleotide AraC (cytarabine) or deoxyuracil, isoguanine, 5-methylisocytosine, ethylene glycol spacers, nucleotides with bulky analogues such as fiuorophores, or unnatural base pair (UBP) "d5SICS-dNaM" nucleic acid analogues. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing target nucleic acids in a sample comprising a plurality of target molecules, the method comprising: creating a library of target nucleic acid molecules from the sample by ligating a single double-stranded adaptor to substantially each double-stranded target molecule

forming a double stranded circular molecule, wherein the adaptor comprises two barcodes, two primer binding sites situated between the two barcodes, wherein the primers annealing to the binding sites are facing away from each other, and at least one modified nucleotide effecting a strand synthesis termination by a nucleic acid polymerase situated between the two primer binding sites; denaturing at least a portion of the double-stranded circular target molecule; annealing a forward primer complementary to the adaptor to one strand of the target molecule; extending the forward primer up to the modified nucleotide, thereby producing a first strand; annealing a reverse primer complementary to the adaptor to the first strand; extending the first primer, thereby producing the second strand and a double-stranded molecule comprising the first strand and the second strand wherein the two barcodes are flanking the target sequence; amplifying the double stranded molecule; and sequencing the amplified products of the double-stranded molecule. In some embodiments, at least one of the forward and the reverse primer comprises a 5'-flap sequence not complementary to the adaptor and comprising an additional primer binding site. In some embodiments, the method further comprises after extending the first primer, annealing an additional primer to the sequence complementary to the flap sequence in the forward primer and extending the additional primer thereby producing a double-stranded molecule comprising two additional primer sites and the two barcodes flanking the target sequence. In some embodiments, amplifying or sequencing may be performed with the additional primers.

[665] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/123316, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a targeted sequencing workflow where an input sample comprising a sufficient quantity of genomic material is provided such that minimal or no amplification processes are required prior to sequencing. In some embodiments, the input sample is derived from an intact tumor or from lymph nodes. In some embodiments, the input sample is obtained through homogenization of an intact tumor sample (whole or partial) and/or one or more lymph nodes obtained from a patient or mammalian subject. In some embodiments, the input sample is derived from a sufficient quantity of blood, including whole blood or any fraction thereof. In some embodiments, the input sample is derived from

cancerous tissue. In some embodiments, the input sample is derived from precancerous tissue. In some embodiments, the targeted sequencing workflow comprises one or more amplification steps (e.g. a pre-capture amplification step, an amplification step post-capture) prior to sequencing, where each amplification step prior to sequencing comprises from 0 to 3 amplification cycles, and wherein an aggregate of amplification cycles prior to sequencing does not exceed 4. In other embodiments, the targeted sequencing workflow comprises one or more amplification steps (e.g. a pre-capture amplification step, an amplification step post-capture) prior to sequencing, where each amplification step prior to sequencing comprises from 0 to 2 amplification cycles, and wherein an aggregate of amplification cycles prior to sequencing does not exceed 3. In yet other embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing (e.g. either a pre-capture amplification step or an amplification step post-capture), where the single amplification step prior to sequencing comprises from 0 to 3 amplification cycles. In further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises from 1 to 3 cycles. In yet further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises 1 cycle. In even further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises 2 cycles. In some embodiments, either or both of the pre-capture amplification step or the amplification step post-capture but prior to sequencing utilizes LM-PCR. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing genomic material within a sample comprising: homogenizing a tumor sample and/or lymph node sample to provide a homogenized sample; isolating at least 0.5 micrograms of genomic material from the homogenized sample; preparing the at least 0.5 micrograms of isolated genomic material for sequencing; and sequencing the prepared genomic material. In some embodiments, the method does not comprise any amplification steps prior to sequencing. In some embodiments, the method comprises at least one pre-capture or post-capture amplification step, wherein an aggregate number of amplification cycles conducted during the at least one pre-capture or post-capture amplification step is at most 4 cycles. In some embodiments, the aggregate number of

amplification cycles is 3. In some embodiments, the aggregate number of amplification cycles is 2. In some embodiments, the preparing of the at least 0.5 micrograms of isolated genomic material for sequencing comprises hybridizing the at least 0.5 micrograms of isolated genomic to capture probes and capturing the hybridized genomic material. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, 1 or 2 amplification cycles are performed on the captured genomic material. In some embodiments, the homogenized sample comprises a representative sampling of cells. In some embodiments, at least 1 microgram of genomic material is isolated from the homogenized samples. In some embodiments, at least 5 micrograms of genomic material is isolated from the homogenized samples. In some embodiments, at least 10 micrograms of genomic material is isolated from the homogenized samples. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing DNA within a sample comprising isolating at least 0.5 micrograms of DNA from a blood sample; preparing the at least 0.5 micrograms of isolated DNA for sequencing, and sequencing the prepared DNA. In some embodiments, the method comprises 0 amplification steps prior to sequencing. In some embodiments, the preparing of the at least 0.5 micrograms of isolated DNA for sequencing comprises hybridizing the at least 0.5 micrograms of isolated genomic to capture probes and capturing the hybridized genomic material. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, 1 or 2 amplification cycles are performed on the captured genomic material. In some embodiments, at least 1 microgram of DNA is isolated from the blood sample. Additionally or alternatively, detection of a genetic biomarker can include a method of targeted representational sequencing comprising: (i) homogenizing at least a portion of a tumor, one or more whole or partial lymph nodes, or any combination thereof to provide a homogenized sample; (ii) extracting genomic material from the homogenized sample; (iii) capturing the extracted genomic material onto beads; and (iv) sequencing the captured genomic material; wherein the targeted representational sequencing comprises performing at most 4 amplification cycles prior to sequencing of the captured genomic material. In some embodiments, the at most 3 amplification cycles may be conducted prior to capture of the extracted genomic material or after capture of the extracted genomic material, or any combination thereof. In some

embodiments, no pre-capture amplification cycles are conducted. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, from 1 to 3 amplification cycles are performed following capture of the extracted genomic material, but prior to sequencing. In some embodiments, at least 0.5 micrograms of genomic material is extracted from the homogenized sample. In some embodiments, at least 100 times more genomic material is derived from the homogenized sample as compared with an amount of input material used in a sequencing method requiring more than 4 amplification cycles. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing DNA within a sample comprising: providing at least 0.5 micrograms of input genomic material, the at least 0.5 micrograms of genomic material derived from a tumor sample, a lymph node sample, or a blood sample, isolating DNA from the input genomic sample, preparing the isolated DNA for sequencing, and sequencing the prepared DNA, wherein the method does not comprise any amplification steps. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from multiple histological and/or biopsy specimens. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from a homogenized tumor sample. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from a homogenized lymph node sample. In some embodiments, the at least 0.5 micrograms of input genomic material is a representative sampling of the tumor sample, lymph node sample, or blood sample from which it is derived. In some embodiments, the sequencing is performed using a next-generation sequencing method. In some embodiments, sequencing is performed using a synthesis sequencing methodology. Additionally or alternatively, detection of a genetic biomarker can include a method of reducing PCR- introduced mutations during sequencing comprising isolating DNA from a sample comprising a sufficient amount of genomic material; preparing the isolated DNA for sequencing; and sequencing the prepared DNA, wherein the method comprises at most 3 amplification cycles prior to sequencing. In some embodiments, the method comprises 1 or 2 amplification cycles prior to sequencing. In some embodiments, sufficient amount of input genomic material is an amount such that no pre-capture amplification cycles are utilized. In some embodiments, the sample is derived from a patient suspected of having cancer. In some embodiments, the sample is derived from a patient

diagnosed with cancer. In some embodiments, the sample is derived from a patient at risk of developing cancer. In some embodiments, the sample is derived from healthy tissue samples. In some embodiments, 0.5 micrograms of DNA is isolated from the sample. In some embodiments, at least 1 microgram of genomic material is isolated from the sample. In some embodiments, at least 5 micrograms of genomic material is isolated from the sample. In some embodiments, at least 10 micrograms of genomic material is isolated from the sample. Additionally or alternatively, detection of a genetic biomarker can include a sequencing method where PCR-introduced mutations are reduced, the sequencing method comprising capturing at least 0.05 micrograms of genomic material, and performing between 0 and 2 amplification cycles prior to sequencing. In some embodiments, 0 amplification cycles are conducted. In other embodiments, 1 amplification cycle is conducted. In yet other embodiments, 2 amplification cycles are conducted. Additionally or alternatively, detection of a genetic biomarker can include a sequence capture method where PCR-introduced biases in the proportional representation of genome content are reduced, the sequencing method comprising providing an input sample comprising at least 0.5 micrograms of genomic material, and where the sequence capture method comprises performing between 0 and 2 amplification cycles prior to sequencing. In some embodiments, 0 amplification cycles are conducted. In other embodiments, 1 amplification cycle is conducted. In yet other embodiments, 2 amplification cycles are conducted. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. Additionally or alternatively, detection of a genetic biomarker can include a sequence capture method where PCR-introduced mutations are eliminated, the sequence capture method comprising preparing an input sample comprising at least 0.5 micrograms of genomic material. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. In another aspect is a sequence capture method where a step of removing PCR-duplicate reads prior to sequencing is eliminated, the sequence capture method comprising providing an input sample comprising at least 0.5 micrograms of

genomic material. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. Additionally or alternatively, detection of a genetic biomarker can include a sequencing method where PCR-introduced mutations are virtually eliminated, the sequencing method comprising capturing at least 0.05 micrograms of genomic material. In some embodiments, about 0.05 micrograms of genomic material are provided after capture of the genomic material. In some embodiments, 1 or 2 post-capture amplification cycles are performed prior to sequencing.

[666] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/132276, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods in which regions of a tumor sample predicted not to respond to a first therapeutic agent are excised from the sample with an automated dissection tool, mutations correlated with predictive biomarkers are detected in the excised region using NGS, and additional samples of the tumor are stained for one or more predictive biomarker(s) identified by NGS. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: obtaining a first sample of a tumor, wherein the first sample is histochemically stained for a first predictive biomarker for a first therapeutic agent; excising one or more region(s) from the first sample with an automated dissection tool, wherein the excised region has a staining pattern for the first predictive biomarker indicating that the region is unlikely to respond to the first therapeutic agent; detecting with a next generation sequencer one or more one or more mutations predictive of a response to one or more additional therapeutic agents in a nucleic acid sample derived from the excised region(s) of the first sample; staining one or more additional samples of the tumor for one or more additional predictive biomarker(s) correlating to the one or more mutations identified in the samples, the one or more additional predictive biomarkers being predictive of a response to one or more of the additional therapeutic agent(s). Additionally or alternatively, detection of a genetic biomarker can include a system comprising: (a) a nucleic acid sample derived from one or more regions excised from a first sample of a tumor, wherein the first sample of the tumor is

stained for a first predictive biomarker, and further wherein the one or more regions excised from the section have a staining pattern of the first predictive biomarker indicating that at least a portion of the tumor is unlikely to respond to a first therapeutic agent; (b) a next generation sequencer adapted to identify the presence or absence of mutations correlating to one or more additional predictive biomarkers; (c) a laboratory information system (LIS) comprising a database, the database containing: (cl) mutation analysis of a nucleic acid sample by next generation sequencing, wherein the mutation analysis indicates at least the presence or absence of mutations in the nucleic acid sample, the mutations correlating to one or more additional predictive biomarker(s) for one or more additional therapeutic agent(s); and (c2) instructions for directing an automated slide stainer to stain a second sample of the tumor with the one or more additional predictive biomarkers identified by the mutation analysis.

[667] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 10,023,917, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include High Resolution Melting (HRM) assays as a prescreening diagnostic method to diagnose mutations in the hot spot regions of the most common genes (KRAS, BRAF, PIK3CA, AKT1) concerning the RAS/RAF/MAPK and PI3K/PTEN/AKT pathway. Additionally or alternatively, detection of a genetic biomarker can include pairs of amplification primers, which are useful for HRM analysis of genes which are important for predicting responsiveness to cancer therapeutic agents. Additionally or alternatively, detection of a genetic biomarker can include the following pairs of amplification primers for amplification and analysis of KRAS, exons 2 and 3, BRAF, exon 15, PIK3CA, exons 7, 9 and 20, and AKT1, exon 2. Additionally or alternatively, detection of a genetic biomarker can include a composition or reaction mixture comprising at least one pair of amplification primers as disclosed above. The composition may be used for PCR amplification of nucleic acids during a nucleic acid amplification reaction, and also PCR amplification and monitoring in real time. According to some embodiments, a mixture comprises at least: a pair of amplification primers as disclosed above; a thermostable DNA Polymerase; a mix of deoxynucleoside triphosphates which is usually dA, dG, dC and dT, or dA, dG, dC and dU; and a buffer. In some further embodiments, when suitable for amplification and detection in real time, of one

or more specific nucleic acid target sequence(s) such a composition additionally comprises a nucleic acid detecting entity such as a fluorescent hybridization probe, or a fluorescent, double stranded DNA binding dye. In some embodiments, such a DNA double stranded Dye is a dye which can be used to perform HRM curve analysis. In some embodiments, the pair of amplification primers is designed to amplify a specific sequence of interest according to standard methods known in the art of molecular biology. In some embodiments, when brought into contact with a sample that shall be analyzed, such a PCR reaction mixture additionally comprises an at least partially purified DNA or other nucleic acid which putatively comprises a specific sequence of interest. Also, in some such embodiments, the concentrations of all reagents included are generally as known to persons skilled in the art and can be optimized for specific adaptations according to standard protocols. In some such embodiments, the concentration of the fluorescent, double stranded DNA binding dye is between approximately 0.1 to 10.0 μg/ml. In some embodiments, a kit is provided. Some illustrative embodiments of kits include at least one pair of amplification primers. Some embodiments of kits may further comprise one, several, or all of the following additional ingredients; a thermostable DNA Polymerase; a mix of deoxynucleoside triphosphates which is usually dA, dG, dC and dT, or dA, dG, dC and dU, and a buffer, and a fluorescent, double stranded DNA binding dye, which may be suited to be used for HRM. Additionally or alternatively, detection of a genetic biomarker can include a method for determining the increased likelihood of a response to a targeted treatment of a cancer disease, comprising the steps of: a) isolating genomic DNA from a patient sample; b) amplifying at least one fragment of said DNA by means of PCR with a specific pair of amplification primers; c) determining, whether said amplified fragment has a wildtype sequence or comprises a mutation by means of a High Resolution Melting Analysis (HRM); and d) correlating the presence or absence of a mutation with an increased likelihood of success of said targeted treatment. In some embodiments, the mutation is identified by means of a hybridization analysis or by means of sequencing. For example, the patient sample may be Formalin Fixed Paraffin Embedded (FFPE) tissue. In some such cases, HRM Analysis may be performed without any spiking of DNA.

[668] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,873,908,

which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods for enriching low abundance alleles (e.g. mutant DNA) in a sample that allows subsequent detection of such alleles. Additionally or alternatively, detection of a genetic biomarker can include a method of enriching a variant of a target nucleic acid in a mixture of nucleic acids from a sample, the target nucleic acid existing in the form of two variant sequences, wherein said variants differ at a single nucleotide position, the method comprising, providing the sample that includes the target nucleic acid wherein the variant to be enriched is present in the sample in low abundance amongst a large excess of the other variant; providing an oligonucleotide that is complementary to one strand of the target nucleic acid at a concentration that is in molar excess to the target nucleic acid, wherein the oligonucleotide is attached with an affinity label and is perfectly matched at the single nucleotide position with the variant to be enriched and has a mismatch at the single nucleotide position with the other variant; providing conditions suitable for hybridization of the oligonucleotide to the target nucleic acid to generate duplex polynucleotides consisting of the oligonucleotide and one strand of either variant of the target nucleic acid; contacting the duplex polynucleotides with a mismatch intercalating compound that preferentially binds to only the duplex polynucleotides that contain a mismatch wherein said compound is further capable of catalyzing cleavage of one strand of the duplex polynucleotide at the mismatch site with light; subjecting the duplex polynucleotides to light resulting in both cleaved and uncleaved duplex polynucleotides; applying both cleaved and uncleaved duplex polynucleotides to an affinity matrix that recognizes and binds to the affinity label on the oligonucleotide; providing conditions whereby only the cleaved duplex polynucleotide is denatured and removing the denatured single strand from the affinity matrix; and providing a buffer under conditions to denature the uncleaved polynucleotide duplex; and collecting the buffer which contains one strand of the enriched variant of the target nucleic acid. In one embodiment, the mismatch intercalating compound is Rh(bpy)2(chrysi)3+ or Rh(bpy)2(phzi)3+ or their respective analogs. Additionally or alternatively, detection of a genetic biomarker can include a further step of amplifying and detecting the enriched variant of the target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a mutant allele of a target nucleic acid in a mixture of nucleic acids from a sample wherein the mutant

allele differs from a wild-type allele at a single nucleotide position and is present in the sample in low abundance amongst a large excess of the wild-type allele, the method comprising enriching the mutant allele in the sample wherein the enrichment is performed by providing an oligonucleotide that is complementary to one strand of the target nucleic acid at a concentration that is in molar excess to the target nucleic acid, wherein the oligonucleotide is attached with an affinity label and is perfectly matched at the single nucleotide position with the mutant allele and has a mismatch at the single nucleotide position with the wild-type allele; providing conditions suitable for hybridization of the oligonucleotide to the target nucleic acid to generate duplex polynucleotides consisting of the oligonucleotide and one strand of either the mutant allele or the wild-type allele; contacting the duplex polynucleotides with a mismatch intercalating compound that preferentially binds to only the duplex polynucleotides that contain a mismatch wherein said compound is further capable of catalyzing cleavage of one strand of the duplex polynucleotide at the mismatch site with light; subjecting the duplex polynucleotides to light resulting in both cleaved and uncleaved duplex polynucleotides; applying both cleaved and uncleaved duplex polynucleotides to an affinity matrix that recognizes and binds to the affinity label on the oligonucleotide; providing conditions whereby only the cleaved duplex polynucleotide is denatured and removing the denatured single strand of the wild-type allele from the affinity matrix; providing a buffer under conditions to denature the uncleaved polynucleotide duplex; and collecting the buffer which contains one strand of the enriched mutant allele of the target nucleic acid; amplifying the enriched mutant allele; and detecting the product of the enriched amplified mutant allele or the signal generated from the enriched amplified mutant allele. In one embodiment, the mismatch intercalating compound is Rh(bpy)2(chrysi)3+ or Rh(bpy)2(phzi)3+ or their respective analogs.

[669] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,399,794, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of detecting the presence or absence of a target nucleic acid in a test sample comprising: inputting into a learning statistical classifier system data from a training set of samples where the amount of the target nucleic acid and a control nucleic acid is known, using the learning statistical classifier system, calculating a plurality of weights for

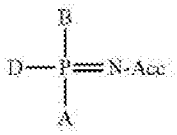
a general linear classifier; building a general linear classifier with the plurality of weights calculated by the learning statistical classifier system; contacting the test sample with a reaction mixture containing reagents necessary to amplify the target and the control nucleic acids by polymerase chain reaction (PCR) under conditions enabling PCR; measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain a test set of data; applying the general linear classifier to the test set of data to classify the test sample as containing or not containing the target nucleic acid, thereby detecting the presence or absence of the target nucleic acid in the test sample. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the amplification-dependent parameter is fluorescence detected during each cycle of amplification. In further variations of this embodiment, the data is cycle-to-threshold (Ct) value. In further variations of this embodiment, the general linear classifier is a piece-wise linear classier. In further variations of this embodiment, a piece-wise function determined by constraints placed upon the amplification-dependent parameter for the control nucleic acid is input into the piece-wise linear classifier. In further variations of this embodiment, the target nucleic acid is a nucleic acid variant of a human sequence. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting the presence or absence of a target nucleic acid in a test sample comprising: inputting into a learning statistical classifier system data from a training set of samples where the amount of the target nucleic acid and a control nucleic acid is known; using the learning statistical classifier system, calculating a plurality of weights for a general linear classifier; building a general linear classifier with the plurality of weights calculated by the learning statistical classifier system; subjecting the sample to polymerase chain reaction (PCR); measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain a test set of data; applying the general linear classifier to the test set of data; classifying the test sample as containing or not containing the target nucleic acid, thereby detecting the presence or absence of the target nucleic acid in the test sample. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the amplification-dependent parameter is fluorescence detected during each cycles of amplification. In further variations of this embodiment, the data is cycle-

to-threshold (Ct) value. In further variations of this embodiment, the general linear classifier is a piece-wise linear classifier. In further variations of this embodiment, a piece-wise function determined by constraints placed upon the amplification-dependent parameter for the control nucleic acid is input into the piece-wise linear classifier. In further variations of this embodiment, the target nucleic acid is a nucleic acid variant of a human sequence. Additionally or alternatively, detection of a genetic biomarker can include a method of determining whether a target nucleic acid is present in a test sample comprising: subjecting a training set of samples wherein the amount of the target nucleic acid and a control nucleic acid is known to polymerase chain reaction (PCR) and measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain a training set of data; inputting the data into a learning statistical classifier system; using the learning statistical classifier system, calculating a plurality of weights for a general linear classifier; building a general linear classifier with the plurality of weights determined by the learning statistical classifier system; subjecting the test sample to PCR and measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain a test set of data; applying the general linear classifier to the test set of data; classifying the test sample as containing or not containing the target nucleic acid. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the amplification-dependent parameter is fluorescence detected during each cycles of amplification. In further variations of this embodiment, the data is cycle-to-threshold (Ct) value. In further variations of this embodiment, the general linear classifier is a piece-wise linear classifier. In further variations of this embodiment, a piece-wise function determined by constraints placed upon the amplification-dependent parameter for the control nucleic acid is input into the piece-wise linear classifier. In further variations of this embodiment, the target nucleic acid is a nucleic acid variant of a human sequence. Additionally or alternatively, detection of a genetic biomarker can include a method of determining whether a target nucleic acid is present in a test sample comprising: subjecting a training set of samples wherein the amount of the target nucleic acid and a control nucleic acid is known to polymerase chain reaction (PCR) and measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain a training set of data; inputting the data into a learning

statistical classifier system; using the learning statistical classifier system, calculating a plurality of weights for a general linear classifier; building a general linear classifier with the plurality of weights determined by the learning statistical classifier system; subjecting the test sample to PCR and measuring at least one amplification-dependent parameter for the target and the control nucleic acids to obtain the test set of data; applying the general linear classifier to the test set of data obtained; classifying the test sample as containing or not containing the target nucleic acid. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the amplification-dependent parameter is fluorescence detected during each cycles of amplification. In further variations of this embodiment, the data is cycle-to-threshold (Ct) value. In further variations of this embodiment, the general linear classifier is a piece-wise linear classifier. In further variations of this embodiment, a piece-wise function determined by constraints placed upon the amplification-dependent parameter for the control nucleic acid is input into the piece-wise linear classifier. In further variations of this embodiment, the target nucleic acid is a nucleic acid variant of a human sequence. Additionally or alternatively, detection of a genetic biomarker can include a computer readable medium including code for controlling one or more processors to classify whether a test sample contains a target nucleic acid, the code including instructions to: apply a learning statistical classifier system to a training data set where the amount of the target nucleic acid and a control nucleic acid is known, in order to build a general linear classifier of Formula I; apply the general linear classifier to a testing data set comprising the data from the test sample to produce a statistically derived decision classifying the test sample as containing or not containing the target nucleic acid. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the data in the datasets is cycle-to-threshold (Ct) value. In further variations of this embodiment, the general linear classifier is a piece-wise linear classifier. In further variations of this embodiment, the target nucleic acid is a nucleic acid variant of a human sequence. Additionally or alternatively, detection of a genetic biomarker can include a system for detecting a target nucleic acid in a test sample comprising: a data acquisition module configured to produce a data set from a training set of samples and one or more test samples, the data set indicating presence and

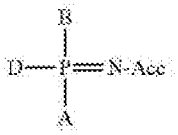
amount of the target nucleic acid and a control nucleic acid; a data processing unit configured to process the data acquired by the acquisition module by applying a learning statistical classifier system to the training data set in order to build a general linear classifier of Formula I, and then apply the general linear classifier of Formula I to the test data set comprising the data from the test sample, to produce a statistically derived decision classifying the test sample as containing or not containing the target nucleic acid; a display module configured to display the data produced by the data processing unit. In variations of this embodiment, the learning statistical classifier system is selected from SVM, LDA and QDA. In further variations of this embodiment, the general linear classifier is a piece-wise linear classifier.

[670] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,382,581, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of allele-specific amplification of a variant of a target sequence, the target existing in the form of several variant sequences, the method comprising, (a) hybridizing a first oligonucleotide and a second oligonucleotide to at least one variant of the target sequence; wherein the first oligonucleotide is at least partially complementary to one or more variants of the target sequence, and the second oligonucleotide is at least partially complementary to one or more variants of the target sequence, and has at least one selective nucleotide complementary to only one variant of the target sequence; wherein said second oligonucleotide comprises both a nucleotide with a base covalently modified at the exocyclic amino group and a modified phosphate having a structure:



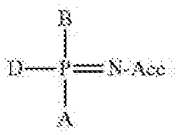
[671] wherein A and B represents a nucleotide chain, D is OH or CH3, and Acc is an electron acceptor or an electron acceptor substituted with a residue R wherein R is an organic substituent, wherein Acc is selected from the group consisting of CN, SO2—R′, in which R′ comprises at least one amino-substituted alkyl, an optionally substituted aryl or an optionally substituted heterocycle, and a six membered N+ heterocycle with at least one alkylated N-atom in ortho- or para-position, said heterocycle selected from the group consisting of pyridinium,

pyrimidinium, and quinolinium; (b) providing conditions suitable for oligonucleotide extension by a nucleic acid polymerase; (c) extending said first oligonucleotide and said second oligonucleotide by said nucleic acid polymerase, wherein said nucleic acid polymerase is capable of extending said second oligonucleotide efficiently when said oligonucleotide is hybridized to a variant of the target sequence which is complementary to said at least one selective nucleotide, and substantially less efficiently when said second oligonucleotide is hybridized to a variant of the target sequence which is not complementary to said at least one selective nucleotide. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a variant of a target sequence, the target existing in the form of several variant sequences, the method comprising, (a) hybridizing a first oligonucleotide and a second oligonucleotide to at least one variant of the target sequence; wherein the first oligonucleotide is at least partially complementary to one or more variants of the target sequence, and the second oligonucleotide is at least partially complementary to one or more variants of the target sequence, and has at least one selective nucleotide complementary to only one variant of the target sequence; wherein said second oligonucleotide comprises both a nucleotide with a base covalently modified at the exocyclic amino group and a modified phosphate having a structure:

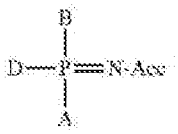


[672] herein A and B represents a nucleotide chain, D is OH or CH3, and Acc is an electron acceptor or an electron acceptor substituted with a residue R wherein R is an organic substituent, wherein Acc is selected from the group consisting of CN, SO2—R′, in which R′ comprises at least one amino-substituted alkyl, an optionally substituted aryl or an optionally substituted heterocycle, and a six membered N+ heterocycle with at least one alkylated N-atom in ortho- or para-position, said heterocycle selected from the group consisting of pyridinium, pyrimidinium, and quinolinium; (b) providing conditions suitable for oligonucleotide extension by a nucleic acid polymerase; (c) extending said first oligonucleotide and said second oligonucleotide by said nucleic acid polymerase, wherein said nucleic acid polymerase is capable of extending said second oligonucleotide efficiently when said oligonucleotide is hybridized to a variant of the target sequence which is complementary to said at least one

selective nucleotide, and substantially less efficiently when said second oligonucleotide is hybridized to a variant of the target sequence which is not complementary to said at least one selective nucleotide; (d) detecting products of said oligonucleotide extension, wherein said extension signifies the presence of the variant of said target sequence to which said second oligonucleotide has a complementary selective nucleotide. Additionally or alternatively, detection of a genetic biomarker can include an oligonucleotide for performing an allele-specific amplification of a target sequence, the target existing in the form of several variant sequences, the oligonucleotide comprising, (a) a sequence at least partially complementary to a portion of one or more variants of said target sequence; (b) at least one selective nucleotide complementary to only one variant of the target sequence; (c) a nucleotide with a base covalently modified at the exocyclic amino group; (d) a modified phosphate having a structure:



[673] wherein A and B represents a nucleotide chain, D is OH or CH3, and Acc is an electron acceptor or an electron acceptor substituted with a residue R wherein R is an organic substituent, wherein Acc is selected from the group consisting of CN, SO2—R′, in which R′ comprises at least one amino-substituted alkyl, an optionally substituted aryl or an optionally substituted heterocycle, and a six membered N+ heterocycle with at least one alkylated N-atom in ortho- or para-position, said heterocycle selected from the group consisting of pyridinium, pyrimidinium, and quinolinium. Additionally or alternatively, detection of a genetic biomarker can include a reaction mixture for allele-specific amplification of a target sequence, the target existing in the form of several variant sequences, the mixture comprising, (a) a first oligonucleotide, at least partially complementary to one or more variant of the target sequence; and (b) a second oligonucleotide, at least partially complementary to one or more variants of the target sequence, and has at least one selective nucleotide complementary to only one variant of the target sequence; wherein said second oligonucleotide comprises both a nucleotide with a base covalently modified at the exocyclic amino group and a modified phosphate having a structure:



[674] wherein A and B represents a nucleotide chain, D is OH or CH3, and Acc is an electron acceptor or an electron acceptor substituted with a residue R wherein R is an organic substituent, wherein Acc is selected from the group consisting of CN, SO2—R′, in which R′ comprises at least one amino-substituted alkyl, an optionally substituted aryl or an optionally substituted heterocycle, and a six membered N+ heterocycle with at least one alkylated N-atom in ortho- or para-position, said heterocycle selected from the group consisting of pyridinium, pyrimidinium, and quinolinium; (c) a nucleic acid polymerase; (d) nucleoside triphosphates; and (e) a buffer suitable for the extension of nucleic acids by the nucleic acid polymerase.

[675] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,279,146, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods and compositions for enriching low abundance alleles (e.g. mutant DNA) in a sample that allows subsequent detection of such alleles. Additionally or alternatively, detection of a genetic biomarker can include a method of enriching a variant of a target nucleic acid sequence in a mixture of nucleic acids from a sample, the target nucleic acid existing in the form of two variant sequences, wherein said variants differ at a single nucleotide position, the method comprising, providing the sample that includes the target nucleic acid sequence wherein the variant to be enriched is present in the sample in low abundance amongst a large excess of the other variant; providing an oligonucleotide that is complementary to one strand of the target nucleic acid sequence, wherein the oligonucleotide has a mismatch at the single nucleotide position with the variant to be enriched and is perfectly matched at the single nucleotide position with the other variant; providing conditions suitable for hybridization of the oligonucleotide to the target nucleic acid to generate duplex polynucleotides consisting of the oligonucleotide and one strand of either variant of the target nucleic acid sequence; contacting the duplex polynucleotides with a mismatch intercalating compound that is attached with an affinity label to generate a reaction mixture, wherein said mismatch intercalating compound is capable of binding to the duplex polynucleotides that

contain a mismatch and is not capable of binding to the duplex polynucleotides that do not contain a mismatch; subjecting the reaction mixture to an affinity matrix that recognizes and binds to the affinity label on the mismatch intercalating compound; washing the reaction mixture and separating the affinity matrix from all material that is not bound to the affinity matrix; and providing a buffer to elute nucleic acid from the affinity matrix, and collecting the eluted buffer which contains the enriched variant of the target nucleic acid sequence. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a mutant allele of a target nucleic acid sequence in a mixture of nucleic acids from a sample wherein the mutant allele differs from a wild-type allele at a single nucleotide position and is present in the sample in low abundance amongst a large excess of the wild-type allele, the method comprising, enriching the mutant allele in the sample wherein the enrichment is performed by providing an oligonucleotide that is complementary to one strand of the target nucleic acid sequence, wherein the oligonucleotide has a mismatch at the single nucleotide position with the mutant allele and is perfectly matched at the single nucleotide position with the wild-type allele; providing conditions suitable for hybridization of the oligonucleotide to the target nucleic acid to generate duplex polynucleotides consisting of the oligonucleotide and one strand of either the mutant allele or the wild-type allele; contacting the duplex polynucleotides with a mismatch intercalating compound that is attached with an affinity label to generate a reaction mixture, wherein the mismatch intercalating compound is capable of binding to the duplex polynucleotides that contain a mismatch and is not capable of binding to the duplex polynucleotides that do not contain a mismatch; subjecting the reaction mixture to a affinity matrix that recognizes and binds to the affinity label on the mismatch intercalating compound; washing the reaction mixture and separating the affinity matrix from all material that is not bound to the affinity matrix; and providing a buffer to elute nucleic acid from the affinity matrix, and collecting the eluted buffer which contains the enriched mutant allele; amplifying the enriched mutant allele; and detecting the product of the enriched amplified mutant allele or the signal generated from the enriched amplified mutant allele. Additionally or alternatively, detection of a genetic biomarker can include a method of enriching a variant of a target nucleic acid sequence in a mixture of nucleic acids from a sample, the target nucleic acid existing in the form of two variant sequences, wherein said variants differ at a single

nucleotide position, the method comprising: providing the sample that includes the target nucleic acid sequence wherein the variant to be enriched is present in the sample in low abundance amongst a large excess of the other variant; heating the sample such that the mixture of nucleic acid is denatured; providing conditions suitable for the reannealing of the target nucleic acid, wherein duplex polynucleotides can be formed between one strand of one variant sequence and one strand of the other variant sequence to generate a mismatch at the single nucleotide position where the variants differ; contacting the duplex polynucleotides with a mismatch intercalating compound that is attached with an affinity label to generate a reaction mixture, wherein said mismatch intercalating compound is capable of binding to the duplex polynucleotides that contain a mismatch and is not capable of binding to the duplex polynucleotides that do not contain a mismatch; subjecting the reaction mixture to an affinity matrix that recognizes and binds to the affinity label on the mismatch intercalating compound; washing the reaction mixture and separating the affinity matrix from all material that is not bound to the affinity matrix; and providing a buffer to elute nucleic acid from the affinity matrix, and collecting the eluted buffer which contains the enriched variant of the target nucleic acid sequence. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting a mutant allele of a target nucleic acid sequence in a mixture of nucleic acids from a sample wherein the mutant allele differs from a wild-type allele at a single nucleotide position and is present in the sample in low abundance amongst a large excess of the wild-type allele, the method comprising: enriching the mutant allele in the sample wherein the enrichment is performed by: heating the sample such that the mixture of nucleic acid is denatured; providing conditions suitable for the reannealing of the target nucleic acid, wherein duplex polynucleotides can be formed between one strand of the mutant allele and one strand of the wild-type allele to generate a mismatch at the single nucleotide position where the alleles differ; contacting the duplex polynucleotides with a mismatch intercalating compound that is attached with an affinity label to generate a reaction mixture, wherein said mismatch intercalating compound is capable of binding to the duplex polynucleotides that contain a mismatch and is not capable of binding to the duplex polynucleotides that do not contain a mismatch; subjecting the reaction mixture to an affinity matrix that recognizes and binds to the affinity label on the mismatch intercalating compound; washing the reaction mixture and

separating the affinity matrix from all material that is not bound to the affinity matrix; and providing a buffer to elute nucleic acid from the affinity matrix, and collecting the eluted buffer which contains the enriched variant of the target nucleic acid sequence; amplifying the enriched mutant allele; and detecting the product of the enriched amplified mutant allele or the signal generated from the enriched amplified mutant allele.

[676] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 9,238,832, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of allele-specific amplification of a variant of a target sequence, the target existing in the form of several variant sequences, the method comprising (a) hybridizing a first and a second oligonucleotides to at least one variant of the target sequence; wherein the first oligonucleotide is at least partially complementary to one or more variants of the target sequence, and the second oligonucleotide is at least partially complementary to one or more variants of the target sequence, and has at least one internal selective nucleotide complementary to only one variant of the target sequence; (b) extending the second oligonucleotide with a nucleic acid polymerase, wherein said polymerase is capable of extending said second oligonucleotide preferentially when said selective nucleotide forms a base pair with the target, and substantially less when said selective nucleotide does not form a base pair with the target. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a variant of a target sequence, the target existing in the form of several variant sequences, the method comprising (a) hybridizing a first and second oligonucleotides to at least one variant of the target sequence; wherein said first oligonucleotide is at least partially complementary to one or more variants of the target sequence and said second oligonucleotide is at least partially complementary to one or more variants of the target sequence, and has at least one internal selective nucleotide complementary to only one variant of the target sequence; (b) extending the second oligonucleotide with a nucleic acid polymerase; wherein said polymerase is capable of extending said second oligonucleotide preferentially when said selective nucleotide forms a base pair with the target, and substantially less when said selective nucleotide does not form a base pair with the target; and (c) detecting the products of said oligonucleotide extension,

wherein the extension signifies the presence of the variant of a target sequence to which the oligonucleotide has a complementary selective nucleotide. Additionally or alternatively, detection of a genetic biomarker can include an oligonucleotide for performing an allele-specific amplification of a target sequence, said target existing in the form of several variant sequences, the oligonucleotide comprising (a) a sequence at least partially complementary to a portion of one or more variants of said target sequence; (b) at least one internal selective nucleotide complementary to only one variant of the target sequence. Additionally or alternatively, detection of a genetic biomarker can include a reaction mixture for allele-specific amplification of a target sequence, said target existing in the form of several variant sequences, the mixture comprising (a) a first oligonucleotide, at least partially complementary to one or more variant of the target sequence; and (b) a second oligonucleotide, at least partially complementary to one or more variants of the target sequence but having at least one internal selective nucleotide complementary to only one variant of the target sequence.

[677] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2016/0092630, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include accurate and fast mapping of sequencing reads obtained from a targeted sequencing. For example, once a target region is selected, alternate regions of the genome that are sufficiently similar to the target region can be identified. If a sequencing read is more similar to the target region than to an alternate region, then the read can be determined as aligning to the target region. The reads aligning to the target region can then be analyzed to determine whether a mutation exists in the target region. Accordingly, a sequencing read can then be compared to the target region and the corresponding alternate regions, and not to the entire genome, thereby providing computational efficiency. Additionally or alternatively, detection of a genetic biomarker can include a method detects variants in a target region of a sample genome of an organism. A plurality of sequence reads are received. The sequence reads are obtained from sequencing genomic segments in a sample obtained from the organism, where the sequencing includes targeting genomic segments from the target region. One or more alternate regions that have a respective first number of variations from the target region of a reference genome are identified. Each

respective first number is greater than one and less than a first threshold number. A computer system performs an alignment of the plurality of sequence reads to the target region of the reference genome to identify a set of sequence reads that align to the target region of the reference genome with less than a second threshold number of variations. Sequence reads that align to one of the alternate regions with a second number of variations that is less than a third threshold number can be removed from the set. The remaining sequence reads of the set are analyzed to determine variants in the target region of the sample genome.

[678] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,977,108, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include approaches for rapidly and reliably detecting and differentiating between mutant and non-mutant forms of nucleic acids that comprise repetitive nucleotide sequences. In certain embodiments, for example, the methods are used to assess microsatellite instability in patients as part of diagnostic or prognostic applications. In many embodiments, various polymorphisms of a given repetitive nucleotide sequence are detected using a single probe nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method of detecting a mutant form of a target nucleic acid. The method includes providing at least one target nucleic acid and/or an amplicon of the target nucleic acid. The target nucleic acid includes at least one repetitive nucleotide sequence. The method also includes binding (e.g., hybridizing, etc.) at least one probe nucleic acid to the target nucleic acid and/or to the amplicon of the target nucleic acid. The probe nucleic acid includes at least a first nucleotide sequence that is at least substantially complementary to at least a portion of a non-mutant form of the repetitive nucleotide sequence. In addition, the method also includes detecting a bimodal dissociation of the probe nucleic acid from the target nucleic acid and/or from the amplicon of the target nucleic acid. In some embodiments, the detected bimodal dissociation comprises a bimodal distribution of melting peaks. Further, the detected bimodal dissociation generally correlates with at least one mutant form of the repetitive nucleotide sequence. In some embodiments, a detected non-bimodal (e.g., a single mode, etc.) dissociation correlates with a non-mutant form the repetitive nucleotide sequence. Typically, the probe nucleic acid, the target nucleic acid, and/or the amplicon of the target nucleic acid includes or is associated with

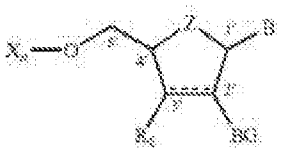
at least one labeling moiety and/or at least one quencher moiety. In these embodiments, the detecting step generally includes detecting a detectable signal produced by the labeling moiety. Moreover, the bimodal dissociation of the probe nucleic acid from the target nucleic acid and/or from the amplicon of the target nucleic acid is typically detected under at least one varied condition, such as a varied temperature or the like. Additionally or alternatively, detection of a genetic biomarker can include a reaction mixture. The reaction mixture includes at least one target nucleic acid and/or an amplicon of the target nucleic acid. The target nucleic acid includes at least one repetitive nucleotide sequence. The reaction mixture also includes at least one probe nucleic acid that includes at least a first nucleotide sequence that is at least substantially complementary to at least a portion of a non-mutant form of the repetitive nucleotide sequence. Further, the probe nucleic acid dissociates bimodally from a bound target nucleic acid that includes at least one mutant form of the repetitive nucleotide sequence under at least one varied condition. In certain embodiments, the reaction mixture also includes various other components. For example, the reaction mixture optionally includes at least one salt (e.g., NaCl, KCl, and/or the like). In some embodiments, the reaction mixture also includes at least one buffer. The buffer typically maintains a pH of the reaction mixture between about 5.5 and about 10.0. The reaction mixture also optionally includes at least one cofactor, such as Mg2+ (e.g., MgSO4, MgCl2, etc.), Mn2+ (e.g., MnSO4, MnCl2, etc.), and/or the like. Additionally or alternatively, detection of a genetic biomarker can include a probe nucleic acid. The probe nucleic acid includes at least a first nucleotide sequence that is at least substantially complementary to at least a portion of a non-mutant form of a repetitive nucleotide sequence. In addition, the probe nucleic acid dissociates bimodally from a bound target nucleic acid that includes at least one mutant form of the repetitive nucleotide sequence under at least one varied condition. Additionally or alternatively, detection of a genetic biomarker can include a system for detecting mutant forms of target nucleic acids. The system includes at least one probe nucleic acid that includes at least a first nucleotide sequence that is at least substantially complementary to a non-mutant form of a repetitive nucleotide sequence. The probe nucleic acid dissociates bimodally from a bound target nucleic acid that comprises at least one mutant form of the repetitive nucleotide sequence under at least one varied condition. Typically, at least one container comprises the probe nucleic acid, e.g., in solution. The system also includes

at least one detector that detects dissociation of the probe nucleic acid from a target nucleic acid and/or from an amplicon of the target nucleic acid when the probe nucleic acid is bound to the target nucleic acid and/or to the amplicon of the target nucleic acid and subjected to one or more varied conditions. In some embodiments, the system also includes at least one thermal modulator that modulates temperatures to which the probe nucleic acid is exposed when the probe nucleic acid is bound to the target nucleic acid and/or to the amplicon of the target nucleic acid to effect the varied conditions. In certain embodiments, the system also includes at least one controller operably connected at least to the detector, which controller correlates detected bimodal dissociations of the probe nucleic acid from bound target nucleic acids and/or bound amplicons of target nucleic acids with diagnoses of at least one genetic disorder and/or at least one disease state for subjects from which the target nucleic acids were obtained. In some embodiments, the target nucleic acid typically comprises a DNA or an RNA, and is generally obtained from at least one subject. Mutant forms of the target nucleic acid typically correlate with a diagnosis of at least one genetic disorder (e.g., Fragile X Syndrome, etc.) and/or at least one disease state (e.g., at least one form of cancer, etc.) for a subject comprising the mutant form of the target nucleic acid. Further, the mutant form of the repetitive nucleotide sequence typically comprises at least one deletion relative to the non-mutant form of the repetitive nucleotide sequence. In some embodiments, for example, the repetitive nucleotide sequence corresponds to a microsatellite marker, a mononucleotide repeat, and/or the like. In some embodiments, the repetitive nucleotide sequence comprises at least one mononucleotide repeat (e.g., An, Tn, Gn, Cn, Un, etc., where n is an integer greater than 1). For example, the mononucleotide repeat optionally comprises a BAT-25 repeat, a BAT-26 repeat, among many others. In certain embodiments, detected mutant forms of the mononucleotide repeat comprise 22 or fewer adenine nucleotides. To further illustrate, the repetitive nucleotide sequence of the target nucleic acid includes at least one AT repeat, at least one GC repeat, at least one CGG repeat, at least one CGC repeat, at least one TAT repeat, at least one ATT repeat, and/or at least one complementary repeat thereof in certain embodiments. In some embodiments, for example, the first nucleotide sequence is longer than the non-mutant form of the repetitive nucleotide sequence. In these embodiments, the portion of the first nucleotide sequence that extends beyond the length of the non-mutant form of the repetitive nucleotide sequence is

typically not substantially complementary to nucleotide sequences of the target nucleic acid that are adjacent to the repetitive nucleotide sequence. While not being constrained to a particular theory, in these embodiments it is thought that at least one segment of the probe nucleic acid forms a triple helix when the probe nucleic acid is bound to the mutant form of the target nucleic acid or to an amplicon of the mutant form of the target nucleic acid under at least one selected condition. In certain embodiments, the probe nucleic acid comprises at least one modified nucleotide. The probe nucleic acids, target nucleic acids, and/or amplicons of the target nucleic acids (e.g., via primer nucleic acids used to produce the amplicons, etc.) optionally comprise or are associated with at least one labeling moiety and/or at least one quencher moiety. To illustrate, the labeling moiety optionally comprises one or more of, e.g., a fluorescent dye, a weakly fluorescent label, a non-fluorescent label, a colorimetric label, a chemiluminescent label, a bioluminescent label, an antibody, an antigen, biotin, a hapten, an enzyme, or the like. To further exemplify, the fluorescent dye is optionally selected from the group consisting of, e.g., Cy3, Cy3.5, Cy5, Cy5.5, JOE, VIC, TET, HEX, FAM, R6G, R110, TAMRA, ROX, SYBR-Green, EtBr, and the like.

[679] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 7,745,125, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods relating to nucleic acid polymerization and amplification. In certain embodiments, for example, the pyrophosphorolysis activated polymerization (PAP)-related methods involve the serial coupling of pyrophosphorolysis and polymerization. These methods can be used, e.g., for SNP analysis and rare somatic mutation detection, among many other applications. In some embodiments, the methods enhance the general specificity of oligonucleotide-mediated synthesis reactions. For example, analogous to other "hot start" methods (e.g., reversible, chemically-modified enzymes, aptamer- or antibody-mediated "hot start"), "zeroth cycle extension" (pre-PCR) is reduced or eliminated. Unlike these other methods, primer activation is effected at each and every new oligonucleotide-mediated synthesis step. This improves the overall specificity of the reaction, minimizing the generation of unwanted side products. Accordingly, the detection of low copy and even single copy sequences is improved. In addition, the performance in multiplex (where several or many

different target are being amplified) amplification reactions is also improved by reducing or eliminating the generation of unintended and undesired, non-specific synthesis products, e.g., primer dimers in the case of PCR. Additionally or alternatively, detection of a genetic biomarker can include a reaction mixture that includes at least one oligonucleotide (e.g., a primer nucleic acid, a probe nucleic acid, etc.) comprising a 2′-terminator nucleotide (e.g., at a 3′-terminus). In certain embodiments, the oligonucleotide comprises the formula:



[680] where Z is O or CH2; B is at least one homocyclic ring, at least one heterocyclic ring, at least one aryl group, or combinations thereof; BG is a blocking group; R1 is H, OH, a hydrophilic group, or a hydrophobic group; X is a nucleotide or a nucleotide analog; n is an integer greater than 0; and, represents a single or double bond. Optionally, the oligonucleotide comprises at least one label. In certain embodiments, at least one nucleotide position in the oligonucleotide corresponds to a polymorphic nucleotide position in a target nucleic acid. In some of these embodiments, for example, the 2′-terminator nucleotide corresponds to the polymorphic nucleotide position in the target nucleic acid. The reaction mixture typically includes additional reagents according to the particular application in which the reaction mixture is utilized. In some embodiments, for example, additional reagents are selected from, e.g., a first biocatalyst comprising a nucleotide removing activity (e.g., a pyrophosphorolysis activity and/or a nuclease activity), a second biocatalyst comprising a nucleotide incorporating activity, a target nucleic acid comprising at least a subsequence that is at least partially complementary to the oligonucleotide, an amplicon, a primer nucleic acid, a probe nucleic acid (e.g., a hybridization probe, a 5′-nuclease probe, a hairpin probe, etc.), an additional nucleotide (e.g., an extendible nucleotide, a terminator nucleotide, a ribonucleoside triphosphate, a deoxyribonucleoside triphosphate, etc.), an additional oligonucleotide (e.g., a primer nucleic acid, a probe nucleic acid, etc.), a soluble light emission modifier, a cosolvent, an intercalating agent, a clinical specimen, a sample, a buffer, a salt, a metal ion, pyrophosphate, glycerol, dimethyl sulfoxide, poly rA, and the like. In some embodiments, the target nucleic acid, the

amplicon, the primer nucleic acid, the probe nucleic acid, the additional nucleotide, and/or the additional oligonucleotide comprises at least one label. In certain embodiments, the buffer comprises N-[Tris(hydroxymethyl)methyl]glycine at a concentration of at least 90 mM (e.g., about 95 mM, about 100 mM, about 105 mM, etc.). In some embodiments, the first biocatalyst comprises a nucleotide incorporating activity (i.e., in addition to the nucleotide removing activity). The nucleotide incorporating activity of the first and/or the second biocatalyst typically comprises a polymerase activity and/or a ligase activity. Optionally, the first and/or the second biocatalyst comprises a nuclease activity. To further illustrate, the first and/or second biocatalyst optionally comprises an enzyme selected from, e.g., a polymerase, a terminal transferase, a reverse transcriptase, a polynucleotide phosphorylase, a ligase, an AP endonuclease, and a telomerase. In certain embodiments, the first and/or second biocatalyst comprises a CS5 DNA polymerase that includes one or more mutations at amino acid positions selected from the group consisting of: G46, L329, Q601, D640, I669, S671, and E678. In some of these embodiments, for example, the mutations comprise a G46E mutation, an L329A mutation, a Q601R mutation, a D640G mutation, an I669F mutation, an S671F mutation, and/or an E678G mutation. In some embodiments, for example, the 2′-terminator nucleotide comprises a 2′-monophosphate-3′-hydroxyl nucleoside. Additionally or alternatively, detection of a genetic biomarker can include a method of removing a nucleotide from an oligonucleotide. The method includes incubating at least one target nucleic acid with: at least a first biocatalyst comprising a nucleotide removing activity (e.g., a pyrophosphorolysis activity and/or a nuclease activity), and at least one oligonucleotide (e.g., a primer nucleic, a probe nucleic acid, etc.) comprising a 2′-terminator nucleotide (e.g., at a 3′-terminus), which oligonucleotide is at least partially complementary to at least a first subsequence of the target nucleic acid, under conditions whereby the first biocatalyst removes at least the 2′-terminator nucleotide from the oligonucleotide to produce a removed 2′-terminator nucleotide and a shortened oligonucleotide, thereby removing the nucleotide from the oligonucleotide. In some embodiments, the method includes incubating the target nucleic acid with the first biocatalyst, the oligonucleotide, and pyrophosphate, which pyrophosphate is added to the removed 2′-terminator nucleotide. In some exemplary embodiments, the target nucleic acid comprises at least one polymorphic nucleotide position, and the method comprises detecting removal of the

2′-terminator nucleotide from the oligonucleotide, which removal correlates with the oligonucleotide comprising at least one nucleotide position that corresponds to the polymorphic nucleotide position. In these embodiments, the 2′-terminator nucleotide typically corresponds to the polymorphic nucleotide position. In certain embodiments, the oligonucleotide comprises at least one label, and the method comprises detecting a detectable signal emitted from the label. In some of these embodiments, the label comprises a donor moiety and/or an acceptor moiety and the detectable signal comprises light emission, and the method comprises incubating the target nucleic acid with the first biocatalyst, the oligonucleotide, and at least one soluble light emission modifier and detecting the light emission from the donor moiety and/or the acceptor moiety. Optionally, the 2′-terminator nucleotide comprises the donor moiety and/or the acceptor moiety. In some embodiments, the first biocatalyst comprises a nucleotide incorporating activity (i.e., in addition to the nucleotide removing activity), and the method comprises incubating the target nucleic acid with the first biocatalyst, the shortened oligonucleotide, and at least one additional nucleotide under conditions whereby the first biocatalyst incorporates the additional nucleotide at a terminus of the shortened oligonucleotide to produce an extended oligonucleotide. Optionally, the method comprises incubating the target nucleic acid with at least a second biocatalyst comprising a nucleotide incorporating activity, the shortened oligonucleotide, and at least one additional nucleotide under conditions whereby the second biocatalyst incorporates the additional nucleotide at a terminus of the shortened oligonucleotide to produce an extended oligonucleotide. To illustrate, the nucleotide incorporating activity typically includes a polymerase activity and/or a ligase activity. The first and/or second biocatalyst typically comprises an enzyme selected from, e.g., a polymerase, a terminal transferase, a reverse transcriptase, a polynucleotide phosphorylase, a ligase, an AP endonuclease, a telomerase, and the like. In certain embodiments, the first and/or second biocatalyst comprises a CS5 DNA polymerase comprising one or more mutations at amino acid positions selected from, e.g., G46, L329, Q601, D640, 1669, S671, and E678. In some of these embodiments, the mutations comprise a G46E mutation, an L329A mutation, a Q601R mutation, a D640G mutation, an I669F mutation, an S671F mutation, and/or an E678G mutation. In some embodiments, one or more nucleotides of the oligonucleotide extend beyond a terminus of the target nucleic acid

when the oligonucleotide and the target nucleic acid hybridize to form a hybridized nucleic acid. In some embodiments, at least one additional oligonucleotide comprises the additional nucleotide. The additional nucleotide comprises an extendible nucleotide and/or a terminator nucleotide. In certain embodiments, the additional nucleotide comprises at least one label, and the method comprises detecting a detectable signal emitted from the label. For example, the label optionally comprises a donor moiety and/or an acceptor moiety and the detectable signal comprises light emission, and the method comprises incubating the target nucleic acid with at least one soluble light emission modifier and detecting the light emission from the label. Additionally or alternatively, detection of a genetic biomarker can include incubating the target nucleic acid with at least one probe nucleic acid that comprises at least one label, which probe nucleic acid is at least partially complementary to at least a second subsequence of the target nucleic acid, and detecting a detectable signal emitted from the label of the probe nucleic acid or a fragment thereof. In some embodiments, the detectable signal comprises light emission, and the method further comprises incubating the target nucleic acid with at least one soluble light emission modifier and detecting the light emission from the label. For example, the probe nucleic acid optionally comprises a 5′-nuclease probe and the first and/or second biocatalyst extends the shortened oligonucleotide in a 5′ to 3′ direction and comprises a 5′ to 3′ exonuclease activity. Optionally, the probe nucleic acid comprises a hybridization probe and/or a hairpin probe. In certain embodiments, the target nucleic acid comprises at least one polymorphic nucleotide position, and the method comprises detecting extension of the shortened oligonucleotide, which extension correlates with the extended oligonucleotide comprising at least one nucleotide position that corresponds to the polymorphic nucleotide position. In some of these embodiments, the 2′-terminator nucleotide corresponds to the polymorphic nucleotide position. Additionally or alternatively, detection of a genetic biomarker can include a system that includes (a) at least one container or support comprising an oligonucleotide that comprises a 2′-terminator nucleotide. The system also includes at least one of: (b) at least one thermal modulator configured to thermally communicate with the container or the support to modulate temperature in the container or on the support; (c) at least one fluid transfer component that transfers fluid to and/or from the container or the support; and, (d) at least one detector configured to detect detectable signals produced in the container or on the support. In some

embodiments, the system includes at least one controller operably connected to: the thermal modulator to effect modulation of the temperature in the container or on the support, the fluid transfer component to effect transfer of the fluid to and/or from the container or on the support, and/or the detector to effect detection of the detectable signals produced in the container or on the support.

[681] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2018/0135103, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include methods based on digital polymerase chain reaction (dPCR) in combination with a reference sample which is used in a double function. First, it is added to a dPCR run as an external standard. Secondly, the same reference sample is used as an internal standard, preferably by adding it to the primary sample. It runs through the whole sample preparation process in the same way as the nucleic acid of interest (target nucleic acid). Both the internal and the external reference are quantified using dPCR. The ratio of internal vs external reference quantification gives the yield of the sample preparation prior to the dPCR. Knowing this yield, the initial target concentration in the primary sample can be calculated. The reference used with dPCR leads to a full understanding of standards used in dPCR and helps preventing miscalculation due to pipetting and dilution errors. Even with non-precise standards, the absolute accuracy of dPCR is further improved and standards may be re-calibrated as a bonus. Additionally or alternatively, detection of a genetic biomarker can include a method for determining the amount or concentration of a nucleic acid of interest in an unprocessed sample, the method comprising the steps of: a) providing an unprocessed sample suspected of containing the nucleic acid of interest and a reference sample known to contain a reference nucleic acid, which is different from the nucleic acid of interest; b) combining the unprocessed sample with a defined amount of the reference sample, thereby obtaining a combined sample; c) processing the combined sample, thereby obtaining a processed sample suitable for digital polymerase chain reaction (dPCR); d) performing dPCR with the processed sample, thereby determining the amount or concentration of the nucleic acid of interest and the amount or concentration of the reference nucleic acid in the processed sample; e) performing the dPCR with a defined amount of the reference sample,

thereby determining the amount or concentration of the reference nucleic acid in the defined amount of the reference sample;

[682] f) comparing the amount or concentration of the reference nucleic acid determined in step d) to that determined in step e), thereby determining the yield of the nucleic acid in step c); and

[683] g) determining the amount or concentration of the nucleic acid of interest in the unprocessed sample based on the amount or concentration of the nucleic acid of interest in the processed sample determined in step d) and the yield determined in step f). Additionally or alternatively, detection of a genetic biomarker can include a method for determining the amount or concentration of a nucleic acid of interest in an unprocessed sample, the method comprising the steps of: a) providing an unprocessed sample suspected of containing the nucleic acid of interest;

[684] b) providing a reference sample known to contain a reference nucleic acid, which is different from the nucleic acid of interest; c) processing the reference sample, thereby obtaining a processed reference sample suitable for dPCR; d) performing the dPCR with the processed reference sample, thereby determining the amount or concentration of the reference nucleic acid in the processed reference sample; e) performing the dPCR with a defined amount of unprocessed reference sample, thereby determining the amount or concentration of the reference nucleic acid in the defined amount of the unprocessed reference sample; f) comparing the amount or concentration of the reference nucleic acid determined in step d) to that determined in step e), thereby determining the yield of the nucleic acid in step c); g) processing the unprocessed sample, thereby obtaining a processed sample suitable for dPCR, wherein the processing steps c) and g) are identical; h) performing the dPCR with the processed sample, thereby determining the amount or concentration of the nucleic acid of interest; and i) determining the amount or concentration of the nucleic acid of interest in the unprocessed sample based on the amount or concentration of the nucleic acid of interest in the processed sample determined in step i) and the yield determined in step f). In some embodiments, (i) the amount or concentration of the reference nucleic acid in the reference sample is compared to a reference value, thereby controlling the reference sample; (ii) the amount or concentration of the reference nucleic acid in the reference sample is unknown or not predetermined; and/or

(iii) the amount or concentration of the reference sample in step e) is identical to that in step b). In addition, the reference nucleic acid has one or more of the following characteristics: (i) is a nucleic acid selected from the group consisting of DNA, cDNA, RNA and a mixture thereof; (ii) has the same primer binding site as the nucleic acid of interest; (iii) has a primer binding site different from that of the nucleic acid of interest; (iv) has a length in nucleic acids that differs from that of the nucleic acid of interest by at most 50%, at most 25%, at most 10% or at most 5%; (v) has a sequence that is at least 50% identical, at least 60%, at least 70% or at least 80% identical to that of the nucleic acid of interest; (vi) has a content of G and C that differs from that of the nucleic acid of interest by at most 50%, at most 25%, at most 10% or at most 5%; and (vii) comprises a part that is not part of the nucleic acid of interest and that is used for detecting the reference nucleic acid. Moreover, the nucleic acid of interest has one or more of the following characteristics: (i) is a nucleic acid selected from the group consisting of DNA, cDNA, RNA and a mixture thereof; (ii) comprises a part that is not part of the reference nucleic acid and that is used for detecting the nucleic acid of interest; and (iii) is indicative of a microorganism, a cell, a virus, a bacterium, a fungus, a mammal species, a genetic status or a disease. Still further, the unprocessed sample has one or more of the following characteristics: (i) has been obtained from a cell culture, a source suspected of being contaminated or a subject, particularly wherein the subject is selected from the group consisting of a human, an animal and a plant, especially a human; and (ii) is selected from the group consisting of a body fluid, blood, blood plasma, blood serum, urine, bile, cerebrospinal fluid, a swab, a clinical specimen, an organ sample and a tissue sample. The processing step can include one or more of the following processes: dilution, lysis, centrifugation, extraction, precipitation, filtration, and purification. In some embodiments, dPCR, is characterized by one or more of the following: (i) is carried out in a liquid, in a gel, in an emulsion, in a droplet, in a microarray of miniaturized chambers, in a chamber of a microfluidic device, in a microwell plate, on a chip, in a capillary, on a nucleic acid binding surface or on a bead, especially in a microarray or on a chip; (ii) is carried out identically in at least 100 reaction areas, particularly at least 1,000 reaction areas, especially at least 5,000 reaction areas; and (iii) is carried out identically in at least 10,000 reaction areas, particularly at least 50,000 reaction areas, especially at least 100,000 reaction areas. More specifically, steps d) and e) are carried out in

the same dPCR run and/or on the same dPCR device. In a further embodiment, dPCR, comprises using one or more fluorescent probes, alone or in combination with a quencher, to detect the nucleic acid of interest and/or the reference nucleic acid. In a specific embodiment, the fluorescent probe comprises fluorescein, rhodamine, or cyanine. In this embodiment, the determining step comprises detecting a fluorescent signal. In some embodiments, an external control is used. In a specific embodiment, the method is used to diagnose the presence or absence of a disease, a pathogen, a rare genetic sequence, a rare mutation, a copy number variation or relative gene expression. Optionally, the method is used to monitor disease progression, therapeutic response, and combinations thereof.

[685] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2014/0128270, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method of interrogating a sequence of a target nucleic acid having a sense and an anti-sense strands by a microarray analysis comprising a sequence determination computation, comprising omitting from the computation a signal from one of the sense and anti-sense strands for one or more nucleotide positions in the target nucleic acid sequence. In variations of this embodiment, omitting the signal from one of the sense and anti-sense strands at a nucleotide position comprises the steps of using a plurality of microarrays, measuring hybridization signals at the nucleotide position using one or more probe sets for each of the sense and the anti-sense strands; for each probe set, determining base discrimination ability by comparing the hybridization signals within each probe set; for each nucleotide position, computing discrimination ability for sense and antisense strand separately using the computed discrimination ability from each of the probe sets; for each nucleotide position, comparing the computed discrimination ability between the sense and the anti-sense strands; omitting the signal from the strand with lower base discrimination ability. In variations of this embodiment, the base discrimination is measured using Formula 1. In further variations of this embodiment, the discrimination ability for sense and antisense strand is computed as a percentile of the discrimination ability for probe sets in the strand at the base position. In yet further variations of this embodiment, the discrimination ability between sense and antisense strand is compared using Formula 3:

(1) $Q_{75} < Q_{25} - T$, for $Q_{25} < PT$

(2) $Q_{75} < A(Q_{25} - B)^2 + PT$, for $Q_{25} \geq PT$ Formula 3

[686] Additionally or alternatively, detection of a genetic biomarker can include a method of detecting the presence or absence of a target nucleic acid having a sense and an anti-sense strands in a test sample using a microarray analysis including a sequence determination or mutation detection computation, comprising omitting from the computation a signal from one of the sense and anti-sense strands for one or more nucleotide positions in the target nucleic acid sequence. In variations of this embodiment, omitting the signal from one of the sense and anti-sense strands at a nucleotide position comprises the steps of: using a plurality of microarrays, measuring hybridization signals at the nucleotide position using one or more probe sets for each of the sense and the anti-sense strands; for each probe set, determining base discrimination by comparing the hybridization signals within each probe set; for each nucleotide position, computing discrimination ability for sense and antisense strand separately using discrimination ability from each of the probe sets; for each nucleotide position, comparing discrimination ability between the sense and the anti-sense strands; omitting the signal from a strand with lower base discrimination ability. In variations of this embodiment, the base discrimination is measured using Formula 1. In further variations of this embodiment, the discrimination ability of the sense and anti-sense strand is computed as a percentile of the discrimination ability for probe sets in the strand at the base position measured using a plurality of microarrays. Additionally or alternatively, detection of a genetic biomarker can include a computer readable medium including code for controlling one or more processors to detect the presence or absence of a target nucleic acid having a sense and an anti-sense strands in a test sample using a microarray analysis that includes a sequence determination or mutation detection computation, comprising omitting from the computation a signal from one of the sense and anti-sense strands for one or more nucleotide positions in the target nucleic acid sequence. In variations of this embodiment, the computer readable medium comprises a code controlling the steps of: using a plurality of microarrays, measuring hybridization signals at the nucleotide position using one or more probe sets for each of the sense and the anti-sense strands; for each probe set, determining base discrimination ability by comparing the

hybridization signals within each probe set; for each nucleotide position, computing discrimination ability for sense and antisense strand separately using discrimination ability from each of the probe sets; for each nucleotide position, comparing discrimination ability between the sense and the anti-sense strands; omitting the signal from a strand with lower base discrimination ability. Additionally or alternatively, detection of a genetic biomarker can include a system for detecting a target nucleic acid in a test sample comprising: a data acquisition module configured to acquire hybridization data from a microarray; a data processing unit configured to process the data to determine a target nucleotide sequence by omitting the signal from one of the sense and anti-sense strands at one or more nucleotide positions in the target sequence via the steps of: using a plurality of microarrays, measuring hybridization signals at the nucleotide position using one or more probe sets for each of the sense and the anti-sense strands; for each probe set, determining base discrimination ability by comparing the hybridization signals within each probe set; for each nucleotide position, computing discrimination ability for sense and antisense strand separately using discrimination ability from each of the probe sets; for each nucleotide position, comparing discrimination ability between the sense and the anti-sense strands; omitting the signal from a strand with lower base discrimination ability; and a display module configured to display the data produced by the data processing unit.

[687] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2002/0160404, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for the amplification of nucleic acid fragments from a sample comprising two or three thermocyclic amplification reactions in which completely randomized primers are used in the first amplification reaction and specific primers are used in the second amplification reaction, characterized in that, to amplify the DNA, a mixture of at least two DNA polymerases is used, at least one of which possesses 3'-5' exonuclease activity. An amplification reaction can comprise about 20 to 60 thermal cycles. The first amplification reaction preferably comprises at least 40 thermal cycles and, most preferably, at least 50 thermal cycles. The second amplification reaction preferably comprises at least 30 thermal cycles, and most preferably, at

least 40 thermal cycles. Each thermal cycle comprises a denaturing phase, an annealing phase, and at least one elongation phase. Denaturation into single strands preferably takes place at temperatures of between 90° C. and 96° C. The annealing phase to hybridize the primers with the target nucleic acid preferably takes place at temperatures of between 30° C. and 50° C. Most preferably, the annealing phase takes place at temperatures of between 35° C. and 45° C. During the first amplification reaction, the annealing phase most preferably takes place at about 37° C. The elongation phase is carried out at temperatures of between 50° C. and 75° C. In a preferred embodiment, the elongation phase of the first amplification reaction takes place at temperatures of between 50° C. and 60° C. A temperature of about 55° C. is especially preferred. It is advantageous for the elongation to be carried out during the first amplification reaction in the majority of cycles using two or more elongation steps, with one elongation carried out at a lower temperature and then continuing the elongation at a higher temperature. Using this approach, populations of especially long amplicons are created during the first amplification reaction. In this embodiment, the first amplification reaction preferably takes place at about 55° C., and the second amplification reaction takes place at about 65° C. to 72° C. A temperature of about 68° C. is optimal. The primers used in the first amplification reaction are completely randomized, i.e., a population of single-stranded oligonucleotides is used in which every single nucleotide on every single position can comprise one of four nucleotide components A, T, G, or C. These primers are preferably 10-20 nucleotides long. Most preferably, the primers are about 15 nucleotides long. The specific primers used in the second amplification reaction are characterized in that they have a sequence that is identical to a sequence of the target nucleic acid or its complementary sequence over a range of at least 10 nucleotides. The specific primers used to carry out a "nested PCR" in a potential third amplification reaction are selected according to the same criteria as the primers used in the second amplification reaction. The sequences of the primers used that are identical to the target nucleic acid or its complement must be a component of the sequence amplified in the second amplification reaction. The mixture of DNA polymerases preferably contains a thermostable DNA polymerase without 3'-5' exonuclease activity such as Taq DNA polymerase, for instance, and another thermostable DNA polymerase with 3'-5' exonuclease activity, such as Pwo DNA polymerase obtained from Pyrokokkus woesii (Boehringer Mannheim order no.

1644947). Other DNA polymerases without 3'-5' exonuclease activity can also be used as a component of the polymerase mixture. Additionally or alternatively, detection of a genetic biomarker can include a method for DNA amplification. To ensure the sensitivity of detecting certain sequences, it is advantageous to carry out the cell analysis of the material to be analyzed using enzymatic protease digestion to obtain the sample DNA. Proteinase K can be used, for instance. Additionally or alternatively, detection of a genetic biomarker can include a method in which RNA is first isolated from the physical material to be analyzed. The sample of physical material can comprise one cell, fewer than 10 cells, or fewer than 100 cells. To obtain RNA, it is preferable to use chemical lysis using buffers that contain guanidinum isothiocynate. A corresponding cDNA is then created using a reverse transcriptase reaction. This cDNA is then used as the starting material for the primer-extension preamplification. The cDNA is preferably obtained via reverse transcription of poly-A RNA. The use of polymerase mixtures in the primer-extension preamplification PCR leads to a surprisingly high sensitivity of DNA detection that cannot be achieved using the methods known from the prior art. Additionally or alternatively, detection of a genetic biomarker can include a method for the amplification of nucleic acid fragments comprising two or three thermocyclic amplification reactions. Completely randomized primers are used in the first amplification reaction and specific primers are used in the second amplification reaction. In addition, the sample contains a quantity of nucleic acid corresponding to an equivalent of no more than 100 cells. In some embodiments, the likelihood of the amplificates forming is greater than 90%. In some embodiments, the likelihood is greater than 90% that amplificates will form from an equivalent of no more than 5-10 cells. In a special embodiment, the likelihood of amplificates forming from the equivalent of one cell is greater than 50%. The method is suitable for use in the amplification of nucleic acid fragments having a length between 100 and 1000 base pairs. The method is especially suited for use in the amplification of nucleic acid fragments having a length between 150 and 550 base pairs.

[688] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,658,572, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a microarray with high density of oligopeptide features, thereby

allowing for the detection of protein interactions across an organism's proteome. An embodiment is a microarray comprising at least 50,000 oligopeptide features per cm2. Another embodiment is a microarray having oligopeptide features representing at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 99%, or 100% of the proteome of a target selected from a virus or organism. Additionally or alternatively, detection of a genetic biomarker can include a microarray comprising at least 50,000 oligopeptide features per cm2 wherein the features represent between about 90% and 100% of a target proteome, the target selected from a virus and an organism, and wherein at least a portion of the features comprise oligopeptides having a terminal 2-(2-nitro-4-benzoyl-phenyl)-propoxycarbonyl(benzoyl-NPPOC)-protected tyrosine residue.

[689] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 8,822,158, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a method for treating multiple nucleic acid molecules of interest comprising in the steps of: (a) providing a plurality of beads, characterized in that each bead comprises at least one pair of sequence specific amplification primers, further characterized in that at least one of said primers is bound to the bead via a photo-cleavable linker, (b) capturing the nucleic acid molecules of interest from a sample, (c) clonally isolating said plurality of beads, (d) photo-cleaving said at least one primer, (e) clonally amplifying said nucleic acid thereby creating multiple amplification products, and (f) analyzing said amplification products. In a first major embodiment, step c) comprises the generation of an emulsion wherein each bead is encapsulated in a single micelle. Preferably, step f) comprises the distribution of said plurality of beads into the cavities of a micro- or picotiter plate and detecting said amplification products. In a first particular embodiment, step f) further comprises a sequencing reaction of said amplification products. Preferably, said sequencing reaction is a sequencing by synthesis reaction, for example a pyrosequencing reaction. In case the multiple nucleic acid molecules are variants of the same type of nucleic acid, such a method may be used for quantitative mutational analysis. In case the plurality of molecules corresponds to a plurality of different cellular RNAs or their corresponding cDNAs, such a method may be used for monitoring gene expression. In a second particular embodiment, the generation of said amplification products

for example by means of PCR is monitored. Preferably, said amplification products are detected by means of a specifically double-stranded DNA binding fluorescent entity, a sequence specific hybridization probe: Furthermore, said amplification products may be analyzed by means of subjecting said amplification products to a thermal gradient. In a second major embodiment, step c) comprises the distribution of said plurality of beads into the cavities of a micro- or picotiter plate. Preferably, steps e) and f) are performed simultaneously by means of Real Time PCR. Subsequent to PCR, a melting curve analysis may be performed. In some embodiments, at least one primer which is bound to the bead via a cleavable linker carries a detectable tag. Preferably, said detectable tag is selected from a group consisting of mass-tag, color label, e-tag and a hapten which is detectable by an antibody. Highly preferred is a fluorescent label which is preferably quenched as long as said labeled primer has not been elongated. Alternatively; the cleavable primer carries a detectable tag. In this case, said amplification products are detected using labeled primers or labeled dNTPs. For example, the detectable tag may be a hapten such as Biotin or Digoxygenin. In a particular embodiment, each member of the plurality of primers which are bound to the bead via a cleavable linker carries a different detectable label.

[690] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent Application Publication No. 2015/0024948, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a system and methods for the enrichment and analysis of nucleic acid sequences. Additionally or alternatively, detection of a genetic biomarker can include the enrichment of targeted sequences in a format by representing one fusion partner gene on a capturing platform and allowing subsequent sequencing of chimeric nucleic acids such as nucleic acid strands that carry information on different DNA regions of a genome. Additionally or alternatively, detection of a genetic biomarker can include a method for detecting balanced chromosomal aberrations in a genome is provided. The method comprises the steps of: (a) exposing fragmented, denatured nucleic acid molecules of said genome to multiple, different oligonucleotide probes located on multiple, different sites of a solid support under hybridizing conditions to capture nucleic acid molecules that specifically hybridize to said probes, wherein said fragmented, denatured nucleic acid molecules have an

average size of about 100 to about 1000 nucleotide residues, preferably about 250 to about 800 nucleotide residues and most preferably about 400 to about 600 nucleotide residues, in particular about 500 nucleotide residues, wherein said oligonucleotide probes have an average size of about 20 to about 100 nucleotides, preferably about 40 to about 85 nucleotides, more preferred about 45 to about 75 nucleotides, in particular about 55 to about 65 nucleotide residues or about 60 nucleotide residues, (b) separating unbound and non-specifically hybridized nucleic acids from the captured molecules; (c) eluting the captured molecules from the solid support, (d) optionally repeating steps (a) to (c) for at least one further cycle with the eluted captured molecules, (e) determining the nucleic acid sequence of the captured molecules, in particular by means of performing sequencing by synthesis reactions, (f) comparing the determined sequence to sequences in a database of the reference genome, (g) identifying sequences in the determined sequence which only partially match or do not match with sequences of the reference genome, (h) detecting at least one balanced chromosomal aberration. Additionally or alternatively, detection of a genetic biomarker can include pre-selected, immobilized nucleic acid probes for capturing target nucleic acid sequences from, for example, a genomic sample by hybridizing the sample to probes on a solid support is provided. According to some embodiments, the captured target nucleic acids may be washed and eluted off of the probes. In some cases, the eluted genomic sequences may be more amenable to detailed genetic analysis than a sample that has not been subjected to the methods. Additionally or alternatively, detection of a genetic biomarker can include the solution based capture method comprising probe derived amplicons wherein said probes for amplification are affixed to a solid support. The solid support comprises support-immobilized nucleic acid probes to capture specific nucleic acid sequences from a genomic sample. Probe amplification provides probe amplicons in solution which are hybridized to target sequences. Following hybridization of probe amplicons to target sequences, target nucleic acid sequences present in the sample are enriched by capturing and washing the probes and eluting the hybridized target nucleic acids from the captured probes. The target nucleic acid sequence(s) may be further amplified using, for example, non-specific ligation-mediated PCR (LM-PCR), resulting in an amplified pool of PCR products of reduced complexity compared to the original target sample which is further analysed by sequencing as described above. Additionally or alternatively, detection of a

genetic biomarker can include a method for detecting balanced chromosomal aberrations in a genome of an organism is provided. The method comprises the steps of exposing fragmented, denatured nucleic acid molecules of the genome to a plurality of oligonucleotide probes bound to different positions of a solid support. The nucleic acid molecules have an average size of about 100 to about 1000 nucleotide residues and the oligonucleotide probes have an average size of about 20 to about 100 nucleotide residues. The method also includes the step of separating nucleic acid molecules bound to one or more of the oligonucleotide probes from nucleic acid molecules not bound to one or more of the oligonucleotide probes and then eluting the nucleic acid molecules bound to one or more of the oligonucleotide probes from the solid support. Thereafter, the nucleic acid molecules which were eluted in the step of eluting are sequenced, thereby getting a determined sequence for the nucleic acid molecules. Also, the method includes the step of comparing the determined sequence to a database comprising a reference genome sequence and identifying sequences in the determined sequence which only partially match or do not match with sequences of the reference genome, thereby detecting at least one balanced chromosomal aberration. In some embodiments, the oligonucleotide probes include a linker for binding to the solid support. In various embodiments, the linker may comprise a chemical linker. In some embodiments, the method may further include the steps of ligating at least one adaptor molecule to at least one end of the nucleic acid molecules prior to step exposing and amplifying the nucleic acid molecules which bound to one or more of the oligonucleotide probes with at least one primer comprising a sequence which specifically hybridizes to the adaptor molecule, whereby the step of amplifying is carried out after the step of eluting. Further, according to some embodiments, the solid support is either a nucleic acid microarray or a population of beads. In some embodiments, the method of detecting balanced chromosomal aberrations in a genome. The method includes the steps of providing a solid support comprising a plurality of different oligonucleotide probes bound to different positions of the solid support, wherein the oligonucleotide probes have an average size of about 20 to about 100 nucleotides, and providing a plurality of fragmented and denatured nucleic acid molecules having an average size of about 100 to about 1000 nucleotide residues. The method also includes the step of amplifying the oligonucleotide probes, thereby generating amplification products including a binding moiety and being maintained in solution.

Thereafter, the method includes the steps of hybridizing the target nucleic acid molecules to the amplification products in solution under specific hybridizing conditions, thereby generating a plurality of hybridization complexes, and separating the hybridization complexes from nucleic acid molecules not hybridized to the amplification products. Next, according to the method, the hybridized target nucleic acid molecules are separated from the amplification product comprising the hybridization complex and sequenced, whereby a determined sequence for the nucleic acid molecules is obtained. According to the method, the determined sequence is compared to a database comprising a reference genome and sequences in the determined sequence which only partially match or do not match with sequences of the reference genome are determined in order for detecting at least one balanced chromosomal aberration. In some embodiments, the binding moiety is a biotin moiety. According to some embodiments, oligonucleotide probes having highly repetitive sequences are not used. Further, in some embodiments, the balanced chromosomal aberrations identified may include translocations or inversions.

[691] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in U.S. Patent No. 6,514,736, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a process for amplifying one or more specific nucleic acid sequences present in a nucleic acid or mixture thereof using primers and a thermostable enzyme. The extension product of one primer when hybridized to the other becomes a template for the production of the desired specific nucleic acid sequence, and vice versa, and the process is repeated as often as is necessary to produce the desired amount of the sequence. The method improves the specificity of the amplification reaction, resulting in a very distinct signal of amplified nucleic acid. In addition, the method eliminates the need for transferring reagents from one vessel to another after each amplification cycle. Such transferring is not required because the thermostable enzyme will withstand the high temperatures required to denature the nucleic acid strands and therefore does not need replacement. The temperature cycling may, in addition, be automated for further reduction in manpower and steps required to effectuate the amplification reaction. Additionally or alternatively, detection of a genetic biomarker can include a process for amplifying at least one specific nucleic acid sequence

contained in a nucleic acid or a mixture of nucleic acids, wherein if the nucleic acid is double-stranded, it consists of two separated complementary strands of equal or unequal length, which process comprises: (a) contacting each nucleic acid strand with four different nucleoside triphosphates and one oligonucleotide primer for each different specific sequence being amplified, wherein each primer is selected to be substantially complementary to different strands of each specific sequence, such that the extension product synthesized from one primer, when it is separated from its complement, can serve as a template for synthesis of the extension product of the other primer, said contacting being at a temperature which promotes hybridization of each primer to its complementary nucleic acid strand; (b) contacting each nucleic acid strand, at the same time as or after step (a), with a thermostable enzyme which enables combination of the; nucleoside triphosphates to form primer extension products complementary to each strand of each nucleic acid; (c) maintaining the mixture from step (b) at an effective temperature for an effective time to activate the enzyme, and to synthesize, for each different sequence being amplified, an extension product of each primer which is complementary to each nucleic acid strand template, but not so high (a temperature) as to separate each extension product from its complementary strand template; (d) heating the mixture from step (c) for an effective time and at an effective temperature to separate the primer extension products from the templates on which they were synthesized to produce single-stranded molecules, but not so high (a temperature) as to denature irreversibly the enzyme; (e) cooling the mixture from step (d) at an effective temperature for an effective time to promote hybridization of each primer to each of the single-stranded molecules produced in step (d); and (f) maintaining the mixture from step (e) at an effective temperature for an effective time to promote the activity of the enzyme and to synthesize, for each different sequence being amplified, an extension product of each primer which is complementary to each nucleic acid strand template produced in step (d), but not so high (a temperature) as to separate each extension product from its complementary strand template, wherein steps (e) and (f) are carried out simultaneously or sequentially. The steps (d), (e) and (f) may be repeated until the desired level of sequence amplification is obtained. The preferred thermostable enzyme is a polymerase extracted from Thermus aquaticus (Taq polymerase). Most preferably, if the enzyme is Taq polymerase, in step (a) the nucleic acid strands are contacted with a buffer

comprising about 1.5-2 mM of a magnesium salt, 150-200 μ M each of the nucleotides, and 1 μM of each primer, steps (a), (e) and (f) are carried out at about 45-58° C., and step (d) is carried out at about 90-100° C. In a preferred embodiment, the nucleic acid(s) are double-stranded and step (a) is accomplished by (i) heating each nucleic acid in the presence of four different nucleoside triphosphates and one oligonucleotide primer for each different specific sequence being amplified, for an effective time and at an effective temperature to denature each nucleic acid, wherein each primer is selected to be substantially complementary to different strands of each specific sequence, such that the extension product synthesized from one primer, when it is separated from its complement, can serve as a template for synthesis of the extension product of the other primer; and (ii) cooling the denatured nucleic acids to a temperature which promotes hybridization of each primer to its complementary nucleic acid strand. Additionally or alternatively, detection of a genetic biomarker can include a process for detecting the presence or absence of at least one specific nucleic acid sequence in a sample containing a nucleic acid or mixture of nucleic acids, or distinguishing between two different sequences in said sample, wherein the sample is suspected of containing said sequence or sequences, and wherein if the nucleic acid(s) are double-stranded, they each consist of two separated complementary strands of equal or unequal length, which process comprises steps (a) to (f) mentioned above, resulting in amplification in quantity of the specific nucleic acid sequence(s), if present; (g) adding to the product of step (f) a labeled oligonucleotide probe, for each sequence being detected, capable of hybridizing to said sequence or to a mutation thereof; and (h) determining whether said hybridization has occurred. Additionally or alternatively, detection of a genetic biomarker can include a process for detecting the presence or absence of at least one nucleotide variation in sequence in one or more nucleic acids contained in a sample, wherein if the nucleic acid is double-stranded it consists of two separated complementary strands of equal or unequal length, which process comprises steps (a)-(f) mentioned above, wherein steps (d), (e) and (f) are repeated a sufficient number of times to result in detectable amplification of the nucleic acid containing the sequence, if present; (g) affixing the product of step (f) to a membrane; (h) treating the membrane under hybridization conditions with a labeled sequence-specific oligonucleotide probe capable of hybridizing with the amplified nucleic acid sequence only if a sequence of the probe is complementary to a

region of the amplified sequence; and (i) detecting whether the probe has hybridized to an amplified sequence in the nucleic acid sample. If the sample comprises cells, preferably they are heated before step (a) to expose the nucleic acids therein to the reagents. This step avoids extraction of the nucleic acids prior to reagent addition. In a variation of this process, the primer(s) and/or nucleoside triphosphates are labeled so that the resulting amplified sequence is labeled. The labeled primer(s) and/or nucleoside triphosphate(s) can be present in the reaction mixture initially or added during a later cycle. The sequence-specific oligonucleotide (unlabeled) is affixed to a membrane and treated under hybridization conditions with the labeled amplification product so that hybridization will occur only if the membrane-bound sequence is present in the amplification product. Additionally or alternatively, detection of a genetic biomarker can include a process for cloning into a cloning vector one or more specific nucleic acid sequences contained in a nucleic acid or a mixture of nucleic acids, which nucleic acid(s) when double-stranded consist of two separated complementary strands, and which nucleic acid(s) are amplified in quantity before cloning, which process comprises steps (a)-(f) mentioned above, with steps (d), (e) and (f) being repeated a sufficient number of times to result in detectable amplification of the nucleic acid(s) containing the sequence(s); (g) adding to the product of step (f) a restriction enzyme for each of said restriction sites to obtain cleaved products in a restriction digest; and (h) ligating the cleaved product(s) of step (g) containing the specific sequencels) to be cloned into one or more cloning vectors containing a promoter and a selectable marker. Additionally or alternatively, detection of a genetic biomarker can include a process for cloning into a cloning vector one or more specific nucleic acid sequences contained in a nucleic acid or mixture of nucleic acids, which nucleic acid(s), when double-stranded, consist of two separated complementary strands of equal or unequal length which nucleic acid(s) are amplified in quantity before cloning, which process comprises steps (a)-(f) mentioned above, with steps (d), (e) and (f) being repeated a sufficient number of times to result in effective amplification of the nucleic acid(s) containing the sequence(s) for blunt-end ligation into one or more cloning vectors; and (g) ligating the amplified specific sequence(s) to be cloned obtained from step (f) into one or more of said cloning vectors in the presence of a ligase, said amplified sequence(s) and vector(s) being present in sufficient amounts to effect the ligation. Additionally or alternatively, detection of a genetic biomarker can include a

composition of matter useful in amplifying at least one specific nucleic acid sequence contained in a nucleic acid or a mixture of nucleic acids, comprising four different nucleoside triphosphates and one oligonucleotide primer for each different specific sequence being amplified, wherein each primer is selected to be substantially complementary to different strands of each specific sequence, such that the extension product synthesized from one primer, when it is separated from its complement, can serve as a template for synthesis of the extension product of the other primer. Additionally or alternatively, detection of a genetic biomarker can include a sample of one or more nucleic acids comprising multiple strands of a specific nucleic acid sequence contained in the nucleic acid(s). The sample may comprise about 10-100 of the strands, about 100-1000 of the strands, or over about 1000 of the strands. Additionally or alternatively, detection of a genetic biomarker can include an amplified nucleic acid sequence from a nucleic acid or mixture of nucleic acids comprising multiple copies of the sequence produced by the amplification above processes.

[692] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/181134, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include techniques for identifying driver genes, mutations, and/or pathways for various types of cancer. For example, the identified driver genes may be used for diagnosis by identifying mutations occurring on the identified driver genes, or for treatment by targeting the identified driver genes. In some embodiments, a driver gene may be identified by determining a gene- specific background mutation rate. In some embodiments, a statistical model for gene- specific background mutation rate may be determined by optimizing parameters estimated from single-gene and cross-genes modeling. In one example, the gene-specific background mutation can be statistically determined by recursively optimizing a gene-specific mean and a gene-specific dispersion using negative binomial regression and Bayesian inference. Genes, mutations, and/or pathways that have significantly more mutations than the expected background mutations across samples may be identified as candidate driver genes, mutations, and/or pathways. Additionally or alternatively, detection of a genetic biomarker can include a method comprising: for each sample of a plurality of samples from different subjects having a same type of cancer, receiving a set of one or more mutations in DNA measured in

the sample, the DNA including a plurality of genes; for each sample of the plurality of samples, determining a sample mutation rate based on a total number of mutations measured in the sample; for each mutation context of a plurality of mutation contexts, determining a context mutation rate based on a first number of mutations identified in the sets of mutations for the mutation context, wherein a mutation context corresponds to a type of substitution or deletion; for each gene of the plurality of genes, determining, for each sample of the plurality of samples, a second number of silent mutations measured in the gene in the sample; determining an expected silent mutation rate using a sum of context mutation rates of silent mutations in the gene, wherein a silent mutation does not cause a change to an amino acid sequence of a translated protein for the gene; determining a probability distribution of gene-specific background mutation rate across the plurality of samples for the gene based on the expected silent mutation rate for the gene and the sample mutation rates of the plurality of samples, wherein determining the probability distribution of gene-specific background mutation rate for the gene includes: optimizing one or more parameters of the probability distribution of gene-specific background mutation rate for the gene to increase a fit of the probability distribution to the second number of silent mutations; determining an expected non-silent mutation rate using a sum of context mutation rates of a subset of non-silent mutations in the gene; determining an expected number of samples having at least one non- silent mutation using the expected non-silent mutation rate and the probability distribution of the gene-specific background mutation rate for the gene; and comparing the expected number to the measured number of samples having at least one non-silent mutation to obtain a likelihood value for the measured number; and identifying a group of genes having likelihood values above a threshold as candidate driver genes.

[693] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/201315, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include an automated nucleic acid amplification method which may comprise the following steps: (a) providing at least two droplets, wherein each droplet comprises primers that anneal to a target nucleic acid; (b) amplifying the target nucleic acid in each said droplet in parallel; (c) quantitating the amplified target nucleic acid in at least one

droplet; and (d) after a desired amount of the target nucleic acid has been obtained, recovering at least one droplet for further analyzing or processing of said at least one droplet. Additionally or alternatively, detection of a genetic biomarker can include an automated nucleic acid amplification method which may comprise the following steps: (a) providing at least two droplets, wherein each droplet comprises a target nucleic acid; (b) amplifying the target nucleic acid in each said droplet in parallel; (c) quantitating the amplified target nucleic acid in at least one droplet; and (d) after a desired amount of the target nucleic acid has been obtained, recovering at least one droplet for further analyzing or processing of said at least one droplet. In an embodiment, said droplets may be provided on an electrowetting-based device. Additionally or alternatively, detection of a genetic biomarker can include an automated nucleic acid amplification method which comprises the following steps: (a) providing an electrowetting- based device; (b) providing at least two droplets on said electrowetting-based device, wherein each droplet comprises primers that anneal to a target nucleic acid; (c) amplifying the target nucleic acid in each said droplet in parallel; (d) quantitating the amplified target nucleic acid in at least one droplet; and (e) after a desired amount of the target nucleic acid has been obtained, recovering at least one droplet using for further analyzing or processing of said at least one droplet. Additionally or alternatively, detection of a genetic biomarker can include an automated nucleic acid amplification method which comprises the following steps: (a) providing an electrowetting-based device; (b) providing at least two droplets on said electrowetting-based device, wherein each droplet comprises a target nucleic acid; (c) amplifying the target nucleic acid in each said droplet in parallel; (d) quantitating the amplified target nucleic acid in at least one droplet; and (e) after a desired amount of the target nucleic acid has been obtained, recovering at least one droplet using for further analyzing or processing of said at least one droplet. In some embodiments, said droplets may each may comprise a different target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method wherein said droplets each may comprise the same target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include to a method wherein said droplet may comprise a mixture of droplets that contain the same target nucleic acid and different target nucleic acids. Additionally or alternatively, detection of a genetic biomarker can include a method wherein the electrowetting-based device may comprise a biplanar

configuration of parallel arrays of electrodes to effect electrowetting-mediated droplet manipulations. Some embodiments relate to a method wherein the electrowetting- based device may comprise a planar configuration of electrodes that effects electrowetting- mediated droplet manipulations. Some embodiments relate to a method wherein the electrowetting-based device may comprise square electrodes, optionally wherein said electrodes are about 5 mm by 5 mm. Some embodiments relate to a method wherein the electrowetting-based device may comprise electrodes, wherein said electrodes are square, triangular, rectangular, circular, trapezoidal, and/or irregularly shaped. Some embodiments relate to a method wherein the electrowetting-based device may comprise electrodes wherein said electrodes may comprise electrode dimensions ranging from about 100 μηι by 100 μηι to about 10 cm by 10 cm. Some embodiments relate to a method wherein the electrowetting- based device may comprise interdigitated electrodes. Some embodiments relate to a method wherein the electrowetting-based device may comprise electrodes, wherein said electrodes may comprise indium tin oxide ("ITO"), transparent conductive oxides ("TCOs"), conductive polymers, carbon nanotubes ("CNT"), graphene, nanowire meshes and/or ultra thin metal films, e.g., ITO. Additionally or alternatively, detection of a genetic biomarker can include a method wherein the detection zone may detect electrochemical and/or fluorescent signals. Additionally or alternatively, detection of a genetic biomarker can include a method wherein said detection zone may detect capacitance of a droplet. An additional embodiment pertains to a method wherein said detection zone may be a fixed location. Another embodiment relates to a method wherein said detection zone may comprise any location within the electrowetting-based device. Yet another embodiment generally pertains to a method wherein the method of amplification may comprise hot start PCR. Additionally or alternatively, detection of a genetic biomarker can include a method wherein said amplification may comprise isothermal amplification. Additionally or alternatively, detection of a genetic biomarker can include a method wherein said amplification may comprise thermocycling. Said thermocycling may comprise temperatures ranging from about 50°C to about 98°C, e.g., about 50°C, about 60°C, about 65°C, about 72°C, about 95°C, or about 98°C. Said thermocycling may comprise times ranging from about 1 s to about 5 min., e.g., about 1 sec, about 5 sec, about 10 sec, about 20 sec, about 30 sec, about 45 sec, about 1 min, and/or about 5 min. Furthermore, said thermocycling may comprise three thermocycle

steps, and said three thermocycle steps may be completed in one minute or less. In some embodiments, each droplet may further comprise a detection agent. Additionally or alternatively, detection of a genetic biomarker can include a method wherein each droplet may contain the same detection agent. Additionally or alternatively, detection of a genetic biomarker can include a method wherein each droplet may contain a different detection agent. Another embodiment generally relates to a method wherein the droplets may comprise a labeled subset of droplets wherein each droplet within the subset contains an agent for detecting the target nucleic acid, and an unlabeled subset of droplets wherein each droplet within the subset does not contain said agent for detecting the target nucleic acid. An additional embodiment generally encompasses a method wherein each droplet within the subset containing a detection agent may comprise a different detection agent. Additionally or alternatively, detection of a genetic biomarker can include a method wherein each droplet within the subset containing a detection agent may comprise the same detection agent. In some embodiments, the nucleic acid polymerase may be a modified naturally occurring Type A polymerase. A further embodiment generally relates to a method wherein the modified Type A polymerase may be selected from any species of the genus Meiothermus, Thermotoga, or Thermomicrobium. Another embodiment generally pertains to a method wherein the polymerase may be isolated from any of Thermus aquaticus (Taq), Thermus thermophilus, Thermus caldophilus, or Thermus flliformis. A further embodiment generally encompasses a method wherein the modified Type A polymerase may be isolated from Bacillus stearothermophilus, Sphaerobacter thermophilus, Dictoglomus thermophilum, or Escherichia coli. Additionally or alternatively, detection of a genetic biomarker can include a method wherein the modified Type A polymerase may be a mutant 7a -E507K polymerase. Another embodiment generally pertains to a method wherein a thermostable polymerase may be used to effect amplification of the target nucleic acid. A further embodiment generally relates to a method wherein the thermostable polymerase may be selected from the following: Thermotoga maritima, Thermus aquaticus, Thermus thermophilus , Thermus flavus, Thermus flliformis, Thermus species Sps 1 7. Thermus species Z05, Thermus caldophilus, Bacillus caldotenax, Thermotoga neopolitana, and Thermosipho africanus. Additionally or alternatively, detection of a genetic biomarker can include a method wherein a modified polymerase may be used to

effect amplification of the target nucleic acid, e.g., wherein said modified polymerase may be selected from the following: G46E E678G CS5 DNA polymerase, G46E L329A E678G CS5 DNA polymerase, G46E L329A D640G S671F CS5 DNA polymerase, G46E L329A D640G S671F E678G CS5 DNA polymerase, a G46E E678G CS6 DNA polymerase, Z05 DNA polymerase, ΔZ05 polymerase, AZ05-Gold polymerase, AZ05R polymerase, E615G Taq DNA polymerase, E678G TMA-25 polymerase, and E678G TMA-30 polymerase. Additionally or alternatively, detection of a genetic biomarker can include a method wherein detection of the detection agent may occur at the end of an amplification cycle. In some embodiments, the method may detect a single nucleotide polymorphism. An additional embodiment generally relates to a method wherein the method may be used for amplicon generation. In some embodiments, the method may be used for a melting curve analysis. In some embodiments, the method may be used for target nucleic acid enrichment. In some embodiments, the method may be used for primer extension target enrichment ("PETE"). In some embodiments, the method may be used to for library amplification In some embodiments, the method may be used quantitate the number of adapter-ligated target nucleic acid molecules during library preparation. Additionally or alternatively, detection of a genetic biomarker can include a method wherein said quantitation of the number of adapter-ligated target nucleic acid molecules may occur (a) after adapter ligation to determine the amount of input material converted to adapter-ligated molecules (conversion rate) and/or the quantity of template used for library amplification; (b) after library amplification, to determine whether a sufficient amount of each library has been generated and/or to ensure equal representation of indexed libraries pooled for target capture or cluster amplification; and/or (c) prior to cluster amplification, to confirm that individual libraries or sample pools are diluted to the optimal concentration for NGS flow cell loading. Additionally, said quantitation of the number of adapter-ligated target nucleic acid molecules may occur after post-ligation cleanup steps (prior to library amplification). In some embodiments, after recovering at least one droplet, said further analyzing or processing of said at least one droplet may comprise a nucleic acid sequencing reaction, a next generation sequencing reaction, whole-genome shotgun sequencing, whole exome or targeted sequencing, amplicon sequencing, mate pair sequencing, RIP-seq/CLIP-seq, ChlP-seq, RNA-seq, transcriptome analysis, and/or methyl-seq.

Additionally or alternatively, detection of a genetic biomarker can include a method wherein the droplets may be surrounded by a filler fluid, e.g., wherein said filler fluid may be an oil. In some embodiments, said oil may comprise a transparent oil. In some embodiments, said oil may comprise liquid polymerized siloxane, silicone oil mineral oil, and/or paraffin oil. Another embodiment generally relates to method wherein the droplets may be surrounded by a gas, e.g., wherein said gas may be air. Yet another embodiment generally relates to a method wherein the method may be used to avoid overamplification bias. Another embodiment generally relates to a method wherein the method may be used to produce a representative sample of a population of mutations. Additionally or alternatively, detection of a genetic biomarker can include a method wherein the method may be used to determine the number of amplification cycles necessary to generate the desired concentration of a target nucleic acid. Additionally or alternatively, detection of a genetic biomarker can include a method wherein the method may be controlled through a computer in communication with the electrowetting-based device. Some embodiments generally relate to a method wherein said method comprises a master mix. In some embodiments, said master mix may comprise a polymerase, dNTP(s), MgCl2, and/or oligonucleotide primer(s). In some embodiments, said master mix may comprise dNTP(s) at a concentration comprising from about 1 mM to about 100 mM, e.g., about 1 mM, about 10 mM, or about 100 mM; MgC12 at a concentration comprising from about 1 mM to about 100 mM, e.g., about 1 mM, about 10 mM, or about 100 mM; and/or a oligonucleotide primer(s) at a concentration comprising from about 1 nM to about 1 mM, e.g., about 1 nM, about 1 μM, or about 1 mM. Additionally or alternatively, detection of a genetic biomarker can include a device for amplification of a target nucleic acid, wherein said device may (a) comprise a biplanar configuration of parallel arrays of electrodes to effect electrowetting-mediated droplet manipulations; (b) comprise or be in contact with at least one heating element; and (c) comprise or be in contact with at least one detection zone. In an embodiment, said heating element may comprise an inductive heating element. Another aspect generally pertains to a device for amplification of a target nucleic acid, wherein said device may (a) comprise a planar configuration of electrodes to effect electrowetting-mediated droplet manipulations; (b) comprise or be in contact with at least one heating element; and (c) comprise or be in contact with at least one detection zone. In an embodiment, said heating element may comprise an

inductive heating element. In some embodiments, said electrodes may comprise square shapes, optionally about 5 mm by 5 mm. In some embodiments, said electrodes may comprise square, triangular, rectangular, circular, trapezoidal, and/or irregularly shapes. In some embodiments, said electrodes may comprise electrode dimensions ranging from about 100 μιτι by 100 μιτι to about 10 cm by 10 cm. In some embodiments, said electrodes may be interdigitated. In some embodiments, said electrodes may comprise indium tin oxide ("ITO"), transparent conductive oxides ("TCOs"), conductive polymers, carbon nanotubes ("CNT"), graphene, nanowire meshes and/or ultra thin metal films, e.g., ITO. In some embodiments, said device may comprise droplets that range in volume from about 1 picoliter to about 5 mL, e.g., about 12.5 μΐ. In some embodiments, said device may comprise a gap between a top plate and a bottom plate of about 0.5 mm. In some embodiments, said device may comprise a plurality of inlet/outlet ports. In some embodiments, said device may comprise between 1 to about 400 inlet/outlet ports for loading and removal of the same sample or of different samples, and/or said device further comprises between 1 to about 100 inlet/out ports for the introduction and removal of filler fluid(s). In some embodiments, said device may comprise inlet/outlet ports wherein the spacing between adj acent ports ranges from about 5 mm to about 500 mm. In a further embodiment, said heating element may comprise a contact heater. An additional aspect relates to an embodiment wherein said amplification comprises thermocy cling. Said thermocycling may comprise three thermocycle steps, and said three thermocycle steps may be completed in one minute or less. In another embodiment, said amplification may comprise isothermal amplification. In a further embodiment, said amplification may comprise hot start PCR. In yet another embodiment, the detection zone may detect electrochemical and/or fluorescent signals. An additional embodiment pertains to a detection zone that may detect capacitance of a droplet. In a further embodiment, said detection zone may be a fixed location. In another embodiment, said detection zone may comprise any location within the electrowetting-based device. In another embodiment, the target nucleic acid may be provided on the device within at least three droplets. In a further embodiment, said droplets may each comprise the same target nucleic acid. In yet another embodiment, said droplets may comprise a mixture of droplets that contain the same target nucleic acid and different target nucleic acids. In another embodiment, each droplet may further comprise a detection agent. In an additional

embodiment, each droplet may contain the same detection agent. In another embodiment, each droplet may contain a different detection agent. Additionally, in another embodiment, the droplets may comprise a labeled subset of droplets that each contain an agent for detecting the target nucleic acid, and an unlabeled subset of droplets that each do not contain said agent for detecting the target nucleic acid. In an additional embodiment, each droplet within the subset containing a detection agent may comprise a different detection agent. In another embodiment, each droplet within the subset containing a detection agent may comprise the same detection agent. In a further embodiment, each subset of droplets may comprise 1 or more, 2 or more, 10 or more, 100 or more, 1,000 or more, or 10,000 or more droplets. In some embodiments, the device may detect a single nucleotide polymorphism. In yet another embodiment, the device may effect amplicon generation. In an additional embodiment, the device may effect a melting curve analysis. In yet another embodiment, the device may effect target nucleic acid enrichment. In yet another embodiment, the device may effect PETE. In an additional embodiment, the device may effect library amplification. In a further embodiment, the device may quantitate the number of adapter-ligated target nucleic acid molecules during library preparation. For example, said quantitation may occur (a) after adapter ligation to determine the amount of input material converted to adapter-ligated molecules (conversion rate) and/or the quantity of template used for library amplification; (b) after library amplification, to determine whether a sufficient amount of each library has been generated and/or to ensure equal representation of indexed libraries pooled for target capture or cluster amplification; and/or (c) prior to cluster amplification, to confirm that individual libraries or sample pools are diluted to the optimal concentration for NGS flow cell loading. Also, said quantitation may occur after post-ligation cleanup steps (prior to library amplification). In yet another embodiment, after a desired amount of the target nucleic acid has been obtained, at least one droplet may be recovered from said device prior to further analysis or processing of said droplet. For example, said further analyzing or processing of said at least one droplet may comprise a nucleic acid sequencing reaction, a next generation sequencing reaction, whole-genome shotgun sequencing, whole exome or targeted sequencing, amplicon sequencing, mate pair sequencing, RIP-seq/CLIP-seq, ChIP-seq, RNA-seq, transcriptome analysis, and/or methyl- seq. Additionally or alternatively, detection of a genetic biomarker can include a

system for automated amplification of a target nucleic acid which may comprise: (a) an electrowetting-based device; (b) at least one heating element that comprises or is in contact with the electrowetting-based device; (c) at least one detection zone that comprises or is in contact with the electrowetting-based device. In an embodiment, said heating element may comprise an inductive heating element. In a further embodiment, said heating element may comprise a contact heater. An additional aspect relates to an embodiment wherein said amplification comprises thermocycling. Said thermocycling may comprise three thermocycle steps, and said three thermocycle steps may be completed in one minute or less. In another embodiment, said amplification may comprise isothermal amplification. In a further embodiment, said amplification may comprise hot start PCR. In yet another embodiment, the detection zone may detect electrochemical and/or fluorescent signals. An additional embodiment pertains to a detection zone that may detect capacitance of a droplet. In a further embodiment, said detection zone may be a fixed location. In another embodiment, said detection zone may comprise any location within the system. In another embodiment, the target nucleic acid may be provided on the system within at least three droplets. In a further embodiment, said droplets may each comprise the same target nucleic acid. In yet another embodiment, said droplets may comprise a mixture of droplets that contain the same target nucleic acid and different target nucleic acids. In another embodiment, each droplet may further comprise a detection agent. In an additional embodiment, each droplet may contain the same detection agent. In another embodiment, each droplet may contain a different detection agent. Additionally, in another embodiment, the droplets may comprise a labeled subset of droplets that each contain an agent for detecting the target nucleic acid, and an unlabeled subset of droplets that each do not contain said agent for detecting the target nucleic acid. In an additional embodiment, each droplet within the subset containing a detection agent may comprise a different detection agent. In another embodiment, each droplet within the subset containing a detection agent may comprise the same detection agent. In a further embodiment, each subset of droplets may comprise 1 or more, 2 or more, 10 or more, 100 or more, 1,000 or more, or 10,000 or more droplets. Additionally or alternatively, detection of a genetic biomarker can include an automated amplification method which may comprise (a) providing an electrowetting-based device with a biplanar configuration of parallel arrays of electrodes to

effect electrowetting-mediated droplet manipulations, and further wherein said device contains at least one inductive heating element and at least one detection zone; (b) providing on said device droplets comprising a target nucleic acid, wherein said droplets comprise a subset of droplets that contains an agent for target nucleic acid detection and a subset of droplets that does not contain said agent for target nucleic acid detection; (c) amplifying the target nucleic acid in each said droplet in parallel; (d) quantitating the amplified target nucleic acid in said subset of droplets containing said agent through detection of said agent; and (e) after a desired amount of said target nucleic acid has been obtained in said subset of droplets containing an agent, recovering at least one droplet from said subset of droplets not containing an agent for further analyzing or processing.

[694] In some embodiments, detection of a genetic biomarker (e.g., one or more genetic biomarkers) can include any of the variety of methods described in P.C.T. Publication No. WO 2017/123316, which is hereby incorporated by reference in its entirety. For example, detection of a genetic biomarker can include a targeted sequencing workflow where an input sample comprising a sufficient quantity of genomic material is provided such that minimal or no amplification processes are required prior to sequencing. In some embodiments, the input sample is derived from an intact tumor or from lymph nodes. In some embodiments, the input sample is obtained through homogenization of an intact tumor sample (whole or partial) and/or one or more lymph nodes obtained from a patient or mammalian subject. In some embodiments, the input sample is derived from a sufficient quantity of blood, including whole blood or any fraction thereof. In some embodiments, the input sample is derived from cancerous tissue. In some embodiments, the input sample is derived from precancerous tissue. In some embodiments, the targeted sequencing workflow comprises one or more amplification steps (e.g. a pre-capture amplification step, an amplification step post-capture) prior to sequencing, where each amplification step prior to sequencing comprises from 0 to 3 amplification cycles, and wherein an aggregate of amplification cycles prior to sequencing does not exceed 4. In other embodiments, the targeted sequencing workflow comprises one or more amplification steps (e.g. a pre-capture amplification step, an amplification step post-capture) prior to sequencing, where each amplification step prior to sequencing comprises from 0 to 2 amplification cycles, and wherein an aggregate of amplification cycles prior to

sequencing does not exceed 3. In yet other embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing (e.g. either a pre-capture amplification step or an amplification step post-capture), where the single amplification step prior to sequencing comprises from 0 to 3 amplification cycles. In further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises from 1 to 3 cycles. In yet further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises 1 cycle. In even further embodiments, the targeted sequencing workflow comprises one amplification step prior to sequencing, where the single amplification step prior to sequencing comprises 2 cycles. In some embodiments, either or both of the pre-capture amplification step or the amplification step post-capture but prior to sequencing utilizes LM-PCR. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing genomic material within a sample comprising: homogenizing a tumor sample and/or lymph node sample to provide a homogenized sample; isolating at least 0.5 micrograms of genomic material from the homogenized sample; preparing the at least 0.5 micrograms of isolated genomic material for sequencing; and sequencing the prepared genomic material. In some embodiments, the method does not comprise any amplification steps prior to sequencing. In some embodiments, the method comprises at least one pre-capture or post-capture amplification step, wherein an aggregate number of amplification cycles conducted during the at least one pre-capture or post-capture amplification step is at most 4 cycles. In some embodiments, the aggregate number of amplification cycles is 3. In some embodiments, the aggregate number of amplification cycles is 2. In some embodiments, the preparing of the at least 0.5 micrograms of isolated genomic material for sequencing comprises hybridizing the at least 0.5 micrograms of isolated genomic to capture probes and capturing the hybridized genomic material. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, 1 or 2 amplification cycles are performed on the captured genomic material. In some embodiments, the homogenized sample comprises a representative sampling of cells. In some embodiments, at least 1 microgram of genomic material is isolated from the homogenized samples. In some embodiments, at least 5 micrograms of genomic material is

isolated from the homogenized samples. In some embodiments, at least 10 micrograms of genomic material is isolated from the homogenized samples. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing DNA within a sample comprising isolating at least 0.5 micrograms of DNA from a blood sample; preparing the at least 0.5 micrograms of isolated DNA for sequencing, and sequencing the prepared DNA. In some embodiments, the method comprises 0 amplification steps prior to sequencing. In some embodiments, the preparing of the at least 0.5 micrograms of isolated DNA for sequencing comprises hybridizing the at least 0.5 micrograms of isolated genomic to capture probes and capturing the hybridized genomic material. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, 1 or 2 amplification cycles are performed on the captured genomic material. In some embodiments, at least 1 microgram of DNA is isolated from the blood sample. Additionally or alternatively, detection of a genetic biomarker can include a method of targeted representational sequencing comprising: (i) homogenizing at least a portion of a tumor, one or more whole or partial lymph nodes, or any combination thereof to provide a homogenized sample; (ii) extracting genomic material from the homogenized sample; (iii) capturing the extracted genomic material onto beads; and (iv) sequencing the captured genomic material; wherein the targeted representational sequencing comprises performing at most 4 amplification cycles prior to sequencing of the captured genomic material. In some embodiments, the at most 3 amplification cycles may be conducted prior to capture of the extracted genomic material or after capture of the extracted genomic material, or any combination thereof. In some embodiments, no pre-capture amplification cycles are conducted. In some embodiments, an amount of captured genomic material ranges from about 90ng to about 900ng. In some embodiments, from 1 to 3 amplification cycles are performed following capture of the extracted genomic material, but prior to sequencing. In some embodiments, at least 0.5 micrograms of genomic material is extracted from the homogenized sample. In some embodiments, at least 100 times more genomic material is derived from the homogenized sample as compared with an amount of input material used in a sequencing method requiring more than 4 amplification cycles. Additionally or alternatively, detection of a genetic biomarker can include a method of sequencing DNA within a sample comprising: providing

at least 0.5 micrograms of input genomic material, the at least 0.5 micrograms of genomic material derived from a tumor sample, a lymph node sample, or a blood sample, isolating DNA from the input genomic sample, preparing the isolated DNA for sequencing, and sequencing the prepared DNA, wherein the method does not comprise any amplification steps. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from multiple histological and/or biopsy specimens. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from a homogenized tumor sample. In some embodiments, the at least 0.5 micrograms of input genomic material is derived from a homogenized lymph node sample. In some embodiments, the at least 0.5 micrograms of input genomic material is a representative sampling of the tumor sample, lymph node sample, or blood sample from which it is derived. In some embodiments, the sequencing is performed using a next-generation sequencing method. In some embodiments, sequencing is performed using a synthesis sequencing methodology. Additionally or alternatively, detection of a genetic biomarker can include a method of reducing PCR- introduced mutations during sequencing comprising isolating DNA from a sample comprising a sufficient amount of genomic material; preparing the isolated DNA for sequencing; and sequencing the prepared DNA, wherein the method comprises at most 3 amplification cycles prior to sequencing. In some embodiments, the method comprises 1 or 2 amplification cycles prior to sequencing. In some embodiments, sufficient amount of input genomic material is an amount such that no pre-capture amplification cycles are utilized. In some embodiments, the sample is derived from a patient suspected of having cancer. In some embodiments, the sample is derived from a patient diagnosed with cancer. In some embodiments, the sample is derived from a patient at risk of developing cancer. In some embodiments, the sample is derived from healthy tissue samples. In some embodiments, 0.5 micrograms of DNA is isolated from the sample. In some embodiments, at least 1 microgram of genomic material is isolated from the sample. In some embodiments, at least 5 micrograms of genomic material is isolated from the sample. In some embodiments, at least 10 micrograms of genomic material is isolated from the sample. Additionally or alternatively, detection of a genetic biomarker can include a sequencing method where PCR-introduced mutations are reduced, the sequencing method comprising capturing at least 0.05 micrograms of genomic material, and performing between 0 and 2

amplification cycles prior to sequencing. In some embodiments, 0 amplification cycles are conducted. In other embodiments, 1 amplification cycle is conducted. In yet other embodiments, 2 amplification cycles are conducted. Additionally or alternatively, detection of a genetic biomarker can include a sequence capture method where PCR-introduced biases in the proportional representation of genome content are reduced, the sequencing method comprising providing an input sample comprising at least 0.5 micrograms of genomic material, and where the sequence capture method comprises performing between 0 and 2 amplification cycles prior to sequencing. In some embodiments, 0 amplification cycles are conducted. In other embodiments, 1 amplification cycle is conducted. In yet other embodiments, 2 amplification cycles are conducted. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. Additionally or alternatively, detection of a genetic biomarker can include a sequence capture method where PCR-introduced mutations are eliminated, the sequence capture method comprising preparing an input sample comprising at least 0.5 micrograms of genomic material. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. Additionally or alternatively, detection of a genetic biomarker can include a sequence capture method where a step of removing PCR-duplicate reads prior to sequencing is eliminated, the sequence capture method comprising providing an input sample comprising at least 0.5 micrograms of genomic material. In some embodiments, the input sample comprises at least 1 microgram of genomic material. In some embodiments, the input sample comprises at least 5 micrograms of genomic material. In some embodiments, the input sample comprises at least 10 micrograms of genomic material. Additionally or alternatively, detection of a genetic biomarker can include a sequencing method where PCR-introduced mutations are virtually eliminated, the sequencing method comprising capturing at least 0.05 micrograms of genomic material. In some embodiments, about 0.05 micrograms of genomic material are provided after capture of the genomic material.

In some embodiments, 1 or 2 post-capture amplification cycles are performed prior to sequencing.

[695] Examples of genetic biomarkers that can be detected using any of the variety of techniques described herein include, without limitation, ABCA7, ABL1, ABL2, ACVR1B, ACVR2A, AJUBA, AKT1, AKT2, ALB, ALDOB, ALK, AMBRA1, AMER1, AMOT, ANKRD46, APC, AR, ARHGAP35, ARHGEF12, ARID1A, ARID1B, ARID2, ARID4B, ARL15, ARMCX1, ASXL1, ASXL2, ATAD2, ATF1, ATG14, ATG5, ATM, ATRX, ATXN2, AXIN1, B2M, BAP1, BCL11A, BCL11B, BCL2, BCL3, BCL6, BCL9, BCLAF1, BCOR, BCR, BIRC6, BIRC8, BLM, BLVRA, BMPR1A, BRAF, BRCA1, BRCA2, BRD7, BRE, BRWD3, BTBD7, BTRC, C11orf70, C12orf57, C2CD5, C3orf62, C8orf34, CAMKV, CAPG, CARD11, CARS, CASP8, CBFA2T3, CBFB, CBLC, CBX4, CCAR1, CCDC117, CCDC88A, CCM2, CCNC, CCND1, CCND2, CCND3, CCR3, CD1D, CD79B, CDC73, CDCP1, CDH1, CDH11, CDK12, CDK4, CDK6, CDKN1A, CDKN1B, CDKN2A, CDX2, CEBPA, CELF1, CENPB, CEP128, CHD2, CHD4, CHD8, CHEK2, CHRDL1, CHUK, CIC, CLEC4C, CMTR2, CNN2, CNOT1, CNOT4, COL11A1, COPS4, COX7B2, CREB1, CREBBP, CSDE1, CSMD3, CTCF, CTDNEP1, CTNNB1, CUL1, CUL2, CYB5B, CYLD, DACH1, DCHS1, DCUN1D1, DDB2, DDIT3, DDX3X, DDX5, DDX6, DEK, DHX15, DHX16, DICER1, DIRC2, DIS3, DIXDC1, DKK2, DNAJB5, DNER, DNM1L, DNMT3A, EED, EGFR, EIF1AX, EIF2AK3, EIF2S2, EIF4A1, EIF4A2, ELF3, ELK4, EMG1, EMR3, EP300, EPB41L4A, EPHA2, EPS8, ERBB2, ERBB3, ERRFI1, ETV4, ETV6, EVI1, EWSR1, EXO5, EXT1, EXT2, EZH2, F5, FANCM, FAT1, FBN2, FBXW7, FCER1G, FEV, FGF2, FGFR1, FGFR1OP, FGFR2, FGFR3, FH, FLT3, FN1, FOXA1, FOXP1, FUBP1, FUS, GALNTL5, GATA3, GGCT, GIGYF2, GK2, GLIPR2, GNAS, GNPTAB, GNRHR, GOLGA5, GOLM1, GOPC, GOT2, GPC3, GPS2, GPX7, GRK1, GSE1, GZMA, HDAC1, HERC1, HERC4, HGF, HIST1H2BO, HLA-A, HLA-B, HMCN1, HMGA1, HMGA2, HNRNPA1, HRAS, HSP90AB1, ID3, IDH1, IDH2, IFNGR2, IFT88, IKZF2, IL2, INO80C, INPP4A, INPPL1, IRF4, IWS1, JAK1, JAK2, JUN, KANSL1, KAT8, KATNAL1, KBTBD7, KCNMB4, KDM5C, KDM6A, KEAP1, KIAA1467, KIT, KLF4, KMT2A, KMT2B, KMT2C, KMT2D, KMT2E, KRAS, KRT15, LAMTOR1, LARP4B, LCK, LMO2, LPAR2, LYN, MAF, MAFB, MAML2, MAP2K1, MAP2K2, MAP2K4, MAP3K1,

MAP4K3, MAPK1, MAX, MB21D2, MBD1, MBD6, MBNL1, MBNL3, MDM2, MDM4, MED12, MED23, MEN1, MET, MGA, MITF, MKLN1, MLH1, MLL, MLLT4, MOAP1, MORC4, MPL, MS4A1, MSH2, MSI1, MTOR, MYB, MYC, MYCL1, MYCN, MYD88, MYL6, MYO1B, MYO6, NAA15, NAA25, NAP1L2, NAP1L4, NCOA2, NCOA4, NCOR1, NEK9, NF1, NF2, NFE2L2, NFE2L3, NFKB2, NIPBL, NIT1, NKX3-1, NME4, NOTCH1, NOTCH2, NPM1, NR4A3, NRAS, NSD1, NTRK1, NUP214, NUP98, PALB2, PAX8, PBRM1, PCBP1, PCOLCE2, PDGFB, PHF6, PIK3CA, PIK3CB, PIK3R1, PIM1, PLAG1, PML, POLA2, POT1, PPARD, PPARG, PPM1D, PPP2R1A, PPP6C, PRKACA, PRKCI, PRPF40A, PSIP1, PTEN, PTH2, PTMS, PTN, PTPN11, RAB18, RAC1, RAF1, RANBP3L, RAPGEF6, RASA1, RB1, RBBP6, RBM10, RBM26, RC3H2, REL, RERE, RET, RFC4, RHEB, RHOA, RIMS2, RIT1, RNF111, RNF43, ROS1, RPL11, RPL5, RQCD1, RRAS2, RUNX1, RXRA, SARM1, SCAF11, SDHB, SDHD, SEC22A, SENP3, SENP8, SETD1B, SETD2, SF3A3, SF3B1, SFPQ, SIN3A, SKAP2, SMAD2, SMAD3, SMAD4, SMARCA4, SMARCB1, SMARCC2, SMO, SNCB, SOCS1, SOS1, SOX4, SOX9, SP3, SPEN, SPOP, SPSB2, SS18, STAG2, STK11, STK31, SUFU, SUFU, SUZ12, SYK, TAF1A, TARDBP, TAS2R30, TBL1XR1, TBX3, TCF12, TCF3, TCF7L2, TCL1A, TET2, TEX11, TFDP2, TFG, TGFBR2, THRAP3, TLX1, TM9SF1, TMCO2, TMED10, TMEM107, TMEM30A, TMPO, TNFAIP3, TNFRSF9, TNRC6B, TP53, TP53BP1, TPR, TRAF3, TRIM8, TRIP12, TSC1, TSC2, TTK, TTR, TUBA3C, U2AF1, UBE2D3, UBR5, UNC13C, UNKL, UPP1, USO1, USP28, USP6, USP9X, VHL, VN1R2, VPS33B, WAC, WDR33, WDR47, WRN, WT1, WWP1, XPO1, YOD1, ZC3H13, ZDHHC4, ZFHX3, ZFP36L1, ZFP36L2, ZGRF1, ZMYM3, ZMYM4, ZNF234, ZNF268, ZNF292, ZNF318, ZNF345, ZNF600, ZNF750, and/or ZNF800.

[696] As used herein, "TP53" refers to the gene and/or the protein encoded by the gene, which is tumor suppressor protein p53 involved in the regulation of cell proliferation. TP53 gene plays a crucial role in preventing cancer formation. TP53 gene encodes proteins that bind to DNA and regulate gene expression to prevent mutations of the genome. Human TP53 sequences are known in the art (e.g., GenBank accession numbers NM_001276761, NM_000546, NM_001126112, NM_001126113, and NM_001126114). One of ordinary skill in the art can identify additional TP53 sequences and variants thereof.

[697] As used herein, "PIK3CA" refers to the gene and/or the protein encoded by the gene, which is the catalytic subunit of Phosphoinositol-3 kinase (PI3K), isoform alpha, also referred to as p110alpha. PIK3CA has been found to be oncogenic and has been implicated in a variety of cancers. Human PIK3CA sequences are known in the art (e.g., GenBank accession number NM_006218). One of ordinary skill in the art can identify additional PIK3CA sequences and variants thereof.

[698] As used herein, the term "FGFR3" refers to the gene and/or the protein encoded by the gene, which is fibroblast growth factor receptor 3 (FGFR3) which belongs to a family of structurally related tyrosine kinase receptors (FGFRs 1-4) encoded by four different genes. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals which ultimately influencing cell mitogenesis and differentiation. Human FGFR3 sequences are known in the art (e.g., GenBank accession numbers NM_000142, NM_001163213, NM_022965, NM_001354809, and NM_001354810). One of ordinary skill in the art can identify additional FGFR3 sequences and variants thereof.

[699] As used herein, the term "KRAS" refers to the gene and/or the protein encoded by the gene known as K-ras or Ki-ras, which is proto-oncogene corresponding to the oncogene first identified in Kirsten rat sarcoma virus and the gene product was first found as a p21 GTPase. Human KRAS sequences are known in the art (e.g., GenBank accession numbers NM_004985 and NM_033360). One of ordinary skill in the art can identify additional KRAS sequences and variants thereof.

[700] As used herein, the term "ErbB2" refers to the gene and/or the protein encoded by the gene, which is also known as v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2, c-erbB2/neu, her2/neu, or Her2. ErbB2 is a member of the epidermal growth factor receptor family of tyrosine kinases. It is amplified and/or overexpressed in several cancers, including breast and ovarian cancer. Human ErbB2 sequences are known in the art (e.g., GenBank accession numbers NM_001005862, NM_001289936, NM_001289937, NM_001289938, and NM_004448). One of ordinary skill in the art can identify additional ErbB2 sequences and variants thereof.

[701] As used herein, "CDKN2A" refers to the gene and/or the protein encoded by the gene, which is known as cyclin-dependent kinase Inhibitor 2A, act as tumor suppressors by regulating the cell cycle. Human CDKN2A sequences are known in the art (e.g., GenBank accession numbers NM_000077, NM_001195132, NM_058195, NM_058196, and NM_058197). One of ordinary skill in the art can identify additional CDKN2A sequences and variants thereof.

[702] As used herein, the term "MLL" refers to the gene and/or the protein encoded by the gene, which is lymphoid or mixed-lineage leukemia 2. MLL is a major mammalian histone H3 lysine 4 (H3K4) mono-methyltransferase. MLL protein co-localizes with lineage determining transcription factors on transcriptional enhancers and is essential for cell differentiation and embryonic development. MLL also plays critical roles in regulating cell fate transition, metabolism, and tumor suppression. Mutations in MLL have been associated with Kabuki Syndrome, congenital heart disease, and various forms of cancer. Human MLL sequences are known in the art (e.g., GenBank accession number NM_003482). One of ordinary skill in the art can identify additional MLL sequences and variants thereof.

[703] As used herein, the term "HRAS" refers to the gene and/or the protein encoded by the gene, which is harvey rat sarcoma viral oncogene homolog, is a small G protein, activating the MAP kinase pathway. HRAS is involved in regulating cell division in response to growth factor stimulation. HRAS has been shown to be a proto-oncogene. When mutated, proto-oncogenes have the potential to cause normal cells to become cancerous. Human HRAS sequences are known in the art (e.g., GenBank accession numbers NM_001130442, NM_005343, NM_176795, and NM_001318054). One of ordinary skill in the art can identify additional HRAS sequences and variants thereof.

[704] As used herein, the term "MET" refers to the gene and/or the protein encoded by the gene. MET gene encodes c-Met, also called tyrosine-protein kinase Met or hepatocyte growth factor receptor (HGFR). MET is a single pass tyrosine kinase receptor essential for embryonic development, organogenesis and wound healing. Hepatocyte growth factor/Scatter Factor (HGF/SF) and its splicing isoform (NK1, NK2) are the only known ligands of the MET receptor. MET is normally expressed by cells of epithelial origin, while expression of HGF/SF is restricted to cells of mesenchymal origin. When HGF/SF binds its

cognate receptor MET it induces its dimerization through a not yet completely understood mechanism leading to its activation. Human MET sequences are known in the art (e.g., GenBank accession numbers NM_000245, NM_001127500, NM_001324401, and NM_001324402). One of ordinary skill in the art can identify additional MET sequences and variants thereof.

[705] As used herein, the term "VHL" refers to the gene and/or the protein encoded by the gene. VHL gene is Von Hippel Lindau tumor suppressor gene. A germline mutation of the VHL gene is the basis of familial inheritance of Von Hippel-Lindau syndrome, a dominantly inherited hereditary cancer syndrome predisposing to a variety of malignant and benign tumors of the eye, brain, spinal cord, kidney, pancreas, and adrenal glands. Human VHL sequences are known in the art (e.g., GenBank accession numbers NM_000551, NM_198156, and NM_001354723). One of ordinary skill in the art can identify additional VHL sequences and variants thereof.

Scoring for Genetic Mutations

[706] The present disclosure provides methods of identifying the presence of cancer in a subject with high sensitivity and specificity based at least in part on the presence of one or more genetic biomarkers. Various methods are provided herein to determine whether the subject has cancer and/or the likelihood that the subject has cancer. In some embodiments, these methods involve various types of statistical techniques and methods, including, e.g., scoring methods, regression analysis, clustering, principal component analysis, nearest neighbor classifier analysis (e.g., k-nearest neighbors algorithm), linear discriminant analysis, neural networks, and support vector machines, etc.

[707] In some embodiments, one or more genetic biomarkers can be used to generate a score. The score can indicate that the likelihood that the subject has a cancer or does not have a cancer. In some embodiments, the likelihood is generated by comparing the mutation allele frequency of each mutation in one or more genetic biomarkers to a reference distribution of mutation allele frequency. As described herein, genomic segments containing one or more biomarkers can be amplified by a set of primers. The set of primers can have one or more

pairs of primers that amplify one or more non-overlapping genomic segments. The same set of primers can be used to amplify template DNA collected from a subject in one or more wells (e.g., equal to, or more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 20, or 30 wells), thus the amplification process can provide duplicate signals for mutants (e.g., rare mutations) that are detectable in multiple wells. In some embodiments, the PCR products can be subject to one or more rounds of additional amplification before sequencing. In some embodiments, reads from a common template molecule can be then grouped, e.g., based on the unique identifier sequences (UIDs) that are incorporated as molecular barcodes. In some embodiments, artifactual mutations that are introduced during the sample preparation or sequencing steps can be reduced by requiring a mutation to be present in e.g., greater than 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of reads in each UID family. In some embodiments, redundant reads arising from optical duplication can be eliminated by requiring reads with the same UID and sample index to be at least 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, or 9000 pixels apart when located on the same tile.

[708] In some embodiments, mutations that meet one or two of the two following criteria are considered (i) present in the Catalogue of Somatic Mutations in Cancer (COSMIC) database, or (ii) predicted to be inactivating in tumor suppressor genes (nonsense mutations, out-of-frame insertions or deletions, canonical splice site mutations). In some embodiments, synonymous mutations, except those at exon ends, and intronic mutations, except for those at splice sites, are excluded. These selected mutations are referred as supermutants. Thus, in some embodiments, supermutants include e.g., mutations present in the Catalogue of Somatic Mutations in Cancer (COSMIC) database, mutations predicted to be inactivating in tumor suppressor genes (nonsense mutations, out-of-frame insertions or deletions, canonical splice site mutations), non-synonymous mutations, mutations that can affect splicing, and/or mutations that can affect expression, etc.

[709] Thus, as used herein, the term "mutant allele frequency" or "MAF" within a sample (e.g., a well, a test sample) refers to the proportion of UIDs in the sample that have such a mutation. The MAF reflects the mutant fraction within each sample (e.g., each well) and represents an independent sampling of the mutant allele frequency in the sample of interest. In some embodiments, the MAF of a mutation in a sample (rather than the well) can be

calculated by the total number of mutants present in all wells for the sample (e.g., a sample collected from a subject) divided by the total number of UIDs.

[710] In some embodiments, MAF normalization is performed. In some embodiments, all mutations that do not have at least one supermutant in at least one well are excluded from the analysis. For example, the mutant allele frequency (MAF) can reflect the ratio between the total number of supermutants in each well from that sample and the total number of UIDs in the same well from that sample. In some embodiments, the MAF is first normalized based on the observed MAFs for each mutation in a set of normal controls comprising the normal plasmas in the training set. In some embodiments, mutations with <100 UIDs are excluded. The normalization can be performed by standard normalization (*i.e.* subtracting the mean and dividing by the standard deviation) or multiplying the MAF with a predetermined ratio. In some embodiments, the normalization is performed by first calculating the average MAF (ave_i) for each mutation i=1, … n, found among the normal controls. Using the 25th percentile of the distribution generated by these averages as the reference value (ave_ref), each MAF can be normalized multiplying it by the ratio ave_ref / ave_i. For example, if the observed average MAF of a mutation in a set of controls is 10 times higher than ave_ref, then each MAF for that mutation can be multiplied by 1/10.

[711] The classification of a sample's genetic biomarker status can be obtained, e.g., from a statistical test by comparing the MAF of one or more mutations in the selected genetic biomarkers to a reference distribution of mutation allele frequency for the mutations in a group of control samples, by comparing the mutation allele frequency of one or more mutations in the selected genetic biomarkers to a first reference distribution of mutation allele frequency in control samples and a second reference distribution of mutation allele frequency in samples collected from subjects having a cancer, or by comparing the mutation allele frequency of one or more mutations in the selected genetic biomarkers to the maximum mutation allele frequency of the mutation in control samples.

[712] The control reference distribution and the maximum mutation allele frequency of the mutation can be determined from controls samples. In some embodiments, the group of control samples has at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or more control subjects. In some embodiments,

the control subjects are healthy subjects, or at least do not have cancer, or are not suspected to have cancer. The control samples collected from these control subjects can be amplified and sequenced. The mutations in one or more selected genetic biomarkers can be determined. Thus, a MAF for a particular mutation in one subject can be determined, and the distribution of MAF in control samples can be determined from the group of control subjects. Similarly, the maximum mutation allele frequency of the mutation can also be determined in control samples.

[713] In some embodiments, the MAF of one or more mutations in the selected genetic biomarkers can be compared against the reference distribution, thereby obtaining a score indicates that the likelihood or the probability that the subject has cancer. In some embodiments, if the score (e.g., likelihood or probability) is equal to or greater than a reference threshold, it can be determined that the subject is likely to have cancer, otherwise, it can be determined that the subject is not likely to have cancer. In some embodiments, the comparison can provide a score that indicates the likelihood or probability that the subject does not have cancer. In some embodiments, if the score (e.g., likelihood or probability) is equal to or less than a reference threshold, thus it can be determined that the subject is likely to have cancer, otherwise, it can be determined that the subject is not likely to have cancer.

[714] In some embodiments, the MAF is first normalized based on the observed MAFs in a set of normal controls for each mutation. Following this mutation-specific normalization, the MAF of each mutation in each well is compared to a reference distribution of MAFs built from normal controls with all mutations included, and a p-value is calculated from this distribution. In some embodiments, the lowest p-value among all mutations detected in a given sample was deemed the "top mutation". The classification of a sample's ctDNA status is based on whether the p-value of this top mutation was below or above a given threshold. The threshold can be selected based on a desired specificity observed among an independent set of normal controls.

[715] In some embodiments, the Stouffer's Z-score is used to combine hypothesis test results from two or more independent tests (e.g., test results from 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 wells). For example, the results of MAF for two or mutations can be combined into one single test. In some embodiments, a sample is scored as positive when Stouffer's Z-score is

greater than a reference threshold. In some embodiments, a sample is scored positive if the ratio of the Stouffer's Z-score to the average of the first few (e.g., 2, 3, 4, 5, 6 7, 8, 9, or 10) highest Stouffer's Z-scores in the controls is greater than a reference threshold.

[716] In some embodiments, the MAF of one or more mutations in the selected genetic biomarkers is compared to maximum mutation allele frequency of the mutation in control samples. If one or more mutations (e.g., equal to or at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200) have a MAF that is greater than the maximum mutation allele frequency of the mutation in control samples, the subject can be determined to have cancer. In some embodiments, a score can be obtained from the comparison. In some embodiments, the score is the total number of mutations that have a MAF that is greater than the maximum mutation allele frequency of the mutation in control samples. If the score is greater than a reference threshold, then it can be determined that the subject is likely to have cancer. In some embodiments, the average MAF of one or more mutations in the selected genetic biomarkers is calculated.

[717] In some embodiments, the MAF of one or more mutations in the selected genetic biomarkers can be compared to a first reference distribution of mutation allele frequency in control samples and a second reference distribution of mutation allele frequency in samples collected from subjects having cancer. In some embodiments, a score is obtained by comparing the mutation frequencies of the sample of interest to the distributions of the mutation frequencies of, respectively, normal and cancer samples in the training set.

[718] In some embodiments, the UID range for each mutation is split in 10 intervals (e.g., <1,000, 1,000 - 2,000, ... , 8,000 -9,000, > 9,000). Depending on the number of UIDs, the MAF of each mutation in each well can be compared to two reference distributions of MAFs built from samples in the corresponding UID range: 1) a distribution built from all the normal control samples in the training set; and 2) a distribution built from the samples from cancer patients in the training set. In some embodiments, the cancer training set includes only those in which the same mutation is present in the sample (e.g., plasma) and in the corresponding primary tumor, with an MAF > 5% in the tumor. Corresponding p-values, pN and pC, can be obtained. The reference distributions for both the normal and cancer samples can be built independently, from the training sets, in each round and each iteration of 10-fold cross-

validation, i.e., 90% of the samples in each iteration are used for training and 10% of the samples are used for testing.

[719] For each mutation, an omega score can be obtained. The log ratio of these two p values, pC / pN can then be calculated. In some embodiments, the minimum and maximum of these log ratios across the replicate wells can be eliminated so that the results will be less sensitive to outliers. In some embodiments, a log-likelihood ratio is used. As compared to the log-likelihood ratio, the log ratio of the p-values can provide some additional advantages, because the relatively low number of data points available do not allow a robust estimation of the densities of the MAF distributions (particularly for pC). Thus, in some embodiments, an "omega" score was then determined according to the following formula:

$$\Omega = \sum_{i=1} w_i * ln \frac{p_i^C}{p_i^N}$$

where wi is the number of UIDs in well i divided by the total number of UIDs for that mutation in the wells that are included in the analysis. In some embodiments, the total number of wells that are included in the analysis is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 20, 30, or more. In some embodiments, the wells with the maximum log ratio and the minimum log ratio can be excluded from the analysis. In some embodiments, the total number of wells are that are included for analysis is 1, thus, the omega score can be obtained by the following formula instead:

$$\Omega = ln \frac{p_i^C}{p_i^N}$$

[720] The log ratio of p-values can be weighted so that those wells containing more template molecules would have a greater impact on the final statistic (the omega score). The rationale for this weighting was that the larger the number of template molecules in a well, the more confidence in the result.

[721] In some embodiments, an Ω score for each mutation can be determined. In some embodiments, mutations with Ω scores greater than a reference score (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) are selected. The total number of mutations with Ω scores greater than a reference

score reflects the mutation burden in a subject. In some embodiments, if the total number of mutations with Ω scores that is greater than a reference score is greater than a reference threshold, it is determined that the subject is likely to have cancer; otherwise, it can be determined that the subject is not likely to have a cancer.

[722] In some embodiments, the mutation with the greatest Ω score is deemed the "top mutation". The Ω score for top mutation can be used to determine whether a subject is likely to have cancer. For example, the Ω score for the top mutation can be compared against a reference threshold, or be combined with some other information (e.g., protein biomarkers) in various methods (e.g., regression analysis) to determine the likelihood that a subject has cancer. In some embodiments, if the Ω score for the top mutation is greater than a reference threshold, it is determined that the subject is likely to have cancer; otherwise, it can be determined that the subject is not likely to have a cancer. In some embodiments, the Ω score is used in a regression analysis (e.g., logistic regression).

Detecting Protein Biomarkers

[723] In some embodiments, the presence of a protein biomarker may be detected in any of a variety of biological samples isolated or obtained from a subject (e.g., a human subject) including, but not limited to blood, plasma, serum, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. Any protein biomarker known in the art may be detected when a threshold value is obtained above which normal, healthy human subjects do not fall, but human subjects with cancer do fall.

[724] Any appropriate method can be used to detect the level of one or more protein biomarkers as described herein. In some embodiments, the level of one or more protein biomarkers is compared to a predetermined threshold. In some embodiments, the predetermined threshold is a general or global threshold. In other cases, the predetermined threshold is a threshold that is relevant to a particular protein biomarker. In some embodiments, the level of the one or more protein biomarkers is compared to an absolute amount of a reference protein biomarker. In some embodiments, the level of the one or more protein biomarkers is relative to an amount of a reference protein biomarker. In some

embodiments, the level of the one or more protein biomarkers is an elevated level. In some embodiments, the level of the one or more protein biomarkers is above a predetermined threshold. In other cases, the level of the one or more protein biomarkers is within a predetermined threshold range. In some embodiments, the level of the one or more protein biomarkers is or approximates a predetermined threshold. In some embodiments, the level of the one or more protein biomarkers is below a predetermined threshold. In some embodiments, the level of the one or more protein biomarkers from a biological sample is lower than a particular threshold. In some embodiments, the level of the one or more protein biomarkers from a biological sample is depressed compared to a predetermined threshold.

[725] In some embodiments, methods provided herein for selecting a subject for further diagnostic testing and/or increased monitoring include detecting a protein biomarker in the biological sample and comparing the amount of protein biomarker in the biological sample to a reference level in a reference sample. In some embodiments, methods for selecting a subject for further diagnostic testing and/or increased monitoring include detecting a protein biomarker in the biological sample and comparing the amount of protein biomarker in the biological sample to a reference level, wherein the reference level is a composite number derived from multiple reference samples. In some embodiments, the protein biomarker in the biological sample is at least 5% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 10% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 15% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 20% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 25% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 30% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 40% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 50% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 60% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 70% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 80% higher

than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 90% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 100% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 200% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 300% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 400% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 500% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 600% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 700% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 800% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 900% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 5% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 10% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 15% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 20% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 25% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 30% to about 1000% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 10% to about 100% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 15% to about 100% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 20% to about 100% higher than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 25% to about 100% higher

than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 30% to about 100% higher than a reference level.

[726] In some embodiments, the protein biomarker is at least 5% lower than a reference level. In some embodiments, the protein biomarker is at least 10% lower than a reference level. In some embodiments, the protein biomarker is at least 15% lower than a reference level. In some embodiments, the protein biomarker is at least 20% lower than a reference level. In some embodiments, the protein biomarker is at least 25% lower than a reference level. In some embodiments, the protein biomarker is at least 30% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 40% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 50% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 60% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 70% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 80% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is at least 90% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 5% to about 100% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 10% to about 100% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 15% to about 100% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 20% to about 100% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 25% to about 100% lower than a reference level. In some embodiments, the protein biomarker in the biological sample is between about 30% to about 100% lower than a reference level.

[727] In some embodiments, the protein biomarker is a cytokine biomarker. In some embodiments, the protein biomarker is a chemokine biomarker. In some embodiments, the protein biomarker is a growth factor biomarker. In some embodiments, the protein biomarker is associated with inflammation. In some embodiments, the protein biomarker is associated with cancer. In some embodiments, the protein biomarker is associated with a

particular type of cancer. Any appropriate cancer can be identified and/or treated as described herein. In some embodiments, the cancer is a common cancer. In some embodiments, the cancer is a cancer where no blood-based test is available. In some embodiments, the cancer is a cancer where no test for early detection is available. In some embodiments, the cancer is a Stage I cancer. In some embodiments, the cancer is a Stage II cancer. In some embodiments, the cancer is a Stage III cancer. In some embodiments, the cancer is a Stage IV cancer. In some embodiments, the cancer is a surgically resectable cancer. In some embodiments, the cancer is a surgically unresectable cancer. Examples of cancers that be identified as described herein (e.g., based at least in part on the presence or absence of one or more first biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more second biomarkers (e.g., peptide biomarkers)) and/or the presence of aneuploidy include, without limitation, liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, and prostate cancer.

[728] In some embodiments, the levels of one or more protein biomarkers can be detected independently (e.g., via singleplex peptide tools). Examples of methods for detecting protein levels include, without limitation, spectrometry methods (e.g., high-performance liquid chromatography (HPLC) and liquid chromatography–mass spectrometry (LC/MS)), antibody dependent methods (e.g., enzyme-linked immunosorbent assay (ELISA), protein immunoprecipitation, immunoelectrophoresis, western blotting, and protein immunostaining), and aptamer dependent methods. In some embodiments, the level of one or more protein biomarkers can be detected as described in the Examples.

[729] Many of the singleplex peptide tools, such as, but not limited to ELISAs or western blotting, can be used sequentially or concurrently to analyze multiple peptide biomarkers. Multiplex peptide tools can include combining singleplex peptide tools or elements of singleplex peptide tools. Additionally or alternatively, detecting the levels of one or more peptide biomarkers can occur via multiplex peptide tools such as "chips," microarrays, or immunoassay systems. In one non-limiting example, multiple analytes can be probed by multiple capture antibodies spotted on microarrays and analyzed via horseradish peroxidase (HRP)-conjugated antibody/chemiluminescence system. In this method, each spot captures a specific target protein, and a second, target-specific detector antibody is used for

quantification. In addition to membrane antibody arrays, glass slides may be used for quantitative antibody arrays. Commercial embodiments of multiplexed ELISAs include, but are not limited to, Q-Plex available from Quansys Biosciences, Mosaic™ available from R&D Systems, Ciraplex® available from Aushon Biosystems, MULTI-ARRAY available from Meso Scale Discovery, FAST Quant available from Whatman Schleicher & Schuell BioScience, A^2 available from Beckman Coulter, and Quantibody® available from RayBiotech. Additionally or alternatively, multiplex assays can be utilize beads or particles to detect one or more protein biomarkers simultaneously. In one non-limiting example, polystyrene or paramagnetic beads are impregnated with dyes of differing wavelengths are used to detect multiple target antibodies simultaneously, wherein each dye or dye combination corresponds with a different target antibody. Sandwich assays are used to measure protein levels. Commercial embodiments of this technique utilize the Luminex® and FirePlex® technology platforms, e.g., Bio-Plex® Multiplex Immunoassay System available from Bio-Rad, FlowCytomix available from eBioscience, ProcartalPlex Immunoassay System available from ThermoFisher Scientific, Novex® Multiplex Assays available from Invitrogen.

[730] In some embodiments, an assay includes detection of thresholded protein biomarkers in a biological sample (e.g., any biological sample described herein such as, without limitation, blood or plasma) without detection of genetic biomarkers (e.g., mutations in circulating tumor DNA (ctDNA)) and/or aneuploidy and/or an additional class of biomarker. In some embodiments, an assay includes detection of thresholded protein biomarkers in a biological sample (e.g., any biological sample described herein such as, without limitation, blood or plasma) with detection of genetic biomarkers (e.g., mutations in circulating tumor DNA (ctDNA)) and/or aneuploidy and/or an additional class of biomarker. For example, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO) in a biological sample. In some embodiments, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO) in a biological sample at any of the threshold levels disclosed herein. As another example, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP,

prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3 in a biological sample. In some embodiments, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3 in a biological sample at any of the threshold levels disclosed herein. As another example, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3 in a biological sample. In some embodiments, an assay may include detection of one or more of (e.g., each of) CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3 in a biological sample at any of the threshold levels disclosed herein. As another example, an assay may include detection of one or more of (e.g., each of) KRAS (e.g., codons 12 and 61), TP53, CDKN2A, and/or SMAD4 in a biological sample. In some embodiments, an assay may include detection of one or more of (e.g., each of) KRAS (e.g., codons 12 and 61), TP53, CDKN2A, and/or SMAD4 in a biological sample at any of the threshold levels disclosed herein. In some embodiments, once an assay that includes detection of thresholded protein biomarkers in a biological sample is performed, subsequent testing or monitoring is performed (e.g., any of the variety of further diagnostic testing or increased monitoring techniques disclosed herein). In some embodiments, once an assay that includes detection of thresholded protein biomarkers in a biological sample is performed, a second assay that includes detecting the presence of one or more genetic biomarkers present in cell-free DNA (e.g., ctDNA, e.g., any of the variety of genetic alterations that are present in cell-free DNA or ctDNA as described herein), the presence of one or more protein biomarkers (e.g., any of the variety of protein biomarkers described herein), the presence of aneuploidy, and/or the presence of one or more additional classes of biomarkers can be performed.

[731] Examples of protein biomarkers that can be detected using any of the variety of techniques described herein include, without limitation, Actin gamma (ACTG1), AFP, Alpha -2- HS glycol protein, Angiopoietin-2, apolipo protein 1, AXL, CA125, CA15-3, carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), Catenin, Caveolin-1, CD44, class B member 1 (HSP90AB1), complement c3a, Cyclin D, CYFRA 21-1, Defensin α 6, DKK1, EAFP, Endoglin, Eukaryotic translation elongation factor 1 gamma (EEF1G), Ferritin, FGF2, follistatin, Galectin-3, G-CSF, GDF15, Glucose regulated protein- 8,

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH), HE4, Heat shock protein 90 kDa alpha (cytosolic), heavy polypeptide 1 (FTH1), hepatocyte growth factor (HGF), IL-6, IL-8, Kallikrein 6, Lamin A/C filament protein, large subunit, Leptin, light polypeptide (FTL), LRG-1, Mesothelin, Midkine, MMPs, muscle (PKM2), Myeloperoxidase, NSE, OPG, osteopontin (OPN), P0 (RPLP0), PAR, prolactin, Pyruvate kinase, Ribosomal protein, Ribosomal protein L3 (RPL3), Ribosomal protein large subunit P0 (RPLP0), S100 P, sEGFR, Serum C-peptide, sFas, SHBG, sHER2/sEGFR2/sErbB2, sPECAM-1, TGFa, thioredoxin like protein-2, Thrombospondin-2, TIMP-1, TIMP-2, Transferrin, Translation elongation factor (EEF1A1), Txl-2 (thioredoxin like protein-2), Vitronectin, α defensing -1,-2,-3, and/or α-1 antitrypsin. Exemplary protein biomarkers detected in various cancer types are shown in Example 2.

Detecting Aneuploidy

[732] Aneuploidy is the presence of an abnormal number of chromosomes in a cell. Aneuploidy usually originates during cell division when the chromosomes do not separate properly between the two cells. Aneuploidy occurs as the result of a weakened mitotic checkpoint, as these checkpoints tend to arrest or delay cell division until all components of the cell are ready to enter the next phase. If a checkpoint is weakened, the cell may fail to notice that a chromosome pair is not lined up on the mitotic plate. In such a case, most chromosomes would separate normally (with one chromatid ending up in each cell), while others could fail to separate at all. This would generate a daughter cell lacking a copy and a daughter cell with an extra copy. Aneuploidy has been consistently observed in many cancers.

[733] Aneuploidy can be detected through karyotyping, a process in which a sample of cells is fixed and stained to create the typical light and dark chromosomal banding pattern and a picture of the chromosomes is analyzed. Other non-limiting techniques for detecting aneuploidy include e.g., Fluorescence In Situ Hybridization (FISH), quantitative PCR of Short Tandem Repeats, quantitative fluorescence PCR (QF-PCR), quantitative PCR dosage analysis, Quantitative Mass Spectrometry of Single Nucleotide Polymorphisms, Comparative

Genomic Hybridization (CGH), microarrays, Sanger sequencing, and massively parallel sequencing methods, etc.

[734] The present disclosure provides methods to detect aneuploidy. For example, the present disclosure provides methods and materials for evaluating sequencing data to identify a mammal as having a disease associated with one or more chromosomal anomalies (e.g., cancer). The sequencing data can be processed to identify significant single chromosomal arm gains or losses, as well as allelic imbalance on chromosome arms, using **W**ithin-Sample **A**neup**L**oidy **D**etecti**O**n (WALDO) method. WALDO incorporates a support vector machine (SVM) to discriminate between aneuploid and euploid samples. The SVM can be trained using aneuploid samples (e.g., synthetic aneuploid samples) and euploid samples (e.g., peripheral white blood cell (WBC)). A sample can be scored as positive (aneuploid), if the SVM discriminant score exceeded a given threshold. In some embodiments, a single primer pair is used to amplify ~38,000 loci of long interspersed nucleotide elements (LINEs) throughout the genome. Massively parallel sequencing is then performed. In some embodiments, one of the primers include an UID to as a molecular barcode, which can be used to reduce error rates associated with PCR and sequencing.

Overview of WALDO

[735] In euploid samples, the number of LINE reads within each 500-kb genomic interval should track with the number of reads in certain other genomic regions. Genomic intervals that track together do so because the amplicons within them amplify to similar extents. Here, these genomic regions that track together are called "clusters." Clusters can be from sequencing data on euploid samples. In a test sample, whether the number of reads in each genomic interval in each predefined cluster is within the expected bound of the other clusters from that same sample is determined. If the reads within a genomic interval are outside the statistically expected bound, and there are many such outsiders on the same chromosome arm, then that chromosome arm is classified as aneuploidy

[736] In brief, while the number of reads at each LINE is not randomly distributed across the genome, the distribution of scaled reads within each cluster is approximately normal. A convenient property of normal distributions is that the sum of multiple normal distributions is

also a normal distribution. The theoretical mean and variance of the summed reads on each chromosome arm can be computed simply by summing the means and variances of all of the clusters represented on that chromosome arm.

[737] WALDO employs several methods that make it applicable to the analysis of PCR-generated amplicons from clinical samples. One of these methods is controlling amplification bias stemming from the strong dependence of the data on the size of the initial template. Another is the use of a Support Vector Machine (SVM) to enable the detection of aneuploidy in samples containing low neoplastic fractions.

[738] As shown in FIG. 36, a single primer pair is used to amplify LINEs. A test sample is then matched to several euploid samples with genomic DNA of similar size. The genome is divided into multiple intervals, and each interval has a similar size (e.g., 100, 200, 300, 400, 500, 600, 700, 800, 900 Kb, or 1 Mb, 2 Mb, 3 Mb, 4 Mb, or 5 Mb). The reads within these genomic intervals in the euploid samples are grouped into clusters. All of the genomic intervals in the clusters have similar read depths. The reads from each of the genomic intervals in the test sample are placed into the predefined clusters. Statistical tests, e.g., an SVM-based algorithm, are used to determine whether the total reads from all of the genomic intervals on each chromosome arm are distributed as expected if the sample is euploid. The statistical tests are based on the observed distribution of reads within the clusters of the test sample, not by comparison with the reads in euploid samples. Germline sequence variants at sites of known common polymorphisms within the LINEs provide information about arm-level allelic imbalance that can also be used to assess aneuploidy of individual chromosome arms. These same polymorphisms can be used to determine whether any two samples are derived from the same individual. When there is a matched normal sample from the same individual available, the methods described herein can detect the number and nature of single base substitutions and insertions and deletions within the LINEs.

Fast-SeqS

[739] For each DNA sample evaluated, FAST-SeqS can be used to amplify approximately 38,000 amplicons with a single primer pair (Kinde I, Papadopoulos N, Kinzler KW, & Vogelstein B (2012) FAST-SeqS: a simple and efficient method for the

detection of aneuploidy by massively parallel sequencing. PloS ONE 7(7):e41162). Massively parallel sequencing can be performed. In some embodiments, degenerate bases at the 5' end of the primer are used as molecular barcodes to uniquely label each DNA template molecule. Thus, each DNA template molecule will be counted only once. In some embodiments, each unique read can be sequenced between 1 and 20 times (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 times)

Sample alignment and genomic interval grouping

[740] Alignment programs (e.g., Bowtie2) can be used to align reads to human reference genome assembly (e.g., GRC37). Exact matches to the reference genome can be identified. These exact matches allow inclusion of common polymorphisms. In light of experimental and stochastic variation, the number of reads that mapped to each genomic region of any euploid sample is expected to be variable. In some embodiments, to minimize this variability, clusters of genomic intervals with similar read depth across all chromosomes in *multiple euploid samples* are identified. This step can estimate the expected variability in read depth in a sample when no aneuploidy is present. In some embodiments, the genomic interval has a size of 100, 200, 300, 400, 500, 600, 700, 800, 900 Kb, or 1 Mb, 2 Mb, 3 Mb, 4 Mb, or 5 Mb. In some embodiments, the genomic interval has a size of 500 kb.

[741] Clustering of the genomic intervals can be performed as follows. Each test sample is matched to euploid samples that have similar amplicon sizes. This is important because smaller amplicons can be over-represented in the amplicons generated from DNA that is of small size prior to amplification. The euploid samples can be derived from WBC or plasma DNA from normal individuals, collectively termed the "euploid reference set". The euploid samples can include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 samples. In some embodiments, the euploid samples does not include more than 5, 6, 7, 8, 9, or 10 samples.

[742] For each test sample p, the samples with the smallest Euclidean distance to p, defined as

$$D(p,q)=\sqrt{\sum_n (q_n - p_n)^2}$$

where, pn and qn are the fraction of amplicons of size *n* in samples p and q, and the sum is over all amplicon sizes in the two samples. In some embodiments, before calculating the Euclidian distances between the test samples from the samples in the euploid reference set, the following amplicons are excluded: (i) Using maximum likelihood estimates, the amplicons are ranked by variance among the euploid samples and the top 1% excluded. (ii), any amplicons with < 10 reads in one sample but > 50 reads in any of the other samples are removed. In each sample, the genomic intervals are scaled by subtracting the mean and dividing by the standard deviation of reads in each sample.

[743] The scaled genomic intervals are then clustered across the selected normal samples. First, each genomic interval ***i*** is assigned to a primary cluster C_i. Next, the reads in genomic interval ***i*** across all samples is compared to the average number of read in the samples in all other genomic intervals ***i'*** that occurred on the remaining autosomal chromosomes. If the average number of reads in genomic interval ***i'*** is not significantly different from the number of reads in genomic interval ***i*** , it is added to cluster C_i. This process is repeated for each genomic interval, yielding multiple clusters (e.g., more than 1000, 2000, 3000, 4000, or 5000 clusters). Every interval ***i*** belongs to its primary cluster but the same interval can also belong to some other clusters. In some embodiments, there are about 4300 clusters.

[744] In some embodiments, scaled reads are not randomly distributed. In some embodiments, the distribution of scaled reads within the genomic intervals in each cluster follows an approximately normal distribution.

Identifying chromosome arm gains or losses in a test sample

[745] The methods described herein can use just a few euploid samples (e.g., about 2, 3, 4, 5 6, 7, 8, 9, or 10 samples) to define clusters of genomic intervals with similar amplification properties. The statistical tests for aneuploidy are based on the read distributions *within* the test sample and independently of the read distributions in any euploid sample. In some embodiments, maximum likelihood is used to estimate the means μ and variances δ^2 of the genomic intervals in each cluster. In some embodiments, the robustness of these estimates can be improved by iteratively removing outlying genomic intervals within the test sample from the clusters. In some embodiments, clusters

containing fewer than 10 genomic intervals are not included in the analysis. In some embodiments, for each cluster, any genomic interval meeting the criteria

$$min(2^{*}\,CDF(\mu, \sigma_i^2), 2^{*}(1\text{-}CDF(\mu, \sigma_i^2)) < 0.01$$

is removed from all clusters. Next, the μ and the variances δ^2 parameters of each cluster is re-estimated by maximum likelihood. The two steps are repeated until no outlying genomic intervals remained. The statistical significance of the total reads from all genomic intervals on the arm is estimated. Because sums of normally distributed random variables are also normally distributed random variables, the calculation is straightforward. For each chromosome arm, it can be calculated

$$\sum_1^I R_i \sim N(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$$

wherein R_i is the scaled reads and i is the number of clusters on the arm. Z-scores can be produced using the quantile function

$$1-\ CDF(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$$

Positive Z-scores > α represents gains and negative Z-scores < -α represents losses. The α value is the selected significance threshold.

Arm level allelic imbalance

[746] Common polymorphisms from 1000 Genomes (including e.g., 24,720 single nucleotide and 1,500 indels, MAF>1%) can be used as candidate heterozygous sites. For each of the normal samples, polymorphic sites can be confidently called as heterozygous and diploid. Polymorphisms can be defined as those with variant-allele frequencies (VAF) (0.4<VAF<0.6), where VAF = #non-reference reads / total reads. VAFs can be modeled at these sites as random variables taken from a normal distribution with μ =0.5; and the variances δ^2 can be estimated by maximum likelihood as a function of read depth.

[747] To determine whether the alleles on a chromosome arm in a test sample is unbalanced, the subset of polymorphic sites at which both alleles are present and in which the sum of the reads on both alleles is >25 are identified.

[748] The observed VAF with the normal distribution, using the expected variance for the observed read depth, yielding a two-sided P- value. All p-values on a chromosome

arm can be Z-transformed and combined with a weighted Stouffer's method, with the observed read depth at each site used as its weight. The formula used for this calculation is

$$Z \sim \frac{\sum_{i=1}^{k} w_i Z_i}{\sqrt{\sum_{i=1}^{k} w_i^2}}$$

where wi is UID depth at variant *i* , Zi is the Z-score of variant i, and *k* is the number of variants observed on the chromosome arm. A chromosome arm is scored as having an allelic imbalance if the resulting Z score is greater than the selected statistical significance threshold α (e.g., by one-sided test).

Generation of synthetic aneuploid samples

[749] Synthetic aneuploid samples can be created by adding (or subtracting) reads from several chromosome arms to the reads from these normal DNA samples. The reads from 1, 5,10,15,20, or 25 randomly selected chromosome arms are added or subtracted to each sample. The additions and subtractions are designed to represent neoplastic cell fractions ranging from 0.5% to 10% and result in synthetic samples containing exactly nine million reads. The reads from each chromosome arm can be added or subtracted uniformly. These synthetically generated samples in which reads from only a single chromosome arm are added or subtracted can be used estimate the performance of WALDO.

Genome-wide aneuploidy detection

[750] The present disclosure provides genome-wide aneuploidy detections. In some embodiments, a two-class support vector machine (SVM) can be trained to discriminate between euploid samples and the synthetic samples. The training set can contain white blood cells (WBC) samples and samples with aneuploidy (e.g., all synthetic samples).

[751] SVM training can be done by various statistical software (e.g., in R, using radial basis kernel and default parameters).

[752] The number of reads from the data on experimental samples can vary widely, particularly when the samples are derived from sources with limited amounts of DNA such as plasma. In some embodiments, samples with low reads can generate artificially high SVM scores if read depth is not taken into account. Thus, read depth can be controlled by

modeling the change in SVM scores as a function of read depth in the normal samples. The average ratio r at each depth decreased monotonically as a function of increasing read depth. The relation between read depth and SVM score can be modeled using the following equation. Thus, raw SVM scores can be corrected by dividing by the ratio *r*, using the formula

$$\log\left(1-\frac{1}{r}\right)=Ax+B$$

[753] To score a sample as aneuploid, whether any single chromosome arm in it is lost or gained in a statistically significant manner is determined. A statistically significant gain of a single chromosome arm is defined as one whose Z-score is above the maximum Z-score observed in the normal samples (e.g., 1σ, 2σ, 3σ, 4σ, or 5σ above). Similarly, a statistically significant loss of a single chromosome arm is defined as one whose Z-score is below the minimum Z-score observed in the normal samples (e.g., 1 σ, 2 σ, 3 σ, 4 σ, or 5 σ below). Allelic imbalance based on SNPs can be defined for a chromosome arm whose Z-score is above the maximum Z-score observed in normal samples (e.g., 1σ, 2σ, 3σ, 4σ, or 5σ above). Only samples in which no single chromosome arm is gained or lost when defined in this way are subjected to SVM analysis. The rationale for this process is that the SVM is designed to identify samples with large numbers of chromosome arm gains or losses but relatively low neoplastic cell fractions. In some embodiments, the SVM is not designed to detect aneuploidy in samples with neoplastic cell fractions >10%, which are easily identified through evaluation of their Z-scores and comparison to the normal samples.

Somatic sequence mutations and microsatellite instability (MSI)

[754] The present disclosure also provides methods to detect somatic sequence mutations and microsatellite instability. When matched normal samples are available, somatic single base substitution (SBS), insertion and deletion (indel) mutations can be detected based on LINE amplicon sequences and alignments. In some embodiments, the molecular barcoding approach for error reduction is used. In some embodiments, the SBS mutations can be identified by directly comparing amplicons from the test sample with

amplicons from the matched normal, and do not require any alignment to the reference genome.

[755] Indels can be called in a similar way. Amplicons are aligned from the test sample and matched normal sample to the reference genome (GRc37). In some embodiments, a somatic indel can be at least ten reads from the test sample differed from any normal read by virtue of the same insertion or deletion.

[756] Microsatellite instability in a test sample can determined by counting the number of somatic indels in mononucleotide tracts of > 3 nucleotides. Somatic indels in monotracts can be rare in a normal sample. Therefore, the null distribution of counts can be modeled as Poisson ($\lambda = 1$), where λ is the mean number of somatic indels in a monotract in a normal sample. A sample is determined as harboring MSI if the number of somatic indels is statistically significant. To evaluate how often normal samples can be scored as MSI using this process, the total reads in normal samples can be randomly split into two equal partitions. The first partition can be used as the reference sample and the second partition can be used as a test sample.

[757] This document provides methods and materials for identifying one or more chromosomal anomalies (e.g., aneuploidies) in a sample. For example, a mammal (e.g., a sample obtained from a mammal) can be assessed for the presence or absence of one or more chromosomal anomalies. In some cases, this document provides methods and materials for using amplicon-based sequencing data to identify a mammal as having a disease associated with one or more chromosomal anomalies (e.g., cancer). For example, the methods and materials described herein can be applied to a sample obtained from a mammal to identify the mammal as having one or more chromosomal anomalies. For example, methods and materials described herein can be applied to a sample obtained from a mammal to identify the mammal as having a disease associated with one or more chromosomal anomalies (e.g., cancer). This document also provides methods and materials for identifying and/or treating a disease or disorder associated with one or more chromosomal anomalies (e.g., one or more chromosomal anomalies identified as described herein). In some cases, the one or more chromosomal anomalies can be identified in DNA (e.g., genomic DNA) obtained from a sample obtained from a mammal. For example, a prenatal mammal (e.g., prenatal human)

can be identified as having a disease or disorder based, at least in part, on the presence of one or more chromosomal anomalies, and, optionally, can be treated with one or more treatments for the disease or disorder. For example, a mammal identified as having cancer based, at least in part, on the presence of one or more chromosomal anomalies can be treated with one or more cancer treatments.

[758] Any appropriate mammal can be assessed and/or treated as described herein. A mammal can be a prenatal mammal (e.g., prenatal human). A mammal can be a mammal suspected of having a disease associated with one or more chromosomal anomalies (e.g., cancer). In some cases, humans or other primates such as monkeys can be assessed for the presence of one or more chromosomal anomalies as described herein. In some cases, dogs, cats, horses, cows, pigs, sheep, mice, and rats can be assessed for the presence of one or more chromosomal anomalies as described herein. For example, a human can be assessed for the presence of one or more chromosomal anomalies as described herein and, optionally, can be treated with one or more cancer treatments as described herein.

[759] Any appropriate sample from a mammal can be assessed as described herein (e.g., assessed for the presence of one or more chromosomal anomalies). A sample can include genomic DNA. In some cases, a sample can include cell-free circulating DNA (e.g., cell-free circulating fetal DNA). In some cases, a sample can include circulating tumor DNA (ctDNA). Examples of samples that can contain DNA include, without limitation, blood (e.g., whole blood, serum, or plasma), amnion, tissue, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, pap smears, cerebral spinal fluid, endo-cervical, endometrial, and fallopian samples. For example, a sample can be a plasma sample. For example, a sample can be a urine sample. For example, a sample can be a saliva sample. For example, a sample can be a cyst fluid sample. For example, a sample can be a sputum sample. In some cases, a sample can include a neoplastic cell fraction (e.g., a low neoplastic cell fraction). In cases where a sample includes a low neoplastic cell fraction, the neoplastic cell fraction can be from about 0.01% to about 10% (e.g., from about 0.05% to about 10%, from about 0.5% to about 10%, from about 1% to about 10%, from about 3% to about 10%, from about 5% to about 10%, from about 7% to about 10%, from about 0.01% to about 8%, from about 0.01% to about 5%, from about

0.01% to about 2%, from about 0.01% to about 1%, from about 0.01% to about 0.5%, from about 0.05% to about 8%, from about 0. 1% to about 4%, or from about 0.5% to about 1%) of the cell content of the entire sample. For example, a sample that includes a low neoplastic cell fraction can be about 1% neoplastic cells. For example, a sample that includes a low neoplastic cell fraction can be about 0.5% neoplastic cells.

[760] In some cases, a sample can be processed to isolate and/or purify DNA from the sample. In some cases, DNA isolation and/or purification can include cell lysis (e.g., using detergents and/or surfactants). In some cases, DNA isolation and/or purification can include removing proteins (e.g., using a protease). In some cases, DNA isolation and/or purification can include removing RNA (e.g., using an RNase).

[761] Methods and materials for identifying one or more chromosomal anomalies can include assessing a genome (e.g., a genome of a mammal) for the presence or absence of one or more chromosomal anomalies (e.g., aneuploidies). The presence or absence of one or more chromosomal anomalies in the genome of a mammal can, for example, be determined by sequencing a plurality of amplicons obtained from a sample obtained from the mammal to obtain sequencing reads, and grouping the sequencing reads into clusters of genomic intervals. In some cases, read counts of genomic intervals can be compared to read counts of other genomic intervals within the same sample. In some cases where read counts of genomic intervals are compared to read counts of other genomic intervals within the same sample, a second (e.g., control or reference) sample is not assayed. For example, when using methods and materials described herein to identify numerical disorders (e.g., aneuploidy) and/or structural abnormalities, genomic intervals can be compared to read counts of other genomic intervals within the same sample. In some cases, read counts of genomic intervals can be compared to read counts of genomic intervals in another sample. For example, when using the methods and materials described herein to identify genetic relatedness, polymorphisms (e.g., somatic mutations), and/or microsatellite instability, genomic intervals can be compared to read counts of genomic intervals in a reference sample. A reference sample can be a synthetic sample. A reference sample can be from a database. In some cases where the methods and materials described herein are used to identify genetic relatedness, a reference sample can be a forensic sample. In some cases where methods and

materials described herein are used to identify genetic relatedness, a reference sample can be obtained from suspected relation. In some cases where the methods and materials described herein are used to identify, anomalies (e.g., aneuploidies), one or more polymorphisms (e.g., somatic mutations), and/or microsatellite instability, a reference sample can be a normal sample obtained from the same cancer patient (e.g., a sample from the cancer patient that does not harbor cancer cells) or a normal sample from another source (e.g., a patient that does not have cancer).

[762] In some cases, methods and materials described herein can be used for detecting aneuploidy in a genome of mammal. For example, a plurality of amplicons obtained from a sample obtained from a mammal can be sequenced, the sequencing reads can be grouped into clusters of genomic intervals, the sums of the distributions of the sequencing reads in each genomic interval can be calculated, a Z-score of a chromosome arm can be calculated, and the presence or absence of an aneuploidy in the genome of the mammal can be identified. The distributions of the sequencing reads in each genomic interval can be summed. For example, sums of distributions of the sequencing reads in each genomic interval can be calculated using the equation $\sum_1^I R_i \sim N(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$, where R_i is the number of sequencing reads, I is the number of clusters on a chromosome arm, N is a Gaussian distribution with parameters μ_i and σ_i^2, μ_i is the mean number of sequencing reads in each genomic interval, and σ_i^2 is the variance of sequencing reads in each genomic interval. a Z-score of a chromosome arm can be calculated using any appropriate technique. For example, a Z-score of a chromosome arm can be calculated using the quantile function 1-CDF$(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$. The presence of an aneuploidy in the genome of the mammal can be identified in the genome of the mammal when the Z-score is outside a predetermined significance threshold, and the absence of an aneuploidy in the genome of the mammal can be identified in the genome of the mammal when the Z-score is within a predetermined significance threshold. The predetermined threshold can correspond to the confidence in the test and the acceptable number of false positives. For example, a significance threshold can be ± 1.96, ± 3, or ± 5.

[763] In some cases, methods and materials described herein can be used for detecting one or more polymorphisms in a genome of a mammal. For example, a plurality of amplicons obtained from a sample obtained from a first mammal (e.g., a test mammal or a mammal

suspected of harboring one or more polymorphisms) can be sequenced, a plurality of amplicons obtained from a sample obtained from a second mammal (e.g., a reference mammal) can be sequenced, variant sequencing reads from the sample obtained from the first mammal can be grouped into clusters of genomic intervals, reference sequencing reads from the sample obtained from the second mammal can be grouped into clusters of genomic intervals, a chromosome arm having a sum of the variant sequencing reads and the reference sequencing reads on both alleles that is greater than about 3 (e.g., greater than about 4, greater than about 5, greater than about 6, greater than about 7, greater than about 8, greater than about 9, greater than about 10, greater than about 12, greater than about 15, greater than about 18, greater than about 20, greater than about 22, greater than about 25, or greater than about 30) can be selected, a variant-allele frequency (VAF) of the selected chromosome arm can be determined, and the presence or absence of one or more polymorphisms on the selected chromosome arm can be identified. A VAF of the selected chromosome arm can be determined using any appropriate technique. For example, a VAF of the selected chromosome arm can be the number of variant sequencing reads / total number of sequencing reads. The presence of one or more polymorphisms in the genome of the mammal can be identified in the genome of the mammal when the VAF is between about 0.2 and about 0.8 (e.g., between about 0.3 and about 0.8, between about 0.4 and about 0.8, between about 0.5 and about 0.8, between about 0.6 and about 0.8, between about 0.2 and about 0.7, between about 0.2 and about 0.6, between about 0.2 and about 0.5, or between about 0.2 and about 0.4), and the absence of one or more polymorphisms in the genome of the mammal can be identified in the genome of the mammal when the VAF is within a predetermined significance threshold. As one non-limiting example, the presence of one or more polymorphisms in the genome of the mammal can be identified in the genome of the mammal when the VAF is between about 0.4 and 0.6.

[764] Methods and materials for identifying one or more chromosomal anomalies as described herein can include using amplicon-based sequencing reads. For example, a plurality of amplicons (e.g., amplicons obtained from a sample obtained from the mammal) can be sequenced. In some cases, each amplicon can be sequenced between about 1 and about 20 (e.g., between about 1 and about 15, between about 1 and about 12, between about 1

and about 10, between about 1 and about 8, between about 1 and about 5, between about 5 and about 20, between about 7 and about 20, between about 10 and about 20, between about 13 and about 20, between about 3 and about 18, between about 5 and about 16, or between about 8 and about 12) times. In some cases, amplicon-based sequencing reads can include continuous sequencing reads. In some cases, amplicons can include long interspersed nucleotide elements (LINEs). In some cases, amplicon-based sequencing reads can include from about 100,000 to about 25 million (e.g., from about 100,000 to about 20 million, from about 100,000 to about 15 million, from about 100,000 to about 12 million, from about 100,000 to about 10 million, from about 100,000 to about 5 million, from about 100,000 to about 1 million, from about 100,000 to about 750,000, from about 100,000 to about 500,000, from about 100,000 to about 250,000, from about 250,000 to about 25 million, from about 500,000 to about 25 million, from about 750,000 to about 25 million, from about 1 million to about 25 million, from about 5 million to about 25 million, from about 10 million to about 25 million, from about 15 million to about 25 million, from about 200,000 to about 20 million, from about 250,000 to about 15 million, from about 500,000 to about 10 million, from about 750,000 to about 5 million, or from about 1 million to about 2 million) sequencing reads. In some cases, methods of sequencing amplicons include, without limitation, a Fast Aneuploidy Screening Test-Sequencing System (FAST-SeqS). For example, sequencing a plurality of amplicons can include assigning a unique identifier (UID) to each template molecule (e.g., to each amplicon), amplifying each uniquely tagged template molecule to create UID-families, and redundantly sequencing the amplification products. For example, sequencing a plurality of amplicons can include calculating a Z-score of a variant on said selected chromosome arm using the equation $Z \sim \frac{\sum_{i=1}^{k} w_i Z_i}{\sqrt{\sum_{i=1}^{k} w_i^2}}$, where w_i is UID depth at a variant i, Z_i is the Z-score of variant i, and k is the number of variants observed on the chromosome arm. In some cases, methods of sequencing amplicons can be as described in Example 6. In some cases, methods of sequencing amplicons can be as described elsewhere (see, e.g., US 2015/0051085; and Kinde et al. 2012 *PloS ONE* 7:e41162).

[765] In some cases, methods and materials for identifying one or more chromosomal anomalies (e.g., aneuploidies) as described herein can include amplification of a plurality of

amplicons. For example, amplification of a plurality of amplicons can be performed using a single primer pair. Methods of amplifying a plurality amplicons include, without limitation, polymerase chain reaction (PCR) assays.

[766] A plurality of amplicons can include any appropriate number of amplicons. In some cases, a plurality of amplicons can include from about 10,000 to about 1,000,000 (e.g., from about 15,000 to about 1,000,000, from about 25,000 to about 1,000,000, from about 35,000 to about 1,000,000, from about 50,000 to about 1,000,000, from about 75,000 to about 1,000,000, from about 100,000 to about 1,000,000, from about 125,000 to about 1,000,000, from about 160,000 to about 1,000,000, from about 180,000 to about 1,000,000, from about 200,000 to about 1,000,000, from about 300,000 to about 1,000,000, from about 500,000 to about 1,000,000, from about 750,000 to about 1,000,000, from about 10,000 to about 800,000, from about 10,000 to about 500,000, from about 10,000 to about 250,000, from about 10,000 to about 150,000, from about 10,000 to about 100,000, from about 10,000 to about 75,000, from about 10,000 to about 50,000, from about 10,000 to about 40,000, from about 10,000 to about 30,000, or from about 10,000 to about 20,000) amplicons. As one non-limiting example, a plurality of amplicons can include about 38,000 amplicons. Amplicons in a plurality of amplicons can be any appropriate length. In some cases, an amplicon can include from about 50 to about 140 (e.g., from about 60 to about 140, from about 76 to about 140, from about 90 to about 140, from about 100 to about 140, from about 130 to about 140, from about 50 to about 130, from about 50 to about 120, from about 50 to about 110, from about 50 to about 100, from about 50 to about 90, from about 50 to about 80, from about 60 to about 130, from about 70 to about 125, from about 80 to about 120, or from about 90 to about 100) nucleotides. As one non-limiting example, an amplicon can include about 100 nucleotides.

[767] Methods and materials for identifying one or more chromosomal anomalies as described herein can include grouping sequencing reads (e.g., from a plurality of amplicons) into clusters (e.g., unique clusters) of genomic intervals. A genomic interval can be included in one or more clusters. In some cases, a genomic interval can belong to from about 100 to about 252 (e.g., from about 125 to about 252, from about 150 to about 252, from about 175 to about 252, from about 200 to about 252, from about 225 to about 252, from about 100 to

about 250, from about 100 to about 225, from about 100 to about 200, from about 100 to about 175, from about 100 to about 150, from about 125 to about 225, from about 150 to about 200, or from about 160 to about 180) clusters. As one non-limiting example, a genomic interval can belong to about 176 clusters. Each cluster can include any appropriate number of genomic intervals. In some cases, each cluster can include the same number of genomic intervals. In some cases, cluster can include varying numbers of genomic clusters. As one non-limiting example, each cluster can include about 200 genomic intervals.

[768] A cluster of genomic intervals can include any appropriate number of genomic intervals. In some cases, a cluster of genomic intervals can include from about 4000 to about 4500 (e.g., from about 4100 to about 4500, from about 4200 to about 4500, from about 4300 to about 4500, from about 4400 to about 4500, from about 4000 to about 4400, from about 4000 to about 4300, from about 4000 to about 4200, from about 4000 to about 4100, from about 4100 to about 4400, or from about 4200 to about 4300) genomic intervals. As one non-limiting example, a cluster of genomic intervals can include about 4361 genomic intervals. A genomic interval can be any appropriate length. For example, a genomic interval can be the length of an amplicon sequenced as described herein. For example, a genomic interval can be the length of a chromosome arm. In some cases, a genomic interval can include from about 100 to about 125,000,000 (e.g., from about 250 to about 125,000,000, from about 500 to about 125,000,000, from about 750 to about 125,000,000, from about 1,000 to about 125,000,000, from about 1,500 to about 125,000,000, from about 2,000 to about 125,000,000, from about 5,000 to about 125,000,000, from about 7,500 to about 125,000,000, from about 10,000 to about 125,000,000, from about 25,000 to about 125,000,000, from about 50,000 to about 125,000,000, from about 100,000 to about 125,000,000, from about 250,000 to about 125,000,000, from about 500,000 to about 125,000,000, from about 100 to about 1,000,000, from about 100 to about 750,000, from about 100 to about 500,000, from about 100 to about 250,000, from about 100 to about 100,000, from about 100 to about 50,000, from about 100 to about 25,000, from about 100 to about 10,000, from about 100 to about 5,000, from about 100 to about 2,500, from about 100 to about 1,000, from about 100 to about 750, from about 100 to about 500, from about 100 to about 250, from about 500 to about 1,000,000, from about 5000 to about 900,000, from about

50,000 to about 800,000, or from about 100,000 to about 750,000) nucleotides. As one non-limiting example, a genomic interval can include about 500,000 nucleotides. Clusters of genomic intervals can be formed using any appropriate method. For example, amplicons of similar size can be clustered. In some cases, clusters of genomic intervals can be formed as described in Example 6.

[769] Methods and materials described herein also can employ supervised machine learning. In some cases, supervised machine learning can detect small changes in one or more chromosome arms. For example, supervised machine learning can detect changes such as chromosome arm gains or losses that are often present in a disease or disorder associated with chromosomal anomalies, such as cancer. In some cases, supervised machine learning can be used to classify samples according to aneuploidy status. For example, supervised machine learning can be employed to make genome-wide aneuploidy calls. In some cases, a support vector machine model can include obtaining an SVM score. An SVM score can be obtained using any appropriate technique. In some cases, an SVM score can be obtained as described elsewhere (see, e.g., Cortes 1995 *Machine learning* 20:273-297; and Meyer et al. 2015 *R package version*:1.6-3). At lower read depths, a sample will typically have a higher raw SVM score. Thus, in some cases, raw SVM probabilities can be corrected based on the read depth of a sample using the equation $\log\left(1-\frac{1}{r}\right) = Ax + B$, where r is the ratio of the SVM score at a particular read depth/minimum SVM score of a particular sample given sufficient read depth. A and B can be determined as described in Example 6. For example, A = -7.076*10^-7, x = the number of unique template molecules for the given sample, and B = -1.946*10^-1.

[770] Methods and materials described herein can be used to identify any appropriate chromosomal anomaly. Examples of chromosomal anomalies include, without limitation, numerical disorders, structural abnormalities, allelic imbalances, and microsatellite instabilities. A chromosomal anomaly can include a numerical disorder. For example, a chromosomal anomaly can include an aneuploidy (e.g., an abnormal number of chromosomes). In some cases, an aneuploidy can include an entire chromosome. In some cases, an aneuploidy can include part of a chromosome (e.g., a chromosome arm gain or a

chromosome arm loss). Examples of aneuploidies include, without limitation, monosomy, trisomy, tetrasomy, and pentasomy. A chromosomal anomaly can include a structural abnormality. Examples of structural abnormalities include, without limitation, deletions, duplications, translocations (e.g., reciprocal translocations and Robertsonian translocations), inversions, insertions, rings, and isochromosomes. Chromosomal anomalies can occur on any chromosome pair (e.g., chromosome 1, chromosome 2, chromosome 3, chromosome 4, chromosome 5, chromosome 6, chromosome 7, chromosome 8, chromosome 9, chromosome 10, chromosome 11, chromosome 12, chromosome 13, chromosome 14, chromosome 15, chromosome 16, chromosome 17, chromosome 18, chromosome 19, chromosome 20, chromosome 21, chromosome 22, and/or one of the sex chromosomes (e.g., an X chromosome or a Y chromosome). For example, aneuploidy can occur, without limitation, in chromosome 13 (e.g., trisomy 13), chromosome 16 (e.g., trisomy 16), chromosome 18 (e.g., trisomy 18), chromosome 21 (e.g., trisomy 21), and/or the sex chromosomes (e.g., X chromosome monosomy; sex chromosome trisomy such as XXX, XXY, and XYY; sex chromosome tetrasomy such as XXXX and XXYY; and sex chromosome pentasomy such as XXXXX, XXXXY, and XYYYY). For example, structural abnormalities can occur, without limitation, in chromosome 4 (e.g., partial deletion of the short arm of chromosome 4), chromosome 11 (e.g., a terminal 11q deletion), chromosome 13 (e.g., Robertsonian translocation at chromosome 13), chromosome 14 (e.g., Robertsonian translocation at chromosome 14), chromosome 15 (e.g., Robertsonian translocation at chromosome 15), chromosome 17 (e.g., duplication of the gene encoding peripheral myelin protein 22), chromosome 21 (e.g., Robertsonian translocation at chromosome 21), and chromosome 22 (e.g., Robertsonian translocation at chromosome 22).

[771] Methods and materials described herein can be used for identifying and/or treating a disease associated with one or more chromosomal anomalies (e.g., one or more chromosomal anomalies identified as described herein, such as, without limitation, an aneuploidy). In some cases, a DNA sample (e.g., a genomic DNA sample) obtained from a mammal can be assessed for the presence or absence of one or more chromosomal anomalies. For example, a prenatal mammal (e.g., prenatal human) can be identified as having a disease based, at least in part, on the presence of one or more chromosomal anomalies can be treated with one or

more cancer treatments. As another example, a mammal identified as having cancer based, at least in part, on the presence of one or more chromosomal anomalies can be treated with one or more cancer treatments.

[772] In some cases, a mammal identified as having a disease associated with one or more chromosomal anomalies as described herein (e.g., based at least in part on the presence of one or more chromosomal anomalies, such as, without limitation, an aneuploidy) can have the disease diagnosis confirmed using any appropriate method. Examples of methods that can be used to confirm the presence of one or more chromosomal anomalies include, without limitation, karyotyping, fluorescence in situ hybridization (FISH), quantitative PCR of short tandem repeats, quantitative fluorescence PCR (QF-PCR), quantitative PCR dosage analysis, quantitative mass spectrometry of SNPs, comparative genomic hybridization (CGH), whole genome sequencing, and exome sequencing.

[773] Once identified as having a disease associated with one or more chromosomal anomalies as described herein (e.g., based at least in part on the presence of one or more chromosomal anomalies, such as, without limitation, an aneuploidy), a mammal can be treated accordingly. For example, when a mammal is identified as having a cancer associated with one or more chromosomal anomalies as described herein, the mammal can be treated with one or more cancer treatments. The one or more cancer treatments can include any appropriate cancer treatments. A cancer treatment can include surgery. A cancer treatment can include radiation therapy. A cancer treatment can include administration of a pharmacotherapy such chemotherapy, hormone therapy, targeted therapy, and/or cytotoxic therapy. Examples of cancer treatments include, without limitation, platinum compounds (such as cisplatin or carboplatin), taxanes (such as paclitaxel or docetaxel), albumin bound paclitaxel (nab-paclitaxel), altretamine, capecitabine, cyclophosphamide, etoposide (vp-16), gemcitabine, ifosfamide, irinotecan (cpt-11), liposomal doxorubicin, melphalan, pemetrexed, topotecan, vinorelbine, luteinizing-hormone-releasing hormone (LHRH) agonists (such as goserelin and leuprolide), anti-estrogen therapy (such as tamoxifen), aromatase inhibitors (such as letrozole, anastrozole, and exemestane), angiogenesis inhibitors (such as bevacizumab), poly(ADP)-ribose polymerase (PARP) inhibitors (such as olaparib, rucaparib,

and niraparib), external beam radiation therapy, brachytherapy, radioactive phosphorus, and any combinations thereof.

[774] Any appropriate disease associated with one or more chromosomal anomalies as described herein (e.g., based at least in part on the presence of one or more chromosomal anomalies, such as, without limitation, an aneuploidy) can be identified and/or treated as described herein. Examples of diseases and conditions that can be associated with one or more chromosomal anomalies include, without limitation, lung cancer (e.g., small cell lung carcinoma or non-small cell lung carcinoma), papillary thyroid cancer, medullary thyroid cancer, differentiated thyroid cancer, recurrent thyroid cancer, refractory differentiated thyroid cancer, lung adenocarcinoma, bronchioles lung cell carcinoma, multiple endocrine neoplasia type 2A or 2B (MEN2A or MEN2B, respectively), pheochromocytoma, parathyroid hyperplasia, breast cancer, colorectal cancer (e.g., metastatic colorectal cancer), papillary renal cell carcinoma, ganglioneuromatosis of the gastroenteric mucosa, inflammatory myofibroblastic tumor, or cervical cancer, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), cancer in adolescents, adrenal cancer, adrenocortical carcinoma, anal cancer, appendix cancer, astrocytoma, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, bladder cancer, bone cancer, brain stem glioma, brain tumor, breast cancer, bronchial tumor, Burkitt lymphoma, carcinoid tumor, unknown primary carcinoma, cardiac tumors, cervical cancer, childhood cancers, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colon cancer, colorectal cancer, craniopharyngioma, cutaneous T-cell lymphoma, bile duct cancer, ductal carcinoma in situ, embryonal tumors, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, extrahepatic bile duct cancer, eye cancer, fallopian tube cancer, fibrous histiocytoma of bone, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), germ cell tumor, gestational trophoblastic disease, glioma, hairy cell tumor, hairy cell leukemia, head and neck cancer, heart cancer, hepatocellular cancer, histiocytosis, Hodgkin's lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, Kaposi sarcoma, kidney cancer, Langerhans cell histiocytosis,

laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer, lymphoma, macroglobulinemia, malignant fibrous histiocytoma of bone, osteocarcinoma, melanoma, Merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer, midline tract carcinoma, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, myeloid leukemia, multiple myeloma, myeloproliferative neoplasms, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin's lymphoma, non-small cell lung cancer, oral cancer, oral cavity cancer, lip cancer, oropharyngeal cancer, osteosarcoma, ovarian cancer, pancreatic cancer, hepatobiliary cancer, upper urinary tract cancer, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromosytoma, pituitary cancer, plasma cell neoplasm, pleuropulmonary blastoma, pregnancy and breast cancer, primary central nervous system lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, Sezary syndrome, skin cancer, small cell lung cancer, small intestine cancer, soft tissue sarcoma, squamous cell carcinoma, squamous neck cancer, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, unknown primary carcinoma, urethral cancer, uterine cancer, uterine sarcoma, vaginal cancer, vulvar cancer, Waldenstrom Macroglobulinemia, Wilms' tumor, 1p36 deletion syndrome, 1q21.1 deletion syndrome, 2q37 deletion syndrome, Wolf-Hirschhorn syndrome, Cri du chat, 5q deletion syndrome, Williams syndrome, Monosomy 8p, Monosomy 8q, Alfi's syndrome, Kleefstra syndrome, Monosomy 10p, Monosomy 10q, Jacobsen syndrome, Patau syndrome, Angelman syndrome, Prader–Willi syndrome, Miller-Dieker syndrome, Smith-Magenis syndrome, Edwards syndrome, Down syndrome, DiGeorge syndrome, Phelan-McDermid syndrome, 22q11.2 distal deletion syndrome, Cat eye syndrome, XYY syndrome, Triple X syndrome, Klinefelter syndrome, Wolf-Hirschhorn syndrome, Jacobsen syndrome, Charcot-Marie-Tooth disease type 1A, and Lynch Syndrome.

[775] In some embodiments, methods provided herein can be used to detect aneuploidy (e.g., monosomy or trisomy) in a sample (e.g., a cervical sample, an endometrial sample, or a

urine sample) obtained from a subject. Aneuploidy can be detected in any region of the genome that is known to be associated with cancer (e.g., endometrial or ovarian cancer). In some embodiments, aneuploidy can be detected in arms 4p, 7q, 8q, and/or 9q. Each of these arms harbors oncogenes and tumor suppressor genes that have been shown to undergo copy number alterations in many cancers, including endometrial or ovarian cancer. In some embodiments, aneuploidy can be detected in arms 5q, 8q, and/or 9p. Each of these arms harbors oncogenes and tumor suppressor genes that have been shown to undergo copy number alterations in many cancers, including bladder cancer. Other appropriate regions for aneuploidy detection, which aneuploidy regions(s) are associated with the presence of cancer in a subject, will be known to those of ordinary skill in the art.

[776] In some embodiments, aneuploidy can be detected by amplifying interspersed nucleotide elements. For example, aneuploidy can be detected by amplifying long interspersed nucleotide elements (LINEs). Additionally or alternatively, aneuploidy can be detected by amplifying short interspersed nucleotide elements (SINEs). In some embodiments, aneuploidy can be detected using a technique in which a single PCR is used to co-amplify a plurality of members (e.g., ~38,000) of a subfamily of long interspersed nucleotide element-1 (L1 retrotransposons, also called LINEs). L1 retrotransposons, like other human repeats, have spread throughout the genome via retrotransposition and are found on all 39 non-acrocentric autosomal arms. In some embodiments, aneuploidy can be detected by any of the variety of methods disclosed in Patent Cooperation Treaty application publication number WO2013148496, the contents of which are incorporated herein by reference in their entirety. Those of ordinary skill in the art will be aware of other suitable methods for detecting aneuploidy. In some embodiments, the sample for detecting aneuploidy is collected using a Pap brush. In some embodiments, the sample for detecting aneuploidy is collected using a Tao brush.

[777] In some embodiments, methods provided herein to detect aneuploidy can be combined with methods to detect the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes selected from the group consisting of: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and the detection of genetic biomarkers (e.g.,

mutations) present in ctDNA, or both (e.g., to determine the presence of an ovarian or endometrial cancer). In some embodiments, methods provided herein to detect aneuploidy can be combined with methods to detect the presence of one or more genetic biomarkers (e.g., mutations) in one or more genes selected from the group consisting of: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A, and the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both (e.g., to determine the presence of an endometrial cancer). In some embodiments, methods provided herein to detect aneuploidy can be combined with methods to detect the presence of one or more genetic biomarkers (e.g., mutations) in TP53, and the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both (e.g., to determine the presence of an ovarian cancer). In some embodiments, combining the detection of aneuploidy with the detection of one or more genetic biomarkers (e.g., mutations) in any of the genes described herein, the detection of genetic biomarkers (e.g., mutations) present in ctDNA, or both can increase the specificity and/or sensitivity of detecting ovarian or endometrial cancer. In some embodiments, the sample is collected using a Pap brush. In some embodiments, the sample is collected using a Tao brush.

Cancers

[778] In some embodiments, methods provided herein can be used to detect the presence of cancer (e.g., the presence of a cancer cell) in a subject. In some embodiments, methods provided herein can be used to detect the presence of cancer at an early stage. In some embodiments, methods provided herein for identifying the presence of cancer in a subject with high sensitivity and specificity are performed prior to having determined that the subject already suffers from cancer, prior to having determined that the subject harbors a cancer cell, and/or prior to the subject exhibiting symptoms associated with cancer. In some embodiments, methods provided herein can be used to detect the presence of a genetic biomarker, a protein biomarker, and/or aneuploidy, which genetic biomarker, a protein biomarker, and/or aneuploidy is indicative that the subject has cancer (e.g., harbors a cancer cell).

[779] Cancer types that can be detected by any of the variety of methods described herein include, without limitation, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenal cancer, adrenocortical carcinoma, AIDS-related cancers, AIDS-related lymphoma, amyotrophic lateral sclerosis or ALS, anal cancer, appendix cancer, astrocytoma, astrocytoma, childhood cerebellar or cerebral, atypical teratoid/rhabdoid tumor, basal cell carcinoma, bile duct cancer, bile duct cancer, extrahepatic (see cholangiocarcinoma), bladder cancer, bone cancer, bone tumor, osteosarcoma/malignant fibrous histiocytoma, brain cancer, brain stem glioma, brain tumor, brain tumor, cerebellar astrocytoma, brain tumor, cerebral astrocytoma/malignant glioma, brain tumor, ependymoma, brain tumor, medulloblastoma, brain tumor, supratentorial primitive neuroectodermal tumors, brain tumor, visual pathway and hypothalamic glioma, brainstem glioma, breast cancer, bronchial adenomas/carcinoids, bronchial tumor, bronchioles lung cell carcinoma, Burkitt lymphoma, cancer in adolescents, carcinoid tumor, carcinoid tumor, childhood, carcinoid tumor, gastrointestinal, carcinoma of unknown primary, cardiac tumors, central nervous system lymphoma, primary, cerebellar astrocytoma, childhood, cerebral astrocytoma/malignant glioma, childhood, cervical cancer, childhood cancers, chondrosarcoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative disorders, chronic myeloproliferative neoplasms, colon cancer, colorectal cancer, colorectal cancer (e.g., metastatic colorectal cancer), craniopharyngioma, cutaneous t-cell lymphoma, desmoplastic small round cell tumor, differentiated thyroid cancer, ductal carcinoma in situ, embryonal tumors, endometrial cancer, ependymoma, epithelioid hemangioendothelioma (EHE), esophageal cancer, esthesioneuroblastoma, Ewing's sarcoma in the Ewing family of tumors, extracranial germ cell tumor, extracranial germ cell tumor, childhood, extragonadal germ cell tumor, extrahepatic bile duct cancer, eye cancer, eye cancer, intraocular melanoma, eye cancer, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, gallbladder cancer, ganglioneuromatosis of the gastroenteric mucosa, gastric (stomach) cancer, gastric (stomach) cancer, gastric carcinoid, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), germ cell tumor, germ cell tumor: extracranial, extragonadal, or ovarian, gestational trophoblastic disease, gestational trophoblastic tumor, glioma, glioma of the brain stem, glioma, childhood cerebral astrocytoma, glioma, childhood visual pathway and

hypothalamic, hairy cell leukemia, hairy cell tumor, head and neck cancer, heart cancer, hepatocellular (liver) cancer, histiocytosis, Hodgkin's lymphoma, hypopharyngeal cancer, hypothalamic and visual pathway glioma, childhood, inflammatory myofibroblastic tumor, intraocular melanoma, intraocular melanoma, Islet cell carcinoma (endocrine pancreas), islet cell tumors, Kaposi sarcoma, kidney cancer (renal cell cancer), Langerhans cell histiocytosis, laryngeal cancer, leukaemia, acute lymphoblastic (also called acute lymphocytic leukaemia), leukaemia, acute myeloid (also called acute myelogenous leukemia), leukaemia, chronic lymphocytic (also called chronic lymphocytic leukemia), leukemia, leukemia, chronic myelogenous (also called chronic myeloid leukemia), leukemia, hairy cell, lip and oral cavity cancer, liposarcoma, liver cancer (e.g., primary), lung adenocarcinoma, lung cancer, lung cancer (e.g., small cell lung carcinoma or non-small cell lung carcinoma), lymphoma, lymphoma, AIDS-related, lymphoma, Burkitt, lymphoma, cutaneous T-Cell, lymphoma, Hodgkin, lymphoma, primary central nervous system, lymphomas, Non-Hodgkin (an old classification of all lymphomas except Hodgkin's), macroglobulinemia, male breast cancer, malignant fibrous histiocytoma of bone, malignant fibrous histiocytoma of bone/osteosarcoma, medullary thyroid cancer, medulloblastoma, childhood, melanoma, melanoma, intraocular (eye), melanoma, intraocular (eye), Merkel cell cancer, Merkel cell carcinoma, mesothelioma, mesothelioma, adult malignant, mesothelioma, childhood, metastatic squamous neck cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma, mouth cancer, multiple endocrine neoplasia syndrome, childhood, multiple endocrine neoplasia syndromes, multiple endocrine neoplasia type 2A or 2B (MEN2A or MEN2B, respectively), multiple myeloma, multiple myeloma/plasma cell neoplasm, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative diseases, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, myelogenous leukemia, chronic, myeloid leukemia, myeloid leukemia, adult acute, myeloid leukemia, childhood acute, myeloma, multiple (cancer of the bone-marrow), myeloproliferative disorders, chronic, myeloproliferative neoplasms, myxoma, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, nasopharyngeal carcinoma, neuroblastoma, oligodendroglioma, oral cancer, oral cavity cancer, oropharyngeal cancer, osteocarcinoma, osteosarcoma, osteosarcoma/malignant fibrous histiocytoma of

bone, ovarian cancer, ovarian epithelial cancer (surface epithelial-stromal tumor), ovarian germ cell tumor, ovarian low malignant potential tumor, pancreatic cancer, pancreatic cancer, islet cell, pancreatic neuroendocrine tumors, papillary renal cell carcinoma, papillary thyroid cancer, papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, parathyroid hyperplasia, penile cancer, pharyngeal cancer, pheochromocytoma, Phyllodes breast tumors, pineal astrocytoma, pineal germinoma, pineoblastoma and supratentorial primitive neuroectodermal tumors, childhood, pituitary adenoma, pituitary cancer, plasma cell neoplasia/multiple myeloma, plasma cell neoplasm, pleuropulmonary blastoma, pregnancy and breast cancer, primary central nervous system lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, recurrent thyroid cancer, refractory differentiated thyroid cancer, renal cell cancer, renal cell carcinoma (kidney cancer), renal pelvis and ureter, transitional cell cancer, retinoblastoma, rhabdomyosarcoma, rhabdomyosarcoma, childhood, salivary gland cancer, sarcoma, sarcoma, Ewing family of tumors, Sarcoma, Kaposi, Sezary syndrome, skin cancer, skin cancer (melanoma), skin cancer (non-melanoma), skin carcinoma, Merkel cell, small intestine cancer, soft tissue sarcoma, squamous cell carcinoma, squamous cell carcinoma - see skin cancer (non-melanoma), squamous neck cancer, squamous neck cancer with occult primary, metastatic, stomach cancer, supratentorial primitive neuroectodermal tumor, childhood, T-cell lymphoma, T-cell lymphoma, cutaneous , testicular cancer, throat cancer, thymoma and thymic carcinoma, Thymoma, childhood, thyroid cancer, thyroid cancer, childhood, transitional cell cancer of the renal pelvis and ureter, trophoblastic tumor, gestational, unknown primary carcinoma, unknown primary site, cancer of, childhood, unknown primary site, carcinoma of, adult, ureter and renal pelvis, transitional cell cancer, urethral cancer, uterine cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, visual pathway and hypothalamic glioma, childhood, vulvar cancer, Waldenstrom macroglobulinemia, and Wilms tumor (kidney cancer).

[780] In some embodiments, methods described herein are used to detect the presence of a single type of cancer. In some embodiments, methods described herein are capable of detecting two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) types of cancer. For example, methods described herein can be used to detect the presence of liver cancer, ovarian cancer,

esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, or breast cancer. As another example, methods described herein can be capable of detecting the presence of each of liver cancer, ovarian cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, and breast cancer (e.g., methods described herein are capable of detecting the presence of each of these types of cancers in a subject, although only one type of cancer may be present in the subject). In some embodiments, various methods described herein can be used to detect cancers selected from the group consisting of: pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, and breast cancer, and combinations thereof. As another example, methods described herein can be used to detect the presence of cervical, endometrial, ovarian, or fallopian tubal cancers. As another example, methods described herein can be capable of detecting the presence of each of cervical, endometrial, ovarian, and fallopian tubal cancers (e.g., methods described herein are capable of detecting the presence of each of these types of cancers in a subject, although only one type of cancer may be present in the subject). As another example, methods described herein can be used to detect the presence of bladder cancer or an upper-tract urothelial carcinoma (UTUC). As another example, methods described herein can be capable of detecting the presence of each of bladder cancer and an upper-tract urothelial carcinoma (UTUC) (e.g., methods described herein are capable of detecting the presence of each of these types of cancers in a subject, although only one type of cancer may be present in the subject).

Further Diagnostic Testing

[781] In some embodiments of diagnosing or identifying the presence of a disease (e.g., cancer) in a subject (e.g., using any of the variety of methods described herein), the subject is also identified as a candidate for further diagnostic testing. Provided herein are methods for selecting a subject for further diagnostic testing. In some embodiments, methods for selecting a subject for further diagnostic testing include detecting the presence of one or more genetic biomarkers in a biological sample isolated from the subject, detecting the presence of one or more protein biomarkers in a biological sample isolated from the subject, and/or detecting the presence of aneuploidy in a biological sample isolated from the subject and

selecting a subject for further diagnostic testing when the presence of one or more genetic biomarkers, one or more protein biomarkers, or aneuploidy is identified. In some embodiments, methods for selecting a subject for further diagnostic testing further include detecting the presence of one or more member of one or more other classes of biomarkers. In some embodiments, the step of detecting is performed prior to having determined that the subject already suffers from cancer (e.g., when the subject is not known to harbor a cancer cell).

[782] In some embodiments, the biological sample is isolated from a subject. Any suitable biological sample that contains one or more genetic biomarkers, protein biomarkers, and/or aneuploidy can be used in accordance with any of the variety of methods described herein. For example, the biological sample can include blood, plasma, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. Methods of isolating biological samples from a subject are known to those of ordinary skill in the art.

[783] In some embodiments, the subject may be selected for further diagnostic testing. In some embodiments, methods provided herein can be used to select a subject for further diagnostic testing at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for further diagnostic testing can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for further diagnostic testing can be administered a diagnostic test (e.g., any of the diagnostic tests described herein) at an increased frequency compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for further diagnostic testing can be administered one or more additional diagnostic tests compared to a subject that has not been selected for further diagnostic testing. For example, a subject selected for further diagnostic testing can be administered two diagnostic tests or more, whereas a subject that has not been selected for

further diagnostic testing is administered only a single diagnostic test (or no diagnostic tests). In some embodiments, the diagnostic testing method can determine the presence of the same type of cancer as the originally detected cancer. Additionally or alternatively, the diagnostic testing method can determine the presence of a different type of cancer from the originally detected cancer.

[784] In some embodiments, the diagnostic testing method is a scan. In some embodiments, the scan is a bone scan, a computed tomography (CT), a CT angiography (CTA), an esophagram (a Barium swallow), a Barium enema, a gallium scan, a magnetic resonance imaging (MRI), a mammography, a monoclonal antibody scan (e.g., ProstaScint® scan for prostate cancer, OncoScint® scan for ovarian cancer, and CEA-Scan® for colon cancer), a multigated acquisition (MUGA) scan, a PET scan, a PET/CT scan, a thyroid scan, an ultrasound (e.g., a breast ultrasound, an endobronchial ultrasound, an endoscopic ultrasound, a transvaginal ultrasound), an X-ray, a DEXA scan.

[785] In some embodiments, the diagnostic testing method is a physical examination, such as, without limitation, an anoscopy, a biopsy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a digital breast tomosynthesis, a digital rectal exam, an endoscopy, including but not limited to a capsule endoscopy, virtual endoscopy, an arthroscopy, a bronchoscopy, a colonoscopy, a colposcopy, a cystoscopy, an esophagoscopy, a gastroscopy, a laparoscopy, a laryngoscopy, a neuroendoscopy, a proctoscopy, a sigmoidoscopy, a skin cancer exam, a thoracoscopy, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a pelvic exam.

[786] In some embodiments, the diagnostic testing method is a biopsy (e.g., a bone marrow aspiration, a tissue biopsy). In some embodiments, the biopsy is performed by fine needle aspiration or by surgical excision. In some embodiments, the diagnostic testing method(s) further include obtaining a biological sample (e.g., a tissue sample, a urine sample, a blood sample, a check swab, a saliva sample, a mucosal sample (e.g., sputum, bronchial secretion), a nipple aspirate, a secretion or an excretion). In some embodiments, the diagnostic testing method(s) include determining exosomal proteins (e.g., an exosomal surface protein (e.g., CD24, CD147, PCA-3)) (Soung et al. (2017) Cancers 9(1):pii:E8). In some embodiments,

the diagnostic testing method is an oncotype DX® test (Baehner (2016) Ecancermedicalscience 10:675).

[787] In some embodiments, the diagnostic testing method is a test, such as without limitation, an alpha-fetoprotein blood test, a bone marrow test, a fecal occult blood test, a human papillomavirus test, low-dose helical computed tomography, a lumbar puncture, a prostate specific antigen (PSA) test, a pap smear, or a tumor marker test.

[788] In some embodiments, the diagnostic testing method includes determining the level of a known protein biomarker (e.g., CA-125 or prostate specific antigen (PSA)). For example, a high amount of CA-125 can be found in subject's blood, which subject has ovarian cancer, endometrial cancer, fallopian tube cancer, pancreatic cancer, stomach cancer, esophageal cancer, colon cancer, liver cancer, breast cancer, or lung cancer. The term "biomarker" as used herein refers to "a biological molecule found in blood, other bodily fluids, or tissues that is a sign of a normal or abnormal process, or of a condition or disease", e.g., as defined by the National Cancer Institute. (see, e.g., the URL www.cancer.gov/publications/dictionaries/cancer-terms?CdrID=45618). A biomarker can include a genetic biomarker such as, without limitation, a nucleic acid (e.g., a DNA molecule, a RNA molecule (e.g., a microRNA, a long non-coding RNA (lncRNA) or other non-coding RNA) A biomarker can include a protein biomarker such as, without limitation, a peptide, a protein, or a fragment thereof.

[789] In some embodiments, the biomarker is FLT3, NPM1, CEBPA, PRAM1, ALK, BRAF, KRAS, EGFR, Kit, NRAS, JAK2, KRAS, HPV virus, ERBB2, BCR-ABL, BRCA1, BRCA2, CEA, AFP, and/or LDH. See e.g., Easton et al. (1995) Am. J. Hum. Genet. 56: 265-271, Hall et al. (1990) Science 250: 1684-1689, Lin et al. (2008) Ann. Intern. Med. 149: 192-199, Allegra et al. (2009) (2009) J. Clin. Oncol. 27: 2091-2096, Paik et al. (2004) N. Engl. J. Med. 351: 2817-2826, Bang et al. (2010) Lancet 376: 687-697, Piccart-Gebhart et al. (2005) N. Engl. J. Med. 353: 1659-1672, Romond et al. (2005) N. Engl. J. Med. 353: 1673-1684, Locker et al. (2006) J. Clin. Oncol. 24: 5313-5327, Giligan et al. (2010) J. Clin. Oncol. 28: 3388-3404, Harris et al. (2007) J. Clin. Oncol. 25: 5287-5312; Henry and Hayes (2012) Mol. Oncol. 6: 140-146. In some embodiments, the biomarker is a biomarker for detection of breast cancer in a subject, such as, without limitation, MUC-1, CEA, p53, urokinase

plasminogen activator, BRCA1, BRCA2, and/or HER2 (Gam (2012) World J. Exp. Med. 2(5): 86-91). In some embodiments, the biomarker is a biomarker for detection of lung cancer in a subject, such as, without limitation, KRAS, EGFR, ALK, MET, and/or ROS1 (Mao (2002) Oncogene 21: 6960-6969; Korpanty et al. (2014) Front Oncol. 4: 204). In some embodiments, the biomarker is a biomarker for detection of ovarian cancer in a subject, such as, without limitation, HPV, CA-125, HE4, CEA, VCAM-1, KLK6/7, GST1, PRSS8, FOLR1, ALDH1 (Nolen and Lokshin (2012) Future Oncol. 8(1): 55-71; Sarojini et al. (2012) J. Oncol. 2012:709049). In some embodiments, the biomarker is a biomarker for detection of colorectal cancer in a subject, such as, without limitation, MLH1, MSH2, MSH6, PMS2, KRAS, and BRAF (Gonzalez-Pons and Cruz-Correa (2015) Biomed. Res. Int. 2015: 149014; Alvarez-Chaver et al. (2014) World J. Gastroenterol. 20(14): 3804-3824). In some embodiments, the diagnostic testing method determines the presence and/or expression level of a nucleic acid (e.g., microRNA (Sethi et al. (2011) J. Carcinog. Mutag. S1-005), RNA, a SNP (Hosein et al. (2013) Lab. Invest doi: 10.1038/labinvest.2013.54; Falzoi et al. (2010) Pharmacogenomics 11: 559-571), methylation status (Castelo-Branco et al. (2013) Lancet Oncol 14: 534-542), a hotspot cancer mutation (Yousem et al. (2013) Chest 143: 1679-1684)). Non-limiting examples of methods of detecting a nucleic acid in a sample include: PCR, RT-PCR, sequencing (e.g., next generation sequencing methods, deep sequencing), a DNA microarray, a microRNA microarray, a SNP microarray, fluorescent in situ hybridization (FISH), restriction fragment length polymorphism (RFLP), gel electrophoresis, Northern blot analysis, Southern blot analysis, chromogenic in situ hybridization (CISH), chromatin immunoprecipitation (ChIP), SNP genotyping, and DNA methylation assay. See, e.g., Meldrum et al. (2011) Clin. Biochem. Rev. 32(4): 177-195; Sidranksy (1997) Science 278(5340): 1054-9.

[790] In some embodiments, the diagnostic testing method includes determining the presence of a protein biomarker in a sample (e.g., a plasma biomarker (Mirus et al. (2015) Clin. Cancer Res. 21(7): 1764-1771)). Non-limiting examples of methods of determining the presence of a protein biomarker include: western blot analysis, immunohistochemistry (IHC), immunofluorescence, mass spectrometry (MS) (e.g., matrix assisted laser desorption/ionization (MALDI)-MS, surface enhanced laser desorption/ionization time-of-

flight (SELDI-TOF)-MS), enzyme-linked immunosorbent assay (ELISA), flow cytometry, proximity assay (e.g., VeraTag proximity assay (Shi et al. (2009) Diagnostic molecular pathology: the American journal of surgical pathology, part B: 18: 11-21, Huang et al. (2010) AM. J. Clin. Pathol. 134: 303-11)), a protein microarray (e.g., an antibody microarray (Ingvarsson et al. (2008) Proteomics 8: 2211-9, Woodbury et al. (2002) J. Proteome Res. 1: 233-237), an IHC-based microarray (Stromberg et al. (2007) Proteomics 7: 2142-50), a microarray ELISA (Schroder et al. (2010) Mol. Cell. Proteomics 9: 1271-80). In some embodiments, the method of determining the presence of a protein biomarker is a functional assay. In some embodiments, the functional assay is a kinase assay (Ghosh et al. (2010) Biosensors & Bioelectronics 26: 424-31, Mizutani et al. (2010) Clin. Cancer Res. 16: 3964-75, Lee et al. (2012) Biomed. Microdevices 14: 247-57), a protease assay (Lowe et al. (2012) ACS nano. 6: 851-7, Fujiwara et al. (2006) Breast cancer 13: 272-8, Darragh et al. (2010) Cancer Res 70: 1505-12). See, e.g., Powers and Palecek (2015) J. Heathc Eng. 3(4): 503-534, for a review of protein analytical assays for diagnosing cancer patients.

[791] In some embodiments, the diagnostic testing method includes detecting the presence of aneuploidy in a biological sample (e.g. detecting whether the biological sample contains cells with an abnormal number of chromosomes). Non-limiting examples of methods of detecting the presence of aneuploidy include karyotyping, digital karyotyping, fluorescence in situ hybridization (FISH), quantitative PCR of short tandem repeats, quantitative fluorescence PCR (QF-PCR), quantitative PCR dosage analysis, quantitative mass spectrometry of single nucleotide polymorphisms, and comparative genomic hybridization (CGH).

[792] In some embodiments, a subject that has been selected for further diagnostic testing can also be selected for increased monitoring. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods described herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the subject and/or to assess the development of additional cancer cell mutations), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell).

[793] In some embodiments, a subject that is selected for further diagnostic testing can also be selected for a therapeutic intervention. Any of the therapeutic interventions described herein or known in the art can be administered. For example, a subject that has been selected for further diagnostic testing can be administered a further diagnostic test, and a therapeutic intervention can be administered if the presence of the cancer cell is confirmed. Additionally or alternatively, a subject that has been selected for further diagnostic testing can be administered a therapeutic intervention, and can be further monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for further diagnostic testing has been administered a therapeutic intervention, the additional testing will reveal the presence of one or more additional genetic biomarkers, the presence of one or more additional protein biomarkers, and/or the presence of aneuploidy. In some embodiments, the presence of one or more additional genetic biomarkers, the presence of one or more additional protein biomarkers, and/or the presence of aneuploidy will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

Increased Monitoring

[794] Also provided herein are methods for selecting a subject for increased monitoring. In some embodiments, methods for selecting a subject for increased monitoring include detecting the presence of one or more genetic biomarkers in a biological sample isolated from the subject, detecting the presence of one or more protein biomarkers in a biological sample isolated from the subject, and/or detecting the presence of aneuploidy in a biological sample isolated from the subject, and selecting a subject for increased monitoring when the presence of one or more genetic biomarkers, one or more protein biomarkers, or aneuploidy is identified. In some embodiments, methods for selecting a subject for increased monitoring further include detecting the presence of one or more member of one or more other classes of biomarkers. In some embodiments, the step of detecting is performed when the subject is not known to harbor a cancer cell (e.g., when the subject is not known to harbor a cancer cell).

[795] In some embodiments, the biological sample is isolated from a subject. Any suitable biological sample that contains one or more genetic biomarkers, protein biomarkers, and/or aneuploidy can be used in accordance with any of the variety of methods disclosed herein. For example, the biological sample can include blood, plasma, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. Methods of isolating biological samples from a subject are known to those of ordinary skill in the art.

[796] In some embodiments, once a subject has been determined to have a cancer, the subject may be selected for increased or additional monitoring. In some embodiments, methods provided herein can be used to select a subject for increased monitoring at a time period prior to the time period when conventional techniques are capable of diagnosing the subject with an early-stage cancer. For example, methods provided herein for selecting a subject for increased monitoring can be used when a subject has not been diagnosed with cancer by conventional methods and/or when a subject is not known to harbor a cancer. In some embodiments, a subject selected for increased monitoring can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some embodiments, a subject selected for increased monitoring can be administered one or more additional diagnostic tests compared to a subject that has not been selected for increased monitoring. For example, a subject selected for increased monitoring can be administered two diagnostic tests, whereas a subject that has not been selected for increased monitoring is administered only a single diagnostic test (or no diagnostic tests).

[797] In some embodiments, a subject that has been selected for increased monitoring can also be selected for further diagnostic testing. Once the presence of a cancer cell has been identified (e.g., by any of the variety of methods described herein), it may be beneficial for the subject to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the subject and/or to assess the development of additional cancer cell mutations),

and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor harboring the cancer cell).

[798] In some embodiments, a subject that is selected for increased monitoring can also be selected for a therapeutic intervention. Any of the therapeutic interventions described herein or known in the art can be administered. For example, a subject that has been selected for increased monitoring can be further monitored, and a therapeutic intervention can be administered if the presence of the cancer cell is maintained throughout the increased monitoring period. Additionally or alternatively, a subject that has been selected for increased monitoring can be administered a therapeutic intervention, and further monitored as the therapeutic intervention progresses. In some embodiments, after a subject that has been selected for increased monitoring has been administered a therapeutic intervention, the increased monitoring will reveal the presence of one or more additional genetic biomarkers, the presence of one or more additional protein biomarkers, and/or the presence of aneuploidy. In some embodiments, the presence of one or more additional genetic biomarkers, the presence of one or more additional protein biomarkers, and/or the presence of aneuploidy will provide cause to administer a different therapeutic intervention (e.g., a resistance mutation may arise in a cancer cell during the therapeutic intervention, which cancer cell harboring the resistance mutation is resistance to the original therapeutic intervention).

Therapeutic Interventions

[799] In some embodiments, once a subject has been determined to have a cancer (e.g., ancercical, endometrial, ovarian, or fallopian tubal cancer), or is suspected of having cancer, the subject may be administered a therapeutic intervention or selected for therapeutic intervention. In some embodiments, wherein the presence of cancer (e.g., a cervical, endometrial, ovarian, or fallopian tubal cancer) been detected in a subject, the subject is administered a therapeutic intervention that specifically targets the subject's cancer (e.g. genetic modifications present in the cervical, endometrial, ovarian, or fallopian tubal cancer). For example, when a subject is determined to have ovarian cancer, a therapeutic intervention appropriate for ovarian cancer can be administered. As another example, when a subject is

determined to have endometrial cancer, a therapeutic intervention appropriate for endometrial cancer can be administered. In some embodiments the therapeutic intervention is chemotherapy (e.g., any of the platinum-based chemotherapeutic agents described herein (e.g., cisplatin, carboplatin), or a taxane (e.g., placitaxel (Taxol®) or docetaxel (Taxotere®). In some embodiments, the chemotherapeutic agent is an albumin-bound paclitaxel (nap-paclitaxel, Abraxane®), altretamine (Hexalen®), capecitabine (Xeloda®), cyclophosphamide (Cytoxan®), etoposide(VP-16), gemcitabine (Gemzar®), ifosfamide (Ifex®), irinotecan (CPT-11, Camptosar®), liposomal doxorubicin (doxil®), melphalan, pemetrexed (alimta®), topotecan, or vinorelbine (navelbine®). In some embodiments, the therapeutic intervention is a combination of chemotherapeutic agents (e.g., paclitaxel, ifosfamide, and cisplatin; vinblastine, ifosfamide and cisplatin; etoposide, ifosfamide and cisplatin). In some embodiments, the therapeutic intervention is an epigenetic therapy (see, e.g., Smith et al. (2017) Gynecol. Oncol. Rep. 20: 81-86). In some embodiments, the epigenetic therapy is a DNA methyltransferase (DNMT) inhibitor (e.g., 5-azacytidine (5-AZA), decitabine (5-aza-2'-deoxycytidine) (Fu et al. (2011) Cancer 117(8): 1661-1669; Falchook et al. (2013) Investig. New Drugs 31(5): 1192-1200; Matei et al. (2012) Cancer Res. 72(9): 2197-2205). In some embodiments, the DNMT1 inhibitor is NY-ESO-1 (Odunsi et al. (2014) Cancer Immunol. Res. 2(1): 37-49). In some embodiments, the epigenetic therapy is a histone deacetylase (HDAC) inhibitor. In some embodiments, the HDAC inhibitor is vorinostat (Modesitt (2008) 109(2): 182-186) or belinostat (Mackay et al. (2010) Eur. J. Cancer 46(9): 1573-1579). In some embodiments, the HDAC inhibitor is given in combination with a chemotherapeutic agent (e.g., carboplatin (paraplatin), cisplatin, paclitaxel or docetaxel (taxotere)) (Mendivil (2013) Int. J. Gynecol. Cancer 23(3): 533-539; Dizon (2012) Gynecol. Oncol. 125(2): 367-371; Dizon (2012) Int J. Gynecol. Cancer 23(3): 533-539). In some embodiments, the therapeutic intervention is an anti-angiogenic agent (e.g., bevacizumab). In some embodiments, the therapeutic intervention is a poly (ADP-ribose) polymerase (PARP)-1 and/or PARP-2 inhibitor. In some embodiments, the PARP-1 and PARP-2 inhibitor is niraparib (zejula) (Scott (2017) Drugs doiL10.1007/s40265-017-0752). In some embodiments, the PARP inhibitor is olaparib (lynparza) or rucaparib (rubraca). In some embodiments, the therapeutic intervention is a hormone (e.g., a luteinizing-hormone-

releasing hormone (LHRH) agonist). In some embodiments, the LHRH agonist is goserelin (Zoladex®) or leuprolide (Lupron®). In some embodiments, the therapeutic intervention is an anti-estrogen compound (e.g., tamoxifen). In some embodiments, the therapeutic intervention is an aromatase inhibitor (e.g., letrozole (Femara®), anastrozole (Arimidex®) or exemestane (Aromasin®). In some embodiments, the therapeutic intervention is surgery (e.g., debulking of the tumor mass, a hysterectomy, a bilateral salpingo-oophorectomy, an omentectomy). The term "debulking" refers to surgical removal of almost the entire tumor ("optimally debulked"). In some embodiments, debulking can include removing a portion of the bladder, the spleen, the gallbladder, the stomach, the liver, and/or pancreas. In some embodiments, adjuvant chemotherapy is further administered to the subject after surgery (e.g., debulking of the tumor mass, a hysterectomy, a bilateral salpingo-oophorectomy, an omentectomy). In some embodiments, adjuvant chemotherapy is administered intra-abdominally (intraperitoneally). In some embodiments, the therapeutic intervention is a prophylactic surgery (e.g., a hysterectomy). In some embodiments, a paracentesis is performed to remove ascites.

[800] In some embodiments, once a subject has been determined to have a cancer (e.g., a bladder cancer or an UTUC) according to any of the variety of methods provided herein, the subject may be administered a therapeutic intervention or selected for therapeutic intervention. For example, when a subject is determined to have bladder cancer, a therapeutic intervention appropriate for bladder cancer can be administered. Examples of such therapeutic interventions that are appropriate for bladder cancer include, without limitation, transuretral resection of the bladder (TURB), intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, cystectomy or cystoprostatectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination of the above. As another example, when a subject is determined to have an UTUC, a therapeutic intervention appropriate for an UTUC can be administered. Examples of such therapeutic interventions that are appropriate for an UTUC include, without limitation, transurethral resection, intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant

chemotherapy, ureterectomy or nephroureterectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination of the above.

[801] In some embodiments, the detected cancer is a low-grade tumor (e.g., a neoplasm of low malignant potential (PUNLMP) or a non-invasive low grade papillary urothelial carcinoma). In some embodiments, once a subject has been determined to have a low-grade tumor, the subject may be administered a therapeutic intervention or selected for therapeutic intervention that includes transuretral resection of the bladder (TURB).

[802] In some embodiments, wherein the presence of colorectal cancer been detected in a subject, the subject is administered a therapeutic intervention that specifically targets the subject's colorectal cancer (e.g. genetic modifications present in the colorectal cancer). In some embodiments, the subject is administered an anti-EGFR monoclonal antibody (e.g., cetuximab or panitumumab) (Cunningham et al. (2004) N. Engl. J. Med. 351(4): 337-345). In some embodiments, the therapeutic invention is an antiangiogenic agent. In some embodiments, the antiangiogenic agent is bevacizumab (Avastin) (Hurwitz et al. (2004) N. Engl. J. Med. 350: 2335-2342). In some embodiments, the antiangiogenic agent is a VEGF inhibitor (e.g., aflibercept (Tang et al. (2008) J. Clin. Oncol 26 (May 20 suppl; abstr 4027); vatalanib (PTK/ZK222584; Hecht et al. (2005) ASCO Annual Meeting Proceedings J. Clin. Oncol. 23: 16S (abstr. LBA3)); sunitinib (Saltz et al. (2007) J. Clin. Oncol. 25: 4793-4799); AZD2171 (Rosen et al. (2007) J. Clin. Oncol. 25: 2369-76); AMG 706 (Drevis et al. (2007) 25: 3045-2054)). In some embodiments, bevacizumb is administered with a chemotherapy treatment (see, e.g., Hurwitz et al. (2004) N. Engl. J. Med. 350: 2335-2342; Gruenberger et al. (2008) J. Clin. Oncol. 26: 1830-1835). Non-limiting examples of chemotherapy treatments that can be used in a subject with colorectal cancer include: 5-FU, leucovorin, oxaliplatin (Eloxatin), capecitabine, celecoxib and sulindac. In some embodiments, a combination of chemotherapeutic agents is used, e.g., FOLFOX (5-FU, leucovorin and oxaliplatin), FOLFIRI (leucovorin, 5-FU and irinotecan (Camptosar), CapeOx (capecitabine (Xeloda) and oxaliplatin). In some embodiments, the therapeutic intervention is a mammalian target of rapamycin (mTOR) inhibitor (e.g., a rapamycin analog (Kesmodel et al. (2007) Gastrointestinal Cancers Symposium (abstr 234)); RAD-001 (Tabernero et al. (2008) J. Clin. Oncol. 26: 1603-1610). In some embodiments, the therapeutic intervention is a

protein kinase C antagonist (e.g., enzastaurin (Camidge et al. (2008) Anticancer Drugs 19:77-84, Resta et al. (2008) J. Clin. Oncol. 26 (May 20 suppl) (abstr 3529)). In some embodiments, the therapeutic intervention is an inhibitor of nonreceptor tyrosine kinase Src (e.g., AZ0530 (Tabernero et al. (2007) J. Clin. Oncol. 25: 18S (abstr 3520))). In some embodiments, the therapeutic intervention is an inhibitor of kinesin spindle protein (KSP) (e.g., ispinesib (SB-715992) (Chu et al. (2004) J. Clin. Oncol. 22:14S (abstr 2078), Burris et al. (2004) J. Clin. Oncol. 22: 128 (abstr 2004))).

[803] In some embodiments, wherein the presence of lung cancer been detected in a subject, the subject is administered a therapeutic intervention that specifically targets the subject's lung cancer (e.g. genetic modifications present in the lung cancer). In some embodiments the therapeutic intervention is chemotherapy (e.g., any of the platinum-based chemotherapeutic agents described herein (e.g., cisplatin, carboplatin), or a taxane (e.g., placitaxel (Taxol®) or docetaxel (Taxotere®). In some embodiments, the chemotherapeutic agent is an albumin-bound paclitaxel (nap-paclitaxel, Abraxane®), altretamine (Hexalen®), capecitabine (Xeloda®), cyclophosphamide (Cytoxan®), etoposide(VP-16), gemcitabine (Gemzar®), ifosfamide (Ifex®), irinotecan (CPT-11, Camptosar®), liposomal doxorubicin (doxil®), melphalan, pemetrexed (alimta®), topotecan, or vinorelbine (navelbine®). In some embodiments, the therapeutic intervention is a combination of chemotherapeutic agents (e.g., paclitaxel, ifosfamide, and cisplatin; vinblastine, ifosfamide and cisplatin; etoposide, ifosfamide and cisplatin). In some embodiments, the therapeutic intervention is an epigenetic therapy (see, e.g., Smith et al. (2017) Gynecol. Oncol. Rep. 20: 81-86). In some embodiments, the epigenetic therapy is a DNA methyltransferase (DNMT) inhibitor (e.g., 5-azacytidine (5-AZA), decitabine (5-aza-2'-deoxycytidine) (Fu et al. (2011) Cancer 117(8): 1661-1669; Falchook et al. (2013) Investig. New Drugs 31(5): 1192-1200; Matei et al. (2012) Cancer Res. 72(9): 2197-2205). In some embodiments, the DNMT1 inhibitor is NY-ESO-1 (Odunsi et al. (2014) Cancer Immunol. Res. 2(1): 37-49). In some embodiments, the epigenetic therapy is a histone deacetylase (HDAC) inhibitor. In some embodiments, the HDAC inhibitor is vorinostat (Modesitt (2008) 109(2): 182-186) or belinostat (Mackay et al. (2010) Eur. J. Cancer 46(9): 1573-1579). In some embodiments, the HDAC inhibitor is given in combination with a chemotherapeutic agent (e.g., carboplatin (paraplatin), cisplatin,

paclitaxel or docetaxel (taxotere)) (Mendivil (2013) Int. J. Gynecol. Cancer 23(3): 533-539; Dizon (2012) Gynecol. Oncol. 125(2): 367-371; Dizon (2012) Int J. Gynecol. Cancer 23(3): 533-539). In some embodiments, the therapeutic intervention is an anti-angiogenic agent (e.g., bevacizumab). In some embodiments, the therapeutic intervention is a poly (ADP-ribose) polymerase (PARP)-1 and/or PARP-2 inhibitor. In some embodiments, the PARP-1 and PARP-2 inhibitor is niraparib (zejula) (Scott (2017) Drugs doiL10.1007/s40265-017-0752). In some embodiments, the PARP inhibitor is olaparib (lynparza) or rucaparib (rubraca). In some embodiments, the therapeutic intervention is a hormone (e.g., a luteinizing-hormone-releasing hormone (LHRH) agonist). In some embodiments, the LHRH agonist is goserelin (Zoladex®) or leuprolide (Lupron®). In some embodiments, the therapeutic intervention is an anti-estrogen compound (e.g., tamoxifen). In some embodiments, the therapeutic intervention is an aromatase inhibitor (e.g., letrozole (Femara®), anastrozole (Arimidex®) or exemestane (Aromasin®). In some embodiments, the therapeutic intervention is surgery (e.g., debulking of the tumor mass, a hysterectomy, a bilateral salpingo-oophorectomy, an omentectomy). The term "debulking" refers to surgical removal of almost the entire tumor ("optimally debulked"). In some embodiments, debulking can include removing a portion of the bladder, the spleen, the gallbladder, the stomach, the liver, and/or pancreas. In some embodiments, adjuvant chemotherapy is further administered to the subject after surgery (e.g., debulking of the tumor mass, a hysterectomy, a bilateral salpingo-oophorectomy, an omentectomy). In some embodiments, adjuvant chemotherapy is administered intra-abdominally (intraperitoneally). In some embodiments, the therapeutic intervention is a prophylactic surgery (e.g., a hysterectomy). In some embodiments, a paracentesis is performed to remove ascites.

[804] In some embodiments, wherein the presence of breast cancer been detected in a subject, the subject is administered a therapeutic intervention that specifically targets the subject's breast cancer (e.g. genetic modifications present in the breast cancer). In some embodiments, the targeted drug therapy is a HER2 inhibitor (e.g., trastuzumab (Herceptin), pertuzumab (perjeta); ado-trastuzumab emtansine (T-DM1; Kadcyla); lapatinib (Tykerb), neratinib). See, e.g., Baselga et al. (2012) N Engl J Med 366: 109-119; Konecny et al. (2006) Cancer Res 66: 1630-1639, Xia et al. (2007) Cancer Res. 67: 1170-1175; Gomez et al. (2008)

J Clin Oncol 26: 2999-30005; Wong et al. (2009) Clin. Cancer Res. 15: 2552-2558; Agus et al. (2002) Cancer Cell 2: 127-137; Lewis Philips et al. (2008) Cancer Res 68: 9280-9290. In some embodiments, the targeted drug therapy is a cyclin-dependent kinase inhibitor (e.g., a CDK4/6 inhibitor (e.g., palbociclib (Ibrance®), ribociclin(Kisqali®), abemaciclib) (Turner et al. (2015) N Engl J Med 373: 209-219; Finn et al. (2016) N Eng J Med 375: 1925-1936; Ehab and Elbaz (2016) Breast Cancer 8: 83-91; Xu et al. (2017) J Hematol. Oncol. 10(1): 97; Corona et al. (2017) Cri Rev Oncol Hematol 112: 208-214; Barroso-Sousa et al. (2016) Breast Care 11(3): 167-173)). In some embodiments, the targeted drug therapy is a PARP inhibitor (e.g., olaparib (AZD2281), veliparib (ABT-888), niraparib (MK-4827), talazoparib (BMN-673), rucaparib (AG-14699), CEP-9722) See, e.g., Audeh et al. (2010) Lancet 376: 245-251; Fong et al. (2009) N Engl J Med 361: 123-134; Livrahi and Garber (2015) BMC Medicine 13: 188; Kaufamn et al. (2015) J Clin. Oncol. 33: 244-250; Gelmon et al. (2011) Lancet Oncol. 12: 852-61; Isakoff et al. (2011) Cancer Res 71:P3-16-05; Sandhu et al. (2013) Lancet Oncol 14:882-92; Tutt et al. (2010) Lancet 376: 235-44; Somlo et al. (2013) J. Clin. Oncol. 31: 1024; Shen et al. (2013) CLin. Cancer Res. 19(18): 5003-15; Awada et al. (2016) Anticancer Drugs 27(4): 342-8. In some embodiments, the targeted drug therapy is a mTOR inhibitor (e.g., everolimus (afinitor)). See, e.g., Gong et al. (2017) Oncotarget doi: 10.18632/oncotarget.16336; Louseberg et al. (2017) Breast Cancer 10: 239-252; Hare and Harvey (2017) Am J Cancer Res 7(3): 383-404. In some embodiments, the targeted drug therapy is a heat shock protein 90 inhibitor (e.g., tanespimycin) (Modi et al. (2008) J. Clin Oncol. 26: s1027; Miller et al. (2007) J. Clin. Oncol. 25:s1115; Schulz et al. (2012) J Exp Med 209(2): 275-89). In some embodiments, the targeted drug therapy further includes a bone-modifying drug (e.g., a bisphosphonate or denosumab (Xgeva)). See, e.g., Ethier et al. (2017) Curr Oncol Rep 19(3): 15; Abdel-Rahman (2016) Expert Rev Anticancer Ther 16(8): 885-91. In some embodiments, the therapeutic intervention is a hormone (e.g., a luteinizing-hormone-releasing hormone (LHRH) agonist). In some embodiments, the LHRH agonist is goserelin (Zoladex®) or leuprolide (Lupron®). In some embodiments, the therapeutic intervention is an anti-estrogen compound (e.g., tamoxifen, fulvestrant (faslodex)). In some embodiments, the therapeutic intervention is an aromatase inhibitor (e.g., letrozole (Femara®), anastrozole (Arimidex®) or exemestane (Aromasin®). In some embodiments,

the therapeutic intervention is surgery (e.g., a lumpectomy, a single mastectomy, a double mastectomy, a total mastectomy, a modified radical mastectomy, a sentinel lymph node biopsy, an axillary lymph node dissection; breast-conserving surgery). The extent of surgical removal will depend on the stage of breast cancer and overall prognosis. In some embodiments, the therapeutic intervention is radiation therapy. In some embodiments, the radiation therapy is partial breast irradiation or intensity-modulated radiation therapy. In some embodiments, the therapeutic intervention is chemotherapy (e.g., capecitabine (xeloda), carboplatin (paraplatin) ,cisplatin (platinol), cyclophosphamide (neosar), docetaxel (docefrez, taxotere), doxorubicin (Adriamycin), pegylated liposomal doxorubicin (doxil), epirubicin (ellence), fluorouracil (5-FU, adrucil), gemcitabine (gemzar), methotrexate, paclitaxel (taxol), protein-bound paclitaxel (abraxane), vinorelbine (navelbine), eribulin (halaven), or ixabepilone (ixempra)). In some embodiments, the therapeutic intervention is a combination of at least two chemotherapeutic agents (e.g., doxorubicin and cyclophosphamide (AC); epirubicin and cyclophosphamide (EC); cyclophosphamide, doxorubicin and 5-FU (CAF); cyclophosphamide, epirubicin and 5-FU (CEF); cyclophosphamide, methotrexate and 5-FU (CMF); epirubicin and cyclophosphamide (EC); docetaxel, doxorubicin and cyclophosphamide (TAC); docetaxel and cyclophosphamide (TC).

[805] In some embodiments, a therapeutic intervention is administered to the subject after a cancer is detected or identified. Any of the therapeutic interventions disclosed herein or known in the art can be administered. Exemplary therapeutic interventions include, without limitation, a kinase inhibitor, an immune checkpoint inhibitor (e.g., a PD-1, a PD-L1, and/or a CTLA-4 immune checkpoint inhibitor), a chemotherapeutic agent, adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors), an antibody, a bispecific antibody or fragments thereof (e.g., BiTEs), chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, cytotoxic therapy, hormone therapy, immunotherapy, a monoclonal antibody, radiation therapy, signal transduction inhibitors, surgery (e.g., surgical resection), a targeted therapy such as administration of kinase inhibitors (e.g., kinase inhibitors that target a particular genetic lesion, such as a translocation or mutation), or any combination of thereof. Such therapeutic interventions can be administered alone or in combination. In some embodiments of any of

the methods described herein, the one or more therapeutic interventions are administered sequentially or simultaneously to the subject after the cancer cell has been detected. In some embodiments, the therapeutic intervention can be administered at a time when the subject has an early-stage cancer, and wherein the therapeutic intervention is more effective that if the therapeutic intervention were to be administered to a subject at a later time. In some embodiments, a therapeutic intervention can reduce the severity of the cancer, reduce a symptom of the cancer, and/or to reduce the number of cancer cells present within the subject.

[806] In some embodiments, the therapeutic intervention can include an immune checkpoint inhibitor. Non-limiting examples of immune checkpoint inhibitors include nivolumab (Opdivo), pembrolizumab (Keytruda), atezolizumab (tecentriq), avelumab (bavencio), durvalumab (imfinzi), ipilimumab (yervoy). See, e.g., Pardoll (2012) Nat. Rev Cancer 12: 252-264; Sun et al. (2017) Eur Rev Med Pharmacol Sci 21(6): 1198-1205; Hamanishi et al. (2015) J. Clin. Oncol. 33(34): 4015-22; Brahmer et al. (2012) N Engl J Med 366(26): 2455-65; Ricciuti et al. (2017) J. Thorac Oncol. 12(5): e51-e55; Ellis et al. (2017) Clin Lung Cancer pii: S1525-7304(17)30043-8; Zou and Awad (2017) Ann Oncol 28(4): 685-687; Sorscher (2017) N Engl J Med 376(10: 996-7; Hui et al. (2017) Ann Oncol 28(4): 874-881; Vansteenkiste et al. (2017) Expert Opin Biol Ther 17(6): 781-789; Hellmann et al. (2017) Lancet Oncol. 18(1): 31-41; Chen (2017) J. Chin Med Assoc 80(1): 7-14.

[807] In some embodiments, the therapeutic intervention is adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors). See, e.g., Rosenberg and Restifo (2015) Science 348(6230): 62-68; Chang and Chen (2017) Trends Mol Med 23(5): 430-450; Yee and Lizee (2016) Cancer J. 23(2): 144-148; Chen et al. (2016) Oncoimmunology 6(2): e1273302; US 2016/0194404; US 2014/0050788; US 2014/0271635; US 9,233,125; incorporated by reference in their entirety herein.

[808] In some embodiments, a therapeutic intervention is a chemotherapeutic agent. Non-limiting examples of chemotherapeutic agents include: amsacrine, azacitidine, axathioprine, bevacizumab (or an antigen-binding fragment thereof), bleomycin, busulfan, carboplatin, capecitabine, chlorambucil, cisplatin, cyclophosphamide, cytarabine, dacarbazine,

daunorubicin, docetaxel, doxifluridine, doxorubicin, epirubicin, erlotinib hydrochlorides, etoposide, fiudarabine, floxuridine, fludarabine, fluorouracil, gemcitabine, hydroxyurea, idarubicin, ifosfamide, irinotecan, lomustine, mechlorethamine, melphalan, mercaptopurine, methotrxate, mitomycin, mitoxantrone, oxaliplatin, paclitaxel, pemetrexed, procarbazine, all-trans retinoic acid, streptozocin, tafluposide, temozolomide, teniposide, tioguanine, topotecan, uramustine, valrubicin, vinblastine, vincristine, vindesine, vinorelbine, and combinations thereof. Additional examples of anti-cancer therapies are known in the art; see, e.g. the guidelines for therapy from the American Society of Clinical Oncology (ASCO), European Society for Medical Oncology (ESMO), or National Comprehensive Cancer Network (NCCN).

[809] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in NRAS, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in NRAS is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in NRAS is one or more of a RAS-targeted therapeutic, a receptor tyrosine kinase inhibitor, a Ras-Raf-MEK-ERK pathway inhibitor, a PI3K-Akt-mTOR pathway inhibitor, and a farnesyl transferase inhibitor. In some embodiments, the Ras-Raf-MEK-ERK pathway inhibitor is one or more of a BRAF inhibitor, a MEK inhibitor, and an ERK inhibitor. In some embodiments, the BRAF inhibitor is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the MEK inhibitor is one or more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-

180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, and ONC201. In some embodiments, the PI3K-Akt-mTOR pathway inhibitor is one or more of a PI3K inhibitor, an AKT inhibitor, and an mTOR inhibitor. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the AKT inhibitor is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-23573), and sirolimus (rapamycin). In some embodiments, the farnesyl transferase inhibitor is one or more of lonafarnib, tipifarnib, BMS-214662, L778123, L744832 and FTI-277. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in NRAS is a MEK inhibitor and a PI3K inhibitor. In some embodiments, the therapeutic intervention administered to the subject having a genetic

biomarker in NRAS is a MEK inhibitor and an ERK inhibitor. Other therapeutic interventions effective for treating a subject having a genetic biomarker in NRAS are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in NRAS is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in NRAS, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[810] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in CTNNB1, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in CTNNB1 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in CTNNB1 is one or more of a β-catenin inhibitor, a WNT/ β-catenin signaling inhibitor, and a spindle assembly checkpoint kinase TTK (MPS1) inhibitor. In some embodiments, the β-catenin inhibitor is one or more of PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin, sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, and iCRT14. In some embodiments, the WNT/ β-catenin signaling inhibitor is one or more of PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin, sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, iCRT14, SM04554, LGK 974, XAV939, curcumin (e.g., Meriva®), quercetin, epigallocatechin gallate

(EGCC), resveratrol, DIF, genistein, celecoxib (CELEBREX®), CWP232291, NSC668036, FJ9, BML-286 (3289-8625), IWP, IWP-1, IWP-2, JW55, G007-LK, pyrvinium, foxy-5, Wnt-5a, ipafricept (OMP-54F28), vantictumab (OMP-18R5), OTSA 101, OTSA101-DTPA-90Y, SM04690, SM04755, nutlin-3a, XAV939, IWR1, JW74, okadaic acid, tautomycin, SB239063, SB203580, adenosine diphosphate (hydroxymethyl)pyrrolidinediol (ADP-HPD), 2-[4-(4-fluorophenyl)piperazin-1-yl]-6-methylpyrimidin-4(3H)-one, PJ34, niclosamide (NICLOCIDETM), cambinol, sulindac (CLINORIL®, Aflodac), J01-017a, NSC668036, filipin, IC261, PF670462, bosutinib (BOSULIF®), PHA665752, imatinib (GLEEVEC®), ICG-001, ethacrynic acid, ethacryinic acid derivatives, pictilisib (GDC-0941), Rp-8-Br-cAMP, SDX-308, WNT974, CGX1321, ETC-1922159, AD-REIC/Dkk3, WIKI4, and windorphen. In some embodiments, the spindle assembly checkpoint kinase TTK (MPS1) inhibitor is one or more of NTRC 0066-0, CFI-402257, a (5,6-dihydro)pyrimido[4,5-e]indolizine, and BOS172722. Other therapeutic interventions effective for treating a subject having a genetic biomarker in CTNNB1 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in CTNNB1 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in CTNNB1, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[811] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in PIK3CA, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in PIK3CA is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PIK3CA is one or

more of a PI3K-alpha inhibitor, a panPI3K inhibitor, and a dual PI3K and mTOR inhibitor. In some embodiments, the PI3K alpha inhibitor is taselisib (GDC-0032, RG7604), GDC-0077, serabelisib (TAK-117, MLN1117, INK 1117), alpelisib (BYL719), and CH5132799. In some embodiments, the panPI3K inhibitor is buparlisib (BKM120), copanlisib (ALIQOPATM, BAY80-6946), sonolisib (PX-866), ZSTK474, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), AMG 511, PKI-402, wortmannin, LY294002, and WX-037. In some embodiments, the PI3K and mTOR dual inhibitor is dactolisib (NVP-BEZ235, BEZ-235), PQR309, SF1126, gedatolisib (PF-05212384, PKI-587), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), and PI-103. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PIK3CA is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. Other therapeutic interventions effective for treating a subject having a genetic biomarker in PIK3CA are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in PIK3CA is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in PIK3CA, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[812] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in FBXW7, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in FBXW7 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in FBXW7 is one or more of an mTOR inhibitor and a MCL-1 inhibitor. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-23573), and sirolimus (rapamycin). In some embodiments, the MCL-1 inhibitor is S63845,AZD5991, AMG 176, 483-LM, and MIK665. Other therapeutic interventions effective for treating a subject having a genetic biomarker in FBXW7 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in FBXW7 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in FBXW7, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[813] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in APC, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in APC is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in APC is one or more of TASIN-1 (Truncated APC

Selective INhibitor) and a WNT/ β-catenin signaling inhibitor. In some embodiments, the WNT/ β-catenin signaling inhibitor is one or more of PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin, sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, iCRT14, PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin, sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, iCRT14, SM04554, LGK 974, XAV939, curcumin (e.g., Meriva®), quercetin, epigallocatechin gallate (EGCC), resveratrol, DIF, genistein, celecoxib (CELEBREX®), CWP232291, NSC668036, FJ9, BML-286 (3289-8625), IWP, IWP-1, IWP-2, JW55, G007-LK, pyrvinium, foxy-5, Wnt-5a, ipafricept (OMP-54F28), vantictumab (OMP-18R5), OTSA 101, OTSA101-DTPA-90Y, SM04690, SM04755, nutlin-3a, XAV939, IWR1, JW74, okadaic acid, tautomycin, SB239063, SB203580, adenosine diphosphate (hydroxymethyl)pyrrolidinediol (ADP-HPD), 2-[4-(4-fluorophenyl)piperazin-1-yl]-6-methylpyrimidin-4(3H)-one, PJ34, niclosamide (NICLOCIDETM), cambinol, sulindac (CLINORIL®, Aflodac), J01-017a, NSC668036, filipin, IC261, PF670462, bosutinib (BOSULIF®), PHA665752, imatinib (GLEEVEC®), ICG-001, ethacrynic acid, ethacryinic acid derivatives, pictilisib (GDC-0941), Rp-8-Br-cAMP, SDX-308, WNT974, CGX1321, ETC-1922159, AD-REIC/Dkk3, WIKI4, and windorphen. Other therapeutic interventions effective for treating a subject having a genetic biomarker in APC are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in APC is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in APC, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[814] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in EGFR, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in EGFR is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in EGFR is one or more of an EGFR-selective inhibitor, a panHER inhibitor, and an anti-EGFR antibody. In some embodiments, the EGFR inhibitor is a covalent inhibitor. In some embodiments, the EGFR inhibitor is a non-covalent inhibitor. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in EGFR is one or more of osimertinib (AZD9291, merelectinib, TAGRISSOTM), erlotinib (TARCEVA®), gefitinib (IRESSA®), cetuximab (ERBITUX®), necitumumab (PORTRAZZATM, IMC-11F8), neratinib (HKI-272, NERLYNX®), lapatinib (TYKERB®), panitumumab (ABX-EGF, VECTIBIX®), vandetanib (CAPRELSA®), rociletinib (CO-1686), olmutinib (OLITATM, HM61713, BI-1482694), naquotinib (ASP8273), nazartinib (EGF816, NVS-816), PF-06747775, icotinib (BPI-2009H), afatinib (BIBW 2992, GILOTRIF®), dacomitinib (PF-00299804, PF-804, PF-299, PF-299804), avitinib (AC0010), AC0010MA EAI045, matuzumab (EMD-7200), nimotuzumab (h-R3, BIOMAb EGFR®), zalutumab, MDX447, depatuxizumab (humanized mAb 806, ABT-806), depatuxizumab mafodotin (ABT-414), ABT-806, mAb 806, canertinib (CI-1033), shikonin, shikonin derivatives (e.g., deoxyshikonin, isobutyrylshikonin, acetylshikonin, β,β-dimethylacrylshikonin and acetylalkannin), poziotinib (NOV120101, HM781-36B), AV-412, ibrutinib, WZ4002, brigatinib (AP26113, ALUNBRIG®), pelitinib (EKB-569), tarloxotinib (TH-4000, PR610), BPI-15086, Hemay022, ZN-e4, tesevatinib (KD019, XL647), YH25448, epitinib (HMPL-813), CK-101, MM-151, AZD3759, ZD6474, PF-06459988, varlintinib (ASLAN001, ARRY-334543), AP32788, HLX07, D-0316, AEE788, HS-10296, avitinib, GW572016, pyrotinib (SHR1258), SCT200, CPGJ602, Sym004, MAb-425, Modotuximab (TAB-H49), futuximab (992 DS), zalutumumab, KL-140, RO5083945, IMGN289, JNJ-61186372, LY3164530, Sym013, AMG 595, EGFRBi-Armed Autologous T Cells, and

EGFR CAR-T Therapy. Other therapeutic interventions effective for treating a subject having a genetic biomarker in EGFR are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in EGFR is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in EGFR, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[815] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in BRAF, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in BRAF is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in BRAF is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in BRAF is a BRAF inhibitor and a MEK inhibitor. In some embodiments, the BRAF inhibitor is vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, or LXH254 and the MEK inhibitor is trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), or hypothemycin. In some embodiments,

the therapeutic intervention administered to the subject having a genetic biomarker in BRAF is a BRAF inhibitor and an ERK inhibitor. In some embodiments, the BRAF inhibitor is vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, or LXH254 and the ERK inhibitor is FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, or ONC201. Other therapeutic interventions effective for treating a subject having a genetic biomarker in BRAF are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in BRAF is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in BRAF, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[816] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in CDNK2A, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in CDNK2A is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in CDNK2A is a CDK4/6 inhibitor. In some embodiments, the CDK4/6 inhibitor is one or more of palbociclib, ribociclib, and abemaciclib. Other therapeutic interventions effective for treating a subject having a genetic biomarker in CDNK2A are known in the art. In some

embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in CDNK2A is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in CDNK2A, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[817] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in CDKN2, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in CDKN2 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in CDKN2 is a CDK4/6 inhibitor. In some embodiments, the CDK4/6 inhibitor is one or more of palbociclib, ribociclib, and abemaciclib Other therapeutic interventions effective for treating a subject having a genetic biomarker in CDKN2 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in CDKN2 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in CDKN2, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[818] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in PTEN, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in PTEN

is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PTEN is one or more of a PI3K/AKT/mTOR signaling pathway inhibitor and a PARP inhibitor. In some embodiments, the PI3K-Akt-mTOR pathway inhibitor is one or more of a PI3K inhibitor, an AKT inhibitor, and an mTOR inhibitor. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the AKT inhibitor is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-23573), and sirolimus (rapamycin). In some embodiments, the farnesyl transferase inhibitor is one or more of lonafarnib, tipifarnib, BMS-214662, L778123, L744832 and FTI-277. In some embodiments, the PARP

inhibitor is one or more of olaparib, veliparib, iniparib, rucaparib, CEP-9722, E7016, or E7449. Other therapeutic interventions effective for treating a subject having a genetic biomarker in PTEN are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in PTEN is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in PTEN, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[819] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in FGFR2, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in FGFR2 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in FGFR2 is one or more of an anti-FGFR2 antibody, an FGFR2 selective inhibitor and a pan-FGFR inhibitor. In some embodiments, the therapeutic intervention is a covalent FGFR2 inhibitor (e.g., PRN1371, BLU9931, FIIN-4, H3B-6527, and FIIN-2). In some embodiments, the therapeutic interventions is a non-covalent FGFR2 inhibitor (e.g., AZD4547, BGJ398, Debio-1347, dovitinib, JNJ-42756493 and LY2874455). In some embodiments, the anti-FGFR2 antibody is GP369, BAY1187982, or FPA144 (bemarituzumab). In some embodiments, the therapeutic intervention is one or more of PRN1371, BLU9931, FIIN-4, H3B-6527, NVP-BGJ398, ARQ087, TAS-120, JNJ-42756493, CH5183284/Debio 1347, INCB054828, GP369, BAY1187982, or FPA144 (bemarituzumab), NVP-BGJ398, JNJ-42756493 (erdafitinib), rogaratinib (BAY1163877), FIIN-2, JNJ-42756493, LY2874455, lenvatinib (E7080), ponatinib (AP24534), regorafenib (BAY 73-4506), dovitinib (TKI258), lucitanib (E3810), cediranib (AZD2171), intedanib (BIBF 1120),

brivanib (BMS-540215), ASP5878, AZD4547, BGJ398 (infigratinib), E7090, HMPL-453, nintedanib (OFEV®, BIBF 1120), MAX-40279, XL999, orantinib (SU6668), pazopanib (VOTRIENT®), anlotinib, AL3818. Other therapeutic interventions effective for treating a subject having a genetic biomarker in FGFR2 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in FGFR2 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in FGFR2, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[820] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in HRAS, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in HRAS is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in HRAS is one or more of a RAS-targeted therapeutic, a receptor tyrosine kinase inhibitor, a Ras-Raf-MEK-ERK pathway inhibitor, a PI3K-Akt-mTOR pathway inhibitor, and a farnesyl transferase inhibitor. In some embodiments, the Ras-Raf-MEK-ERK pathway inhibitor is one or more of a BRAF inhibitor, a MEK inhibitor, and an ERK inhibitor. In some embodiments, the BRAF inhibitor is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the MEK inhibitor is one or more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390,

TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, and ONC201. In some embodiments, the PI3K-Akt-mTOR pathway inhibitor is one or more of a PI3K inhibitor, an AKT inhibitor, and a mTOR inhibitor. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the AKT inhibitor is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-23573), and sirolimus (rapamycin). In some embodiments, the farnesyl transferase inhibitor is one or more of lonafarnib, tipifarnib, BMS-214662, L778123, L744832 and FTI-277. In

some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in HRAS is a MEK inhibitor and a PI3K inhibitor. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in HRAS is a MEK inhibitor and an ERK inhibitor. Other therapeutic interventions effective for treating a subject having a genetic biomarker in HRAS are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in HRAS is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in HRAS, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[821] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in KRAS, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in KRAS is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in KRAS is one or more of a RAS-targeted therapeutic, a receptor tyrosine kinase inhibitor, a Ras-Raf-MEK-ERK pathway inhibitor, a PI3K-Akt-mTOR pathway inhibitor, and a farnesyl transferase inhibitor. In some embodiments, the RAS-targeted therapeutic is one or more of SML-10-70-4 and AA12. In some embodiments, the Ras-Raf-MEK-ERK pathway inhibitor is one or more of a BRAF inhibitor, a MEK inhibitor, and an ERK inhibitor. In some embodiments, the BRAF inhibitor is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the MEK inhibitor is one or

more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, and ONC201. In some embodiments, the PI3K-Akt-mTOR pathway inhibitor is one or more of a PI3K inhibitor, an AKT inhibitor, and a mTOR inhibitor. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the AKT inhibitor is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-

23573), and sirolimus (rapamycin). In some embodiments, the farnesyl transferase inhibitor is one or more of lonafarnib, tipifarnib, BMS-214662, L778123, L744832 and FTI-277. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in KRAS is a MEK inhibitor and a PI3K inhibitor. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in KRAS is a MEK inhibitor and an ERK inhibitor. Other therapeutic interventions effective for treating a subject having a genetic biomarker in KRAS are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in KRAS is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in KRAS, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[822] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in AKT1, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in AKT1 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in AKT1 is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-

vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. Other therapeutic interventions effective for treating a subject having a genetic biomarker in AKT1 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in AKT1 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in AKT1, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[823] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in TP53, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in TP53 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in TP53 is one or more of p53 reactivation and induction of massive apoptosis-1 (PRIMA-1), APR-246 (PRIMA-1^{MET}), 2-sulfonylpyrimidines such as PK11007, pyrazoles such as PK7088, zinc metallochaperone-1 (ZMC1; NSC319726/ZMC 1), a thiosemicarbazone (e.g., COTI-2), CP-31398, STIMA-1 (SH Group-Targeting Compound That Induces Massive Apoptosis), MIRA-1 (NSC19630) and its analogs MIRA-2 and -3, RITA (NSC652287), Chetomin (CTM), PK7088, Stictic acid (NSC87511), p53R3, SCH529074, WR-1065, Hsp90 inhibitors (e.g., 17-AAG, geldanamycin, ganetespib, AUY922, IPI-504), HDAC inhibitors (e.g., vorinostat/SAHA, romidepsin/depsipeptide, HBI-8000), arsenic compounds, gambogic acid, spautin-1, YK-3-237, NSC59984, disulfiram (DSF), gentamicin, G418, and amikamicin, reactivate transcriptional activity (RETRA), PD0166285, inhibitors of MDM2 (e.g., RG7112 (RO5045337), RO5503781, MI-773 (SAR405838), DS-3032b, AM-8553, AMG 232, MI-219, MI-713, MI-888, TDP521252, NSC279287, PXN822, SAH-8 (stapled peptides), ATSP-7041, spiroligomer, PK083,

PK5174, PK5196, PK7088, nutlin 3a, RG7388, Ro-2443, stictic acid, and NSC319726), and inhibitors of MDM4. Other therapeutic interventions effective for treating a subject having a genetic biomarker in TP53 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in TP53 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in TP53, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[824] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in PPP2R1A, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in PPP2R1A is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PPP2R1A is one or more of activators of PP2A such as SET inhibitors (e.g., FTY-720, ceramide, and OP449). Other therapeutic interventions effective for treating a subject having a genetic biomarker in PPP2R1A are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in PPP2R1A is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in PPP2R1A, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[825] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in GNAS, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in GNAS is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in GNAS is one or more of a Ras-Raf-MEK-ERK pathway inhibitor and a WNT/ β-catenin signaling inhibitor. In some embodiments, the Ras-Raf-MEK-ERK pathway inhibitor is one or more of a BRAF inhibitor, a MEK inhibitor, and an ERK inhibitor. In some embodiments, the BRAF inhibitor is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the MEK inhibitor is one or more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, and ONC201. In some embodiments, the WNT/ β-catenin signaling inhibitor is one or more of PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin, sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, iCRT14, PRI-724, CWP232291, PNU74654, 2,4 diamino-quinazoline, PKF115-584, PKF118-744, PKF118-310, PFK222-815, CGP 049090, ZTM000990, BC21, vitamin D, retinoid acid, aspirin,

sulindac (CLINORIL®, Aflodac), 2,4 diamino-quinazoline derivatives, methyl 3-{[(4-methylphenyl)sulfonyl]amino}benzoate (MSAB), AV65, iCRT3, iCRT5, iCRT14, SM04554, LGK 974, XAV939, curcumin (e.g., Meriva®), quercetin, epigallocatechin gallate (EGCC), resveratrol, DIF, genistein, celecoxib (CELEBREX®), CWP232291, NSC668036, FJ9, BML-286 (3289-8625), IWP, IWP-1, IWP-2, JW55, G007-LK, pyrvinium, foxy-5, Wnt-5a, ipafricept (OMP-54F28), vantictumab (OMP-18R5), OTSA 101, OTSA101-DTPA-90Y, SM04690, SM04755, nutlin-3a, XAV939, IWR1, JW74, okadaic acid, tautomycin, SB239063, SB203580, adenosine diphosphate (hydroxymethyl)pyrrolidinediol (ADP-HPD), 2-[4-(4-fluorophenyl)piperazin-1-yl]-6-methylpyrimidin-4(3H)-one, PJ34, niclosamide (NICLOCIDETM), cambinol, sulindac (CLINORIL®, Aflodac), J01-017a, NSC668036, filipin, IC261, PF670462, bosutinib (BOSULIF®), PHA665752, imatinib (GLEEVEC®), ICG-001, ethacrynic acid, ethacryinic acid derivatives, pictilisib (GDC-0941), Rp-8-Br-cAMP, SDX-308, WNT974, CGX1321, ETC-1922159, AD-REIC/Dkk3, WIKI4, and windorphen. Other therapeutic interventions effective for treating a subject having a genetic biomarker in GNAS are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in GNAS is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in GNAS, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[826] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in SMAD4, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in SMAD4 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic

intervention administered to the subject having a genetic biomarker in SMAD4 is one or more of a PI3K inhibitor, antiangiogenic therapy, and 5-FU-based chemotherapy. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the antiangiogenic therapy is an inhibitor of one or more of VEGFR1, VEGFR, VEGFR2, VEGFA, CDH5, EDNRA, ANGPT2, CD34, and ANGPT. In some embodiments, the antiangiogenic therapy is one or more of vatalanib (PTK787/ZK222584), TKI-538, sunitinib (SU11248, SUTENT®), pazopanib (VOTRIENT®), bevacizumab (AVASTIN®), thalidomide, lenalidomide (REVLIMID®), ranibizumab, EYE001, and axitinib (AG013736, INLYTA®). Other therapeutic interventions effective for treating a subject having a genetic biomarker in SMAD4 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in SMAD4 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in SMAD4, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[827] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in POLE, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in POLE

is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in POLE is one or more of immunotherapy and an immune checkpoint inhibitor. Other therapeutic interventions effective for treating a subject having a genetic biomarker in POLE are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in POLE is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in POLE, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[828] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in RNF43, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in RNF43 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in RNF43 is one or more of autologous RNF43 peptide-pulsed dendritic cells (DCs), RNF43 peptide-pulsed DCs, systemic low dose interleukin-2, and PORCN inhibitors. In some embodiments, the PORCN inhibitor is one or more of RXC0004, ETC-1922159, ETC-159, IWP-2, LGK974, and WNT-C59. Other therapeutic interventions effective for treating a subject having a genetic biomarker in RNF43 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in RNF43 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a

subject having a genetic biomarker in RNF43, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[829] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in MAPK1, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in MAPK1 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in MAPK1 is one or more of an ERK inhibitor, a MEK inhibitor, an ERBB-receptor inhibitor (e.g., an EGFR inhibitor or a HER2 inhibitor), or PI3K-Akt-mTOR pathway inhibitor. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, ONC201. In some embodiments, the MEK inhibitor is one or more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162), selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the PI3K-Akt-mTOR pathway inhibitor is one or more of a PI3K inhibitor, an AKT inhibitor, and an mTOR inhibitor. In some embodiments, the PI3K inhibitor is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-

05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the AKT inhibitor is one or more of miltefosine (IMPADIVO®), wortmannin, NL-71-101, H-89, GSK690693, CCT128930, AZD5363, ipatasertib (GDC-0068, RG7440), A-674563, A-443654, AT7867, AT13148, uprosertib, afuresertib, DC120, 2-[4-(2-aminoprop-2-yl)phenyl]-3-phenylquinoxaline, MK-2206, edelfosine, miltefosine, perifosine, erucylphophocholine, erufosine, SR13668, OSU-A9, PH-316, PHT-427, PIT-1, DM-PIT-1, triciribine (Triciribine Phosphate Monohydrate), API-1, N-(4-(5-(3-acetamidophenyl)-2-(2-aminopyridin-3-yl)-3H-imidazo[4,5-b] pyridin-3-yl)benzyl)-3-fluorobenzamide, ARQ092, BAY 1125976, 3-oxo-tirucallic acid, lactoquinomycin, boc-Phe-vinyl ketone, Perifosine (D-21266), TCN, TCN-P, GSK2141795, and ONC201. In some embodiments, the mTOR inhibitor is one or more of MLN0128, AZD-2014, CC-223, AZD2014, CC-115, everolimus (RAD001), temsirolimus (CCI-779), ridaforolimus (AP-23573), and sirolimus (rapamycin). In some embodiments, the HER2 inhibitor is one or more of AZD8931, AST1306, AEE788, CP724714, CUDC101, TAK285, dacomitinib, pelitinib, AC480, trastuzumab (HERCEPTIN®), pertuzumab (PERJETA®), trastuzumab-dkst (OGIVRI®), DXL-702, E-75, PX-104.1, ZW25, CP-724714, irbinitinib (ARRY-380, ONT-380), TAS0728, lapatinib (TYKERB®, TYVERB®), AST-1306, AEE-788, perlitinib (EKB-569), afatinib (BIBW 2992, GILOTRIF®), neratinib (HKI-272, NERLYNX®, PKI-166, D-69491, HKI-357, AP32788, GW572016, canertinib (CI-1033), AC-480 (BMS-599626), dacomitinib (PF299804, PF299), RB-200h, ARRY-334543 (ARRY-543, ASLAN001), poziotinib (NOV120101), CUDC-101, emodin, IDM-1, ado-trastuzumab emtansine (KADCYLA®), Zemab, DS-8201a, T-DM1, anti-HER2 CAR-T therapy, HER2-Peptid-Vakzine, and HER2Bi-Armed Activated T Cells. In some embodiments, the EGFR inhibitor is osimertinib (AZD9291, merelectinib, TAGRISSOTM), erlotinib (TARCEVA®), gefitinib (IRESSA®), cetuximab (ERBITUX®), necitumumab (PORTRAZZATM, IMC-11F8), neratinib (HKI-272, NERLYNX®), lapatinib (TYKERB®), panitumumab (ABX-EGF,

VECTIBIX®), vandetanib (CAPRELSA®), rociletinib (CO-1686), olmutinib (OLITATM, HM61713, BI-1482694), naquotinib (ASP8273), nazartinib (EGF816, NVS-816), PF-06747775, icotinib (BPI-2009H), afatinib (BIBW 2992, GILOTRIF®), dacomitinib (PF-00299804, PF-804, PF-299, PF-299804), avitinib (AC0010), AC0010MA EAI045, matuzumab (EMD-7200), nimotuzumab (h-R3, BIOMAb EGFR®), zalutumab, MDX447, depatuxizumab (humanized mAb 806, ABT-806), depatuxizumab mafodotin (ABT-414), ABT-806, mAb 806, canertinib (CI-1033), shikonin, shikonin derivatives (e.g., deoxyshikonin, isobutyrylshikonin, acetylshikonin, β,β-dimethylacrylshikonin and acetylalkannin), poziotinib (NOV120101, HM781-36B), AV-412, ibrutinib, WZ4002, brigatinib (AP26113, ALUNBRIG®), pelitinib (EKB-569), tarloxotinib (TH-4000, PR610), BPI-15086, Hemay022, ZN-e4, tesevatinib (KD019, XL647), YH25448, epitinib (HMPL-813), CK-101, MM-151, AZD3759, ZD6474, PF-06459988, varlintinib (ASLAN001, ARRY-334543), AP32788, HLX07, D-0316, AEE788, HS-10296, avitinib, GW572016, pyrotinib (SHR1258), SCT200, CPGJ602, Sym004, MAb-425, Modotuximab (TAB-H49), futuximab (992 DS), zalutumumab, KL-140, RO5083945, IMGN289, JNJ-61186372, LY3164530, Sym013, AMG 595, EGFRBi-Armed Autologous T Cells, and EGFR CAR-T Therapy. Other therapeutic interventions effective for treating a subject having a genetic biomarker in MAPK1 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in MAPK1 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in MAPK1, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[830] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in PI3KR1, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in PI3KR1 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either

alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PI3KR1 is one or more of one or more of a panPI3K inhibitor, a dual PI3K and mTOR inhibitor, and a Ras-Raf-MEK-ERK pathway inhibitor. In some embodiments, the panPI3K inhibitor is buparlisib (BKM120), copanlisib (ALIQOPATM, BAY80-6946), sonolisib (PX-866), ZSTK474, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), AMG 511, PKI-402, wortmannin, LY294002, and WX-037. In some embodiments, the PI3K and mTOR dual inhibitor is dactolisib (NVP-BEZ235, BEZ-235), PQR309, SF1126, gedatolisib (PF-05212384, PKI-587), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), and PI-103. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in PIK3CA is one or more of buparlisib (BKM120), alpelisib (BYL719), WX-037, copanlisib (ALIQOPATM, BAY80-6946), dactolisib (NVP-BEZ235, BEZ-235), taselisib (GDC-0032, RG7604), sonolisib (PX-866), CUDC-907, PQR309, ZSTK474, SF1126, AZD8835, GDC-0077, ASN003, pictilisib (GDC-0941), pilaralisib (XL147, SAR245408), gedatolisib (PF-05212384, PKI-587), serabelisib (TAK-117, MLN1117, INK 1117), BGT-226 (NVP-BGT226), PF-04691502, apitolisib (GDC-0980), omipalisib (GSK2126458, GSK458), voxtalisib (XL756, SAR245409), AMG 511, CH5132799, GSK1059615, GDC-0084 (RG7666), VS-5584 (SB2343), PKI-402, wortmannin, LY294002, PI-103, rigosertib, XL-765, LY2023414, SAR260301, KIN-193 (AZD-6428), GS-9820, AMG319, and GSK2636771. In some embodiments, the Ras-Raf-MEK-ERK pathway inhibitor is one or more of a BRAF inhibitor, a MEK inhibitor, and an ERK inhibitor. In some embodiments, the BRAF inhibitor is one or more of vemurafenib (ZELBORAF®), dabrafenib (TAFINLAR®), and encorafenib (BRAFTOVITM), BMS-908662 (XL281), sorafenib, LGX818, PLX3603, RAF265, RO5185426, GSK2118436, ARQ 736, GDC-0879, PLX-4720, AZ304, PLX-8394, HM95573, RO5126766, and LXH254. In some embodiments, the MEK inhibitor is one or more of trametinib (MEKINIST®, GSK1120212), cobimetinib (COTELLIC®), binimetinib (MEKTOVI®, MEK162),

selumetinib (AZD6244), PD0325901, MSC1936369B, SHR7390, TAK-733, RO5126766, CS3006, WX-554, PD98059, CI1040 (PD184352), and hypothemycin. In some embodiments, the ERK inhibitor is one or more of FRI-20 (ON-01060), VTX-11e, 25-OH-D3-3-BE (B3CD, bromoacetoxycalcidiol), FR-180204, AEZ-131 (AEZS-131), AEZS-136, AZ-13767370, BL-EI-001, LY-3214996, LTT-462, KO-947, KO-947, MK-8353 (SCH900353), SCH772984, ulixertinib (BVD-523), CC-90003, GDC-0994 (RG-7482), ASN007, FR148083, 5-7-Oxozeaenol, 5-iodotubercidin, GDC0994, and ONC201. Other therapeutic interventions effective for treating a subject having a genetic biomarker in PI3KR1 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in PI3KR1 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in PI3KR1, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[831] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in FGFR3, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in FGFR3 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in FGFR3 is one or more of an anti-FGFR3 antibody, an FGFR3 selective inhibitor and a pan-FGFR inhibitor. In some embodiments, the therapeutic intervention is a covalent FGFR inhibitor (e.g., PRN1371, BLU9931, FIIN-4, H3B-6527, and FIIN-2). In some embodiments, the therapeutic interventions is a non-covalent FGFR inhibitor (e.g., AZD4547, BGJ398, Debio-1347, dovitinib, JNJ-42756493 and LY2874455). In some embodiments, the anti-FGFR3 antibody is), MFGR1877S or B-701. In some

embodiments, the therapeutic intervention is one or more of MFGR1877S, B-701, FP-1039 (GSK230), NVP-BGJ398, JNJ-42756493 (erdafitinib), rogaratinib (BAY1163877), FIIN-2, JNJ-42756493, LY2874455, lenvatinib (E7080), ponatinib (AP24534), regorafenib (BAY 73-4506), dovitinib (TKI258), lucitanib (E3810), cediranib (AZD2171), intedanib (BIBF 1120), brivanib (BMS-540215), ASP5878, AZD4547, BGJ398 (infigratinib), Debio-1347, dovitinib, E7090, HMPL-453, nintedanib (OFEV®, BIBF 1120), MAX-40279, XL999, orantinib (SU6668), pazopanib (VOTRIENT®), anlotinib, and AL3818. Other therapeutic interventions effective for treating a subject having a genetic biomarker in FGFR3 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in FGFR3 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in FGFR3, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[832] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in ERBB2, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in ERBB2 is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in ERBB2 is one or more of an anti-ERBB2 antibody, a selective ERBB2 inhibitor, and a pan-ERBB inhibitor. In some embodiments, the therapeutic intervention is a covalent ERBB2 inhibitor. In some embodiments, the therapeutic intervention is a non-covalent ERBB2 inhibitor. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in ERBB2 is one or more of AZD8931, AST1306, AEE788, CP724714, CUDC101, TAK285, dacomitinib, pelitinib, AC480, trastuzumab (HERCEPTIN®), pertuzumab (PERJETA®), trastuzumab-

dkst (OGIVRI®), DXL-702, E-75, PX-104.1, ZW25, CP-724714, irbinitinib (ARRY-380, ONT-380), TAS0728, lapatinib (TYKERB®, TYVERB®), AST-1306, AEE-788, perlitinib (EKB-569), afatinib (BIBW 2992, GILOTRIF®), neratinib (HKI-272, NERLYNX®, PKI-166, D-69491, HKI-357, AP32788, GW572016, canertinib (CI-1033), AC-480 (BMS-599626), dacomitinib (PF299804, PF299), RB-200h, ARRY-334543 (ARRY-543, ASLAN001), poziotinib (NOV120101), CUDC-101, emodin, IDM-1, ado-trastuzumab emtansine (KADCYLA®), Zemab, DS-8201a, T-DM1, anti-HER2 CAR-T therapy, HER2-Peptid-Vakzine, and HER2Bi-Armed Activated T Cells. Other therapeutic interventions effective for treating a subject having a genetic biomarker in ERBB2 are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in ERBB2 is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in ERBB2, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[833] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in MLL, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in MLL is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in MLL is one or more of cytosine arabinoside, all-*trans* retinoic acid (ATRA), an HDAC inhibitor (e.g., valproic acid and HBI-8000), a DNA methyltransferase inhibitor (e.g,. decitabine), an LSD1 inhibitor (e.g., ORY1001 (RG6016), ORY1001 (RG6016), GSK2879552, GSK2879552, INCB059872, IMG7289, and CC90011), menin 1 inhibitors (e.g., MI1, MI2, MI3, Mi2-2 (MI-2-2), MI463, MI503, MIV-6R), DOLT1 (histone–lysine KMT) inhibitors (e.g,. EPZ004777, EPZ-5676, SGC0946, CN-SAH, SYC-

522, SAH, and SYC-534), and WDR5-MLL antagonists (e.g., MM-101, MM-102, MM-103, MM-401, WDR5-0101, WDR5-0102, WDR5-0103, and OICR-9429). Other therapeutic interventions effective for treating a subject having a genetic biomarker in MLL are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in MLL is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in MLL, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[834] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in MET, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in MET is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in MET is a MET inhibitor, an HGF antagonist, an anti-HGF antibody (e.g., rilotumumab (AMG102), ficlatuzumab (AV-299), and TAK701, YYB101), and a multikinase inhibitor (e.g., tivantinib (ARQ 197), golvatinib (E7050), cabozantinib (XL 184, BMS-907351), foretinib (GSK1363089), crizotinib (PF-02341066), MK-2461, BPI-9016M, BPI-9016M, TQ-B3139, MGCD265, and MK-8033). In some embodiments, the MET inhibitor is one or more of capmatinib (INC280, INCB28060), onartuzumab (MetMAb), Savolitinib, tepotinib (MSC2156119J, EMD1214063), CE-35562, AMG-337, AMG-458, Foretinib, PHA-665725, MK-2461, PF-04217903 and SU11274, SU11274 and PHA-665752, SAIT301, HS-10241, ARGX-111, MSC2156119J, glumetinib (SCC244), EMD 1204831, AZD6094 (savolitinib, volitinib, HMPL-504), PLB1001, ABT-700, AMG 208, INCB028060, AL2846, and PF-04217903. In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in MET is

one or more of capmatinib (INC280, INCB28060), onartuzumab (MetMAb), Savolitinib, tepotinib (MSC2156119J, EMD1214063), CE-35562, AMG-337, AMG-458, Foretinib, PHA-665725, MK-2461, PF-04217903 and SU11274, SU11274 and PHA-665752, SAIT301, HS-10241, ARGX-111, MSC2156119J, glumetinib (SCC244), EMD 1204831, AZD6094 (savolitinib, volitinib, HMPL-504), PLB1001, ABT-700, AMG 208, INCB028060, AL2846, PF-04217903, rilotumumab (AMG102), ficlatuzumab (AV-299), and TAK701, YYB101, tivantinib (ARQ 197), Golvatinib (E7050), Cabozantinib (XL 184, BMS-907351), Foretinib (GSK1363089), Crizotinib (PF-02341066), MK-2461, BPI-9016M, BPI-9016M, TQ-B3139, MGCD265, MK-8033, ABBV-399, HTI-1066, and JNJ-61186372. Other therapeutic interventions effective for treating a subject having a genetic biomarker in MET are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in MET is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in MET, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[835] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in VHL, the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in VHL is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in VHL is one or more of an antiangiogenic therapy (e.g., inhibitors of one or more of VEGFR1, VEGFR, VEGFR2, VEGFA, CDH5, EDNRA, ANGPT2, CD34, and ANGPT) vatalanib (PTK787/ZK222584), TKI-538, sunitinib (SU11248, SUTENT®), pazopanib (VOTRIENT®), bevacizumab (AVASTIN®), thalidomide, lenalidomide (REVLIMID®), ranibizumab, EYE001, axitinib (AG013736,

INLYTA®), a c-KIT inhibitor (e.g., dovitinib (TKI258)), an HDAC inhibitor (e.g., vorinostat and HBI-8000), a HIF-2alpha inhibitor (e.g., PT2385 and PT2977), a Hsp90 inhibitor (e.g., 17 allylamino-17-demethoxygeldanamycin, AUY922, and IPI-504), and growth factor and receptor inhibitors (e.g, E10030). Other therapeutic interventions effective for treating a subject having a genetic biomarker in VHL are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in VHL is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in VHL, the number of cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[836] In some embodiments, when a subject is identified as having a genetic biomarker (e.g., a mutation) in TERT (e.g., in a TERT promoter), the subject is administered a therapeutic intervention. In some embodiments, a subject identified as having a genetic biomarker (e.g., a mutation) in TERT (e.g., in a TERT promoter) is identified as having a cancer (e.g., based on the presence of the genetic biomarker, either alone or in combination with the presence of other genetic biomarkers and/or the presence of one or more members of other classes of biomarkers and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject having a genetic biomarker in TERT (e.g., in a TERT promoter) is one or more of eribulin, an hTERT mRNA transfected dendritic cell vaccine (e.g., AST-VAC1 (hTERT-DC, GRNVAC1)), INO-1400, INO-1401, GX301, dendritic cells transfected with hTERT-, survivin- and tumor cell derived mRNA, and arsenic trioxide. Other therapeutic interventions effective for treating a subject having a genetic biomarker in TERT (e.g., in a TERT promoter) are known in the art. In some embodiments, a therapeutic intervention administered to the subject having a genetic biomarker in TERT (e.g., in a TERT promoter) is effective in treating a cancer in the subject. For example, after administration of a therapeutic intervention that is effective in treating a subject having a genetic biomarker in TERT (e.g., in a TERT promoter), the number of

cancer cells in the subject can be reduced, the size of one or more tumors in the subject can be reduced, the rate or extent of metastasis can be reduced, symptoms associated with the disease or disorder or condition can be wholly or partly alleviated, the state of the disease can be stabilized (i.e., not worsened), and/or survival can be prolonged as compared to expected survival if not receiving treatment.

[837] In some embodiments, when a subject is identified as being at risk (e.g., increased risk) of developing a disease (e.g., using any of the variety of methods described herein), the subject is administered a therapeutic intervention. In some embodiments, a subject identified as being at risk (e.g., increased risk) of developing a disease (e.g., using any of the variety of methods described herein) is identified as being at risk of developing cancer (e.g., based on the presence of one or more genetic biomarkers, the presence of one or more protein biomarkers, the presence of one or more other biomarkers, and/or the presence of aneuploidy as described herein). In some embodiments, the therapeutic intervention administered to the subject identified as being at risk of developing cancer is a chemopreventive. Non-limiting examples of chemopreventives include a non-steroidal anti-inflammatory drug (e.g., aspirin, tolfenamic acid, indomethacin, celecoxib, sulindac sulfide, diclofenac, indomethacin, ibuprofen, flurbiprofen, piroxicam, diflunisal, etodolac, ketoprofen, ketorolac, nabumetone, naproxen, oxaprozin, salsalate, and tolmetin), a selective estrogen receptor modulator (e.g., tamoxifen (NOLVADEX®, SOLTAMOX™) and raloxifene (EVISTA®)), instillational BCG, valrubicin, finasteride, dutasteride, curcumin, bisdemethoxycurcumin, metformin, an aromatase inhibitor (e.g., exemestane), resveratrol, lunasin, vitamin A, isothiocyanate, green tea, luteolin, genistein, lycopene, bitter melon, withaferin A, guggulsterone, selenides, diselenides, crocetin, piperine, a statin (a 3-hydroxy-3-methylglutaryl coenzyme A reductase inhibitor), a carotenoid, vitamin A, a retinoid, folic acid, vitamin C, vitamin D, vitamin E, calcium, a flavonoid, and an anti-cancer vaccine. In some embodiments, tamoxifen and/or raloxifene is administered to a subject identified as being at risk of developing breast cancer. In some embodiments, instillational BCG and/or valrubicin is administered to a subject identified as being at risk of developing bladder cancer. In some embodiments, finasteride and/or dutasteride is administered to a subject identified as being at risk of developing

prostate cancer. In some embodiments, celecoxib is administered to a subject identified as being at risk of developing colorectal neoplasia.

[838] In some embodiments, the therapeutic intervention can result in an early onset of remission of a cancer in a subject. In some embodiments, the therapeutic intervention can result in an increase in the time of remission of a cancer in a subject. In some embodiments, the therapeutic intervention can result in an increase in the time of survival of a subject. In some embodiments, the therapeutic intervention can result in decreasing the size of a solid primary tumor in a subject. In some embodiments, the therapeutic intervention can result in decreasing the volume of a solid primary tumor in a subject. In some embodiments, the therapeutic intervention can result in decreasing the size of a metastasis in a subject. In some embodiments, the therapeutic intervention can result in decreasing the volume of a metastasis in a subject. In some embodiments, the therapeutic intervention can result in decreasing the tumor burden in a subject.

[839] In some embodiments, the therapeutic intervention can result in improving the prognosis of a subject. In some embodiments, the therapeutic intervention can result in decreasing the risk of developing a metastasis in a subject. In some embodiments, the therapeutic intervention can result in decreasing the risk of developing an additional metastasis in a subject. In some embodiments, the therapeutic intervention can result in decreasing cancer cell migration in a subject. In some embodiments, the therapeutic intervention can result in decreasing cancer cell invasion in a subject. In some embodiments, the therapeutic intervention can result in a decrease in the time of hospitalization of a subject. In some embodiments, the therapeutic intervention can result in a decrease of the presence of cancer stem cells within a tumor in a subject.

[840] In some embodiments, the therapeutic intervention can result in an increase in immune cell infiltration within the tumor microenvironment in a subject. In some embodiments, the therapeutic intervention can result in altering the immune cell composition within the tumor microenvironment of a tumor in a subject. In some embodiments, the therapeutic intervention can result in modulating a previously immunosuppressive tumor microenvironment into an immunogenic, inflammatory tumor microenvironment. In some

embodiments, the therapeutic intervention can result in a reversal of the immunosuppressive tumor microenvironment in a subject.

[841] In some embodiments, the therapeutic intervention can halt tumor progression in a subject. In some embodiments, the therapeutic intervention can delay tumor progression in a subject. In some embodiments, the therapeutic intervention can inhibit tumor progression in a subject. In some embodiments, the therapeutic intervention can inhibit immune checkpoint pathways of a tumor in a subject. In some embodiments, the therapeutic intervention can immuno-modulate the tumor microenvironment of a tumor in a subject. In some embodiments, the therapeutic intervention can immuno-modulate the tumor macroenvironment of a tumor in a subject.

[842] In some embodiments, a therapeutic intervention can reduce the number of cancer cells present in a subject. For example, a therapeutic intervention can reduce the number of cancer cells present in a subject by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or more. In some embodiments, a therapeutic intervention can reduce the number of cancer cells present in a subject such that no cancer cells are observable. In some embodiments, a therapeutic intervention can reduce the observable tumors present in a subject.

[843] In some embodiments, one or more therapeutic interventions (e.g., a chemotherapy or any of the other appropriate therapeutic interventions discloses herein) can be administered to a subject once or multiple times over a period of time ranging from days to weeks. In some embodiments, one or more therapeutic interventions can be formulated into a pharmaceutically acceptable composition for administration to a subject having cancer. For example, a therapeutically effective amount of a therapeutic intervention (e.g. a chemotherapeutic or immunotherapeutic agent) can be formulated together with one or more pharmaceutically acceptable carriers (additives) and/or diluents. A pharmaceutical composition can be formulated for administration in solid or liquid form including, without limitation, sterile solutions, suspensions, sustained-release formulations, tablets, capsules, pills, powders, and granules.

[844] Pharmaceutically acceptable carriers, fillers, and vehicles that may be used in a pharmaceutical composition described herein include, without limitation, ion exchangers,

alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat.

[845] A pharmaceutical composition containing one or more therapeutic interventions can be designed for oral or parenteral (including subcutaneous, intramuscular, intravenous, and intradermal) administration. When being administered orally, a pharmaceutical composition can be in the form of a pill, tablet, or capsule. Compositions suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that can contain anti-oxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient. The formulations can be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials, and may be stored in a freeze dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules, and tablets.

[846] In some embodiments, a pharmaceutically acceptable composition including one or more therapeutic interventions can be administered locally or systemically. For example, a composition provided herein can be administered locally by injection into tumors. In some embodiments, a composition provided herein can be administered systemically, orally, or by injection to a subject (e.g., a human).

[847] Effective doses can vary depending on the severity of the cancer, the route of administration, the age and general health condition of the subject, excipient usage, the possibility of co-usage with other therapeutic treatments such as use of other agents, and the judgment of the treating physician.

[848] An effective amount of a composition containing one or more therapeutic interventions can be any amount that reduces the number of cancer cells present within the subject without producing significant toxicity to the subject. If a particular subject fails to

respond to a particular amount, then the amount of a therapeutic intervention can be increased by, for example, two fold. After receiving this higher amount, the subject can be monitored for both responsiveness to the treatment and toxicity symptoms, and adjustments made accordingly. The effective amount can remain constant or can be adjusted as a sliding scale or variable dose depending on the subject response to treatment. Various factors can influence the actual effective amount used for a particular application. For example, the frequency of administration, duration of treatment, use of multiple treatment agents, route of administration, and severity of the condition (e.g., cancer) may require an increase or decrease in the actual effective amount administered.

[849] The frequency of administration of one or more therapeutic interventions can be any amount that reduces the number of cancer cells present within the subject without producing significant toxicity to the subject. For example, the frequency of administration of one or more therapeutic interventions can be from about two to about three times a week to about two to about three times a month. The frequency of administration of one or more therapeutic interventions can remain constant or can be variable during the duration of treatment. A course of treatment with a composition containing one or more therapeutic interventions can include rest periods. For example, a composition containing one or more therapeutic interventions can be administered daily over a two-week period followed by a two week rest period, and such a regimen can be repeated multiple times. As with the effective amount, various factors can influence the actual frequency of administration used for a particular application. For example, the effective amount, duration of treatment, use of multiple treatment agents, route of administration, and severity of the condition (e.g., cancer) may require an increase or decrease in administration frequency.

[850] An effective duration for administering a composition containing one or more therapeutic interventions can be any duration that reduces the number of cancer cells present within the subject without producing significant toxicity to the subject. In some embodiments, the effective duration can vary from several days to several weeks. In general, the effective duration for reducing the number of cancer cells present within the subject can range in duration from about one week to about four weeks. Multiple factors can influence the actual effective duration used for a particular treatment. For example, an effective

duration can vary with the frequency of administration, effective amount, use of multiple treatment agents, route of administration, and severity of the condition being treated.

Exemplary Embodiments

[851] In some embodiments, provided herein are methods of detecting biomarkers, which methods include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject. In some embodiments of methods of detecting biomarkers, the methods further include detecting the presence of aneuploidy in the sample obtained from the subject. In some embodiments of methods of detecting biomarkers, the first class of biomarkers includes genetic biomarkers. In some embodiments of methods of detecting biomarkers, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of detecting biomarkers, the second class of biomarkers includes protein biomarkers. In some embodiments of methods of detecting biomarkers, members of the second class of biomarkers are associated with the presence of cancer.

[852] In some embodiments, provided herein are methods of detecting biomarkers, which methods include: detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject; detecting the presence of aneuploidy in the sample obtained from the subject. In some embodiments of methods of detecting biomarkers, the methods further include detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject. In some embodiments of methods of id detecting biomarkers, the first class of biomarkers comprises genetic biomarkers. In some embodiments of methods of detecting biomarkers, the first class of biomarkers comprises protein biomarkers. In some embodiments of methods of detecting biomarkers, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of detecting biomarkers in which the first class of biomarkers comprises protein biomarkers, the second class of biomarkers comprises genetic biomarkers. In some embodiments of methods of detecting biomarkers in which the first

class of biomarkers comprises protein biomarkers, members of the second class of biomarkers are associated with the presence of cancer.

[853] In some embodiments, provided herein are methods of identifying a subject as having cancer, which methods include: detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject; detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject; and identifying the subject as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, or both. In some embodiments of methods of identifying a subject as having cancer, the methods further include detecting the presence of aneuploidy in the sample obtained from the subject; wherein the subject is identified as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, the presence aneuploidy is detected in the sample, or combinations thereof. In some embodiments of methods of identifying a subject as having cancer, the first class of biomarkers includes genetic biomarkers. In some embodiments of methods of identifying a subject as having cancer, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of identifying a subject as having cancer, the second class of biomarkers includes protein biomarkers. In some embodiments of methods of identifying a subject as having cancer, members of the second class of biomarkers are associated with the presence of cancer.

[854] In some embodiments, provided herein are methods of identifying a subject as having cancer, which methods include: detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject; detecting the presence of aneuploidy in the sample obtained from the subject; and identifying the subject as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of aneuploidy is detected in the sample, or both. In some embodiments of methods of identifying a subject as having cancer, the methods further include detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject; wherein the subject is identified as having cancer when the

presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, the presence aneuploidy is detected in the sample, or combinations thereof. In some embodiments of methods of identifying a subject as having cancer, the first class of biomarkers comprises genetic biomarkers. In some embodiments of methods of identifying a subject as having cancer, the first class of biomarkers comprises protein biomarkers. In some embodiments of methods of identifying a subject as having cancer, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of identifying a subject as having cancer in which the first class of biomarkers comprises protein biomarkers, the second class of biomarkers comprises genetic biomarkers. In some embodiments of methods of identifying a subject as having cancer in which the first class of biomarkers comprises protein biomarkers, members of the second class of biomarkers are associated with the presence of cancer.

[855] In some embodiments of methods of identifying a subject as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject, the sensitivity of detecting the presence of cancer is increased as compared to methods which include detecting the presence of one or more members of only a single class of biomarkers. In some embodiments of methods of identifying a subject as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject, the specificity of detecting the presence of cancer is increased as compared to methods which include detecting the presence of one or more members of only a single class of biomarkers. In some embodiments of methods of identifying a subject as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of aneuploidy in the sample obtained from the subject, the sensitivity of detecting the presence of cancer is increased as compared to methods which include detecting only one or more members of the class of biomarkers or only the presence of

aneuploidy. In some embodiments of methods of identifying a subject as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of aneuploidy in the sample obtained from the subject, the specificity of detecting the presence of cancer is increased as compared to methods in which include detecting only one or more members of the class of biomarkers or only the presence of aneuploidy.

[856] In some embodiments, provided herein are methods of treating a subject identified as having cancer, which methods include: detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject; detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject; identifying the subject as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, or both; and administering to the subject a therapeutic intervention. In some embodiments of methods of treating a subject identified as having cancer, the methods further include detecting the presence of aneuploidy in the sample obtained from the subject; wherein the subject is identified as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, the presence aneuploidy is detected in the sample, or combinations thereof. In some embodiments of methods of treating a subject identified as having cancer, the first class of biomarkers includes genetic biomarkers. In some embodiments of methods of treating a subject identified as having cancer, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of treating a subject identified as having cancer, the second class of biomarkers includes protein biomarkers. In some embodiments of methods of treating a subject identified as having cancer, members of the second class of biomarkers are associated with the presence of cancer.

[857] In some embodiments, provided herein are methods of treating a subject identified as having cancer, which methods include: detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject; detecting the presence of aneuploidy in the sample obtained from the subject; identifying the subject as having cancer

when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of aneuploidy is detected in the sample, or both; and administering to the subject a therapeutic intervention. In some embodiments of methods of treating a subject identified as having cancer, the methods further include detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject; wherein the subject is identified as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, the presence aneuploidy is detected in the sample, or combinations thereof. In some embodiments of methods of treating a subject identified as having cancer, the first class of biomarkers comprises genetic biomarkers. In some embodiments of methods of treating a subject identified as having cancer, the first class of biomarkers comprises protein biomarkers. In some embodiments of methods of treating a subject identified as having cancer, members of the first class of biomarkers are associated with the presence of cancer. In some embodiments of methods of treating a subject identified as having cancer in which the first class of biomarkers comprises protein biomarkers, the second class of biomarkers comprises genetic biomarkers. In some embodiments of methods of treating a subject identified as having cancer in which the first class of biomarkers comprises protein biomarkers, members of the second class of biomarkers are associated with the presence of cancer.

[858] In some embodiments of methods of treating a subject identified as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject, the sensitivity of detecting the presence of cancer is increased as compared to methods which include detecting the presence of one or more members of only a single class of biomarkers. In some embodiments of methods of treating a subject identified as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of one or more members of a second class of biomarkers in the sample obtained from the subject, the specificity of detecting the presence of cancer is increased as compared to methods which include detecting the presence

of one or more members of only a single class of biomarkers. In some embodiments of methods of treating a subject identified as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of aneuploidy in the sample obtained from the subject, the sensitivity of detecting the presence of cancer is increased as compared to methods which include detecting only one or more members of the class of biomarkers or only the presence of aneuploidy. In some embodiments of methods of treating a subject identified as having cancer that include detecting the presence of one or more members of a first class of biomarkers in a sample obtained from the subject and detecting the presence of aneuploidy in the sample obtained from the subject, the specificity of detecting the presence of cancer is increased as compared to methods in which include detecting only one or more members of the class of biomarkers or only the presence of aneuploidy.

[859] In some embodiments of methods of treating a subject identified as having cancer, any of the variety of therapeutic interventions described herein (e.g., surgery, chemotherapy, hormone therapy, targeted therapy, radiation therapy, and combinations thereof) can be administered to the subject.

[860] In some embodiments, provided herein are methods of identifying a subject as having cancer that include: detecting the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject; detecting the presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject; and identifying the subject as having cancer when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated level of one or more peptide biomarkers is detected in said blood sample, or both. In some embodiments, provided herein are methods of treating a subject having cancer that include: detecting the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject; detecting the presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject; and administering one or more therapeutic interventions (e.g., one or more of surgery, chemotherapy, hormone therapy, targeted therapy, and radiation therapy) to said subject when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated

level of one or more peptide biomarkers is detected in said blood sample, or both. In some embodiments, provided herein are methods of identifying the location of a cancer in a subject, said method comprising: detecting the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject; detecting the presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject; and identifying the location of the cancer in the subject when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated level of one or more peptide biomarkers is detected in said blood sample, or both.

[861] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the subject is a human. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, said blood sample is a plasma sample. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, the cancer is a Stage I cancer. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, the one or more genetic biomarkers comprise one or more modifications in one or more genes. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, the one or more modifications comprise inactivating modifications, and wherein said one or more genes comprise tumor suppressor genes. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, the one or more modifications include a modification independently selected from single base substitutions, insertions, or deletions, translocations, fusions, breaks, duplications, or amplifications.

[862] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said

subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer and in which the one or more genetic biomarkers are genes, the one or more genes are one or more of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the one or more genes one or more of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS, the one or more protein biomarkers are one or more of CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, or myeloperoxidase (MPO). In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the one or more genes one or more of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS, the one or more protein biomarkers are one or more of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, or CA15-3. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the one or more genes one or more of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS, the one or more protein biomarkers are one or more of CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, or CA15-3. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the one or more genes one or more of: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS, the one or more modifications are independently selected from the modifications set forth in Table 3.

[863] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the cancer is pancreatic cancer. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the cancer is pancreatic cancer and in which the one or more genetic biomarkers are genes, the one or more genes are one or more of KRAS, TP53, CDKN2A, or SMAD4. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject in which the one or more genes one or more of: KRAS, TP53, CDKN2A, or SMAD4, the one or more protein biomarkers are one or more of CA19-9, CEA, HGF, or OPN.

[864] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the step of detecting the presence of one or more genetic biomarkers is performed using a method that includes a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments, the multiplex PCR-based sequencing assay includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products.

[865] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the step of elevated level of one or more protein biomarkers is performed using a multiplex immunoassay system.

[866] In some embodiments of identifying a subject as having cancer, the methods further include identifying a location of the cancer. In some embodiments of identifying a subject as having cancer, the methods further include administering to the subject one or more therapeutic interventions. In some embodiments, the one or more therapeutic interventions are one or more of: surgery, chemotherapy, hormone therapy, targeted therapy, or radiation therapy.

[867] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the methods further include: a) determining a mutation allele frequency in the blood sample for two or more of the genetic biomarkers; b) obtaining a score that indicates the likelihood that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers to a first reference distribution of mutation allele frequency in control samples and a second reference distribution of mutation allele frequency in samples collected from subjects having a cancer; and c) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some embodiments, obtaining the score includes calculating the ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genetic biomarkers. In some embodiments, the score is determined by calculating the weighted average of the log ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genetic biomarkers. In some embodiments, detecting the presence of one or more genetic biomarkers is performed in two or more test samples using an assay comprising: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments, the score is calculated by the following formula:

$$\Omega = \sum_{i=1} w_i * ln \frac{p_i^C}{p_i^N}$$

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wherein w_i is the number of unique identifier sequences (UIDs) in a test sample i divided by the total number of UIDs for that mutation in all test samples, pi^N is the probability of the mutation allele frequency in the first reference distribution, and pi^C is the probability of the mutation allele frequency in the second reference distribution.

[868] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the sensitivity of identifying a subject as having cancer is increased as compared to: 1) the sensitivity obtained when the presence of one or more members of only a single class of biomarkers in the sample obtained from the subject is detected. In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject, the specificity of identifying a subject as having cancer is increased as compared to: 1) the specificity obtained when the presence of one or more members of only a single class of biomarkers in the sample obtained from the subject is detected.

[869] In some embodiments of identifying a subject as having cancer, treating a subject having cancer, or identifying the location of a cancer in a subject (e.g., based on the presence of one or more genetic biomarkers in circulating DNA in a blood sample obtained from said subject and/or presence of an elevated level of one or more peptide biomarkers in the blood sample obtained from a subject), the methods further include: detecting the presence of aneuploidy in the sample obtained from the subject, wherein the subject is identified as having cancer when the presence of one or more members of the first class of biomarkers are detected in the sample, the presence of one or more members of the second class of biomarkers are detected in the sample, the presence aneuploidy is detected in the sample, or combinations thereof.

[870] In some embodiments, provided herein are method of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in a sample collected from the patient for each mutation in one or more of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, or GNAS; b) obtaining a score that indicates the likelihood that the patient has a cancer by comparing the mutation allele frequency of each mutation in the selected genes to a first reference distribution of mutation allele frequency in control samples and a second reference distribution of mutation allele frequency in samples collected from patients having a cancer; and c) identifying the patient as having a cancer when the score is higher than a reference value for the score is higher than a reference value for the score. In some embodiments, such methods further include measuring the concentration of one or more of the following proteins: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, or myeloperoxidase (MPO) and determining that the concentration of at least one protein is higher than a reference value. In some embodiments, such methods further include measuring the concentration of one or more of the following proteins: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, or CA15-3 and determining that the concentration of at least one protein is higher than a reference value. In some embodiments, such methods further include measuring the concentration of one or more of the following proteins: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, or CA15-3 and determining that the concentration of at least one protein is higher than a reference value. In some embodiments, obtaining the score comprises calculating the ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments, the score is determined by calculating the weighted average of the log ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments, the sample is assayed in two or more test samples using a method that includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c.

redundantly sequencing the amplification products. In some embodiments, the score is calculated by the following formula:

$$\Omega = \sum_{i=1} w_i * ln \frac{p_i^C}{p_i^N}$$

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wherein w_i is the number of unique identifier sequences (UIDs) in a test sample i divided by the total number of UIDs for that mutation in all test samples, pi^N is the probability of the mutation allele frequency in the first reference distribution, and pi^C is the probability of the mutation allele frequency in the second reference distribution. In some embodiments, the blood sample is a plasma sample. In some embodiments, the cancer is a Stage I cancer. In some embodiments, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments, the at least one mutation comprises an inactivating modifications, and wherein the at least one mutation is in a tumor suppressor gene. In some embodiments, the at least one mutation comprises a mutation that is a single base substitution, an insertion, or a deletion. In some embodiments, the at least one mutation is a mutation set forth in Table 3. In some embodiments, the step of detecting the level of one or more proteins is performed using a multiplex immunoassay system. In some embodiments, the methods further include identifying a location of the cancer. In some embodiments, the methods further include comprising administering to the mammal one or more therapeutic interventions. In some embodiments, the one or more therapeutic interventions are one or more of: surgery, chemotherapy, hormone therapy, targeted therapy, or radiation therapy.

[871] In some embodiments, provided herein are method of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in a sample collected from the patient for each mutation in one or more of the following genes: KRAS, TP53, CDKN2A, or SMAD4; b) obtaining a score that indicates the likelihood that the patient has a cancer by comparing the mutation allele frequency of each mutation in the selected genes to a first reference distribution of mutation allele frequency in control samples and a second reference distribution of mutation allele frequency in samples collected from patients having a cancer;

and c) identifying the patient as having a cancer when the score is higher than a reference value for the score is higher than a reference value for the score. In some embodiments, such methods further include measuring the concentration of one or more of the following proteins: CA19-9, CEA, HGF, or OPN and determining that the concentration of at least one protein is higher than a reference value. In some embodiments, obtaining the score comprises calculating the ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments, the score is determined by calculating the weighted average of the log ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments, the sample is assayed in two or more test samples using a method that includes: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments, the score is calculated by the following formula:

$$\Omega = \sum_{i=1} w_i * ln \frac{p_i^C}{p_i^N}$$

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wherein w_i is the number of unique identifier sequences (UIDs) in a test sample i divided by the total number of UIDs for that mutation in all test samples, pi^N is the probability of the mutation allele frequency in the first reference distribution, and pi^C is the probability of the mutation allele frequency in the second reference distribution. In some embodiments, the blood sample is a plasma sample. In some embodiments, the cancer is a Stage I cancer. In some embodiments, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments, the at least one mutation comprises an inactivating modifications, and wherein the at least one mutation is in a tumor suppressor gene. In some embodiments, the at least one mutation comprises a mutation that is a single base substitution, an insertion, or a

deletion. In some embodiments, the step of detecting the level of one or more proteins is performed using a multiplex immunoassay system. In some embodiments, the methods further include identifying a location of the cancer. In some embodiments, the methods further include comprising administering to the mammal one or more therapeutic interventions. In some embodiments, the one or more therapeutic interventions are one or more of: surgery, chemotherapy, hormone therapy, targeted therapy, or radiation therapy.

[872] In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value.

[873] In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS, TP53, CDKN2A, and/or SMAD4; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in

control samples for each mutation in the set of genes; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value.

[874] In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not

higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[875] In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS, TP53, CDKN2A, and/or SMAD4; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[876] In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a set of genes in a

biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[877] In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS, TP53, CDKN2A, and/or SMAD4; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each

mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[878] In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, calculating the score comprises calculating the ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the score is calculated by calculating the weighted average of the log ratio of the probability of the mutation allele frequency in the first reference distribution to the probability of the mutation allele frequency in the second reference distribution for each mutation in the selected genes. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the

computer database comprises test sample data, the test sample data includes assignment of a unique identifier (UID) to each of a plurality of template molecules present in the sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the score is calculated by the following formula:

$$\Omega = \sum_{i=1} w_i * ln \frac{p_i^C}{p_i^N}$$

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wherein w_i is the number of unique identifier sequences (UIDs) in a test sample i divided by the total number of UIDs for that mutation in all test samples, pi^N is the probability of the mutation allele frequency in the first reference distribution, and pi^C is the probability of the mutation allele frequency in the second reference distribution. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the device configured to assay a set of genes comprises a device that employs a includes a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the multiplex PCR-based sequencing assay comprises: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased

monitoring, further diagnostic testing, or both, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO). In some embodiments of systems for generating a report for a patient, systems for

generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, or 4) of: CA19-9, CEA, HGF, and/or OPN. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device

configured to assay one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS, TP53, CDKN2A, and/or SMAD4, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, or 4) of: CA19-9, CEA, HGF, and/or OPN. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the sensitivity of the system in identifying a subject as having cancer is improved as compared to conventional systems for generating a report for a patient. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the specificity of the system in identifying a subject as having cancer is improved as compared to conventional systems for generating a report for a patient. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the first and second reference distribution of mutation allele frequency values are input into the system from a location that is remote from the at least one computer database. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, first and second reference distribution of mutation allele frequency values are input into the system over an internet connection. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the report is in electronic or paper format. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a

patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the cancer is any of the variety of cancer types described herein (see, e.g., section entitled "Cancers"). In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS and at least one a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or 8) of: CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or myeloperoxidase (MPO), the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS and at least one a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and/or CA15-3, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device

configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS and at least one a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, or 9) of: CA19-9, CEA, HGF, OPN, CA125, AFP, prolactin, TIMP-1, and/or CA15-3, the cancer is liver cancer, ovary cancer, esophageal cancer, stomach cancer, pancreatic cancer, colorectal cancer, lung cancer, breast cancer, or prostate cancer. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, or 4) of the following genes: KRAS, TP53, CDKN2A, and/or SMAD4 and at least one a device (e.g., a device that includes a multiplex immunoassay system) configured to detect a level of one or more protein biomarkers in a biological sample, wherein the protein biomarkers are one or more (e.g., 1, 2, 3, or 4) of: CA19-9, CEA, HGF, and/or OPN, the cancer is pancreatic cancer. In some embodiments of systems for generating a report for a patient or systems for generating a report to identify a cancer treatment for a patient, the patient is identified as a candidate for increased monitoring, further diagnostic testing, or both (e.g. any of the variety of increased monitoring or further diagnostic methods described herein).

[879] In some embodiments, provided herein are methods of identifying a subject as having cancer that include: detecting the presence of one or more genetic biomarkers in a first sample obtained from said subject; detecting the presence of aneuploidy in a second sample obtained from said subject; and identifying the subject as having cancer when the presence of one or more genetic biomarkers is detected in the first sample, when the presence of aneuploidy is detected in the second sample, or both. In some embodiments, provided herein are methods of treating a subject having cancer that include: detecting the presence of one or more genetic biomarkers in a first sample obtained from said subject; detecting the presence of aneuploidy in a second sample obtained from said subject; and administering one or more

therapeutic interventions to said subject when the presence of one or more genetic biomarkers is detected in the first sample, when the presence of aneuploidy is detected in the second sample, or both.

[880] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the step of detecting the presence of one or more genetic biomarkers comprises a method that includes a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments, the step of detecting the presence of one or more genetic biomarkers comprises a method that increases the sensitivity of massively parallel sequencing instruments with an error reduction technique comprising: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products.

[881] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the step of detecting the presence of aneuploidy includes: amplifying long interspersed nucleotide elements (LINEs) across the genome of the second sample, thereby obtaining a plurality of amplicons; sequencing the plurality of amplicons to obtain sequencing reads; placing the sequencing reads into pre-defined clusters of genomic intervals; and determining the presence of aneuploidy in the second sample when the number of sequencing reads of a genomic region within a pre-defined cluster is significantly different from the expected number of sequencing reads of the genomic region within the pre-defined cluster. In some embodiments, the pre-defined clusters of genomic intervals are created by grouping genomic intervals based on read depths of sequencing reads of two or more euploid samples. In some embodiments, determining that the number of sequencing reads of a genomic region within a pre-defined cluster is significantly different from the expected

number of sequencing reads of the genomic region within the pre-defined cluster includes: calculating the distribution of sequencing reads of all genomic intervals in the pre-defined cluster, wherein the sequence reads of all genomic intervals in the pre-defined cluster are obtained by sequencing the amplicons derived from the second sample; and determining the number of sequencing reads of the genomic region is outside a significance threshold of the distribution. In some embodiments, determining that the number of sequencing reads of a genomic region within a pre-defined cluster is significantly different from the expected number of sequencing reads of the genomic region within the pre-defined cluster includes: calculating sums of distributions of the sequencing reads in each genomic interval using the equation $\sum_1^I R_i \sim N(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$, wherein R_i is the number of sequencing reads, I is the number of clusters on a chromosome arm, N is a Gaussian distribution with parameters μ_i and σ_i^2, where μ_i is the mean number of sequencing reads in each genomic interval, and where σ_i^2 is the variance of sequencing reads in each genomic interval; calculating a Z-score of a chromosome arm using the quantile function 1-CDF($\sum_1^I \mu_i, \sum_1^I \sigma_i^2$); and identifying the presence of an aneuploidy in the tissue of the mammal when the Z-score is outside a significance threshold.

[882] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the step of detecting the presence of aneuploidy includes: sequencing a plurality of amplicons obtained from a second sample to obtain variant sequencing reads for a plurality of polymorphic sites; selecting a chromosome arm having the variant sequencing reads and the reference sequencing reads on both alleles that is greater than about 3; determining a variant-allele frequency (VAF) of each polymorphic site in the selected chromosome arm, wherein said VAF is the number of variant sequencing reads / total number of sequencing reads; and identifying the presence of aneuploidy on the selected chromosome arm if the VAF of one or more polymorphic sites is outside a significance threshold of a normal distribution, wherein the expected VAF is 0.5. In some embodiments, the step of sequencing includes: a. assigning a unique identifier (UID) to each of a plurality of amplicons, b. amplifying each uniquely tagged amplicon to create UID-families, and c.

redundantly sequencing the amplification products. In some embodiments, the step of identifying the presence of aneuploidy on the selected chromosome arm includes: calculating a Z-score for one or more polymorphic sites on said selected chromosome arm using the equation $Z \sim \frac{\sum_{i=1}^{k} w_i Z_i}{\sqrt{\sum_{i=1}^{k} w_i^2}}$, where w_i is UID depth at a variant i, Z_i is the Z-score of VAF for variant i, and k is the number of variants observed on the chromosome arm.

[883] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the methods further include performing cytology on the first sample, the second sample, or both, and identifying the subject as having cancer when the presence of one or more genetic biomarkers is detected in the first sample, when the presence of aneuploidy is detected in the second sample, a positive cytology indicates that the subject has cancer, or combinations thereof.

[884] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the cancer is a bladder cancer or an upper tract urothelial carcinoma; the one or more genetic biomarkers are one or more of: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL; the method further includes detecting the presence of at least one genetic biomarker (e.g., a mutation) in a TERT promoter; and the presence of one or more genetic biomarkers in one or more of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, the presence of the at least one genetic biomarker (e.g., a mutation) in the TERT promoter, or the presence of aneuploidy indicates that the subject has bladder cancer. In some embodiments, the presence of one or more genetic biomarkers in one or more of TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, the presence of the at least one genetic biomarker (e.g., a mutation) in the TERT promoter, and the presence of aneuploidy indicates that the subject has bladder cancer. In some embodiments, the one or more genetic biomarkers are TP53, FGFR3, or both. In some embodiments, the step of detecting the

presence of aneuploidy comprises detecting the presence of aneuploidy on one or more of chromosome arms 5q, 8q, and 9p. In some embodiments, the one or more genetic biomarkers, the one or more genetic biomarkers (e.g., a mutations) in the TERT promoter, or both, are present in 0.03% or fewer of the urinary cells in the sample. In some embodiments, the step of detecting the presence of at least one genetic biomarker (e.g., a mutation) in the TERT promoter is performed using a PCR based multiplex assay, a Sanger Sequencing assay, or a next generation sequencing assay. In some embodiments, the step of detecting the presence of at least one genetic biomarker (e.g., a mutation) in the TERT promoter is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique including: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products.

[885] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the method includes detecting bladder cancer and further includes administering transuretral resection of the bladder (TURB), intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, cystectomy or cystoprostatectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination thereof.

[886] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the method includes detecting an upper tract urothelial carcinoma and further includes administering transurethral resection, intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, ureterectomy or nephroureterectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination thereof.

[887] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the cancer is an ovarian or endometrial cancer; the one or more genetic biomarkers are one or more of NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A; and the presence of one or more mutations in one or more of NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A, the presence of aneuploidy, or both indicates that the subject has ovarian or endometrial cancer. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the cancer is an endometrial cancer; the one or more genetic biomarkers are one or more of PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, or PPP2R1A; and the presence of one or more mutations in one or more of PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, or PPP2R1A, the presence of aneuploidy, or both indicates that the subject has endometrial cancer. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the cancer is a high-grade serous carcinoma; the one or more genetic biomarkers in TP53; and the presence of one or more genetic biomarkers in TP53, the presence of aneuploidy, or both indicates that the subject has a high-grade serous carcinoma. In some embodiments, the step of detecting the presence of aneuploidy includes detecting the presence of aneuploidy on one or more of chromosome arms 4p, 7q, 8q, and 9q. In some embodiments, the first sample, the second sample, or both are collected via intrauterine sampling. In some embodiments, the first sample, the second sample, or both are collected with a Tao brush. In some embodiments, the methods further include detecting in a circulating tumor DNA (ctDNA) sample obtained from the subject the presence of at least

one genetic biomarker in one or more of the following genes: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, or TP53. In some embodiments, the methods further include administering to the subject a therapy, wherein the therapy includes: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, or combinations thereof.

[888] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the genetic biomarker is a mutation in a gene.

[889] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the first sample and the second sample are the same. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the first sample and the second sample are different. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the first sample is a blood sample.

[890] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the methods further include a) determining a mutation allele frequency in the sample for two or more of the genetic biomarkers; b) obtaining a score that indicates the likelihood that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution

of mutation allele frequency for each mutation in control samples; and c) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some embodiments, the methods further include selecting one genetic biomarker with the highest score that indicates the probability that the subject has a cancer from the two or more genetic biomarkers; and comparing the score for the selected genetic biomarker to the reference value. In some embodiments, the score is Stouffer's Z-score.

[891] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the methods further include a) determining a mutation allele frequency in the sample for two or more of the genetic biomarkers; and b) comparing the mutation allele frequency of each mutation in the selected genetic biomarkers to the maximum mutation allele frequency of each mutation for each mutation in control samples.

[892] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the sensitivity of identifying a subject as having cancer is increased as compared to: 1) the sensitivity obtained when only the presence of one or more genetic biomarkers in the sample obtained from the subject is detected, or 2) the sensitivity obtained when the presence of only aneuploidy in the sample obtained from the subject is detected. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the specificity of identifying a subject as having cancer is increased as compared to: 1) the specificity obtained when only the presence of one or more genetic biomarkers in the sample obtained from the subject is detected, or 2) the specificity obtained when the presence of only aneuploidy in the sample obtained from the subject is detected.

[893] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first

sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the methods further include detecting the presence of a detecting one or more protein biomarkers in a sample obtained from the subject, wherein the sample is the first sample, the second sample, or a third sample. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), subject is a human. In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the cancer is a Stage I cancer.

[894] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject), the one or more genetic biomarkers comprise one or more modifications in one or more genes. In some embodiments, the one or more modifications comprise inactivating modifications, and wherein said one or more genes comprise tumor suppressor genes. In some embodiments, the one or more modifications include a modification independently selected from single base substitutions, insertions, or deletions, translocations, fusions, breaks, duplications, or amplifications.

[895] In some embodiments of identifying a subject as having cancer or treating a subject having cancer (e.g., based on the presence of one or more genetic biomarkers in a first sample obtained from said subject and/or the presence of aneuploidy in a second sample obtained from the subject),

[896] In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in a sample collected from the patient for each mutation in one or more of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A; b) obtaining a score that indicates the likelihood

that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and c) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in a sample collected from the patient for each mutation in one or more of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, or PPP2R1A; b) obtaining a score that indicates the likelihood that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and c) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some embodiments, the methods further include selecting one genetic biomarker with the highest score that indicates the probability that the subject has a cancer from the two or more genetic biomarkers; and comparing the score for the selected genetic biomarker to the reference value. In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in the sample for one or more of the genetic biomarkers; b) obtaining a score that indicates the probability that the subject does not have a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and c) identifying the subject as not having a cancer when the score is lower than a reference value for the score. In some embodiments, the methods further include selecting one genetic biomarker with the lowest score that indicates the probability that the subject does not have a cancer; and comparing the score for the selected genetic biomarker to the reference value. In some embodiments, the score is Stouffer's Z-score. In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in the blood sample for two or more of the genetic biomarkers; and b) comparing the mutation allele frequency of each mutation in the selected genetic biomarkers to the maximum mutation allele frequency of each mutation for each mutation in control samples. In some

embodiments, provided herein are methods of identifying a patient as having a cancer described in the preceding paragraph, the sample is assayed in two or more test samples using a method comprising: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of identifying a patient as having a cancer, the methods further include detecting the presence of aneuploidy in the sample (e.g., the presence of aneuploidy on one or more of chromosome arms 4p, 7q, 8q, and 9q). In some embodiments of identifying a patient as having a cancer, the methods further include detecting in a circulating tumor DNA (ctDNA) sample obtained from the subject the presence of at least one genetic biomarker in one or more of the following genes: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, or TP53. In some embodiments, the cancer is a Stage I cancer. In some embodiments, the cancer is cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer. In some embodiments, the at least one mutation comprises an inactivating modification, and wherein the at least one mutation is in a tumor suppressor gene. In some embodiments, the modifications are independently selected from single base substitutions, insertions, deletions, translocations, fusions, breaks, duplications, or amplifications. In some embodiments, the methods further include administering to the subject one or more therapeutic interventions (e.g., one or more of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, or combinations thereof).

[897] In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in a sample collected from the patient for each mutation in one or more of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL; b) obtaining a score that indicates the likelihood that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and c) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some

embodiments, the methods further include selecting one genetic biomarker with the highest score that indicates the probability that the subject has a cancer from the two or more genetic biomarkers; and comparing the score for the selected genetic biomarker to the reference value. In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in the sample for one or more of the genetic biomarkers; b) obtaining a score that indicates the probability that the subject does not have a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and c) identifying the subject as not having a cancer when the score is lower than a reference value for the score. In some embodiments, the methods further include selecting one genetic biomarker with the lowest score that indicates the probability that the subject does not have a cancer; and comparing the score for the selected genetic biomarker to the reference value. In some embodiments, the score is Stouffer's Z-score. In some embodiments, provided herein are methods of identifying a patient as having a cancer that include: a) determining a mutation allele frequency in the blood sample for two or more of the genetic biomarkers; and b) comparing the mutation allele frequency of each mutation in the selected genetic biomarkers to the maximum mutation allele frequency of each mutation for each mutation in control samples. In some embodiments, provided herein are methods of identifying a patient as having a cancer described in the preceding paragraph, the sample is assayed in two or more test samples using a method comprising: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments, the methods further include detecting the presence of at least one genetic biomarker (e.g., a mutation) in a TERT promoter in the sample. In some embodiments of identifying a patient as having a cancer, the methods further include detecting the presence of aneuploidy in the sample (e.g., the presence of aneuploidy on one or more of chromosome arms 5q, 8q, and 9p). In some embodiments of identifying a patient as having a cancer, the methods further include detecting in a circulating tumor DNA (ctDNA) sample obtained from the subject the presence of at least one genetic biomarker in

one or more of the following genes: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, or TP53. In some embodiments, the cancer is a Stage I cancer. In some embodiments, the cancer is bladder cancer or an upper-tract urothelial cancer (UTUC). In some embodiments, the at least one mutation comprises an inactivating modification, and wherein the at least one mutation is in a tumor suppressor gene. In some embodiments, the modifications are independently selected from single base substitutions, insertions, deletions, translocations, fusions, breaks, duplications, or amplifications. In some embodiments, the methods further include administering to the subject one or more therapeutic interventions (e.g., one or more of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, or combinations thereof).

[898] In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value. In some embodiments of systems for generating a report for a patient, the systems further include at

least one device configured to detect the presence of at least one genetic biomarker (e.g., at least one mutation) in a TERT promoter.

[899] In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value. In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; c) a computer-readable program code comprising instructions to

execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value. In some embodiments, provided herein are systems for generating a report for a patient that include: at least one device configured to assay a TP53 gene in a biological sample collected from the patient to determine mutation allele frequency of TP53; b) at least one computer database including: i) a first reference distribution of mutation allele frequency in control samples for TP53; and ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for TP53; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of TP53; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value.

[900] In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the

set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments of systems for generating a report to identify a cancer treatment for a patient, the systems further include at least one device configured to detect the presence of at least one genetic biomarker (e.g., at least one mutation) in a TERT promoter.

[901] In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing

the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the

calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments, provided herein are systems for generating a report to identify a cancer treatment for a patient that include: a) at least one device configured to assay a TP53 gene in a biological sample collected from the patient to determine mutation allele frequency of TP53; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for TP53; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for TP53; and iii) a listing of cancer treatment with efficacy linked to a biological state of TP53; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of TP53; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[902] In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected

from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments of systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the systems further include at least one device configured to detect the presence of at least one genetic biomarker (e.g., at least one mutation) in a TERT promoter.

[903] In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes in a sample collected from the patient, wherein the set of genes in a sample collected from the patient, wherein the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing

of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a set of genes in a biological sample to determine mutation allele frequency of each mutation in the set of genes comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for each mutation in the set of genes; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for each mutation in the set of genes; and iii) a listing of cancer treatment with efficacy linked to a biological state of at least one member of the set of genes; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of each mutation in the set of genes; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient

as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient. In some embodiments, provided herein are systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: a) at least one device configured to assay a TP53 gene in a biological sample collected from the patient to determine mutation allele frequency of TP53; b) at least one computer database comprising: i) a first reference distribution of mutation allele frequency in control samples for TP53; ii) a second reference distribution of mutation allele frequency in samples collected from patients having a cancer for TP53; and iii) a listing of cancer treatment with efficacy linked to a biological state of TP53; c) a computer-readable program code comprising instructions to execute the following: i) inputting the mutation allele frequency in the biological sample of TP53; ii) comparing the mutation allele frequency to the first reference distribution; iii) comparing the mutation allele frequency to the second reference distribution; and iv) calculating a score that indicates the likelihood that the patient has a cancer; d) a computer-readable program code comprising instructions to generate a report that indicates the patient as having a cancer if the score is higher than a reference value; or a report that indicates the patient as not having a cancer if the score is not higher than the reference value; and e) a computer-readable program code comprising instructions to identify for the patient at least one cancer treatment from the listing of cancer treatments in (b)(iii) when the patient is identified as having a cancer in step (d), wherein the calculated score provides an indication that the identified cancer treatment will be effective in the patient.

[904] In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the systems further include a computer-readable program code comprising instructions to execute the following: i) determining a mutation allele frequency

in the sample for two or more of the genetic biomarkers; ii) obtaining a score that indicates the likelihood that the subject has a cancer by comparing the mutation allele frequency of each mutation in the selected genetic biomarkers against a reference distribution of mutation allele frequency for each mutation in control samples; and ii) identifying the subject as having a cancer when the score is higher than a reference value for the score. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the systems further include a computer-readable program code comprising instructions to execute the following instructions: i) selecting one genetic biomarker with the highest score that indicates the probability that the subject has a cancer from the two or more genetic biomarkers; and ii) comparing the score for the selected genetic biomarker to the reference value. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the score is Stouffer's Z-score. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the systems further include a computer-readable program code comprising instructions to execute the following instructions: i) determining a mutation allele frequency in the sample for two or more of the genetic biomarkers; and ii) comparing the mutation allele frequency of each mutation in the selected genetic biomarkers to the maximum mutation allele frequency of each mutation for each mutation in control samples.

[905] In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the device configured to assay a set of genes comprises a device that employs a includes a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-

generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the multiplex PCR-based sequencing assay comprises: a. assigning a unique identifier (UID) to each of a plurality of template molecules present in the sample; b. amplifying each uniquely tagged template molecule to create UID-families; and c. redundantly sequencing the amplification products. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the system further includes a device configured to detect the presence of aneuploidy in a biological sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect the presence of aneuploidy in a biological sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include: 1) at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, or 16) of the following genes: NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS, and 2) at least one device configured to detect the presence of a genetic biomarker (e.g., at least one mutation) in a TERT promoter, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect the presence of aneuploidy in a

biological sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect the presence of aneuploidy in a biological sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect the presence of aneuploidy in a biological sample. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay TP53, the system further includes a device (e.g., a device that includes a multiplex immunoassay system) configured to detect the presence of aneuploidy in a biological sample. The presence of aneuploidy can be detected on one or more chromosomes or chromosomal arms that are associated with cancer. In some embodiments, the presence of aneuploidy is detected on one or more of chromosomal arms 5q, 8q, and/or 9p. In some embodiments, the presence of aneuploidy is detected on one or more of chromosomal arms 4p, 7q, 8q, and/or 9q

[906] In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further

diagnostic testing, or both, the sensitivity of the system in identifying a subject as having cancer is improved as compared to conventional systems for generating a report for a patient. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the specificity of the system in identifying a subject as having cancer is improved as compared to conventional systems for generating a report for a patient. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the first and second reference distribution of mutation allele frequency values are input into the system from a location that is remote from the at least one computer database. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, first and second reference distribution of mutation allele frequency values are input into the system over an internet connection. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the report is in electronic or paper format.

[907] In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both, the cancer is any of the variety of cancer types described herein (see, e.g., section entitled "Cancers"). In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) of the

following genes: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and/or VHL and at least one a device configured to detect the presence of aneuploidy in a biological sample, the cancer is bladder cancer or an upper-tract urothelial carcinoma. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the following genes: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and/or CDKN2A and at least one a device configured to detect the presence of aneuploidy in a biological sample, the cancer is cervical cancer, endometrial cancer, ovarian cancer, or fallopian tubal cancer. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following genes: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and/or PPP2R1A and at least one a device configured to detect the presence of aneuploidy in a biological sample, the cancer is endometrial cancer. In some embodiments of systems for generating a report for a patient, systems for generating a report to identify a cancer treatment for a patient, or systems for generating a report for a patient to identify the patient as a candidate for increased monitoring, further diagnostic testing, or both that include at least one device configured to assay TP53 and at least one a device configured to detect the presence of aneuploidy in a biological sample, the cancer is a high-grade serous carcinoma. In some embodiments of systems for generating a report for a patient or systems for generating a report to identify a cancer treatment for a patient, the patient is identified as a candidate for increased monitoring, further diagnostic testing, or both (e.g. any of the variety of increased monitoring or further diagnostic methods described herein).

[908] Many of the currently approved tests for earlier cancer detection are procedural in nature, and include colonoscopy, mammography, and cervical cytology analysis. To date, the vast majority of cancer patients evaluated with mutation-based liquid biopsies have advanced stage disease. Yet another issue with liquid biopsies is the identification of the underlying organ of origin. Because the same gene mutations drive multiple tumor types, liquid biopsies based on such alterations cannot generally identify the location of the primary tumor giving rise to a positive blood test. Described herein is a non-invasive combinatorial blood test (e.g., a test that combines DNA markers and protein markers) for the early detection and localization of many common cancers.

[909] This document provides methods and materials for assessing and/or treating mammals (e.g., humans) having, or suspected of having, cancer. In some embodiments, this document provides methods and materials for identifying a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the presence or absence of one or more biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more biomarkers (e.g., peptide biomarkers). In some embodiments, this document provides methods and materials for identifying the location (e.g., the anatomic site) of a cancer in a mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine the location of the cancer in the mammal based, at least in part, on the presence or absence of one or more biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more biomarkers (e.g., peptide biomarkers). In some embodiments, this document provides methods and materials for identifying a mammal as having cancer, and administering one or more pharmacological interventions to treat the mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the presence or absence of one or more biomarkers (e.g., genetic biomarkers) and/or an elevated level of one or more biomarkers (e.g., peptide biomarkers), and administering one or more cancer treatments to the mammal.

[910] As demonstrated herein, an analysis of only 2,001 bp of genomic DNA could detect at least one mutation in 82% of eight common cancer types. A test (CancerSEEK) was

designed which assessed the levels of 10 circulating proteins as well as mutations of these 2,001 bp in circulating cell-free DNA. This test was applied to 1,005 patients with cancers of the liver, ovary, esophagus, stomach, pancreas, colorectum, lung, or breast. CancerSEEK tests were positive in a median of 70% of the eight cancer types, while fewer than 1% of 812 normal individuals scored positively. The sensitivities ranged from 69% to 98% for the detection of five cancer types (liver, ovary, esophagus, stomach, and pancreas) for which there are no screening tests available for average-risk individuals. Moreover, the source of the cancer could be localized to a small number of anatomic sites in a median of 84% of the patients scoring positive in the CancerSEEK assay.

[911] Having the ability to use a blood test having very high specificity (e.g., by combining DNA markers and protein markers) can allow clinicians to detect cancers at earlier stages resulting in earlier treatment with fewer unnecessary follow-up procedures, less anxiety, and/or reduced cancer deaths.

[912] In general, one aspect of this document features a method for identifying a mammal as having cancer. The method can include, or consist essentially of, detecting one or more genetic biomarkers in circulating DNA in a blood sample obtained from a mammal; detecting an elevated level of one or more peptide biomarkers in the blood sample obtained from a mammal; and identifying the mammal as having cancer when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated level of one or more peptide biomarkers is detected in said blood sample, or both. The mammal can be a human. The blood sample can be a plasma sample. The cancer can be a Stage I cancer. The cancer can be a liver cancer, an ovary cancer, an esophageal cancer, a stomach cancer, a pancreatic cancer, a colorectal cancer, a lung cancer, a breast cancer, or a prostate cancer. The one or more genetic biomarkers can include one or more modifications in one or more genes. The one or more modifications can include inactivating modifications, and the one or more genes can include tumor suppressor genes. The one or more modifications can independently be selected from single base substitutions, insertions, and deletions. The one or more genes are can include NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A,

and/or GNAS. The one or more modifications can independently be selected from the modifications set forth in Table 5. The step of detecting the presence of one or more genetic biomarkers can be performed using a multiplex PCR-based sequencing assay. The multiplex PCR-based sequencing assay can include assigning a unique identifier (UID) to each template molecule; amplifying each uniquely tagged template molecule to create UID-families; and redundantly sequencing the amplification products. The one or more peptide biomarkers can include prolactin, OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and/or TIMP-1. The step of detecting the level of one or more peptide biomarkers can be performed using a multiplex immunoassay system. The method also can include identifying a location of said cancer. The method also can include administering to the mammal one or more cancer treatments. The one or more cancer treatments can include surgery, chemotherapy, hormone therapy, targeted therapy, radiation therapy, and combinations thereof.

[913] In another aspect, this document features a method for treating a mammal having cancer. The method can include, or consist essentially of, detecting one or more genetic biomarkers in circulating DNA in a blood sample obtained from a mammal; detecting an elevated level of one or more peptide biomarkers in the blood sample obtained from a mammal; and administering one or more cancer treatments to said mammal when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated level of one or more peptide biomarkers is detected in said blood sample, or both. The one or more cancer treatments can include surgery, chemotherapy, hormone therapy, targeted therapy, radiation therapy, and combinations thereof. The mammal can be a human. The blood sample can be a plasma sample. The cancer can be a Stage I cancer. The cancer can be a liver cancer, an ovary cancer, an esophageal cancer, a stomach cancer, a pancreatic cancer, a colorectal cancer, a lung cancer, a breast cancer, or a prostate cancer. The one or more genetic biomarkers can include one or more modifications in one or more genes. The one or more modifications can include inactivating modifications, and the one or more genes can include tumor suppressor genes. The one or more modifications can independently be selected from single base substitutions, insertions, and deletions. The one or more genes are can include NRAS, CTNNB1, PIK3CA, FBXW7,

APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS. The one or more modifications can independently be selected from the modifications set forth in Table 5. The step of detecting the presence of one or more genetic biomarkers can be performed using a multiplex PCR-based sequencing assay. The multiplex PCR-based sequencing assay can include assigning a unique identifier (UID) to each template molecule; amplifying each uniquely tagged template molecule to create UID-families; and redundantly sequencing the amplification products. The one or more peptide biomarkers can include prolactin, OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and/or TIMP-1. The step of detecting the level of one or more peptide biomarkers can be performed using a multiplex immunoassay system.

[914] In another aspect, this document features a method for identifying the location of a cancer in a mammal. The method can include, or consist essentially of, detecting one or more genetic biomarkers in circulating DNA in a blood sample obtained from a mammal; detecting an elevated level of one or more peptide biomarkers in the blood sample obtained from a mammal; and identifying the location of the cancer in the mammal when the presence of one or more genetic biomarkers is detected in circulating DNA in said blood sample, when an elevated level of one or more peptide biomarkers is detected in said blood sample, or both. The mammal can be a human. The blood sample can be a plasma sample. The cancer can be a Stage I cancer. The cancer can be a liver cancer, an ovary cancer, an esophageal cancer, a stomach cancer, a pancreatic cancer, a colorectal cancer, a lung cancer, a breast cancer, or a prostate cancer. The one or more genetic biomarkers can include one or more modifications in one or more genes. The one or more modifications can include inactivating modifications, and the one or more genes can include tumor suppressor genes. The one or more modifications can independently be selected from single base substitutions, insertions, and deletions. The one or more genes are can include NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS. The one or more modifications can independently be selected from the modifications set forth in Table 5. The step of detecting the presence of one or more genetic biomarkers can be performed using a multiplex PCR-based sequencing assay. The multiplex PCR-based sequencing assay can include assigning a unique identifier (UID) to each

template molecule; amplifying each uniquely tagged template molecule to create UID-families; and redundantly sequencing the amplification products. The one or more peptide biomarkers can include prolactin, OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and/or TIMP-1. The step of detecting the level of one or more peptide biomarkers can be performed using a multiplex immunoassay system.

[915] Provided herein are methods for identifying the presence of a cancer in a human subject comprising: detecting in a first biological sample isolated from the human subject the presence of one or more genetic alterations in cell-free DNA derived from a gene selected from the group consisting of: AKT1, APC, BRAF, CDKN2, CTNNB1, FBXW7, FGFR2, GNAS, HRAS, KRAS, PPP2R1A, TP53, PTEN, PIK3CA, EGFR and NRAS, and combinations thereof; detecting a level of one or more protein biomarkers in a second biological sample isolated from the human subject, wherein the protein biomarker is selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3, and combinations thereof; comparing the detected levels of the one or more protein biomarkers to one or more reference levels of the protein biomarkers; and identifying the presence of the cancer in the human subject when the presence of one or more genetic alterations in the cell-free DNA is detected, the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers, or both. In some embodiments, the first biological sample comprises blood, plasma, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, the first biological sample, the second biological sample, or both comprises plasma. In some embodiments, the first and second biological samples are the same.

[916] In some embodiments of identifying the presence of a cancer in a human subject, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample comprises amplifying an amplicon comprising codons and their surrounding splice sites, wherein the codons are selected from the group consisting of: codons 16-18 of AKT1; codons 1304-1311 or 1450-1459 of APC; codons 591-602 of BRAF;

codons 51-58 or 76-88 of CDKN2A; codons 31-39 or 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, or 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, or 143-148 of KRAS; codons 3-15 or 54-63 of NRAS; codons 80-90, 343-348, 541-551, or 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; codons 90-98, 125-132, 133-146, 145-154 of PTEN; codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, or 374-386 of TP53, and combinations thereof. In some embodiments, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample comprises sequencing gene regions comprising codons and their surrounding splice sites, wherein the codons are selected from the group consisting of: codons 16-18 of AKT1; codons 1304-1311 or 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58 or 76-88 of CDKN2A; codons 31-39 or 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, or 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, or 143-148 of KRAS; codons 3-15 or 54-63 of NRAS; codons 80-90, 343-348, 541-551, or 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; codons 90-98, 125-132, 133-146, 145-154 of PTEN; codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, or 374-386 of TP53, and combinations thereof. In some embodiments, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample comprises sequencing gene regions comprising codons and their surrounding splice from each of: codons 16-18 of AKT1; codons 1304-1311 and 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58 and 76-88 of CDKN2A; codons 31-39 and 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, and 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, and 143-148 of KRAS; codons 3-15 and 54-63 of NRAS; codons 80-90, 343-348, 541-551, and 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A;

codons 90-98, 125-132, 133-146, 145-154 of PTEN; codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, and 374-386 of TP53, and combinations thereof.

[917] In some embodiments of identifying the presence of a cancer in a human subject, the one or more protein biomarkers include CA19-9. In some embodiments, the reference level of the CA19-9 protein biomarker is 92 U/mL. In some embodiments, the one or more protein biomarkers include CEA. In some embodiments, the reference level of the CEA protein biomarker is 7.5 ng/mL. In some embodiments, the one or more protein biomarkers include HGF. In some embodiments, the reference level of the HGF protein biomarker is 0.89 ng/mL. In some embodiments, the one or more protein biomarkers include OPN. In some embodiments, the reference level of the OPN protein biomarker is 158 ng/mL. In some embodiments, the one or more protein biomarkers include CA125. In some embodiments, the reference level of the CA125 protein biomarker is 577 U/mL. In some embodiments, the one or more protein biomarkers include AFP. In some embodiments, the reference level of the AFP protein biomarker is 21 ng/mL. In some embodiments, the one or more protein biomarkers include prolactin. In some embodiments, the reference level of the prolactin protein biomarker is 145 ng/mL. In some embodiments, the one or more protein biomarkers include TIMP-1. In some embodiments, the reference level of the TIMP-1 protein biomarker is 177ng/mL. In some embodiments, the one or more protein biomarkers include follistatin. In some embodiments, the reference level of the follistatin protein biomarker is 2 ng/mL In some embodiments, the one or more protein biomarkers include G-CSF. In some embodiments, the reference level of the G-CSF protein biomarker is 800 pg/mL. In some embodiments, the one or more protein biomarkers include CA15-3. In some embodiments, the reference level of the CA15-3 protein biomarker is 98 U/mL.

[918] In some embodiments of identifying the presence of a cancer in a human subject, the presence of the cancer in the human subject is identified when: (i) the presence of one or more genetic alterations in cell-free DNA derived is detected, and (ii) the detected levels of

the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers.

[919] In some embodiments of identifying the presence of a cancer in a human subject, the presence of one or more genetic alterations in cell-free DNA in the first biological sample is detected by amplifying the cell-free DNA to form families of amplicons in which each member of a family is derived from a single template molecule in the cell-free DNA, wherein each member of a family is marked by a common oligonucleotide barcode, and wherein each family is marked by a distinct oligonucleotide barcode. In some embodiments, the oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers which collectively contain a plurality of oligonucleotide barcodes. In some embodiments, the oligonucleotide barcode is endogenous to the template molecule, and an adapter comprising a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the oligonucleotide barcode.

[920] In some embodiments of identifying the presence of a cancer in a human subject, a therapeutic intervention is administered to the subject when the presence of cancer is identified. In some embodiments, the therapeutic intervention is selected from the group consisting of: adoptive T cell therapy, radiation therapy, surgery, administration of a chemotherapeutic agent, administration of an immune checkpoint inhibitor, administration of a targeted therapy, administration of a kinase inhibitor, administration of a signal transduction inhibitor, administration of a bispecific antibody, administration of a monoclonal antibody, and combinations thereof. In some embodiments, cancer, and wherein the therapeutic intervention is more effective than if the therapeutic intervention were to be administered to a human subject at a later time.

[921] In some embodiments of identifying the presence of a cancer in a human subject, the presence of cancer in the human subject is detected at a time prior to diagnosis of the human subject with cancer. In some embodiments, the presence of cancer in the human subject is detected at a time prior to the human subject exhibiting symptoms associated with cancer.

[922] In some embodiments of identifying the presence of a cancer in a human subject, the human subject is human subjected to a radiologic scanning of an organ or body region to

identify the location of the cancer. In some embodiments, the human subject is human subjected to whole body radiologic scanning to identify the location of the cancer. In some embodiments, the scanning is a Positron emission tomography-computed tomography (PET-CT) scan.

[923] In some embodiments, the cancer is selected from the group consisting of: pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, and breast cancer, and combinations thereof.

[924] Also provided herein are methods for identifying the presence of cancer in a human subject comprising: detecting a level of one or more protein biomarkers in a first biological sample isolated from the human subject, wherein the one or more protein biomarkers are selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3, and combinations thereof; comparing the detected levels of the one or more protein biomarkers to one or more reference levels of the protein biomarkers; and identifying the presence of cancer in the human subject when the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers.

[925] Provided herein are methods for identifying the presence of pancreatic cancer in a human subject comprising: detecting in a first biological sample isolated from the human subject the presence of one or more genetic alterations in cell-free DNA derived from a gene selected from the group consisting of: KRAS, TP53, CDKN2A, SMAD4, and combinations thereof; detecting a level of one or more protein biomarkers in a second biological sample isolated from the human subject, wherein the one or more protein biomarkers are selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), and combinations thereof; comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of pancreatic cancer in the human subject when the presence of one or more genetic alterations in the cell-free DNA is detected, the detected levels of the one or more protein biomarkers are higher than the

reference levels of the one or more protein biomarkers, or both. In some embodiments, the first biological sample comprises blood, plasma, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, the first biological sample, the second biological sample, or both comprises plasma. In some embodiments, the first and second biological samples are the same.

[926] In some embodiments of methods for identifying the presence of pancreatic cancer in a human subject, the one or more genetic alterations occur in codons 12 or 61 of the KRAS gene. In some embodiments, the one or more protein biomarkers include CA19-9. In some embodiments, the reference level of the CA19-9 protein biomarker is 100 U/mL. In some embodiments, the one or more protein biomarkers include CEA. In some embodiments, the reference level of the CEA protein biomarker is 7.5 ng/mL. In some embodiments, the one or more protein biomarkers include HGF. In some embodiments, the reference level of the HGF protein biomarker is 0.92 ng/mL. In some embodiments, the one or more protein biomarkers include OPN. In some embodiments, the reference level of the OPN protein biomarker is 158 ng/mL. In some embodiments, detecting the level of the one or more protein biomarkers comprises detecting the levels of each of CA19-9, CEA, HGF, and OPN; and comparing the detected levels of the one or more protein biomarkers to one or more reference levels of the protein biomarker comprises comparing the detected levels of each of CA19-9, CEA, HGF, and OPN to a reference level of each of CA19-9, CEA, HGF, and OPN.

[927] [09] In some embodiments of methods for identifying the presence of pancreatic cancer in a human subject, the presence of pancreatic cancer in the human subject is identified when: (i) the presence of one or more genetic alterations in cell-free DNA derived from the KRAS gene are detected, and (ii) the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers. In some embodiments of methods for identifying the presence of pancreatic cancer in a human subject, the one or more genetic alterations are detected by amplifying the cell-free DNA to form families of amplicons in which each member of a family is derived from a single template molecule in the cell-free DNA, wherein each member of a family is marked by a

common oligonucleotide barcode, and wherein each family is marked by a distinct oligonucleotide barcode. In some embodiments, the oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers which collectively contain a plurality of oligonucleotide barcodes. In some embodiments, the oligonucleotide barcode is endogenous to the template molecule, and an adapter comprising a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the oligonucleotide barcode.

[928] In some embodiments, a therapeutic intervention to the human subject when the presence of pancreatic cancer is identified. In some embodiments, the therapeutic intervention is selected from the group consisting of: adoptive T cell therapy, radiation therapy, surgery, administration of a chemotherapeutic agent, administration of an immune checkpoint inhibitor, administration of a targeted therapy, administration of a kinase inhibitor, administration of a signal transduction inhibitor, administration of a bispecific antibody, administration of a monoclonal antibody, and combinations thereof. In some embodiments, the therapeutic intervention is administered at a time when the human subject has an early-stage pancreatic cancer, and wherein the therapeutic intervention is more effective than if the therapeutic intervention were to be administered to a human subject at a later time.

[929] In some embodiments, the presence of pancreatic cancer in the human subject is detected at a time prior to diagnosis of the human subject with pancreatic cancer. In some embodiments, the presence of pancreatic cancer in the human subject is detected at a time prior to the human subject exhibiting symptoms associated with pancreatic cancer.

[930] Also provided herein are methods for identifying the presence of pancreatic cancer in a human subject comprising: detecting a level of one or more protein biomarkers in a first biological sample isolated from the human subject, wherein the one or more protein biomarkers are selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), and combinations thereof; comparing the detected levels of the one or more protein biomarker to one or more reference levels of the protein biomarkers; and identifying the presence of

pancreatic cancer in the human subject when the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more protein biomarkers.

[931] Provided herein are methods for identifying the presence of a cancer in a human subject comprising: detecting in a first biological sample isolated from the subject the presence of one or more genetic alterations in cell-free DNA derived from a gene selected from the group consisting of: AKT1, APC, BRAF, CDKN2, CTNNB1, FBXW7, FGFR2, GNAS, HRAS, KRAS, PPP2R1A, TP53, PTEN, PIK3CA, EGFR and NRAS, and combinations thereof; detecting in a second biological sample isolated from the subject the absence of one or more genetic alterations in DNA derived from a gene selected from the group consisting of: AKT1, APC, BRAF, CDKN2, CTNNB1, FBXW7, FGFR2, GNAS, HRAS, KRAS, PPP2R1A, TP53, PTEN, PIK3CA, EGFR and NRAS, and combinations thereof, wherein the second biological sample is isolated from white blood cells of the subject; identifying the presence of the cancer in the subject when the one or more genetic alterations that are detected in the first sample are not detected in the second sample. In some embodiments, the first biological sample, the second biological sample, or both comprise blood, plasma, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, and combinations thereof. In some embodiments, the first biological sample, the second biological sample, or both comprises plasma. In some embodiments, the first and second biological samples are the same. In some embodiments of identifying the presence of a cancer in a human subject, the methods further comprise detecting a level of one or more protein biomarkers in a third biological sample isolated from the subject, wherein the protein biomarker is selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, and CA15-3 and combinations thereof; comparing the detected levels of the one or more protein biomarkers to one or more reference levels of the protein biomarkers; and identifying the presence of the cancer in the subject when the presence of one or more genetic alterations in the cell-free DNA is detected in the first sample, the absence of one or more genetic alterations is detected in DNA from the second sample, and the detected levels of the one or more protein biomarkers are higher than the reference levels of the one or more

protein biomarkers. In some embodiments, the third biological sample is the same as the first biological sample.

[932] In some embodiments of identifying the presence of a cancer in a human subject, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample, the step of detecting the absence of one or more genetic alterations in DNA in the second biological sample, or both comprises amplifying an amplicon comprising codons and their surrounding splice sites, wherein the codons are selected from the group consisting of: codons 16-18 of AKT1; codons 1304-1311 or 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58 or 76-88 of CDKN2A; codons 31-39 or 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, or 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, or 143-148 of KRAS; codons 3-15 or 54-63 of NRAS; codons 80-90, 343-348, 541-551, or 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; and codons 90-98, 125-132, 133-146, 145-154 of PTEN; and codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, or 374-386 of TP53. In some embodiments, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample, the step of detecting the absence of one or more genetic alterations in DNA in the second biological sample, or both comprises sequencing gene regions comprising codons and their surrounding splice sites, wherein the codons are selected from the group consisting of: codons 16-18 of AKT1; codons 1304-1311 or 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58 or 76-88 of CDKN2A; codons 31-39 or 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, or 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, or 143-148 of KRAS; codons 3-15 or 54-63 of NRAS; codons 80-90, 343-348, 541-551, or 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; and codons 90-98, 125-132, 133-146, 145-154 of PTEN; and codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307,

307-314, 323-331, 333-344, 344-355, 367-375, or 374-386 of TP53. In some embodiments, the step of detecting the presence of one or more genetic alterations in cell-free DNA in the first biological sample, the step of detecting the absence of one or more genetic alterations in DNA in the second biological sample, or both comprises sequencing gene regions comprising codons and their surrounding splice from each of: codons 16-18 of AKT1; codons 1304-1311 and 1450-1459 of APC; codons 591-602 of BRAF; codons 51-58 and 76-88 of CDKN2A; codons 31-39 and 38-47 of CTNNB1; codons 856-868 of EGFR; codons 361-371, 464-473, 473-483, and 498-507 of FBXW7; codons 250-256 of FGFR2; codons 199-208 of GNAS; codons 7-19 of HRAS; codons 7-14, 57-65, and 143-148 of KRAS; codons 3-15 and 54-63 of NRAS; codons 80-90, 343-348, 541-551, and 1038-1050 of PIK3CA; codons 175-187 of PPP2R1A; and codons 90-98, 125-132, 133-146, 145-154 of PTEN; and codons 10-22, 25-32, 33-40, 40-52, 52-64, 82-94, 97-110, 112-125, 123-125, 126-132, 132-142, 150-163, 167-177, 175-186, 187-195, 195-206, 207-219, 219-224, 226-237, 232-245, 248-261, 261-268, 272-283, 279-290, 298-307, 307-314, 323-331, 333-344, 344-355, 367-375, and 374-386 of TP53.

[933] In some embodiments of identifying the presence of a cancer in a human subject, the one or more protein biomarkers include CA19-9. In some embodiments, the reference level of the CA19-9 protein biomarker is 92 U/mL. In some embodiments, the one or more protein biomarkers include CEA. In some embodiments, the reference level of the CEA protein biomarker is 7.5 ng/mL. In some embodiments, the one or more protein biomarkers include HGF. In some embodiments, the reference level of the HGF protein biomarker is 0.89 ng/mL. In some embodiments, the one or more protein biomarkers include OPN. In some embodiments, the reference level of the OPN protein biomarker is 158 ng/mL. In some embodiments, the one or more protein biomarkers include CA125. In some embodiments, the reference level of the CA125 protein biomarker is 577 U/mL. In some embodiments, the one or more protein biomarkers include AFP. In some embodiments, the reference level of the AFP protein biomarker is 21 ng/mL. In some embodiments, the one or more protein biomarkers include prolactin. In some embodiments, the reference level of the prolactin protein biomarker is 145 ng/mL. In some embodiments, the one or more protein biomarkers include TIMP-1. In some embodiments, the reference level of the TIMP-1 protein biomarker

is 177ng/mL. In some embodiments, the one or more protein biomarkers include follistatin. In some embodiments, the reference level of the follistatin protein biomarker is 2 ng/mL. In some embodiments, the one or more protein biomarkers include G-CSF. In some embodiments, the reference level of the G-CSF protein biomarker is 800 pg/mL. In some embodiments, the one or more protein biomarkers include CA15-3. In some embodiments, the reference level of the CA15-3 protein biomarker is 98 U/mL.

[934] In some embodiments of identifying the presence of a cancer in a human subject, the presence of one or more genetic alterations in cell-free DNA in the first biological sample, the absence of one or more genetic alterations in DNA in the second biological sample, or both are detected by amplifying the cell-free DNA to form families of amplicons in which each member of a family is derived from a single template molecule in the cell-free DNA, wherein each member of a family is marked by a common oligonucleotide barcode, and wherein each family is marked by a distinct oligonucleotide barcode. In some embodiments, the oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers which collectively contain a plurality of oligonucleotide barcodes. In some embodiments, the oligonucleotide barcode is endogenous to the template molecule, and an adapter comprising a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the oligonucleotide barcode.

[935] In some embodiments, a therapeutic intervention is administered to the subject when the presence of cancer is identified. In some embodiments, the therapeutic intervention is selected from the group consisting of: adoptive T cell therapy, radiation therapy, surgery, administration of a chemotherapeutic agent, administration of an immune checkpoint inhibitor, administration of a targeted therapy, administration of a kinase inhibitor, administration of a signal transduction inhibitor, administration of a bispecific antibody, administration of a monoclonal antibody, and combinations thereof. In some embodiments, the therapeutic intervention is administered at a time when the subject has an early-stage cancer, and wherein the therapeutic intervention is more effective than if the therapeutic intervention were to be administered to a subject at a later time.

[936] In some embodiments of identifying the presence of a cancer in a human subject, the presence of cancer in the subject is detected at a time prior to diagnosis of the subject with cancer. In some embodiments, the presence of cancer in the subject is detected at a time prior to the subject exhibiting symptoms associated with cancer.

[937] In some embodiments of identifying the presence of a cancer in a human subject, the human subject is human subjected to a radiologic scanning of an organ or body region to identify the location of the cancer. In some embodiments, the human subject is human subjected to whole body radiologic scanning to identify the location of the cancer. In some embodiments, the scanning is a Positron emission tomography-computed tomography (PET-CT) scan.

[938] In some embodiments of identifying the presence of a cancer in a human subject, the cancer is selected from the group consisting of: pancreatic cancer, colon cancer, esophageal cancer, stomach cancer, ovarian cancer, liver cancer, lung cancer, and breast cancer, and combinations thereof.

[939] As described in more detail herein, it has been shown that DNA from sampled fluid (e.g., fluid containing cells sampled from the endocervical canal) can be used in an assay (e.g., a PCR-based, multiplex test) to simultaneously assess genetic alterations that commonly occur in endometrial or ovarian cancers (Fig. 19). Additionally, as described in more detail herein and without limitation, two ways to increase sensitivity were identified. First, intrauterine sampling (with a "Tao brush") was tested, a method that allows sample collection closer to the anatomical site of the tumors. Second, in a recent study, it was shown that testing for mutations in both saliva and plasma from the same individual increased the sensitivity of detecting head and neck tumors (Wang et al., Detection of somatic mutations and HPV in the saliva and plasma of patients with head and neck squamous cell carcinomas. Sci Transl Med 7, 293ra104 (2015)). Based on this precedent, it was shown that testing for mutations in both the plasma and Pap test fluid can increase sensitivity for cancers (e.g., ovarian cancers).

[940] In some aspects, provided herein are methods of detecting endometrial and ovarian cancers based on genetic analyses of DNA recovered from fluids (e.g., fluids obtained during

a routine Papanicolaou (Pap) test). In some embodiments, this new test, called PapSEEK, incorporates assays for mutations in one or more of 18 genes and/or an assay for aneuploidy. In some embodiment, method provided herein to detect gynecologic cancers are used at a stage when the cancers are more likely to be curable. In some embodiments, PapSEEK can be combined with assays for mutations in one or more genes in nucleic acids present in a plasma sample.

[941] In some embodiments, provided herein are methods of detecting ovarian or endometrial cancer in a subject that include detecting in a sample obtained from the subject the presence of one or more mutations in one or more genes selected from the group consisting of: NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, and CDKN2A, detecting in the sample the presence of aneuploidy, or both, wherein the presence of one or more mutations in NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A, the presence of aneuploidy, or both indicates that the subject has ovarian or endometrial cancer. In some embodiments, the step of detecting the presence of one or more mutations in NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, CDKN2A is performed using a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments, the step of detecting the presence of one or more mutations in NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, CDKN2A is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that allows for the detection of rare mutant alleles in a range of 1 mutant template among 100 to 1,000,000 wild-type templates. For example, the step of detecting one or more mutations can be performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique comprising: a) molecularly assigning a unique identifier (UID) to each template molecule, b) amplifying each uniquely tagged template molecule to create

UID-families, and c) redundantly sequencing the amplification products. In some embodiments, methods provided herein further include conducting cytology on the sample, wherein presence of the one or more mutations in NRAS, PTEN, FGFR2, KRAS, POLE, AKT1, TP53, RNF43, PPP2R1A, MAPK1, CTNNB1, PIK3CA, FBXW7, PIK3R1, APC, EGFR, BRAF, or CDKN2A, the presence of aneuploidy, and/or a positive cytology indicates that the subject has ovarian or endometrial cancer. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises detecting the presence of one or more alterations on one or more of chromosome arms 4p, 7q, 8q, and 9q. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises amplifying interspersed nucleotide elements. In some embodiments, methods provided herein further include detecting in a second sample comprising circulating tumor DNA (ctDNA) the presence of at least one mutation in one or more genes selected from the group consisting of: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and TP53. In some embodiments, the second sample includes plasma. In some embodiments, the sample is collected via intrauterine sampling. In some embodiments, the sample is collected with a Tao brush. In some embodiments, methods further include administering to the subject a therapy (e.g., adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, and combinations thereof).

[942] In some embodiments, provided herein are methods of detecting endometrial cancer in a subject that include detecting in a sample obtained from the subject the presence of one or more mutations in one or more genes selected from the group consisting of: PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A, detecting in the sample the presence of aneuploidy, or both, wherein the presence of one or more mutations in PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A, the presence of aneuploidy, or both indicates that the subject has endometrial cancer. In some embodiments, the step of detecting the presence of one or more mutations in PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A is performed using a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital

PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments, the step of detecting the presence of one or more mutations in PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that allows for the detection of rare mutant alleles in a range of 1 mutant template among 100 to 1,000,000 wild-type templates. For example, the step of detecting one or more mutations can be performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique comprising: a) molecularly assigning a unique identifier (UID) to each template molecule, b) amplifying each uniquely tagged template molecule to create UID-families, and c) redundantly sequencing the amplification products. In some embodiments, methods provided herein further include conducting cytology on the sample, wherein presence of the one or more mutations in PTEN, TP53, PIK3CA, PIK3R1, CTNNB1, KRAS, FGFR2, POLE, APC, FBXW7, RNF43, and PPP2R1A, the presence of aneuploidy, and/or a positive cytology indicates that the subject has endometrial cancer. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises detecting the presence of one or more alterations on one or more of chromosome arms 4p, 7q, 8q, and 9q. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises amplifying interspersed nucleotide elements. In some embodiments, methods provided herein further include detecting in a second sample comprising circulating tumor DNA (ctDNA) the presence of at least one mutation in one or more genes selected from the group consisting of: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and TP53. In some embodiments, the second sample includes plasma. In some embodiments, the sample is collected via intrauterine sampling. In some embodiments, the sample is collected with a Tao brush. In some embodiments, methods further include administering to the subject a therapy (e.g., adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, and combinations thereof).

[943] In some embodiments, provided herein are methods of detecting ovarian cancer in a subject that include detecting in a sample obtained from the subject the presence of one or more mutations in TP53, detecting in the sample the presence of aneuploidy, or both, wherein the presence of one or more mutations in TP53, the presence of aneuploidy, or both indicates that the subject has ovarian cancer. In some embodiments, the step of detecting the presence of one or more mutations in TP53 is performed using a PCR-based multiplex assay, using a PCR-based singleplex assay, a digital PCR assay, a droplet digital PCR (ddPCR) assay, a microarray assay, a next-generation sequencing assay, a Sanger sequencing assay, a quantitative PCR assay, or a ligation assay. In some embodiments, the step of detecting the presence of one or more mutations in TP53 is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that allows for the detection of rare mutant alleles in a range of 1 mutant template among 100 to 1,000,000 wild-type templates. For example, the step of detecting one or mutations can be performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique comprising: a) molecularly assigning a unique identifier (UID) to each template molecule, b) amplifying each uniquely tagged template molecule to create UID-families, and c) redundantly sequencing the amplification products. In some embodiments, methods provided herein further include conducting cytology on the sample, wherein presence of the one or more mutations in TP53, the presence of aneuploidy, and/or a positive cytology indicates that the subject has ovarian cancer. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises detecting the presence of one or more alterations on one or more of chromosome arms 4p, 7q, 8q, and 9q. In some embodiments, the step of detecting in the sample the presence of aneuploidy comprises amplifying interspersed nucleotide elements. In some embodiments, methods provided herein further include detecting in a second sample comprising circulating tumor DNA (ctDNA) the presence of at least one mutation in one or more genes selected from the group consisting of: AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN, and TP53. In some embodiments, the second sample includes plasma. In some embodiments, the sample is collected via intrauterine sampling. In some embodiments, the sample is collected with a Tao brush. In

some embodiments, methods further include administering to the subject a therapy (e.g., adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, immunotherapy, targeted therapy, immune checkpoint inhibitors, and combinations thereof).

[944] Provided herein are methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject that include: detecting in a urinary sample obtained from the subject the presence of one or more mutations in one or more genes selected from the group consisting of: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, detecting in the sample the presence of at least one mutation in a TERT promoter, and detecting in the sample the presence of aneuploidy, wherein presence of one or more mutations in the group consisting of: TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, and VHL, the presence of the at least one mutation in the TERT promoter, or the presence of aneuploidy indicates that the subject has bladder cancer. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the one or more genes are TP53, FGFR3, or both. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL, the one or more mutations in the TERT promoter, or both, are present in 0.03% or fewer of the urinary cells in the sample.

[945] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a PCR based multiplex assay, a Sanger sequencing assay, a next-generation sequencing assay, a quantitative PCR assay, a droplet digital PCR (ddPCR) assay, or a microarray technique. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a Sanger Sequencing assay. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence

of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a next generation sequencing assay.

[946] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting in the sample the presence of aneuploidy comprises detecting the presence of one or more alterations on one or more of chromosome arms 5q, 8q, and 9p. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence of aneuploidy comprises amplifying long interspersed nucleotide elements (LINESs).

[947] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that allows for the detection of rare mutant alleles in a range of 1 mutant template among 5,000 to 1,000,000 wild-type templates. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that includes: a) assigning a unique identifier (UID) to each template molecule, b) amplifying each uniquely tagged template molecule to create UID-families, and c) redundantly sequencing the amplification products.

[948] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the method further includes performing cytology on the sample, wherein presence of the one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the presence of the at least one mutation in the TERT promoter, the presence of aneuploidy, or a positive cytology indicates that the subject has bladder cancer.

[949] In some embodiments of methods of detecting bladder cancer in a subject, the method further includes administering transuretral resection of the bladder (TURB), intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, cystectomy or cystoprostatectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination thereof.

[950] In some embodiments of methods of detecting an upper tract urothelial carcinoma in a subject, the method further includes administering transurethral resection, intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, ureterectomy or nephroureterectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination thereof.

[951] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the cancer is a low-grade tumor. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the cancer is a low-grade tumor, the low-grade tumor is a papillary urothelial neoplasms of low malignant potential (PUNLMP) or a non-invasive low grade papillary urothelial carcinoma. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the cancer is a low-grade tumor, the method further includes administering transuretral resection of the bladder (TURB).

[952] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject, the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the method includes detecting in a urinary sample obtained from the subject the presence of one or more mutations in TP53, FGFR3, or both. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, or VHL, one or more mutations in the TERT promoter, or both, are present in 0.03% or fewer of the urinary cells in the sample. In some embodiments of methods of detecting

bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a PCR based multiplex assay. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a Sanger Sequencing assay. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed using a next generation sequencing assay.

[953] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting in the sample the presence of aneuploidy comprises detecting the presence of one or more alterations on one or more of chromosome arms 5q, 8q, and 9p. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of aneuploidy comprises amplifying long interspersed nucleotide elements (LINESs).

[954] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS,

MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that allows for the detection of rare mutant alleles in a range of 1 mutant template among 5,000 to 1,000,000 wild-type templates. In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the step of detecting the presence of one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the step of detecting the presence of at least one mutation in the TERT promoter, or both is performed by increasing the sensitivity of massively parallel sequencing instruments with an error reduction technique that includes: a) assigning a unique identifier (UID) to each template molecule, b) amplifying each uniquely tagged template molecule to create UID-families, and c) redundantly sequencing the amplification products.

[955] In some embodiments of methods of detecting bladder cancer or an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the method further includes conducting cytology on the sample, wherein presence of the one or more mutations in TP53, PIK3CA, FGFR3, KRAS, ERBB2, CDKN2A, MLL, HRAS, MET, VHL, the presence of the at least one mutation in the TERT promoter, the presence of aneuploidy, or a positive cytology indicates that the subject has bladder cancer.

[956] In some embodiments of methods of detecting bladder cancer in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the method further includes administering transuretral resection of the bladder (TURB), intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant chemotherapy, neoadjuvant chemotherapy, cystectomy or cystoprostatectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combinations of the above.

[957] In some embodiments of methods of detecting an upper tract urothelial carcinoma in a subject in which the subject has previously undergone treatment for bladder cancer or an upper tract urothelial carcinoma, the method further includes administering transurethral resection, intravesical BCG (Bacillus Calmette-Guerin), intravesical chemotherapy, adjuvant

chemotherapy, neoadjuvant chemotherapy, ureterectomy or nephroureterectomy, radiation therapy, immunotherapy, immune checkpoint inhibitors, or any combination thereof.

[958] This document provides methods and materials for identifying one or more chromosomal anomalies (e.g., aneuploidy). In some cases, this document provides methods and materials for using amplicon-based sequencing data to identify a mammal as having a disease or disorder associated with one or more chromosomal anomalies. For example, methods and materials described herein can be applied to a sample obtained from a mammal to identify the mammal as having one or more chromosomal anomalies. For example, methods and materials described herein can be applied to a sample obtained from a mammal to identify the mammal as having a disease or disorder associated with one or more chromosomal anomalies. For example, a prenatal mammal can be identified as having a disease or disorder based, at least in part, on the presence of one or more aneuploidies. This document also provides methods and materials for identifying and/or treating a disease associated with one or more chromosomal anomalies. In some cases, one or more chromosomal anomalies can be identified in DNA obtained from a sample obtained from a mammal. For example, a mammal identified as having cancer based, at least in part, on the presence of one or more chromosomal anomalies can be treated with one or more cancer treatments.

[959] As demonstrated herein, a new approach (called WALDO for **W**ithin-**S**ample-**A**neup**L**oidy-**D**etecti**O**n, can be used to evaluate the sequencing data obtained from amplicons to identify the presence of one or more chromosomal anomalies (e.g., aneuploidy). For example, WALDO can employ supervised machine learning to detect the small changes in multiple chromosome arms that are often present in cancers. As described herein, WALDO was used to search for chromosome arm gains and losses in 1,677 tumors as well as in 1,522 liquid biopsies of blood from cancer patients or normal individuals. Aneuploidy was detected in 95% of cancer biopsies and in 22% of liquid biopsies. Using single nucleotide polymorphisms (SNPs) within the amplified interspersed nucleotide elements (LINEs), WALDO concomitantly assessed allelic imbalances, microsatellite instability, and sample identification. WALDO can be used on samples containing only a few nanograms (ng) of DNA and having as little as 1% neoplastic content.

[960] Having the ability to use amplicon-based sequencing reads to detect one or more chromosomal anomalies provides a unique and unrealized opportunity to achieve high coverage depth with improved sensitivity at relatively low cost. Moreover, the ability to use amplicon-based sequencing reads allows the detection of one or more chromosomal anomalies (e.g., aneuploidies) from samples containing limited amounts of DNA. This approach can be used in a variety of applications including, but not limited to, diagnostics (e.g., prenatal diagnostics and/or cancer diagnostics) and forensic science.

[961] In general, one aspect of this document features a method for detecting aneuploidy in a genome of a mammal. The method includes, or consists essentially of, sequencing a plurality of amplicons obtained from a sample obtained from the mammal to obtain sequencing reads; grouping the sequencing reads into clusters of genomic intervals; calculating sums of distributions of the sequencing reads in each genomic interval using the equation $\sum_1^I R_i \sim N(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$, where R_i is the number of sequencing reads, I is the number of clusters on a chromosome arm, N is a Gaussian distribution with parameters μ_i and σ_i^2, where μ_i is the mean number of sequencing reads in each genomic interval, and where σ_i^2 is the variance of sequencing reads in each genomic interval; calculating a Z-score of a chromosome arm using the quantile function 1-CDF($\sum_1^I \mu_i, \sum_1^I \sigma_i^2$); and identifying the presence of an aneuploidy in the genome of the mammal when the Z-score is outside a significance threshold. The plurality of amplicons can include from about 10,000 amplicons to about 1,000,000 amplicons (e.g., the plurality of amplicons can include about 38,000 amplicons). The genomic intervals can include from about 100 nucleotides to about 125,000,000 nucleotides (e.g., the genomic intervals can include about 500,000 nucleotides). The mammal can be a human. The sample can be a liquid biopsy. The liquid biopsy can be blood, urine, saliva, cyst fluid, sputum, tissue, stool, pap smears, or cerebral spinal fluid. The liquid biopsy can be a blood sample (e.g., a plasma sample). The blood sample can include cell free fetal DNA. The sample can include a neoplastic cell fraction. The neoplastic cell fraction in the sample can include less than about 1% (e.g., less than about 0.5%) of the entire sample. The amplicons can include unique long interspersed nucleotide elements (LINEs). The sequencing step also can include amplifying DNA from the sample obtained from the mammal to obtain the amplicons. The amplifying can be performed using a single

primer pair. The amplicons can include about 100 to about 140 base pairs. Each amplicon can be sequenced between 1 and 20 times. The method can include about 100,000 to about 25 million sequencing reads. Each cluster can include about two hundred genomic intervals. The method also can include supervised machine learning. The supervised machine learning can employ a support vector machine model.

[962] In another aspect, this document features a method for detecting one or more polymorphisms in a genome of a mammal. The method includes, or consists essentially of, sequencing a plurality of amplicons obtained from a sample from the mammal to obtain variant sequencing reads; sequencing a plurality of amplicons obtained from a reference sample from the mammal to obtain reference sequencing reads; grouping the variant sequencing reads and the reference sequencing reads into clusters of genomic intervals; selecting a chromosome arm having a sum of the variant sequencing reads and the reference sequencing reads on both alleles that is greater than about 3; determining a variant-allele frequency (VAF) of the selected chromosome arm, wherein said VAF is the number of variant sequencing reads / total number of sequencing reads; and identifying the presence of one or more polymorphisms on said selected chromosome arm of the mammal if the VAF is between about 0.2 and about 0.8. The sequencing step can include assigning a unique identifier (UID) to each amplicon, amplifying each uniquely tagged amplicon to create UID-families, and redundantly sequencing the amplification products. The sequencing step can further include calculating a Z-score of a variant on said selected chromosome arm using the equation $Z \sim \frac{\sum_{i=1}^{k} w_i Z_i}{\sqrt{\sum_{i=1}^{k} w_i^2}}$, where w_i is UID depth at a variant i, Z_i is the Z-score of variant i, and k is the number of variants observed on the chromosome arm. The one or more polymorphisms can include single base substitutions, insertions, deletions, indels, and/or combinations thereof. The pluralities of amplicons can include from about 10,000 amplicons to about 1,000,000 amplicons (e.g., the pluralities of amplicons can include about 38,000 amplicons). The genomic intervals can include from about 100 nucleotides to about 125,000,000 nucleotides (e.g., the genomic intervals can include about 500,000 nucleotides). The mammal can be a human. The sample can be a liquid biopsy. The liquid biopsy can be blood, urine, saliva, cyst fluid, sputum, tissue, stool, pap smears, or cerebral spinal fluid. The

liquid biopsy can be a blood sample (e.g., a plasma sample). The blood sample can include cell free fetal DNA. The sample can include a neoplastic cell fraction. The neoplastic cell fraction in the sample can include less than about 1% (e.g., less than about 0.5%) of the entire sample. The amplicons can include unique long interspersed nucleotide elements (LINEs). The sequencing step also can include amplifying DNA from the sample obtained from the mammal to obtain the amplicons. The amplifying can be performed using a single primer pair. The amplicons can include about 100 to about 140 base pairs. Each amplicon can be sequenced between 1 and 20 times. The method can include about 100,000 to about 25 million sequencing reads. Each cluster can include about two hundred genomic intervals. The method also can include supervised machine learning. The supervised machine learning can employ a support vector machine model.

OTHER EMBODIMENTS

[963] It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

EXAMPLES

Example 1: Detection and localization of surgically resectable cancers with a multi-analyte liquid biopsy

[964] Many of the currently approved tests for earlier cancer detection are procedural in nature, and include colonoscopy, mammography, and cervical cytology analysis. To date, the vast majority of cancer patients evaluated with mutation-based liquid biopsies have advanced stage disease. Yet another issue with liquid biopsies is the identification of the underlying organ of origin. Because the same gene mutations drive multiple tumor types, liquid biopsies based on such alterations cannot generally identify the location of the primary tumor giving rise to a positive blood test.

[965] This Example describes a new blood test, called CancerSEEK, which addresses the problematic issues described above. The test utilizes combined assays for genetic alterations and protein biomarkers and has the capacity not only to identify the presence of relatively early cancers but also to pinpoint the organ of origin of these cancers (Fig. 1).

[966] CancerSEEK is a widely applicable, non-invasive test for most cancers. The eight cancer types studied here account for 360,000 (60%) of the estimated cancer deaths in the U.S. in 2017 and their earlier detection could conceivably reduce deaths from these diseases. At the time of this disclosure, the cost of CancerSEEK is less than $500, which is comparable or lower than other screening tests for *single* cancers, such as colonoscopy, while this test can detect at least eight different cancer types.

Materials and Methods

Plasma, white blood cell and tumor DNA samples

[967] The study was approved by the Institutional Review Boards for Human Research at each institution, and samples were obtained after informed consent was obtained. Patients with stage I to III cancer, who had undergone surgical resection at the participating institutions were included in the study. Blood was collected from patients before any therapy was undertaken (i.e., before neoadjuvant therapy in those patients receiving neoadjuvant therapy) and before surgery in all patients. If sample was drawn on the day of surgery, then care was taken to ensure that the blood was collected prior to the administration of anesthesia, as anesthesia can increase the levels of circulating biomarkers (Cohen *et al.*, 2017 *Proc Natl Acad Sci U S A* 114:10202-10207). General demographics, surgical pathology, and AJCC stage (7^{th} edition) were documented. The 'healthy' cohort consisted of peripheral blood samples obtained from 812 individuals of median age 55 (IQR interquartile range 28 to 65) with no history of cancer. The cancer and healthy control samples were processed in an identical manner. Plasma samples from 46 of the 1,005 cancer patients and 181 of the 812 normal samples had been previously evaluated with a different approach (Cohen *et al.*, 2017 *Proc Natl Acad Sci U S A* 114:10202-10207) (Table 2).

[968] DNA was purified from an average of 7.5 mL plasma using a QIASymphony circulating DNA kit (cat # 1091063), as specified by the manufacturer. DNA from peripheral WBCs was also purified with the QIAsymphony DP DNA Midi Kit (Cat # 937255) as specified by the manufacturer. Tumor tissues were formalin-fixed and paraffin-embedded (FFPE) according to standard histopathologic procedures and also purified with a QIAsymphony DP DNA Midi Kit (Cat # 937255).

Mutation detection and analysis

[969] For amplification of DNA from plasma, 61 primer pairs were designed (see below) to amplify 66 to 80 bp segments containing regions of interest from 16 genes.

[970] The 61 primer pairs were divided into two non-overlapping sets each containing either 28 or 33 primer pairs. Each of these two primer sets were used to amplify DNA in six independent 25 µl reactions as described elsewhere (see, e.g., Wang *et al.*, 2016 *Elife* 5) except that 15 cycles were used for the initial amplification. The PCR products were purified with AMPure XP beads (Beckman Coulter, PA, USA) and 1% of the purified PCR products were then amplified in a second round of PCR as described elsewhere (see, e.g., Wang *et al.*, 2016 *Elife* 5), but using 21 cycles. PCR products from the second round of amplification were then purified with AMPure and sequenced on an Illumina MiSeq or HiSeq 4000 instrument.

[971] The template-specific portion of the reads was matched to reference sequences using custom scripts written in SQL and C#. Reads from a common template molecule were then grouped based on the unique identifier sequences (UIDs) that were incorporated as molecular barcodes as described elsewhere (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535). Artefactual mutations introduced during the sample preparation or sequencing steps were reduced by requiring a mutation to be present in > 90% of reads in each UID family. Redundant reads arising from optical duplication were eliminated by requiring reads with the same UID and sample index to be at least 5,000 pixels apart when located on the same tile. Mutations that met one of the two following criteria were considered (i) present in the COSMIC database (Forbes *et al.*, 2017 *Nucleic Acids Res* 45:D777-D783), or (ii) predicted to be inactivating in tumor suppressor genes (nonsense mutations, out-of-

frame insertions or deletions, canonical splice site mutations). Synonymous mutations, except those at exon ends, and intronic mutations, except for those at splice sites, were excluded.

Evaluation of plasma proteins

[972] The Bioplex 200 platform (Biorad, Hercules CA) was used to determine the concentration of multiple target proteins in the plasma samples. Luminex bead based immunoassays (Millipore, Bilerica NY) were performed following the manufacturers protocols and concentrations were determined using 5 parameter log curve fits (using Bioplex Manager 6.0) with vendor provided standards and quality controls. The HCCBP1MAG-58K panel was used to detect FGF2, Osteopontin, sFas, IL-8/CXCL8, Prolactin, HE4, HGF, AFP, CA125, IL6, CA15-3, TGFa, CYFRA21-1, CEA, CA19-9 and Leptin. The HANG2MAG-12K panel was used to detect PAR, sPECAM-1, TSP-2, sEGFR, AXL and sHER2/sEGFR2/sErbB2. The HCMBMAG-22K panel was used to detect DKK1, GDF15, Osteoprotegerin (OPG) and Neuron-specific enolase (NSE). The HCCBP4MAG-58K panels was used to detect Kallikrein-6, CD44, Midkine and Mesothelin. The HAGP1MAG-12K panel was used to detect Follistatin, G-CSF, Angiopoietin-2 and Endoglin. The HCCBP3MAG-58K panel was used to detect SHBG, Galectin and Myeloperoxidase. The HTMP1MAG-54K panel was used to detect TIMP-1 and TIMP-2. LRG-1 and Vitronectin were not included in this study since they could not be reproducibly evaluated with a single immunoassay platform.

Algorithm for classifying ctDNA status

[973] The classification of a sample's ctDNA status was obtained from a statistical test comparing the normalized mutation frequencies of the sample of interest to the distributions of the normalized mutation frequencies of, respectively, normal and cancer samples in the training set. Specifically, the mutant allele frequency (MAF), defined as the ratio between the number of supermutants and the number of UIDs, was first normalized based on the observed

MAFs for each mutation in a set of normal controls. Following this mutation-specific normalization, the MAF of each mutation in each well was compared to two reference distributions of MAFs: 1) a distribution built from the normal control plasmas in the training set plus a set of 188 WBCs from unrelated, healthy individuals 2) a distribution built from the cancers' samples in a training set that included only mutations found in plasma that were also present with MAF > 5% in the corresponding primary tumors. Corresponding p-values, p^N and p^C, were thus obtained. For each mutation, the log ratio of these two p-values was calculated, and the minimum and maximum of these log ratios across the six wells were eliminated so that the results would be less sensitive to outliers. An "omega" score was then determined according to the following formula:

$$\Omega = \sum_{i=1}^{4} w_i * \ log \frac{p_i^C}{p_i^N} ,$$

where w_i is the proportion of UIDs in well i out of the total number of UIDs for that mutation present across the four wells. When a mutation identified in a plasma sample had $\Omega > 1$, and was not identified in the primary tumor of the patient, DNA from white blood cells (WBCs) of the same patient whenever WBCs were available (23% of the cancer patients was evaluated. WBC DNA was tested with the same 61-amplicon panel to ensure that the plasma mutation was not a result of Clonal Hematopoiesis of Indeterminate Potential (Jaiswal et al., 2014 *N Engl J Med* 371:2488-2498). WBCs from the normal individuals were evaluated identically whenever a mutation with $\Omega > 1$ was found in the plasma. Any mutation that was identified in the WBCs as well as in the plasma was excluded from the analysis. The requirement for exclusion was that the ratio between the max MAF in the plasma and the max MAF in the WBC was less than 100.

[974] The mutation with the greatest Ω score in each patient or normal control was then deemed the "top mutation" and is listed in Table 3. This score was used in the logistic regression as well as the concentrations of the following 10 proteins, selected via an optimization step, Prolactin, OPN, IL6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and TIMP-1. To be conservative, a non-linear transformation was applied to the

features used by Logistic Regression. Specifically, if a protein's concentration in the sample of interest was lower than the 95th percentile of the concentration found for that same protein among the normal samples in the training set, then the protein's concentration was set equal to zero; otherwise the log of that concentration was used. For the Ω score, the same log-threshold transformation was used but with a constant threshold equal to 1. The *R glmnet* package (version 2.10-13) was then used to perform the Logistic Regression, with the lambda parameter set to zero as described elsewhere (see, e.g., Friedman et al., 2010 *Journal of Statistical Software* 33:74862). The importance of each feature was evaluated by multiplying its coefficient (see below) times the difference of the feature's mean between normal and cancer samples. Ten rounds of 10-fold cross-validations were performed. The classification calls obtained in an average round of 10-fold cross-validation (CV) are listed for each of the 812 normal individuals and 1,005 cancer patients in Table 2.

Logistic regression model coefficients and importance scores.

Feature	**Logistic Regression Coefficient**	**Importance Score**
Ω score	1.77E+00	7.55E+00
CA-125	4.15E-02	1.37E+00
CEA	2.33E-04	1.17E+00
CA19-9	1.20E-02	5.18E-01
Prolactin	3.51E-05	4.76E-01
HGF	2.45E-03	3.03E-01
OPN	1.45E-05	1.72E-01
Myeloperoxidase	5.40E-03	9.31E-02
TIMP-1	7.34E-06	7.05E-02

[975] For prediction of cancer type, the same 11 features (mutation score and levels of ten proteins) were used plus patient gender and the other 29 proteins evaluated in this study. Cancer type prediction was performed only on the cancer samples that were correctly classified as cancer by Logistic Regression. Random Forest, as implemented in the *randomForest* package (version 4.6-12) (see, e.g., Liaw et al., 2001 *R news* 2:18-22) was

used for this prediction. Ten rounds of 10-fold CV were performed and, for consistency, in each round and in each fold the same partition used by Logistic Regression was used by Random Forest. The classification calls obtained in an average round of 10-fold CV (the same round for which cancer status is reported in Table 3), are listed in Table 6.

[976] For determining the concordance between mutations identified in the plasma with those identified in primary tumors (Table 5), only the 155 cases in which a mutation could be identified with high confidence in the plasma were considered (Ω score > 3, Table 3) and in which the primary tumor contained any mutation that was present at a mutant allele fraction of > 5% (Table 1). This approach allowed us to avoid scoring tumors that had low neoplastic contents.

Sample identification

[977] To confirm that plasma, WBC, and primary tumor DNA samples originated from the same patient primers were utilized that could be used to amplify ~38,000 unique long interspersed nucleotide elements (LINEs) from throughout the genome as described elsewhere (see, e.g., Kinde et al., 2012 *PloS one* 7:e41162). These ~38,000 LINEs contain 26,220 common polymorphisms which can establish or refute sample identity among plasma, white blood cell and tumor samples. The genotype at each polymorphic location was identified, and the percent concordance between the samples of interest was calculated. Concordance was defined as the number of matched polymorphic sites that were identical in both samples divided by the total number of genotypes that had adequate coverage in both samples. Two samples were considered a match if concordance was > 0.99 and at least 5,000 amplicons had adequate coverage.

Statistical analysis

Continuous variables were reported as means and standard deviations or medians and range as deemed necessary while categorical variables were reported as whole numbers and percentages. Confidence intervals (CI) for sensitivities were calculated using a binomial

distribution. P-values were calculated with a one sided binomial test using the R *stats* package (version 3.3.1).

Results

[978] To identify a panel of protein and gene markers that might be used to detect many solid tumors at a stage prior to the emergence of distant metastases, a PCR-based assay was designing that could simultaneously assess multiple regions of driver genes that are commonly mutated in a variety of cancer types. Four challenges confronted this design. First, the test must query a sufficient number of bases to allow a large number of cancers to be detected. Second, each queried base must be sequenced thousands of times to detect mutations present at low prevalence. Third, the more bases that are queried the more likely that artifactual mutations will be identified, reducing the signal-to-noise ratio. And fourth, a test that can be implemented in a screening setting must be cost effective and high throughput, limiting the amount of sequencing that must be performed. To meet these contrasting challenges, a minimum number of short amplicons was identified that would allow detection of at least one driver gene in each of the eight tumor types evaluated. Using Publicly available sequencing data was used to determine that there was a fractional power law relationship between the number of amplicons required and the sensitivity of detection, with a plateau at ~ 60 amplicons (Fig. 2). Raising the number of amplicons above a threshold level would not detect substantially more cancers but would increase the probability of false positive results. This decreasing marginal utility defined the optimal number of amplicons.

[979] Based on these data, a 61-amplicon panel was designed with each amplicon querying an average of 33 bp within one of 16 genes (see Materials and Methods). As shown in Fig. 2, this panel would theoretically detect 41% (liver) to 95% (pancreas) of the cancers in the Catalog of Somatic Mutations in Cancer (COSMIC) dataset (Forbes *et al.*, 2017 *Nucleic Acids Res* 45:D777-D783). In practice, the panel performed considerably better, detecting at least one mutation in 82%, two mutations in 47%, and more than two mutations in 8% of the 805 cancers evaluated in our study (dots in Fig. 2, Fig. 3, and Table 1). A larger fraction of tumors was detected than predicted by the COSMIC dataset because the PCR-based

sequencing assay was more sensitive for detecting mutations than conventional genome-wide sequencing. Based on this analysis of the DNA from primary tumor tissues, the predicted maximum detection capability of circulating tumor DNA (ctDNA) varied by tumor type, ranging from 60% for liver cancers to 100% for ovarian cancers (Fig. 2).

[980] Armed with this small but robust panel of amplicons, two approaches were developed that enabled the detection of the rare mutations expected to be present in plasma. First, a multiplex-PCR was used to directly and uniquely label each original template molecule with a DNA barcode. This design minimized the errors inherent to massively parallel sequencing and made efficient use of the small amount of cell-free DNA present in plasma. Additionally, the total amount of DNA recovered from plasma was divided into multiple aliquots and independent assays were performed on each replicate. This decreased the number of DNA molecules per well; however, it increased the fraction of each mutant molecule per well making it easier to assay. Because the sensitivity of detection is often limited by the fraction of mutant alleles in each replicate, this partitioning strategy allowed an increase in the signal-to-noise ratio and identification of mutations present at lower prevalence than possible if all of the plasma DNA was evaluated at once.

[981] The second component of CancerSEEK is based on protein biomarkers. The literature was searched to find proteins potentially useful for early detection and cancer diagnosis in at least one of the eight cancer types described above with sensitivities > 10% and specificities > 99%. 41 potential protein biomarkers were identified and evaluated in preliminary studies on plasma samples from individuals without cancer and from cancer patients. 39 of these proteins could be reproducibly evaluated through a single immunoassay platform and these were then used to assay all plasma samples. Ten of these 39 proteins proved to be useful for discriminating cancer patients from healthy controls, and are set forth below.

Protein biomarkers analyzed and included in exemplary CancerSEEK test.

Protein	Evaluated in this study	Included in exemplary CancerSEEK test	Used for cancer type identification
AFP	Yes	No	Yes
Angiopoietin-2	Yes	No	Yes
AXL	Yes	No	Yes
CA125	Yes	Yes	Yes
CA15-3	Yes	No	Yes
CA19-9	Yes	Yes	Yes
CD44	Yes	No	Yes
CEA	Yes	Yes	Yes
CYFRA 21-1	Yes	No	Yes
DKK1	Yes	No	Yes
Endoglin	Yes	No	Yes
FGF2	Yes	No	Yes
Follistatin	Yes	No	Yes
Galectin-3	Yes	No	Yes
G-CSF	Yes	No	Yes
GDF15	Yes	No	Yes
HE4	Yes	No	Yes
HGF	Yes	Yes	Yes
IL-6	Yes	Yes	Yes
IL-8	Yes	No	Yes
Kallikrein-6	Yes	No	Yes
Leptin	Yes	No	Yes
LRG-1	No	No	No
Mesothelin	Yes	No	Yes
Midkine	Yes	Yes	Yes
Myeloperoxidase	Yes	Yes	Yes
NSE	Yes	No	Yes
OPG	Yes	No	Yes
OPN	Yes	Yes	Yes
PAR	Yes	No	Yes
Prolactin	Yes	Yes	Yes
sEGFR	Yes	No	Yes
sFas	Yes	No	Yes
SHBG	Yes	No	Yes
sHER2/sEGFR2/sErbB2	Yes	No	Yes
sPECAM-1	Yes	No	Yes

TGFa	Yes	No	Yes
Thrombospondin-2	Yes	No	Yes
TIMP-1	Yes	Yes	Yes
TIMP-2	Yes	No	Yes
Vitronectin	No	No	No

[982] This study included 1,005 patients with Stage I to III cancers of the ovary, liver, esophagus, pancreas, stomach, colorectum, lung, or breast. No patient received neo-adjuvant chemotherapy prior to blood sample collection. None had evident distant metastasis at the time of study entry and all underwent surgical resection with the intent to cure. The median age at diagnosis was 64 (range 22 to 93). The eight cancer types were chosen because they are common and because no blood-based tests for earlier detection of them are in common clinical use. The histopathological and clinical characteristics of the patients are summarized in Table 2.

[983] The most common stage at presentation was American Joint Commission on Cancer (AJCC) stage II, accounting for 49% of patients, with the remaining patients harboring stage I (20%), or stage III (31%) disease. The number of samples per stage for each of the eight tumor types is summarized below. A total of 812 individuals of median age 55 (range 17 to 88) with no known history of cancer, high-grade dysplasia, autoimmune disease, or chronic kidney disease acted as the healthy control cohort.

Cancer patients evaluated in this study by tumor type and stage.

Tumor Type	AJCC Stage	Patients (n)	Proportion of cases (%)
Breast	I	32	15
	II	114	55
	III	63	30
	I-III	209	--
Colorectum	I	77	20
	II	191	49
	III	120	31
	I-III	388	--
Esophagus	I	5	11
	II	29	64
	III	11	24

	I-III	45	--
Liver	I	5	11
	II	19	43
	III	20	45
	I-III	44	--
Lung	I	46	44
	II	27	26
	III	31	30
	I-III	104	--
Ovary	I	9	17
	II	4	7
	III	41	76
	I-III	54	--
Pancreas	I	4	4
	II	83	89
	III	6	6
	I-III	93	--
Stomach	I	21	31
	II	30	44
	III	17	25
	I-III	68	--

[984] CancerSEEK evaluates levels of 10 proteins and mutations in 2,001 genomic positions; each genomic position could be mutated in several ways (single base substitutions, insertions, or deletions). The presence of a mutation in an assayed gene or an elevation in the level of any of these proteins would classify a patient as positive. Rigorous statistical methods were employed to ensure the accuracy of the test. Log ratios were used to evaluate mutations and incorporated them into a logistic regression algorithm that took into account both mutation data and protein biomarker levels to score CancerSEEK test results. The mean sensitivities and specificities were determined by ten iterations of 10-fold cross-validations. The receiver operating characteristic (ROC) curves for the entire cohort of cancer patients and controls in one representative iteration is shown in Fig. 4A.

[985] The median sensitivity of CancerSEEK among the eight cancer types evaluated was 70% ($p < 10^{-96}$ one-sided binomial test) and ranged from 98% in liver cancers to 33% in breast cancers (Fig. 4C). At this sensitivity, the specificity was > 99%, i.e., only 6 of the individuals without known cancers scored positive.

[986] The features of the test that were most important to the algorithm were the presence of a ctDNA mutation followed by elevations of Prolactin, OPN, IL-6, CEA, CA125, HGF, Myeloperoxidase, CA19-9, Midkine, and TIMP-1 protein levels. Waterfall plots for each of the ctDNA and protein features used in CancerSEEK illustrate their distribution among individuals with and without cancer (Fig. 4). The importance ranking of the ctDNA and protein features used in CancerSEEK are provided below and a principal component analysis displaying the clustering of individuals with and without cancer is shown in Fig. 5. The complete dataset, including the levels of all proteins studied and the mutations identified in the plasma samples, are provided in Table 3 and Table 4. The probabilistic rather than deterministic nature of the approach used here to call a sample positive is evident from Fig. 6; each panel represents the sensitivity of CancerSEEK when one specific feature was excluded from the analysis.

[987] A screening test is advantageously able to detect cancers at early stages. The median sensitivity of CancerSEEK was 73% for the most common stage evaluated (Stage II), similar (78%) for Stage III cancers, and lower (43%) for Stage I cancers (Fig. 4B). The sensitivities for the earliest stage cancers (Stage I) were highest for liver (100%) and lowest for esophageal cancer (20%).

[988] The basis of liquid biopsy is that mutant DNA templates in plasma are derived from dying cancer cells and thus serve as exquisitely specific markers for neoplasia. To test this expectation, tumor tissue from 155 patients in whom ctDNA could be detected at statistically significant levels and in whom primary tumors were available were evaluated. The mutation in the plasma was identical to a mutation found in the primary tumor of the same individual in 138 (90%) of these 155 cases (Table 5). This concordance between plasma and primary tumor was evident in all 8 cancer types, and ranged from 100% in ovarian and pancreatic cancers to 82% in stomach cancers.

[989] A major limitation of conventional liquid biopsies is their inability to determine the cancer type in patients who test positive, thereby posing challenges for clinical follow-up. In addition to increasing the sensitivity of detection, the combination of protein biomarkers and ctDNA helped identify the type of cancer that might exist with a positive CancerSEEK test. Supervised machine learning was used to predict the underlying cancer type in patients with

positive CancerSEEK tests. The input algorithm took into account the gender of the patient and the protein and ctDNA biomarker data. One of the main purposes of such predictions is to determine the most appropriate follow up test for cancer diagnosis or monitoring after a positive CancerSEEK test. Patients with esophageal and gastric cancers were grouped together, as the optimal follow-up for individuals potentially affected with these two cancers would be endoscopy.

[990] An algorithm was used to study the 617 patients scoring positive in the CancerSEEK Test. Without any clinical information about the patients, the source of the cancer was localized to two anatomic sites in a median of 83% of these patients (Fig. 8, Table 6; $p < 10^{-77}$ one-sided binomial test). Furthermore, the source of the positive test was localized to a single organ in a median of 63% these patients (Fig. 8, Table 6; $p < 10^{-47}$ one-sided binomial test). The accuracy of prediction varied with tumor type and was best for colorectal cancers and lowest for lung cancers as shown below (see, also, Fig. 8).

Confusion matrix of top predictions from cancer type localization results.

		Breast	Colorectum	Liver	Lung	Ovary	Pancreas	Upper GI
Predicted cancer type	**Breast**	63%	3%	2%	8%	4%	3%	3%
	Colorectum	26%	84%	30%	48%	15%	15%	44%
	Liver	0%	1%	44%	2%	0%	0%	4%
	Lung	4%	2%	0%	39%	2%	1%	4%
	Ovary	3%	0%	0%	2%	79%	0%	0%
	Pancreas	4%	2%	9%	2%	0%	81%	0%
	Upper GI	0%	9%	14%	0%	0%	0%	46%

[991] The results described herein demonstrate that a blood test based on genes and proteins can be used to detect a major fraction (median of 70%) of eight major cancer types. In the majority of the samples that scored positive, the underlying cancer type could be predicted simply from the test results without any prior knowledge of the patient's medical history or disease status. The specificity of CancerSEEK was high, with less than 1% of 812 individuals without known cancers scoring positive.

Example 2: Combination approach to liquid biopsy cancer screening tests with increased sensitivity and high specificity

[992] There is a strong correlation between tumor stage and prognosis in many cancers (see, e.g., Ansari et al., 2017 *Br J Surg* 104(5):600-607). Very few patients with cancers of the lung, colon, esophagus, or stomach who have distant metastasis at the time of diagnosis survive for more than five years (see, e.g., Howlader et al., 2016 SEER Cancer Statistics Review, 1975-2013, National Cancer Institute. Bethesda, MD). It is therefore evident that earlier detection of cancers is one key to reducing deaths from these diseases.

[993] Biomarkers in the circulation provide one of the best ways, in principle, to detect cancers at an earlier stage. Historically, the type of biomarkers used to monitor cancers were proteins (see, e.g., Liotta et al., 2003 *Clin Adv Hematol Oncol* 1(8):460-462). More recently, mutant DNA has been explored as a biomarker as DNA released from the dying cells can escape into bodily fluids such as urine, stool, and plasma (see, e.g., Haber et al., 2014 *Cancer Discov* 4(6):650-661; Dawson et al., 2013 *N Engl J Med* 368(13):1199-1209; Bettegowda et al., 2014 *Science translational medicine* 6(224):224ra224; Kinde et al., 2013 *Science translational medicine* 5(167):167ra164; Wang et al., 2015 *Science translational medicine* 7(293):293ra104; Wang et al., 2015 *Proc Natl Acad Sci U S A* 112(31):9704-9709; Wang et al., 2016 *Elife* 5; Springer et al., 2015 *Gastroenterology* 149(6):1501-1510; Forshew et al., 2012 *Science translational medicine* 4(136):136ra168; Vogelstein et al., 1999 *Proc Natl Acad Sci U S A* 96(16):9236-9241; and Dressman et al., 2003 *Proc Natl Acad Sci U S A* 100(15):8817-8822). The concept underlying this approach, often called "liquid biopsies" is that cancer cells, like normal self-renewing cells, turn over frequently. However, studies of circulating tumor DNA (ctDNA) indicate that while ctDNA is elevated in >85% of patients with advanced forms of many cancer types, a considerably smaller fraction of patients with earlier stages of cancer have detectable levels of ctDNA in their plasma (see, e.g., Bettegowda et al., 2014 *Science translational medicine* 6(224):224ra224; and Wang et al., 2015 *Science translational medicine* 7(293):293ra104).

[994] This Example describes using a combination approach to cancer screening tests which increases the sensitivity of detection of resectable or otherwise treatable cancers under

conditions that preserve high specificity. For example, the assays described in this Example combine detection of mutations in ctDNA with detection of threshold protein markers in plasma.

Materials and Methods

Plasma, white blood cell and tumor DNA samples

[995] DNA was purified from plasma using a QIASymphony circulating DNA kit (Qiagen, cat # 1091063). Custom primers containing a unique identifier (UID) and amplicon specific sequences (Table 38) were used to amplify plasma DNA, and the resulting products were sequenced on an Illumina MiSeq or HiSeq instrument. Protein biomarker plasma concentrations were determined using Luminex bead based immunoassays on the Bioplex 200 platform (Biorad, Hercules CA). Plasma samples were scored as positive if the sample contained a KRAS mutation or if the concentration of CA19-9, CEA, HGF, or OPN was greater than 100 U/mL, 7.5 ng/mL, 0.92 ng/mL, or 158 ng/mL, respectively. All samples were obtained following approval by the Institutional Review Boards for Human Research at each institution and informed consent.

[996] Samples were obtained following approval by the Institutional Review Boards for Human Research at each institution and informed consent. Patients with Stage IA, IB, IIA or IIB (considered resectable) who had had peripheral blood collected prior to surgery, had not received neoadjuvant therapy, and had undergone surgical resection at the participating institutions between April 2011 and May 2016 were included in the study. General demographics, surgical pathology, and AJCC stage (7th edition) were documented. The 'healthy' cohort consisted of peripheral blood samples obtained from 185 individuals of average age 64 with no history of cancer. The pancreatic cancer and healthy control samples were collected and processed in an identical manner.

[997] DNA was purified from 3.75 mL plasma using a QIASymphony circulating DNA kit (cat # 1091063), as specified by the manufacturer. Tumor tissues were formalin-fixed and paraffin embedded (FFPE) according to standard histopathologic procedures and macro-dissected under a microscope to ensure a neoplastic cellularity of >30%. DNA was purified

with a QIAsymphony DP DNA Midi Kit (Cat # 937255) as specified by the manufacturer. DNA concentrations were assessed by fluorescence using SYBR Green I (Thermo Cat # S7585).

Mutation detection and analysis

[998] For amplification of DNA from plasma, primer pairs were designed to amplify 66 to 80 bp segments containing regions of interest from the KRAS and TP53 genes (Table 11 and Table 12). These primers were used to amplify DNA in six independent 25 µl reactions as described elsewhere (see, e.g., Wang et al., 2015 *Proc Natl Acad Sci U S A* 112(31):9704-9709). Reactions were purified with AMPure XP beds (Beckman Coulter, PA, USA) and eluted in 50 µl of Buffer EB (Qiagen). A fraction (5 µl) of purified PCR products were then amplified in a second round of PCR, as described elsewhere (see, e.g., Wang et al., 2015 *Proc Natl Acad Sci U S A* 112(31):9704-9709). The PCR products were purified with AMPure and sequenced on an Illumina MiSeq or HiSeq 4000 instrument.

[999] The template-specific portion of the reads was matched to reference sequences using custom scripts written in SQL and C#. Reads from a common template molecule were then grouped based on the unique identifier sequences (UIDs) that were incorporated as molecular barcodes (see, e.g., Allen et al., 2017 *Ann Surg* 265(1):185-191). Artefactual mutations introduced during the sample preparation or sequencing steps were reduced by requiring a mutation to be present in >90% of reads in each UID family.

Evaluation of plasma proteins

[1000] The Bioplex 200 platform (Biorad, Hercules CA) was used to determine the concentration of multiple target proteins in the plasma samples. Luminex bead based immunoassays were performed following the manufacturers protocols and concentrations were determined using 5 parameter log curve fits (using Bioplex Manager 6.0) with vendor provided standards and quality controls. Plasma samples were diluted 6-fold for assay of CA19-9, CEA, HGF, OPN and prolactin and 5-fold for assay of midkine. Plasma samples

were scored as positive if the concentration of CA19-9, CEA, HGF, or OPN was greater than 100 U/mL, 7.5 ng/mL, 0.92 ng/mL, or 158 ng/mL, respectively. The dynamic ranges of these immunoassays for CA19-9, CEA, HGF, OPN, prolactin, and midkine were 2.74 - 2,000 U/mL, 78.19 - 57,000 pg/mL, 27.43 - 20,000 pg/mL, 548.7 - 400,000 pg/mL, 137.17 - 100,000 pg/mL, and 13.72 - 10,000 pg/mL, respectively.

Algorithm for classifying ctDNA status

[1001] The classification of a sample's ctDNA status was obtained from a statistical test comparing the normalized mutation frequencies of the sample of interest to a distribution of normal controls. Specifically, the MAF, defined as the ratio between the number of supermutants and the number of UIDs, was first normalized based on the observed MAFs in a set of normal controls for each mutation. Following this mutation-specific normalization, the MAF of each mutation in each well was compared to a reference distribution of MAFs built from normal controls with all mutations included, and a p-value was calculated from this distribution. The lowest p-value among all mutations detected in a given sample was deemed the "top mutation". The classification of a sample's ctDNA status was based on whether the p-value of this top mutation was below or above a given threshold. The threshold was selected based on a desired specificity observed among an independent set of normal controls. Thus, no training was performed on any other sample except these controls; in particular, neither the 182 healthy controls nor the 221 pancreatic cancer patients described in the main text were included in the controls used for training the algorithm.

Statistical analysis

[1002] Continuous variables were reported as means and standard deviations or medians and range as deemed necessary while categorical variables were reported as whole numbers and percentages. Confidence intervals (CI) for sensitivities were calculated using a binomial distribution. Survival curves were estimated using Kaplan-Meier method and differences between curves were investigated with the log-rank test. Statistically significant variables in

the univariate analyses were subjected to multivariable Cox proportional hazard regression model.

[1003] Hazard ratio (HR) and 95% confidence interval (CI) for variables included in the multivariable model were reported. A p-value < 0.05 was considered to be statistically significant.

Results

Characteristics of patients with PDAC and presumed healthy controls

[1004] Two hundred and twenty-one patients with surgically resectable pancreatic cancer were evaluated in this study. The histopathological and clinical characteristics of these patients are summarized in Table 7. A total of 182 individuals of similar age with no known history of cancer, autoimmune disease, or chronic kidney disease acted as the healthy control cohort.

[1005] Twenty percent of the patients had no symptoms typically associated with pancreatic cancer. The size of the primary tumors at presentation ranged from 0.6 cm to 13 cm, with a median size of 3.0 cm. The most common stage at presentation was American Joint Commission on cancer stage (AJCC) Stage IIB, accounting for 77% of patients, with the remaining patients harboring Stage IA (5%), Stage IB (8%) or Stage IIA (10%) (Table 7). Patient survival correlated with stage, as graphically depicted in Fig. 12 and as expected from prior clinical studies (see, e.g., Allen et al., 2017 *Ann Surg* 265(1):185-191).

PCR-based assay to identify tumor-specific KRAS mutations in plasma samples

[1006] A PCR-based assay was designed that could simultaneously assess the two codons (codons 12 and 61) of the KRAS gene that are most frequently mutated in PDAC as well as surrounding codons. The assay employed a sensitive technology called the Safe-Sequencing System (Safe-SeqS) (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108(23):9530-9535). Safe-SeqS incorporates molecular barcodes that uniquely label each template molecule, thereby drastically minimizing the errors that routinely occur in massively parallel

sequencing. This approach can identify one mutant template among as many as 10,000 normal templates. Using this technology, KRAS mutations in the plasma of 66 of the 221 (30%: 95% CI 24—36%) pancreatic cancer cases (see below, and Table 8) were identified. Sixty-two (94%) and four (6%) of the mutations were at codons 12, and 61, respectively, with G>T transversions most commonly observed (Table 8). Mutations were found more frequently in Stage II patients than in Stage I patients (see below, Table 8, and Fig. 9A). Additionally, while the mutant allele frequency did not correlate with tumor size (Table 8, and Fig. 11A), mutations were found more frequently in larger tumors than in smaller tumors (see below, Table 8, and Fig. 9B).

Proportion of samples stratified by AJCC stage detected with each individual assay and all combinations thereof.

	Proportion of samples detected (95% confidence interval)				
Assay Type	Stage IA (12 cases)	Stage IB (17 cases)	Stage IIA (22 cases)	Stage IIB (170 cases)	Stage I&II (221 cases)
KRAS ctDNA	25% (5-57%)	0% (0-20%)	18% (5-40%)	35% (28-42%)	30% (24-36%)
CA19-9	17% (2-48%)	41% (18-67%)	36% (17-59%)	54% (46-62%)	49% (43-56%)
CEA + HGF + OPN	25% (5-57%)	6% (0-29%)	14% (3-35%)	19% (14-26%)	18% (13-24%)
KRAS ctDNA + CA19-9	33% (10-65%)	41% (18-67%)	50% (28-72%)	65% (58-72%)	60% (53-67%)
KRAS ctDNA Mutations + CEA + HGF + OPN	33% (10-65%)	6% (0-29%)	32% (14-55%)	47% (39-55%)	42% (35-48%)
CA19-9 + CEA + HGF + OPN	25% (5-57%)	47% (23-72%)	36% (17-59%)	59% (52-67%)	54% (47-61%)
Combination Assay	33% (10-65%)	47% (23-72%)	50% (28-72%)	69% (62-76%)	64% (57-70%)

Proportion of samples stratified by tumor size detected with each individual assay and all combinations thereof.

	Proportion of samples detected (95% confidence interval)						
Assay Type	≤ 1.5 cm (24 cases)	1.5-2.0 cm (12 cases)	2.0-2.5 cm (47 cases)	2.5-3.0 cm (38 cases)	3.0-3.5 cm (36 cases)	3.5-4.0 cm (22 cases)	> 4.0 cm (42 cases)
KRAS ctDNA	21% (7-42%)	17% (2-48%)	9% (2-20%)	32% (18-49%)	42% (26-59%)	45% (24-68%)	43% (28-59%)
CA19-9	25% (10-47%)	33% (10-65%)	43% (28-58%)	45% (29-62%)	58% (41-74%)	59% (36-79%)	67% (50-80%)
CEA + HGF + OPN	25% (10-47%)	8% (0-38%)	17% (8-31%)	21% (10-37%)	8% (2-22%)	18% (5-40%)	24% (12-39%)
KRAS ctDNA + CA19-9	38% (19-59%)	50% (21-79%)	47% (32-62%)	55% (38-71%)	78% (61-90%)	73% (50-89%)	74% (58-86%)
KRAS ctDNA Mutations + CEA + HGF + OPN	38% (19-59%)	25% (5-57%)	26% (14-40%)	47% (31-64%)	47% (30-65%)	55% (32-76%)	50% (34-66%)
CA19-9 + CEA + HGF + OPN	38% (19-59%)	33% (10-65%)	47% (32-62%)	53% (36-69%)	64% (46-79%)	64% (41-83%)	67% (50-80%)
Combination Assay	46% (26-67%)	50% (21-79%)	51% (36-66%)	61% (43-76%)	81% (64-92%)	77% (55-92%)	74% (58-86%)

Protein biomarkers in various cancer types.

Cancer Type	# Cases	% CA19-9	% CEA	% CA125	% AFP	% Prolactin	% HGF	% OPN	% TIMP-1	% Follistatin	% G-CSF	% CA15-3
Breast	150	3%	4%	1%	1%	8%	3%	3%	0%	1%	3%	1%
CRC	322	5%	17%	0%	1%	10%	11%	8%	8%	10%	9%	0%
Esophagus	43	7%	5%	0%	0%	2%	33%	19%	26%	2%	14%	5%
Gastric	65	11%	15%	0%	5%	3%	34%	20%	11%	8%	8%	3%
Liver	53	21%	9%	6%	40%	11%	25%	28%	17%	8%	6%	6%
Lung	109	4%	13%	0%	1%	11%	1%	2%	0%	0%	0%	3%
Ovarian	86	13%	1%	12%	3%	20%	3%	3%	10%	1%	0%	19%
Pancreas	412	52%	8%	0%	0%	0%	7%	6%	7%	8%	1%	0%

[1007] The number of mutant templates in the plasma could be calculated from the mutant allele fraction and the concentration of DNA in each plasma sample (Table 8). This number was often very low, with 15 (23%) of the patients with detectable KRAS mutations having < 2 mutant templates per ml of plasma. The average number of mutant templates per mL of plasma was 9.4 (Table 8). These results emphasize that extremely sensitive techniques can be used to detect the mutations in early stage pancreatic cancer patients. KRAS mutations were only observed in one of the 221 individuals in the presumed healthy cohort, a 69-year-old male with no known cancer.

[1008] The basis for the liquid biopsy concept is that the mutant DNA templates identified in the circulation are derived from cancers. It was therefore important to determine whether the KRAS mutations identified in these patients' plasma samples were also present in their primary carcinomas. Primary carcinomas from 50 of the 66 patients with detectable KRAS mutations in their plasma were obtained. In all 50 cases, the mutation found in the plasma was identical to that found in the primary carcinoma, providing another, orthogonal measure of specificity.

Simultaneous assessment of CA19-9 and KRAS mutations in plasma

[1009] It was sought to determine whether a combination of the KRAS ctDNA test with CA19-9, the PDAC biomarker, would result in improved sensitivity compared with the KRAS ctDNA test alone. Recent studies have shown that CA19-9 can be elevated in patients with pancreatic cancer two years prior to diagnosis (see, e.g., O'Brien et al., 2015 *Clin Cancer Res* 21(3):622-631). However, CA19-9 elevations have also been observed in non-malignant conditions, and 5% of the population cannot produce the CA19-9 antigen due to germline genetic variation, limiting its use for screening purposes (see, e.g., Lennon et al., 2010 Diagnostic and Therapeutic Response Markers. *Pancreatic Cancer*, (Springer New York, New York, NY), pp 675-701). However, it was reasoned that CA19-9 might prove useful as a screening biomarker if the threshold for scoring a result as positive was sufficiently high. A threshold of 100 U/mL was chosen based on prior data that this level is

not found among healthy individuals who do not have a clinical history of pancreaticobiliary disease (see, Kim et al., 2004 *J Gastroenterol Hepatol* 19(2):182-186).

[1010] Using this predefined high threshold, CA19-9 was detected in 109 of the 221 (49%: 95% CI 43—56%) patients with pancreatic cancer, and in none of the 182 healthy controls, confirming its specificity when used in this way (Table 8, and Table 9). As expected, the number of patients with detectable CA19-9 levels increased with stage and tumor size (Fig. 9, and Table 8). A question addressed in the current study was whether these two biomarkers – KRAS mutations and a positive CA19-9 score – were independent indicators of the presence of disease. It was found that the overlap was only partial, as indicated in the Venn diagram in Fig. 10. Though 42 patients (19%) had elevated CA19-9 levels as well as detectable KRAS mutations in their plasma, 91 additional patients had either mutations in KRAS or elevated CA19-9, but not both (Fig. 10). Thus, the combined sensitivity of these analyses was 60% (95% CI 53—67%), higher than the sensitivity of either alone (Fig. 9). As such, this Example demonstrates that the two assays could be combined without substantially increasing the false positive rate because each was extremely specific at the thresholds used.

Increasing sensitivity by inclusion of other protein biomarkers

[1011] Encouraged by the results described above, it was sought to further increase sensitivity by combining ctDNA KRAS mutations and CA19-9 with other protein biomarkers (Table 10). In a pilot study on a small number of pancreatic cancer samples independent from those studied here, the potential utility of other proteins that had been found to be elevated in cancer, including alpha-fetoprotein (AFP), CA15-3, leptin, IL-6, carcinoembryonic antigen (CEA), CA-125, interleukin 8 (IL-8), sFas, prolactin, osteopontin (OPN), basic fibroblast growth factor (FGF2), hepatocyte growth factor (HGF), cytokeratin-19 fragment (CYFRA 21-1), human epididymis protein 4 (HE4), transforming growth factor alpha (TGF-α), growth/differentiation factor 15 (GDF15), dickkopf-related protein 1 (DKK1), neuron specific enolase (NSE), osteoprotegerin (OPG), TIMP metallopeptidase inhibitor 1 (TIMP-1), TIMP metallopeptidase inhibitor 2 (TIMP-2), mesothelin, midkine, kallikrein-6, CD44, AXL receptor tyrosine kinase, soluble human epidermal growth factor receptor 2 (sHER2),

soluble epidermal growth factor receptor (sEGFR), soluble urokinase-type plasminogen activator receptor (suPAR), and soluble platelet endothelial cell adhesion molecule (sPECAM-1) was evaluated. Of these 29 protein biomarkers, five—CEA (see, e.g., Nazli et al., 2000 *Hepatogastroenterology* 47(36):1750-1752), HGF (see, e.g., Di Renzo et al., 1995 *Cancer Res* 55(5):1129-1138), midkine (see, e.g., Ikematsu et al., 2000 *Br J Cancer* 83(6):701-706), OPN (see, e.g., Koopmann et al., 2004 *Cancer Epidemiol Biomarkers Prev* 13(3):487-491), and prolactin (see, e.g., Levina et al., 2009 *Cancer Res* 69(12):5226-5233)—were chosen for further analysis.

[1012] When the levels of these five markers were evaluated in plasmas from the 221 patient pancreatic cancer cohort, an association between the plasma concentrations of prolactin and midkine and surgical site ($P < 0.01$, $\chi 2$ test, degrees of freedom = 5) was observed, suggesting that blood collection conditions might have elevated the levels of these two markers. There was no significant correlation between CA19-9, CEA, HGF, or OPN levels and collection sites, nor was there any correlation between the presence of KRAS ctDNA mutations and collection site ($P > 0.01$, $\chi 2$ test, degrees of freedom = 5). Upon further investigation, it was noted that the levels of prolactin and midkine were significantly elevated in samples that were collected after the administration of anesthesia but before surgical excision (Fig. 14). The results on prolactin were consistent with previous studies showing that anesthetics elevate the levels of this protein (see, e.g., Thorpe et al., 2007 *PLoS One* 2(12):e1281). To ensure that anesthesia did not affect the levels of the other protein biomarkers described above, paired plasma samples were collected before and immediately after the administration of anesthesia in 29 new patients. The only proteins found to be elevated by anesthesia were prolactin and midkine (Fig. 15), in perfect accordance with the correlation between collection site and protein levels noted above. Prolactin and midkine were therefore excluded from further analysis.

[1013] Unlike CA19-9, no predefined threshold exists for the use of CEA, HGF, or OPN as markers for pancreatic cancer. As a result, appropriate thresholds were determined in an independent set of 273 plasma samples from healthy controls. To be conservative, thresholds for each protein that were 10% higher than the maximum values observed in any of the 273 normal plasma samples were chosen. Notably, when these thresholds were applied to the

independent test set of 182 plasma samples, all three protein markers maintained 100% specificity (Table 9). The sensitivity of each of these three markers was less than that obtained with KRAS mutations or CA19-9 when each marker was used alone, but their levels were less dependent on stage and size than KRAS mutations or CA19-9 (Fig. 13, and Table 8). In combination with KRAS mutations and CA19-9 assays, this five-member biomarker panel ("combination assay") detected 141 (64%: 95% CI 57—70%) of the 221 resectable cancers (Table 7, Fig. 9A, Fig. 10, and Table 8).

[1014] Some of the patients detectable by the combination assay were of particular note. Forty-five (20%) patients had no symptoms classically associated with pancreatic cancer (Table 8). The combination assay identified 27 (60%) of these individuals, of whom 19 (70%) had no evidence of recurrence with a median follow up of 12 (range 3 – 16) months (Table 8). Of the 29 patients with the earliest stages of disease (Stages IA and IB) recognized by the AJCC, 12 (41%) were detectable using the combination assay (Fig. 9A), of whom 7 (58%) had no evidence of recurrence at the study termination with a median follow up of 19 (range 2 – 25) months.

[1015] Another notable but sobering result from this study was that patients with poorer survival were more likely to have a positive test. Of the entire 221 pancreatic cancer patients studied, 122 (56%) patients were alive at the termination of the study, with a median follow-up of 13 (7 – 21) months. It was found that the combination assay provided prognostic value that was independent of conventional clinical and histopathologic features. In particular, multivariate analyses showed that the independent predictors of overall survival were combination assay status (HR = 1.76, 95% CI, 1.10–2.84, p = 0.018), increasing age (HR = 1.04, 95% CI 1.02-1.06, p = 0.001), grade of differentiation (poorly differentiated, HR = 1.72, 95% CI 1.11–2.66, p = 0.015), lymphovascular invasion (present, HR = 1.81, 95% CI 1.06 – 3.09, p = 0.028), nodal disease (present, HR = 2.35, 95% CI 1.20 – 4.61, p = 0.013), and margin status (HR = 1.59, 95% CI 1.01 – 2.55, p = 0.050) (Table 7, Fig. 16).

TP53 in a multiplex assay

[1016] While nearly all pancreatic cancers harbor mutations within KRAS, a large fraction (~75%) also contains mutations in TP53 (see, e.g., Jones et al., 2008 *Science* 321(5897):1801-1806; Biankin et al., 2012 Nature 491(7424):399-405; and Waddell et al., 2015 *Nature* 518(7540):495-501). Furthermore, TP53 is the mostly commonly mutated gene in cancer (see, e.g., Vogelstein et al., 2013 *Science* 339(6127):1546-1558), making it an attractive target for ctDNA detection in future studies involving other tumor types. To determine whether the mutant allele frequencies of TP53 in the plasma correlated with those of KRAS, and also to determine whether a mutant TP53 assay in plasma might add to the sensitivity of the mutant KRAS assay, the 152 carcinomas for which matched tumor and plasma samples were available were evaluated. Mutations at one of the "hotspots" identified in genome-wide studies of PDAC (see, e.g., Jones et al., 2008 *Science* 321(5897):1801-1806) were first searched for. A total of 64 (42%) carcinomas contained a TP53 mutation at one of these positions. It was then determined whether these same mutations could be identified in the plasma of these 64 patients, using Safe-SeqS-based assays similar to that described above for KRAS but using primers specific for particular TP53 mutations.

[1017] TP53 mutations in 13 (20%) of the 64 plasma samples (see below) were identified. Two observations were of interest. First, 12 of the 13 plasma samples containing a detectable TP53 mutation also contained a detectable KRAS mutation. Thus, TP53 mutation assays did not substantially increase sensitivity for pancreatic cancer detection, as expected from the high prevalence of KRAS mutations noted above. Second, there was a strong correlation between the mutant allele frequencies of TP53 and KRAS mutations in the plasma of the 12 patients whose plasma contained detectable amounts of both mutations (Fig. 3, Pearson's r = 0.885). This provides yet another validation of the reliability of the ctDNA assay and its quantitative nature.

List of exemplary TP53 mutations detected in PDAC patients

Sample ID #	Plasma DNA concentration (ng/mL)	Mutation identified in plasma	Mutant mean allele frequency (%)	Mutant fragments/ mL plasma
PANC 335	13.28	TP53 p.R196*, c.586C>T	0.795	32.5
PANC 336	13.67	TP53 p.G266E, c.797G>A	0.929	39.1
PANC 552	19.44	TP53 p.R175H, c.524G>A	0.673	40.3
PANC 387	11.11	TP53 p.R175H, c.524G>A	0.195	6.7
PANC 467	6.76	TP53 p.R248Q, c.743G>A	0.344	7.2
PANC 468	10.28	TP53 p.S241F, c.722C>T	0.139	4.4
PANC 469	5.98	TP53 p.C238F, c.713G>T	0.051	0.9
PANC 545	12.23	TP53 p.Y236C, c.707A>G	0.137	5.2
PANC 547	10.73	TP53 p.Y234C, c.701A>G	0.069	2.3
PANC 552	10.00	TP53 p.C238Y, c.713G>A	0.317	9.8
PANC 692	9.83	TP53 p.V272M, c.814G>A	0.101	3.1
PANCA 1105	11.49	TP53 p.H193Y, c.577C>T	0.098	3.5
PANCA 1109	27.57	TP53 p.Y234C, c.701A>G	0.351	29.8

List of exemplary CDKN2A mutations detected in PDAC patients

Sample ID #	Mutation identified in plasma	Mutation identified in tumor tissue	Mutant mean allele frequency (%)
PANC 335 PLS1	CDKN2A p.R58*, c.172C>T	CDKN2A p.R58*, c.172C>T	0.432
PANC 552 PLS 1	CDKN2A p.D84G, c.251A>G	CDKN2A p.D84G, c.251A>G	0.166
PANC 641 PLS 1	CDKN2A g.21971208G>T (splice site)	CDKN2A g.21971208G>T (splice site)	0.143
PANC 447 PLS	CDKN2A p.R80*, c.238C>T	CDKN2A p.R80*, c.238C>T	0.102
PANC 398 PLS 1	CDKN2A p.V51D, c.152T>A	CDKN2A p.V51D, c.152T>A	0.091
PANC 609 PLS 1	CDKN2A p.R80*, c.238C>T	CDKN2A p.R80*, c.238C>T	0.071
PANC 455 PLS	CDKN2A p.H83Y, c.247C>T	CDKN2A p.H83Y, c.247C>T	0.061
PANC 517 PLS 1A	CDKN2A p.R58*, c.172C>T	CDKN2A p.R58*, c.172C>T	0.026
PANC 547 PLS 1	CDKN2A p.R58*, c.172C>T	CDKN2A p.R58*, c.172C>T	0.026
PANC 648 PLS 1	CDKN2A p.A76T, c.226G>A	CDKN2A p.A76T, c.226G>A	0.016
PANC 715 PLS 1	CDKN2A p.M54fs, c.162>G	CDKN2A p.M54fs, c.162>G	0.014
PANC 763 PLS 1	CDKN2A p.H83Y, c.247C>T	CDKN2A p.H83Y, c.247C>T	0.013
PANC 509 PLS 1	CDKN2A p.H83Y, c.247C>T	CDKN2A p.H83Y, c.247C>T	0.012
PANC 545 PLS 1	CDKN2A p.R80fs, c.239ACCCG>	CDKN2A p.R80fs, c.239ACCCG>	0.011
PANC 634 PLS 1	CDKN2A p.A76T, c.226G>A	CDKN2A p.A76T, c.226G>A	0.006

Example 3: Sensitivity and specificity of ctDNA and protein biomarkers

Materials and Methods

Phase A

[1018] Healthy Cohort: Ten thousand non-symptomatic women are recruited. The age range of participants is 65 to 75 years, as this range captures patients at maximum risk for cancers of the eight types that are the target of detection. Women with oophorectomies, known cancer of any type other than non-melanoma skin cancer, are excluded from the study. Plasma from each participant is obtained at study entry. In participants who test positive, as well as in a random sample of participants with negative tests, one additional sample of plasma is drawn at 3 months following the first test. When both tests are positive for the same mutation, a whole body PET/CT scan is performed. If the PET/CT exam is positive, patients are managed as deemed appropriate by their physicians. This management includes yearly follow-up ctDNA tests. Yearly follow-up of patients via electronic questionnaires, combined with phone interviews when necessary, are obtained on all individuals, whether their tests are positive or negative.

[1019] Management Cohorts: Two hundred patients with Stage III colon cancers and 50 patients with resectable pancreatic cancers are recruited from at least 10 sites across Australia, New Zealand and Singapore. Tumor samples are tested to identify mutations that can be used for subsequent ctDNA tests. Plasma samples are collected on all patients prior to surgery (including those randomized to receive routine care). Additional plasma samples are collected at 3, 6, and 12 months in patients whose ctDNA tests are positive prior to surgery. No further ctDNA analyses are performed in ctDNA-negative patients or those randomized to receive routine care. Patients are randomized 1:1 to ctDNA-informed management (with treatment escalation or de-escalation compared to standard of care, or to routine care [blinded to ctDNA test results]).

Phase B

[1020] Healthy Cohort: Forty thousand more non-symptomatic women are recruited. The inclusion and exclusion criteria are the same as in Phase A. Other than the longer follow-up and larger number of patients, there are at least two other differences between Phase A and Phase B. First, protein biomarkers that passed the specificity threshold (>99.5%) in Phase A samples are included. Patients who test positive for one or more of these protein biomarkers are managed identically to those with positive ctDNA results. Second, a "control" Healthy Cohort is added. These represents individuals recruited from the same population but in whom no blood samples are taken to assess disease or guide management. These controls are used to assess the ability of the screening tests to detect disease before they would ordinarily be detected on the basis of symptoms or standard medical care of healthy individuals. Comparisons between stage and survival in the screened and control cohorts are also made.

[1021] Management Cohorts: One thousand more patients with Stage III colon cancers (a total of 1200 patients) and 210 more patients with resectable pancreatic cancers (for a total of 250 patients) are recruited, but now at 30 sites rather than 10 sites. Similarly, to Phase A, tumor samples are collected at surgery in all new patients and mutations identified so that they can be used in subsequent ctDNA tests. Additionally, protein biomarkers for colorectal or pancreatic cancers that passed the specificity threshold (>99.5%) in Phase A are included. Patients who test positive for these protein biomarkers are managed identically to those with positive ctDNA results. Plasma samples are collected on all patients prior to surgery and at 3, 6, and 12 months in patients whose ctDNA tests are positive prior to surgery. Patients are randomized 1:1 to ctDNA-informed management (with treatment escalation or de-escalation compared to standard of care, or to routine care [blinded to ctDNA result]).

Evaluations

[1022] The Safe-SeqS-based ctDNA test that is used in the Healthy Cohort incorporates 61 amplicons representing the most commonly mutated regions of cancer driver genes. It is

estimated that ~70% of the eight cancer types to be targeted have mutations in at least one of the regions covered by these amplicons. The fraction of plasmas that have mutations in at least one of these amplicons is less than 70% because not all cancers give rise to ctDNA (see Bettegowda et al., Sci Transl Med. 2014 Feb 19;6(224):224ra24. doi: 10.1126/scitranslmed.3007094.).

[1023] For the Management Cohort, a targeted sequencing assay is first used to identify at least one mutation in the FFPE-cancer obtained from surgery or biopsy. This Safe-SeqS-based test employs 128 amplicons and we have used it to detect at least one pathogenic driver gene mutation in 395 of 401 colorectal cancers and in 200 of 200 pancreatic cancers tested. One specific amplicon that detects a mutation in each individual patient's tumor is then used to evaluate the plasma from that patient at the specified time points – in other words, a fully personalized assay.

[1024] In addition to the tests on circulating tumor DNA (ctDNA), a panel of ~25 protein biomarkers is assessed using a Luminex platform on a subset of plasma samples from the Healthy Cohort. The assays for these proteins have been well-established. If the thresholds for positivity are set to a high level, they provide additional information that can be combined with the ctDNA test results to improve sensitivity without compromising specificity. Markers that exhibit >99.5% specificity in Phase A are incorporated into Phase B of the study.

Example 4: Detecting gynecologic malignancies using a combination approach cancer screening tests

[1025] Diagnosis of gynecologic malignancy (e.g., cervical cancers, ovarian cancers, and endometrial cancers) often includes the Papanicolaou (Pap) test, transvaginal ultrasound (TVUS), and/or detection of the CA-25 biomarker. However, screening with current diagnostic approaches is not recommended for the general population, as it leads to "important harms, including major surgical interventions in women who do not have cancer" (see, e.g., Moyer, 2012 *Annals of internal medicine* 157:900-904). Thus, new diagnostic approaches are urgently needed.

[1026] This Example describes a new blood test, called PapSEEK, which addresses the problematic issues described above. In this test, DNA from sampled fluid (e.g., fluid containing cells sampled from the endocervical canal) can be used in an assay (e.g., a PCR-based, multiplex test) to simultaneously assess genetic alterations that commonly occur in endometrial or ovarian cancers (Fig. 19). Overall, 1915 samples from 1658 individuals were included in the studies described herein, including 656 patients with endometrial or ovarian cancers and 1002 healthy controls. The age, race, histopathologic diagnosis, stage and other clinical information for the cancer patients are provided in Table 13. The samples tested from these patients are listed in Table 14.

Materials and Methods

Patient Samples

[1027] All samples for this study were obtained according to protocols approved by the Institutional Review Boards of the Johns Hopkins Medical Institutions (Baltimore, MD), McGill University (Montreal, QC, Canada), Gothenburg University (Gothenburg, Sweden), BioreclamationIVT (Chestertown, MD), Memorial Sloan Kettering Cancer Center (New York City, NY), and the Danish Scientific Ethical Committee (Copenhagen, Denmark). Demographic, clinical, and pathologic staging data were collected for each patient with cancer are listed in Table 13. The average age of 714 women without cancer used for Pap brush analysis was 34 (range: 17 to 67 years). The average age of 125 women without cancer used for Tao brush analysis was 29 (range: 18 to 74 years). All histopathology was re-reviewed by board-certified pathologists. DNA was extracted from tumors, Pap smear fluid, and plasma as described elsewhere (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535; and Bettegowda et al., 2014 *Sci Transl Med* 6:224ra224). For intrauterine sampling, Tao Brush IUMC Endometrial Sampler (Cook Medical Inc., Bloomington, IN) was gently inserted to the level of the uterine fundus. The outer sheath was then pulled back and the brush was rotated 360 degrees clockwise and then counterclockwise. Then the outer sheath was pushed again and the device was removed. The sample was placed into Thin-Prep

buffer, from which DNA was purified using an AllPrep DNA kit (Qiagen, Germany) according to the manufacturer's instructions. Purified DNA from all samples was quantified as described elsewhere (see, e.g., Rago et al., 2007 *Cancer research* 67:9364-9370).

[1028] Healthy controls included patients with normal cytology findings on Pap smears and no history of gynecologic tumors. Ovarian cancer patients with history of tubal ligation were excluded from the study.

Somatic mutation detection and analysis

[1029] DNA from Pap smear fluid, Tao brush samples, or primary tumors was amplified in three multiplex PCR reactions consisting of 139 primer pairs that were designed to amplify 110 to 142 bp segments, as described elsewhere (see, e.g., Wang et al., 2016 *Elife* 5). These segments contain regions of interest from the following 18 genes: *AKT1*, *APC*, *BRAF*, *CDKN2A*, *CTNNB1*, *EGFR*, *FBXW7*, *FGFR2*, *KRAS*, *MAPK1*, *NRAS*, *PIK3CA*, *PIK3R1*, *POLE*, *PPP2R1A*, *PTEN*, *RNF43*, and *TP53*. For each sample, three multiplex reactions, each containing non-overlapping amplicons, were performed, as described elsewhere (see, e.g., Wang et al., 2016 *Elife* 5). Each sample was assessed in two duplicate wells. DNA from plasma was amplified in two multiplex PCR reactions consisting of 61 primer pairs that were designed to amplify 67 to 81 bp segments. Each sample was assessed in six duplicate wells. These segments contained regions of interest from the following genes: *AKT1, APC, BRAF, CDKN2A, CTNNB1, EGFR, FBXW7, FGFR2, GNAS, HRAS, KRAS, NRAS, PIK3CA, PPP2R1A, PTEN,* and *TP53*.

[1030] Safe-SeqS, an error-reduction technology for detection of low frequency mutations (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535), was used for all sequencing analyses. One primer in each pair included a unique identifier sequence (UIDs), consisting of 14 degenerate bases with an equal chance of being an A, C, T, or G. High quality sequence reads were selected based on quality scores, which were generated by the sequencing instrument to indicate the probability a base was called in error. Reads from a common template molecule were then grouped based on the UIDs that were incorporated as molecular barcodes. Artifactual mutations introduced during the sample preparation or

sequencing steps were reduced by requiring a mutation to be present in >90% of reads in each UID family (i.e., to be scored as a "supermutant") (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535).

Statistical analysis of sequencing data

[1031] All Pap brush and Tao brush samples were analyzed using a mutant allele fraction (MAF)-based approach. Mutations that met one of the two following criteria were considered (i) present in the COSMIC database (see, e.g., Forbes et al., 2017 *Nucleic Acids Res* 45:D777-D783), or (ii) predicted to be inactivating in tumor suppressor genes (nonsense mutations, out-of-frame insertions or deletions, canonical splice site mutations). Synonymous mutations, except those at exon ends (see, e.g., Jung et al., 2015 *Nat Genet* 47:1242-1248), and intronic mutations, except for those at splice sites, were excluded. The MAF in the sample of interest was first normalized based on the distribution of MAFs for the same mutation in the control group. Following this mutation-specific normalization, a p-value was obtained by comparing the MAF of each mutation in each well with a reference distribution of MAFs built from normal controls where all mutations were included. The Stouffer's Z-score was then calculated from the p-values of two wells, weighted by their number of UIDs.

[1032] A sample was scored as positive when any of its mutations had a value above the corresponding thresholds for any of the following three criteria: 1) the difference between its MAF and the corresponding maximum MAF observed for that mutation in the controls, 2) the ratio of its Stouffer's Z-score to the average of the highest six non-zero Stouffer's Z-scores for the same mutation in the controls, or 3) its Stouffer's Z-score alone when the mutation was not seen in the controls.

[1033] Sensitivity and specificity were obtained from a 10-fold cross validation. In each round, Pap brush samples from 90% of the 714 women without cancer served as controls. In each of the ten rounds, the remaining 10% of the Pap brush samples from women without cancer were scored to obtain specificity. All other samples were scored once in each of the 10 rounds for a total of ten times, and were considered to be positive overall if they scored

positive more than half of the time (i.e. 5 or more rounds). The mutations in the samples that scored positive are listed in Table 15.

[1034] The analysis of the plasma samples was done using an empirical Bayes approach. A Beta distribution was first fitted based on the MAFs in a set of controls using maximum likelihood estimation. The MAFs of all mutations were then adjusted accordingly. A p-value was calculated for each mutation in each well by comparison to the distribution of adjusted MAFs among the controls. An overall p-value for every mutation was obtained as the product of the p-values from all 6 wells. Sensitivity and specificity were obtained from a 10-fold cross validation. In each round, normal plasma samples from 192 healthy individuals served as controls, as for the Pap brush samples described above. A sample was considered to be positive if it was positive in 5 or more rounds. The mutations in the samples that scored positive are listed in Table 17.

[1035] Confidence intervals for sensitivities and specificities were calculated assuming binomial distributions with the actual sensitivities and specificities set as the corresponding success probabilities.

Aneuploidy detection and analysis

[1036] For each sample, a single primer pair was used to amplify ~38,000 loci of long interspersed nucleotide elements (LINEs) throughout the genome (see, e.g., Kinde et al., 2012 *PLoS One* 7:e41162). Massively parallel sequencing was performed on Illumina instruments. One of the primers include an UID to as a molecular barcode as described above to reduce error rates associated with PCR and sequencing. The sequencing data were then processed to identify significant single chromosomal arm gains or losses, as well as allelic imbalance on 39 chromosome arms, using **W**ithin-**S**ample **A**neup**L**oidy **D**etecti**O**n (WALDO) software (see, e.g., Example 6). WALDO incorporates a support vector machine (SVM) to discriminate between aneuploid and euploid samples. The SVM was trained using 3150 synthetic aneuploid samples with low neoplastic content and 677 euploid peripheral white blood cell (WBC) samples. A sample was scored as positive (aneuploid), if the SVM discriminant score exceeded a given threshold, or if significant gains of chromosome arms 7q

and 8q were observed. These chromosome arms are frequently gained in both endometrial and ovarian cancers (see, e.g., Cancer Genome Atlas Research, 2013 *Nature* 497:67-73; and Cancer Genome Atlas Research, 2011 *Nature* 474:609-615).

Results

Evaluation of somatic mutations in Pap brush samples from patients with endometrial or ovarian cancer

[1037] The amount of DNA shed from neoplastic cells was expected to be a minor fraction of the total DNA in the Pap brush samples, with most DNA emanating from normal cells. Therefore, a sensitive, PCR-based error-reduction technology, called Safe-Sequencing System (Safe-SeqS), was used to identify mutations in these samples (see Methods and Materials). In brief, primers were designed to amplify 139 regions, covering 9,392 distinct nucleotide positions within the 18 genes of interest (Table 39). Three multiplex PCR reactions, each containing non-overlapping amplicons, were then performed on each sample.

[1038] This assay was applied to Pap brush samples of 382 women with endometrial cancer, 245 women with ovarian cancer, and 714 women without cancer. It was found that 81% of the patients with endometrial cancers had detectable mutations, including 78% of patients with early-stage (stages I and II) disease and 89% of the patients with late-stage disease (stages III and IV; Table S2**)**. The most commonly mutated genes were *PTEN* (64%), *TP53* (41%), *PIK3CA* (31%), *PIK3R1* (29%), *CTNNB1* (21%), *KRAS* (18%), *FGFR2* (11%), *POLE* (9%), *APC* (9%), *FBXW7* (8%), *RNF43* (7%), and *PPP2R1A* (5%). The median mutant allele fraction (MAF) was 4.0% (95% confidence interval (CI): 3.5% to 4.5%) (Table 15).

[1039] Twenty-nine percent of 245 ovarian cancer patients harbored detectable mutations in their Pap brush samples. These included 28% of patients with early-stage disease and 30% of patients with late-stage disease (Table 14). The most commonly mutated genes were *TP53* (74%). The median MAF was 0.54% (95% CI: 0.4%% to 0.87%) (Table 15). This assay was also applied to 714 women without cancer and found that 1.3% had a detectable mutation, yielding a specificity of 98.7% (95% CI: 97.6% to 99.4%) (Fig. 20).

[1040] Tumor tissue was available from 83% and 84% of endometrial and ovarian cancer patients who donated Pap brush samples, respectively. Using the same multiplex assay applied to the Pap brush samples, a driver gene mutation was identified in 98% and 82% of the endometrial and ovarian cancer tissues, respectively (Table 16). Of the endometrial and ovarian cancer patients with a driver mutation identified in their primary tumor, 85% and 29%, respectively, had mutations in their Pap brush samples. Conversely, of the positive Pap brush samples from patients with endometrial or ovarian cancers, 93% contained at least one driver gene mutation that was identical to that observed in their primary tumor. The fraction of Pap brush samples with mutations that were also found in the primary tumors was higher in endometrial cancer patients (97%) than in ovarian cancer patients (73%).

Evaluation of aneuploidy in Pap brush samples

[1041] In addition to somatic mutations, aneuploidy is found in the great majority of endometrial and ovarian cancers (see, e.g., Cancer Genome Atlas Research, 2013 *Nature* 497:67-73; Cancer Genome Atlas Research, 2011 *Nature* 474:609-615; and Vogelstein et al., 2013 *Science* 339:1546-1558). To assess aneuploidy, a PCR-based was used method to amplify ~38,000 loci of long interspersed nucleotide elements (LINEs) with a single primer pair. LINEs have spread throughout the genome via retrotransposition and are found on all 39 non-acrocentric autosomal arms. After sequencing, the data was processed to identify gains or losses on single chromosome arms.

[1042] Aneuploidy was detected in the Pap brush samples of 38% (n = 382) of patients with endometrial cancer, including 34% and 51% of those with early- and late-stage disease, respectively (Table 14). Aneuploidy was also detected in the Pap brush samples of 11% (n = 245) of ovarian cancer patients, including 15% and 9.3% of those with early- and late-stage disease, respectively (Table 14). In endometrial and ovarian cancers, the most commonly altered arms were 4p, 7q, 8q, and 9q. In contrast, when the aneuploidy assay was applied to the Pap brush samples of 714 women without cancer, only one woman was positive (Fig. 20).

[1043] Even if a sample does not contain a genetic alteration in one of the 18 genes assessed, it might still be aneuploid and detectable by methods provided herein. This conjecture was

supported by identification of six patients (three with endometrial and three with ovarian cancers) who had no mutations in their Pap brush samples or primary tumors (when available), but whose Pap brush samples displayed aneuploidy. The combined test incorporating the above-described assays for mutations plus aneuploidy, was dubbed "PapSEEK." PapSEEK scores a sample as positive if it either harbors a mutation or an abnormal chromosome arm number. Eighty-one percent of the Pap brush samples from women with endometrial cancers were PapSEEK-positive, including 78% of patients with early-stage disease and 92% of patients with late-stage disease (Fig. 21 and Fig. 22). Thirty-three percent of the Pap brush samples from women with ovarian cancers were PapSEEK-positive, including 34% of patients with early-stage disease and 33% of patients with late-stage disease (Fig. 21 and Fig. 22). Only 1.4% of the Pap brush samples from 714 women without cancer were PapSEEK-positive, yielding a specificity of 98.6% (95% CI: 97.4% to 99.3%) (Fig. 20).

Evaluation of Tao brush samples from patients with ovarian or endometrial cancers

[1044] A more direct, minimally invasive sampling of the intrauterine cavity (rather than the endocervical canal) might increase the sensitivity of this approach for detecting gynecologic cancers. To explore this possibility, intrauterine samples were collected using a Tao brush, which is a flexible, narrow brush covered by a retractable outer sheath that allows direct sampling of the entire endometrial cavity without injury to the myometrium or contamination from the cervical canal. It has been approved by the Food and Drug Administration for endometrial sampling and can be used in an outpatient setting without the need for anesthesia. Advantageous to a potential screening test, it is well-tolerated by patients.

[1045] PapSEEK was applied to Tao brush samples collected from 123 patients with endometrial cancers, 51 patients with ovarian cancers, and 125 women without cancer. Ninety-three percent of the Tao brush samples from endometrial cancer patients contained genetic alterations detected by PapSEEK, including 90% and 98% of patients with early-, and late-stage disease, respectively (Fig. 22). The most commonly mutated genes in the Tao brush samples were *PTEN* (63%), *TP53* (42%), *PIK3CA* (36%), *PIK3R1* (20%), *KRAS*

(17%), *CTNNB1* (15%), *FGFR2* (15%), *RNF43* (11%), *PPP2R1A* (7%), *POLE* (7%), and *FBXW7* (6%), similar to that observed in the Pap brush samples. The median MAF was 24.7% (95% CI: 21.3% to 26.9%), considerably higher than observed in the Pap brush samples, in which the median MAF was 4.0% (95% CI: 3.5% to 4.5%; Table S4).

[1046] Genetic alterations detectable by PapSEEK were found in 45% (95% CI: 31% to 60%) of the Tao brush samples from 51 women with ovarian cancers, including 47% and 44% of patients with early-, and late-stage, respectively (Fig. 22). The most commonly mutated genes were *TP53* (86%), consistent with the data on Pap brush samples. The median MAF was 0.88% (95% CI: 0.61% to 2.8%), which was higher than in the Pap brush samples (median 0.54%; 95% CI: 0.4% to 0.87%; Table 15).

[1047] PapSEEK was applied to the Tao brush samples from 125 women without cancer. None (0%) of these women tested positive for mutations, yielding a specificity of 100% (95% CI: 97% to 100%; Fig. 20).

[1048] Tao brush and Pap brush samples were available from the same women in 145 patients (103 with endometrial and 42 with ovarian cancers). In endometrial cancers, PapSEEK was positive in 91% of the Tao brush samples and in 81% of the Pap brush samples ($p = 0.02$, mid-P McNemar test). Similarly, the fraction of ovarian cancer patients with a positive PapSEEK test was higher for Tao brush (45%) than for Pap brush (17%; $p = 0.002$, mid-P McNemar test; Table 13).

[1049] Tumor tissue was available from 90% and 88% of patients with endometrial and ovarian cancers who donated Tao brush samples, respectively. PapSEEK identified driver gene mutations in 97% and 80% of the endometrial and ovarian cancer tissues, respectively (Table 16). Of the endometrial and ovarian cancer patients with a driver mutation identified in their primary tumor, 93% and 42%, respectively, had mutations detectable in their Tao brush samples. Conversely, of the positive Tao brush samples from patients with endometrial or ovarian cancers, 91% contained at least one driver gene mutation that was identical to that observed in their primary tumor. The fraction of Tao brush samples with mutations that were also found in the primary tumors was higher in endometrial cancer patients (97%) than in ovarian cancer patients (53%).

Evaluation of ctDNA in patients with ovarian cancers

[1050] Ovarian cancers that were inaccessible by Pap or Tao brush sampling due to anatomical or other factors might be detectable by circulating tumor DNA (ctDNA) in plasma. This was tested in 83 ovarian cancer patients who had donated both Pap brush and plasma samples. Due to the smaller size of degraded ctDNA, primers were designed to amplify short 67 to 81 bp DNA fragments, covering 1,931 distinct nucleotide positions within 16 genes of interest. To demonstrate the specificity of this assay, it was applied it to plasma samples from 192 healthy individuals; none (0%) tested positive, yielding a specificity of 100% (95% CI: 98% to 100%).

[1051] It was found that 43% (95% CI: 33% to 55%) of the plasma from the 83 patients with ovarian cancers had detectable ctDNA. The mutations detected are listed in Table 17. As expected, the sensitivity for ctDNA in plasma was higher in patients with late-stage tumors than early-stage tumors (56% vs. 35%; Fig. 23). For early-stage disease, the median MAF in the plasma was 0.85%, which was less than the median MAF (5.7%) in the Pap smears. At least one of the mutations identified in the plasma could be identified in 88% of the corresponding primary tumor.

[1052] In the Pap brush samples from this same cohort of 83 patients, 40% were positive by the PapSEEK test. The individuals scoring positive in their Pap brush and plasma samples only partially overlapped (Fig. 21). As a result, 63% (95% CI: 51% to 73%) of patients were positive with at least one of the two tests. Those who tested positive included 54% of patients with early-stage disease and 75% with late-stage disease, respectively (Table 13, Fig. 23).

Discussion

[1053] As described herein, a multiplex PCR-based test (PapSEEK) was designed and applied to detect genetic alterations in Pap brush or Tao brush samples. These samples are minimally invasively and conveniently obtained during routine office visits. The majority of endometrial cancers could be detected with PapSEEK: 93% with Tao Brush and 81% with

Pap brush. A substantial fraction of ovarian cancers could also be detected with PapSEEK: 45% with Tao Brush and 33% with Pap brush. The specificity of PapSEEK was high, with only 0% and 1.4% of women without cancer testing positive with Tao and Pap brush samples, respectively (Fig. 24). It was also demonstrated that assays for ctDNA in plasma could be used in conjunction with PapSEEK on Pap brush samples, increasing the sensitivity of detecting ovarian cancer to 63%.

[1054] It was notable that the sensitivity for detecting early-stage ovarian cancers was as high as that for late-stage disease (47% vs. 44% for Tao; 34 % vs. 33% for Pap). Without wishing to be bound by theory, there are at least two possible explanations for this unexpected but enticing finding. First, it has been shown that some ovarian cancers originate in the fallopian tubes, which could facilitate their early detection with PapSEEK when tumor cells are shed into the uterine cavity. Second, in late-stage tumors, the fallopian tubes are often matted and obliterated by the disease and thus less likely to serve as a conduit for tumor cells to pass into the uterus or endocervical canal. In this setting, the addition of ctDNA analysis in plasma to Pap or Tao brush sampling may be particularly beneficial.

[1055] A subset of samples tested herein was composed of high-grade, early-stage cancers. Currently available diagnostic modalities have low sensitivities for these lesions (see, e.g., Fishman et al., 2005 *Am J Obstet Gynecol* 192:1214-1221; Sharma et al., 2012 *Ultrasound Obstet Gynecol* 40:338-344; and Hamilton et al., 2006 *British journal of cancer* 94:642-646). Though the high-grade subtypes comprise only about 10% of incident endometrial cancers, they account for more than 40% of deaths from the disease (see, e.g., Moore et al., 2011 *Clin Obstet Gynecol* 54:278-291). As these high-grade cancers often arise from a background of atrophic endometrium and can metastasize prior to visible abnormalities on imaging, transvaginal ultrasound has a limited role in screening and early diagnosis. Thus it was encouraging that PapSEEK detected 85% (n=34) and 89% (n=9) of high-grade endometrial cancers confined to the endometrium in the Pap and Tao brush samples, respectively. In the case of ovarian cancers, the tested cohort included only a small number of early-stage, high-grade cases, consistent with the unfortunate fact that these cancers are often diagnosed only at advanced stages. Nevertheless, the finding that 36% (n=11) were positive with combined

Pap and plasma sample testing, and that 80% (n=5) were positive in Tao brush samples, is notable.

[1056] The study described herein was retrospective. The samples that were examined were derived from patients with known cancers, even though a substantial fraction was from patients with early-stage lesions. In a screening setting, the cancers would advantageously be at an earlier stage, and the sensitivities for detection would be expected to be closer to the sensitivity for early-stage cancers observed in the present study. Moreover, the age ranges of the controls and cases are typically better matched in a prospective study than in the present retrospective study. Some of the ovarian cancer patients who had mutations detectable in their Pap brush or Tao brush samples did not have the identical mutations in their primary tumors. This was not an issue with endometrial cancers, wherein at least one mutation in the brush samples was nearly always (97%) found in the corresponding primary tumors. But this phenomenon was observed in ovarian cancer patients, particularly with the Tao brush. At least one mutation identifiable in the Pap brush could be identified in 73% of the corresponding primary ovarian tumors, while the same was true for only 53% of the Tao brush samples.

[1057] Without wishing to be bound by theory, one possible explanation for the discordance between the mutations in brush samples and ovarian cancers from the same patients is that the assay detects mutations that do not exist *in vivo*, representing technical artifacts. It is not believed that this is likely, however, given that the specificity of the assays was 100% and 99% in Tao brush and Pap brush samples, respectively, from women without cancer. Another possible explanation is tumor heterogeneity. Only a small part of the tumors that were analyzed was sampled and sequenced, and the additional mutations found in the Pap smear or intrauterine samples could represent mutations from other parts of the tumor. It is also possible that some mutations were from small synchronous endometrial cancers or early, premalignant endometrial lesions that were unnoted by the pathologist. A significant proportion of women with ovarian cancer have synchronous endometrial cancer, with risk factors including Lynch syndrome, polycystic ovarian syndrome, perimenopause, obesity, nulliparity, and unopposed estrogen replacement therapy (see, e.g., Al Hilli et al., 2012 *Gynecologic oncology* 125:109-113; Walsh et al., 2005 *Obstetrics and gynecology* 106:693-

699; Zaino et al., 2001 *Gynecologic oncology* 83:355-362; and Song et al., 2014 *Int J Gynecol Cancer* 24:520-527).

[1058] Though tumor heterogeneity, or multiple synchronous tumors are feasible explanations that are often used to explain discordances in liquid biopsy studies, without wishing to be bound by theory, it is possible that clonal expansions of non-malignant cells may play a role in the present observations. Clonal proliferations that are not considered neoplastic have been described in the uterine lavage, bone marrow, skin, and other tissues (see, e.g., Steensma et al., 2015 *Blood* 126:9-16; Coombs et al., 2017 *Cell Stem Cell* 21(3):374-382; Young et al., 2016 *Nat Commun* 7:12484; Krimmel et al., 2016 *Proc Natl Acad Sci U S A* 113:6005-6010; and Nair et al., 2016 *PLoS Med* 13:e1002206). Of particular interest are the clonal proliferations of endometrial cells that cause endometriosis, a sometimes debilitating condition that affects millions of women. It has recently been shown that these lesions, which can occur throughout the abdomen and are derived from endometrium, are clonal proliferations that can be driven by the same mutations detected in endometrial cancers (see, e.g., Anglesio et al., 2017 *N Engl J Med* 376:1835-1848). Without wishing to be bound by theory, it is possible that the hormonal and physiologic changes contributing to or resulting from ovarian cancers stimulate or select for such clonal proliferations in the endometrial lining. On one hand, this possibility argues against the exquisite specificity that is the conceptual basis for all liquid biopsies. On the other hand, it could actually enhance the sensitivity of detection of ovarian cancers, without diminishing specificity, if large clonal proliferations are almost exclusively found in women with gynecologic malignancies. Clonal proliferations that account for >0.03% of the total cells in the endometrial lining are detectable by methods provided herein.

Example 5: Detecting urologic malignancies using a combination approach cancer screening tests

[1059] According to the American Cancer Society, 79,030 new cases of bladder cancer (BC) and 18,540 deaths are estimated to occur in the United States alone in 2017 (see, e.g., Siegel et al., 2017 *CA Cancer J Clin* 67:7-30), with many BC patients suffer with multiple relapses

prior to progression, providing ample lead-time for early detection and treatment prior to metastasis (see, e.g., Netto, 2013 *Adv Anat Pathol* 20:175-203). Urine cytology and cystoscopy with transurethral biopsy (TURB) are currently the gold standard for diagnosis and follow-up in bladder cancer. While urine cytology has value for the detection of high-grade neoplasms, it is unable to detect the vast majority of low-grade tumors (see, e.g., Netto et al., 2016 *Urol Clin North Am* 43:63-76; Lotan et al., 2003 *Urology* 61:109-18; and Zhang et al., 2016 *Cancer Cytopathol* 124:552-564). This fact, together with the high cost and invasive nature of repeated cystoscopy and TURB procedures, have led to many attempts to develop novel noninvasive strategies including urine or serum based genetic and protein assays for screening and surveillance (see, e.g., Kawauchi et al., 2009 *Hum Pathol* 40:1783-1789; Kruger et al., 2003 *Int J Oncol* 23:41-48; Skacel et al., 2003 *J Urol* 169:2101-2105; Sarosdy et al., 2006 *J Urol* 176:44-47; Moonen et al., 2007 *Eur Urol* 51:1275-80; Fradet et al., 1997 *Can J Urol* 4:400-405; Yafi et al., 2015 *Urol Oncol* 33:66.e25-66.e31; Serizawa et al., 2010 *Int J Cancer* 129(1):78-87; Kinde et al., 2013 *Cancer Res* 73:7162-7167; Hurst et al., 2014 *Eur Urol* 65:367-369; Wang et al., 2014 *Oncotarget* 5:12428-12439; Ralla et al., 2014 *Crit Rev Clin Lab Sci* 51:200-231; Ellinger et al., 2015 *Expert Rev Mol Diagn* 15:505-516; Bansal et al., 2014 *Clin Chim Acta* 436:97-103; Goodison et al., 2012 *PLoS One* 7:e47469; and Allory et al., 2014 *Eur Urol* 65:360-366). Currently available U.S. Food and Drug Administration (FDA) approved assays include ImmunoCyt test (Scimedx Corp), nuclear matrix protein 22 (NMP22) immunoassay test (Matritech), and multitarget FISH (UroVysion) (see, e.g., Kawauchi et al., 2009 *Hum Pathol* 40:1783-1789; Kruger et al., 2003 *Int J Oncol* 23:41-48; Skacel et al., 2003 *J Urol* 169:2101-2105; Sarosdy et al., 2006 *J Urol* 176:44-47; Moonen et al., 2007 *Eur Urol* 51:1275-80; Fradet et al., 1997 *Can J Urol* 4:400-405; and Yafi et al., 2015 *Urol Oncol* 33:66.e25-66.e31). Sensitivities between 62% and 69% and specificities between 79% and 89% have been reported for some of these tests; however, due to assay performance inconsistencies, cost or required technical expertise, integration of such assays into routine clinical practice has not yet occurred. Further, because urine cytology is relatively insensitive for the detection of recurrence, cystoscopies are performed as often as every three months in such patients in the U.S, and the cost of managing these

patients is in aggregate higher than the cost of managing any other type of cancer, and amounts to 3 billion dollars annually (see, e.g., Netto et al., 2010 *Pathology* 42:384-394).

[1060] Further, the annual incidence of these upper tract urothelial carcinomas (UTUCs) in Western countries is 1-2 cases per 100,000, but occurs at a much higher rate in populations exposed to aristolochic acid (AA) (Chen et al., 2012 *Proc Natl Acad Sci U S A*, 109(21):8241-8246; and Grollman et al., 2013 *Environ Mol Mutagen*, 54(1):1-7; and Lai et al., 2010 *J Natl Cancer Inst*, 102(3):179-186). Nephroureterectomy can be curative for patients with UTUC when it is detected at an early stage (Li et al., 2008 *Eur Urol.* 54(5):1127-34). However, these cancers are largely silent until the onset of overt clinical symptoms, typically hematuria, and as a result, most patients are diagnosed only at an advanced stage (Roupret et al., 2015 *Eur Urol.* 68(5):868-79). Diagnostic tests for the detection of early-stage UTUC are not currently available.

[1061] A broadly applicable approach for non-invasive detection of cancer (e.g., an early-stage cancer such as BCs or UTUCs) could be both medically and economically important.

[1062] This Example describes a new blood test, called UroSEEK, which addresses the problematic issues described above. In this test, DNA from urine samples can be used in an assay (e.g., a PCR-based, multiplex test) to simultaneously assess genetic alterations that commonly occur in BCs or UTUCs. A schematic of the approach used in the bladder cancer study is provided in Fig. 25, and a schematic of the approach used in the UTUC study is provided in Fig. 31.

Materials and Methods

Patients and Samples

[1063] Urine samples were collected prospectively from patients in four participating institutions including Johns Hopkins Hospital, Baltimore, MD, USA; A.C. Camargo Cancer Center, Sao Paulo, Brazil; Osaka University Hospital, Osaka, Japan; and Hacettepe University Hospital, Ankara, Turkey. The study was approved by the institutional Review Boards of Johns Hopkins Hospital and all other participating institutions. Proper material

transfer agreements were obtained. Patients with a known history of malignancy other than bladder cancer were excluded from the study. The study included two cohorts of patients.

[1064] The Early Detection cohort comprised 570 patients who were referred to a urology clinic in one of the above hospitals because of hematuria or lower urinary tract symptoms (Table 18). The second cohort (322 patients) represented patients with prior established diagnosis of Bladder Cancer (BC) who are on surveillance for disease recurrence (Surveillance Cohort). These patients' primary tumors harbored mutations in at least one of the 11 genes assessed through the multiplex or singleplex assays. A minimum follow-up of 12 months was from date of urine collection was required for cases with no evidence of incident or recurrent tumors in the Early Detection or Surveillance cohorts, respectively. Urine samples were collected prior to any procedures, such as cystoscopy, performed during the patients' visits. A total of 892 urine samples were analyzed in the study, composed of two type of samples. The first was residual urinary cells after processing with standard BD SurePath™ liquid-based cytology protocols (Becton Dickinson and Company; Franklin Lakes, NJ, USA). To allow for standard-of-care, residual SurePath® fluids were kept refrigerated for 6-8 weeks prior to submission for DNA purification to allow for any potential need for repeat cytology processing of the same sample. The second sample type was composed of bio-banked fresh urine samples in which 15 - 25 mL of voided urine samples were stored at 4°C for up to 60 min prior to centrifugation (10 min at 500 g) and the pellets stored at minus 80°C prior to DNA purification. Urines from 188 healthy individuals of average age 26 were also obtained and processed identically to the bio-banked fresh urine samples.

[1065] Formalin-fixed paraffin-embedded (FFPE) tumor tissue samples from trans-urethral resections (TURB) or cystectomies were collected in 413 of the 892 cases. When several different tumors from the same patient were available (because of recurrences), the earliest tumor tissue obtained following the donation of the urine sample was used in the Early Detection Cohort. In the surveillance cohort, the tumors preceding the donation of the urine sample was used in 146 of the 322 patients. In the other 176 Surveillance cases, the earliest tissue obtained following the donation of the urine sample was used. A genitourinary pathologist reviewed all histologic slides to confirm the diagnosis and select a representative

tumor area with as high tumor cellularity as possible for that case. Corresponding FFPE blocks were cored with a sterile 16-gauge needle. One to three cores were obtained per tumor and placed in 1.5mL sterile tubes for DNA purification, as described elsewhere (see, e.g., Kinde et al., 2013 *Cancer Res* 73:7162-7167). Electronic medical records were reviewed to obtain medical history and follow up data in all patients.

UTUC Cohort Studied

[1066] Sequential patients with UTUC scheduled to undergo a radical unilateral nephroureterectomy at National Taiwan University Hospital in 2012-2016 were asked to participate in the study. All patients provided informed consent using the consent form and study design reviewed and approved by the Institutional Review Boards at National Taiwan University and Stony Brook University. A total of 56 UTUC patients were enrolled in the study after excluding four patients with gross hematuria and one patient with a tumor-urine DNA mismatch by identity testing. Urinary cell DNA from 188 urine samples donated by healthy individuals in the U.S. of average age 40, range 19 to 60 years old, was used to assess the specificity of the UroSEEK test. White blood cell (WBC) DNA from 94 normal individuals from the U.S. was used to evaluate the technical specificity of the PCR analysis.

Biological samples – UTUC Cohort

[1067] Urine samples were obtained from patients one day prior to surgery. Urinary cells were isolated by centrifugation at 581g for 10 minutes at room temperature, washed thrice in saline using the same centrifugation conditions, and stored frozen until DNA was isolated using a Qiagen kit #937255 (Germantown, MD). DNA was purified from fresh-frozen resected samples of upper tract tumors and renal cortex by standard phenol-chloroform extraction procedures as described elsewhere (see, e.g., Chen et al., 2012 *Proc Natl Acad Sci USA*, 109(21):8241-8246; and Jelakovic et al., 2012 *Kidney Int.* 81(6):559-67). One upper urinary tract tumor per patient was analyzed; for cases with tumors at multiple sites, renal pelvic tumors were preferentially selected whenever available. Formalin-fixed, paraffin-

embedded tumor samples were staged and graded by a urologic pathologist, and the presence of one or more upper tract urothelial carcinomas was confirmed by histopathology for each enrolled subject. Pertinent clinical and demographic data were obtained by a chart review of each subject. eGFR was calculated by the MDRD equation (see, e.g., Levey et al., 2006 *Ann Intern Med.* 145(4):247-54) and used to determine CKD stage (see, e.g., Levey et al., 2005 *Kidney Int.* 67(6):2089-100).

DNA adduct analysis

[1068] AL-DNA adduct (7-(deoxyadenosin-N6-yl) aristolactam I; dA-AL-I) levels in 2 μg of DNA from the normal renal cortex of UTUC patients were quantified by ultra-performance liquid chromatography–electrospray ionization/multistage mass spectrometry (UPLC-ESI/MSn) with a linear quadrupole ion trap mass spectrometer (LTQ Velos Pro, Thermo Fisher Scientific, San Jose, CA) as described elsewhere (see, e.g., Yun et al., 2012 *Chem Res Toxicol.* 2012 25(5):1119-31).

Mutation analysis

[1069] Three separate assays were used to search for abnormalities in urinary cell DNA. First, a multiplex PCR was used to detect mutations in regions of ten genes commonly mutated in urologic malignancies CDKN2A, ERBB2, FGFR3, HRAS, KRAS, MET, MLL, PIK3CA, TP53, and VHL (see, e.g., Netto, 2011 *Nat Rev Urol* 9:41-51; Mo et al., 2007 *J Clin Invest* 117:314-325; Sarkis et al., 1993 *J Natl Cancer Inst* 85:53-59; Lin et al., 2010 *Urol Oncol* 28:597-602; Sarkis et al., 1994 *J Urol* 152:388-392; Sarkis et al., 1995 *J Clin Oncol* 13:1384-1390; Wu, 2005 *Nat Rev Cancer* 5:713-725; and Cancer Genome Atlas Research Network, 2014 *Nature* 507:315-322). The primer pairs used for this multiplex PCR were divided in a total of three multiplex reactions, each containing non-overlapping amplicons (see below). These primers were used to amplify DNA in 25 μL reactions as described elsewhere (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535) except that 15 cycles were used for the initial amplification. Second, the *TERT* promoter

region was evaluated. A single amplification primer was used to amplify a 73-bp segment containing the region of the *TERT* promoter known to harbor mutations in BC (see, e.g., Kinde et al., 2013 *Cancer Res* 73:7162-7167). The conditions used to amplify it were the same as used in the multiplex reactions described above except that Phusion GC Buffer (Thermo-Fisher) instead of HF buffer was used and 20 cycles were used for the initial amplification. The *TERT* promoter region could not be included in the multiplex PCR because of the high GC content of the former. PCR products were purified with AMPure XP beads (Beckman Coulter, PA, USA) and 0.25% of the purified PCR products (multiplex) or 0.0125% of the PCR products (*TERT* singleplex) were then amplified in a second round of PCR, as described elsewhere (see, e.g., Wang et al., 2016 *Elife* 5:10.7554/eLife.15175). The PCR products from the second round of amplification were then purified with AMPure and sequenced on an Illumina instrument. For each mutation identified, the mutant allele frequency (MAF) was determined by dividing the number of uniquely identified reads with mutations (see, e.g., Kinde et al., 2011 *Proc Natl Acad Sci U S A* 108:9530-9535) by the number of total uniquely identified reads. Each DNA sample was assessed in two independent PCRs, for both the *TERT* promoter and multiplex assays, and samples were scored as positive only if both PCRs showed the same mutation. The mutant allele frequencies and number of UIDs listed in Table 19, Table 20, Table 22, and Table 23 refer to the average of the two independent assays.

[1070] To evaluate the statistical significance of putative mutations, DNA from white blood cells of 188 unrelated normal individuals were assessed. A variant observed in the samples from cancer patient was only scored as a mutation if it was observed at a much higher MAF than observed in normal WBCs. Specifically, the classification of a sample's ctDNA status was based on two complementary criteria applied to each mutation: 1) the difference between the average MAF in the sample of interest and the corresponding maximum MAF observed for that same mutation in a set of controls, and 2) the Stouffer's Z-score obtained by comparing the MAF in the sample of interest to a distribution of normal controls. To calculate the Z-score, the MAF in the sample of interest was first normalized based on the mutation-specific distributions of MAFs observed among all controls. Following this mutation-specific normalization, a P-value was obtained by comparing the MAF of each

mutation in each well with a reference distribution of MAFs built from normal controls where all mutations were included. The Stouffer's Z-score was then calculated from the p-values of two wells, weighted by their number of UIDs. The sample was classified as positive if either the difference or the Stouffer's Z-score of its mutations was above the thresholds determined from the normal WBCs. The threshold for the difference parameter was defined by the highest MAF observed in any normal WBCs. The threshold for the Stouffer's Z-score was chosen to allow one false positive among the 188 normal urine samples studied.

Analysis of aneuploidy.

[1071] Aneuploidy was assessed with Fast-SeqS, which uses a single primer pair to amplify ~38,000 loci scattered throughout the genome (see, e.g., Kinde et al., 2012 *PLoS One* 7:e41162). After massively parallel sequencing, gains or losses of each of the 39 chromosome arms covered by the assay were determined using a bespoke statistical learning method. A Support vector machine (SVM) was used to discriminate between aneuploid and euploid samples. The SVM was trained using 3150 low neoplastic cell fraction synthetic aneuploid samples and 677 euploid peripheral white blood cell (WBC) samples. Samples were scored as positive when the genome-wide aneuploidy score was >0.7 and there was at least one gain or loss of a chromosome arm.

Identity checks.

[1072] A multiplex reaction containing 26 primers detecting 31 common SNPs on chromosomes 10 and 20 was performed using the amplification conditions described above for the multiplex PCR. The primers used for this identity evaluation are listed in Fig. 34 (Table 42) for bladder cancer cohorts and Fig. 33 (Table 41) for UTUC cohorts.

Statistical Analysis

[1073] Performance characteristics of urine cytology, UroSEEK and its three components was calculated using MedCalc statistical software (medcalc.org/calc/diagnostic_test.php).

Results

Early Detection Cohort characteristics.

[1074] A flow diagram indicating the number of patients evaluated in this study and the major results is provided in Fig. 26.

[1075] A total 570 patients were included in the Early Detection cohort, each with one urine sample analyzed. 90% of the patients had hematuria, 3% had lower urinary tract symptoms (LUTS), and 9% had other indications suggesting they were at risk for BC. The median age of the participants was 58 years (range 5 to 89) (Table 18). 70% of the patients were male. 175 (31%) of patients developed BC after a median follow-up period of 18 months (range 0 to 40 months). For each patient who developed BC, two other patients were selected who presented with similar symptoms but did not develop BC during the follow-up period. By design, then, the fraction of cases in this cohort developing BC was higher than the fraction (5%) of patients with similar presentations that would have developed BC in standard clinical practice. The characteristics of the tumors developing in the 570 patients are summarized below.

Demographic, clinical and genetic features of the early detection cohort.

Gender	n	%	Ten-gene multiplex positive	TERT positive	Aneuploidy positive	UroSEEK positive	Cytology Positive*	UroSEEK or Cytology positive*
Males without recurrence	172	59%	3 (2%)	10 (6%)	2 (1%)	13 (8%)	0 (0%)	13 (8%)
Males with recurrence	32	11%	26 (81%)	21 (66%)	19 (59%)	29 (91%)	16 (50%)	30 (94%)
Females without recurrence	81	28%	2 (2%)	2 (2%)	1 (1%)	5 (6%)	0 (0%)	5 (6%)
Females with recurrence	9	3%	4 (44%)	4 (44%)	3 (33%)	6 (67%)	1 (11%)	6 (67%)
Indication								
Hematuria without recurrence	346	61%	6 (2%)	15 (4%)	5 (1%)	22 (6%)	0 (0%)	17 (5%)
Hematuria with recurrence	163	29%	108 (66%)	90 (55%)	76 (47%)	134 (82%)	18 (11%)	32 (2%)
LUTS without recurrence	11	2%	0 (0%)	2 (18%)	0 (0%)	2 (18%)	0 (0%)	2 (18%)
LUTS with recurrence	3	1%	2 (67%)	1 (33%)	0 (0%)	2 (67%)	1 (33%)	2 (67%)
Other without recurrence	38	7%	1 (3%)	0 (0%)	1 (3%)	2 (5%)	0 (0%)	2 (5%)
Other with recurrence	9	2%	9 (100%)	8 (89%)	5 (56%)	9 (100%)	2 (22%)	9 (100%)
Detected Tumor Diagnosis								
PUNLMP	2	1%	0 (0%)	1 (50%)	0 (0%)	1 (50%)	0 (0%)	0 (0%)
CIS	7	5%	4 (57%)	4 (57%)	1 (14%)	6 (86%)	3 (43%)	6 (86%)
LGTCC	31	21%	15 (48%)	18 (58%)	9 (29%)	22 (71%)	0 (0%)	4 (13%)
HGTCC	49	33%	34 (69%)	28 (57%)	26 (53%)	40 (82%)	4 (8%)	11 (22%)
INTCC	61	41%	48 (79%)	36 (59%)	35 (57%)	57 (93%)	9 (15%)	16 (26%)

*Cytology diagnosis**								
Positive	21	6%	16 (76%)	12 (57%)	16 (76%)	20 (95%)	N/A	N/A
Atypical	105	30%	21 (20%)	21 (30%)	12 (11%)	30 (29%)	N/A	N/A
Negative	221	64%	4 (2%)	9 (4%)	1 (0.4%)	12 (5%)	N/A	N/A

*Cytology was available on only a subset of cases.

N/A Not Available.

Genetic analysis in bladder cancer cohorts.

[1076] Three separate tests were performed for genetic abnormalities that might be found in urinary cells derived from BC (Fig. 26). First, mutations were evaluated in selected regions of ten genes that have been shown to be frequently altered in urothelial tumors (Table 19). For this purpose, a specific set of primers were designed that allowed detection of mutations in as few as 0.03% of urinary cells. The capacity to detect such low mutant fractions was a result of the incorporation of molecular barcodes in each of the primers, thereby substantially reducing the artifacts associated with massively parallel sequencing. Second, *TERT* promoter mutations were evaluated. A singleplex PCR was used for this analysis because the unusually high GC-content of the *TERT* promoter precluded its inclusion in the multiplex PCR design. Third, the extent of aneuploidy was evaluated using a technique in which a single PCR is used to co-amplify ~38,000 members of a subfamily of long interspersed nucleotide element-1 (L1 retrotransposons, also called LINEs). L1 retrotransposons, like other human repeats, have spread throughout the genome via retrotransposition and are found on all 39 non-acrocentric autosomal arms.

[1077] The multiplex assay detected mutations in 68% of the 175 urinary cell samples from the individuals that developed BC during the course of this study (95% CI 61% to 75%) (Table 19). A total of 246 mutations were detected in 8 of the ten target genes (Fig. 27A and Table 19). The mean mutant allele frequency in the urinary cells with detectable mutations was 18% and ranged from 0.17% to 99%. The most commonly altered genes were TP53 (45% of the total mutations) and FGFR3 (20% of the total mutations; Fig. 27A). At the thresholds used, 1.7% of the 395 patients in the Early Detection Cohort who did not develop BC during the course of the study had a detectable mutation in any of the ten genes. At the same thresholds, none of the 188 urinary cell samples from healthy individuals had any mutation in any of the ten genes assayed (100% specificity, 95% CI 98% to 100%).

[1078] Mutations in the *TERT* promoter were detected in 57% of the 175 urinary cell samples from the patients that developed cancer during the study interval (95% CI 49% to

64%; Table 20). The mean *TERT* mutant allele frequency in the urinary cells was 14% and ranged from 0.18% to 78%. Mutations were detected in 3 positions: 98% of the mutations were at hg1295228 (79%) and hg 1295250 (19%), which are 66 and 88 bp upstream of the transcription start site, respectively. These positions have been previously shown to be involved in the appropriate transcriptional regulation of *TERT*. In particular, the mutant alleles recruit the GABPA/B1 transcription factor, resulting in the H3K4me2/3 mark of active chromatin and reversing the epigenetic silencing present in normal cells. 4% of the 395 patients in this cohort who did not develop BC during the course of the study had a detectable mutation in the *TERT* promoter. Only one of the 188 urinary samples from healthy individuals harbored a *TERT* promoter mutation.

[1079] Aneuploidy was detected in 46% (95% CI 39% to 54%) of the 175 urinary cell samples from the patients that developed BC during the course of the study (Table 20 and Table 21). The most commonly altered arms were 5q, 8q, and 9p. All three of these arms harbor well-known oncogenes and tumor suppressor genes which have been shown to undergo copy number alterations in many cancers, including BC. 1.5% of the urinary cell samples from the 395 patients who did not develop BC during the course of the study exhibited aneuploidy. None of the 188 urinary samples from healthy individuals exhibited aneuploidy when assessed with the same technology.

Comparison with primary tumors

[1080] Tumor samples from 102 of the patients enrolled in this cohort were available for comparison and were studied with the same three assays used to study the urinary cell samples (Table 20). In 91 (89%) of these 102 cancers, at least one mutation in the eleven genes studied were mutated (in the 10-gene panel or in the *TERT* promoter). Moreover, at least one of the mutations identified in the urine samples from these 102 patients was also identified in 83% of the corresponding BC (Table 19, and Table 20). Analysis of the BCs also shed light on the basis for "false negatives", i.e., the reason that 21% of urine samples from patients who developed BC had no detectable mutations in the 11 genes tested. The reason could either have been that the corresponding BC did not harbor a mutation in these

11 genes or that it did, but the fraction of neoplastic cells in the urine sample was not high enough to allow its detection with the assays used. At least one mutation in at least one of the 11 genes in 62% of the primary tumors was identified from patients with false negative urine tests for mutations (Table 22, and Table 23). The results indicate that 38% of the 29 false negative tests for mutations were due to the fact that none of the queried mutations were present in the tumor and that the other 62% of the false negatives were due to insufficient amounts of cancer cells in the urine.

UroSEEK: biomarkers in combination.

[1081] As noted above, the ten-gene multiplex assay, the *TERT* singleplex assay, and the aneuploidy assays yielded 68%, 57%, and 46% sensitivities, respectively, when used separately (Table 19, Table 20, and Table 21). 45 samples without *TERT* promoter mutations could be detected by mutations in one of the other ten genes (Fig. 28A and Table 19). Conversely, 35 samples without detectable mutations in the multiplex assay could be detected by virtue of *TERT* promoter mutations (Fig. 28A and Table 20). Ten of the urinary cell samples without any detectable mutations in the 11 genes could be detected by the assay for aneuploidy (Fig. 28A and Table 21). Thus, when the three assays were used together (test termed "UroSEEK"), and a positive result in either assay was sufficient to score a sample as positive, the sensitivity rose to 83% (95% CI 76% to 88 %). Only one of the 188 samples from healthy individuals was scored positive by UroSEEK (specificity 99.5%, CI 97% to 100%). Twenty-six (6.5%) of the 395 patients in this cohort who did not develop BC during the course of the study scored positive by the UroSEEK test (specificity 93%, CI 91% to 96%). On average, UroSEEK positivity preceded the diagnosis of BC by 2.3 months, and in eight cases by more than a year (Fig. 29A and Table 18).

UroSEEK plus cytology

[1082] As both cytology and UroSEEK tests are non-invasive and can be performed on the same urine sample, their performance in combination was assessed. There were 347 patients

in the Early Detection cohort in whom cytology was available (Table 18). Among the 40 patients who developed biopsy-proven cancer in this cohort, 17 were positive by cytology (43% sensitivity). None of the 299 patients that did not develop cancer were positive by cytology (100% specificity). UroSEEK was positive in 100% of the 17 cancer patients whose urines were positive by cytology and in 95% of the 23 cancer patients whose urines were negative by cytology. Thus, in combination, UroSEEK plus cytology afforded 95% (95% CI 83% to 99%) sensitivity, a 12% increase over UroSEEK and a 52% increase over cytology. Among the 299 patients in the early detection cohort who did not develop BC during the course of the study, 20 (6.6%) were positive by UroSEEK or cytology, giving the combination of UroSEEK and cytology a specificity of 93% (95% CI 90% to 96%).

Surveillance Cohort characteristics

[1083] The strategy for surveillance was different than the one used for early detection. Patients in whom a BC was surgically excised for treatment and diagnosis generally have tumor tissue available, and in most such tumors, a mutation can be identified. For example, it was found during the course of this study that a mutation in at least one of the 11 queried genes was present in 95.2% of BCs evaluated. All patients selected for the surveillance study had biopsy confirmed BC and had a urine sample collected 0 - 5 years after surgery. A total of 322 patients that donated urines and whose BC contained a mutation in at least one of the 11 genes analyzed were evaluated. It was determined whether a single urine sample taken a relatively short time following surgical excision of the BC could reveal residual disease in these 322 patients, as evidenced by later recurrence. 187 (58%) of the 322 patients developed clinically evident BC after a median follow-up period of 10.7 months (range 0 to 51 months). The histopathologic types and tumor stages of these patients are summarized below and detailed Table 24. The median age of the participants was 62 (range 20 to 93). As expected from the demographics of BC, 75% of the patients were male.

Demographic, clinical and genetic features of the Surveillance cohort.

Gender	n	%	Ten-gene multiplex positive	TERT positive	Aneuploidy positive	UroSEEK positive	Cytology Positive*	UroSEEK or Cytology positive*
Males without recurrence	59	30%	3 (5%)	8 (14%)	3 (5%)	10 (17%)	0 (0%)	8 (14%)
Males with recurrence	90	45%	45 (50%)	53 (59%)	20 (22%)	59 (66%)	20 (22%)	53 (59%)
Females without recurrence	17	9%	5 (29%)	3 (18%)	0 (0%)	6 (35%)	0 (0%)	6 (35%)
Females with recurrence	33	17%	15 (45%)	19 (58%)	11 (33%)	33 (100%)	6 (18%)	19 (58%)
Original Tumor Diagnosis								
PUNLMP	12	4%	5 (42%)	2 (17%)	1 (8%)	6 (50%)	0 (0%)	2 (17%)
CIS	25	8%	11 (44%)	13 (52%)	6 (24%)	14 (56%)	5 (20%)	10 (40%)
LGTCC	107	35%	27 (25%)	34 (32%)	8 (7%)	41 (38%)	0 (0%)	59 (55%)
HGTCC	62	20%	22 (36%)	24 (39%)	10 (16%)	30 (49%)	4 (7%)	16 (26%)
INTCC	104	34%	39 (38%)	47 (45%)	29 (28%)	54 (52%)	20 (19%)	34 (33%)
Original Tumor Stage								
pTis	25	8%	11 (44%)	13 (52%)	6 (24%)	14 (56%)	5 (20%)	10 (40%)
pTa	181	58%	54 (30%)	60 (33%)	19 (19%)	77 (43%)	4 (2%)	77 (43%)
pT1	71	23%	28 (39%)	35 (49%)	22 (31%)	39 (55%)	14 (20%)	23 (32%)
pT2	23	7%	9 (9%)	9 (39%)	7 (30%)	12 (52%)	5 (22%)	10 (43%)
pT3	9	3%	1 (11%)	2 (22%)	0	2 (22%)	1 (11%)	1 (11%)
pT4	1	0.3%	1 (100%)	1 (100%)	0	1 (100%)	N/A	N/A

*Routine cytology diagnosis**								
Positive	30	15%	21 (21%)	25 (83%)	20 (67%)	27 (90%)	N/A	N/A
Atypical	95	48%	38 (40%)	43 (45%)	18 (19%)	50 (53%)	N/A	N/A
Negative	71	36%	12 (17%)	13 (18%)	3 (4%)	19 (27%)	N/A	N/A

*Cytology was available on only a subset of cases.

N/A Not Available.

Genetic analysis of Surveillance Cohort

[1084] The multiplex assay in urinary cells detected mutations in 49% of the urinary cell samples from patients that developed recurrent BC during the study interval (95% CI 45% to 60%; Table 24 and Table 25). The mean mutant allele frequency in the urinary cells with detectable mutations was 16% and ranged from 0.08% to 93%. The most commonly altered genes were FGFR3 (43% of the 134 mutations) and TP53 (30% of the 134 mutations; Fig. 27B). Seven percent of the 135 patients who did not develop recurrent BC during the course of the study had a detectable mutation in their urinary cell sample (these are considered to be false positives; see Discussion). The mean interval between a positive multiplex assay test and the diagnosis of recurrent BC was 7 months (range 0 to 51 months).

[1085] Mutations in the *TERT* promoter were detected in 51% of the urinary cell samples from patients that developed recurrent BC during the study interval (95% CI 44% to 58%; Table 26). The mean *TERT* mutant allele frequency in the urinary cells with detectable mutations was 6% and ranged from 0.23% to 43%. Mutations were detected in the same three positions observed in the urinary cells of the Early Detection cohort. 10% (95% CI 83% to 94%) of the 135 patients who did not develop recurrent BC during the course of the study had a detectable *TERT* promoter mutation in their urine sample (false positives). The mean interval between a positive *TERT* test and the diagnosis of recurrent BC was 7 months (range 0 to 40 months).

[1086] Aneuploidy was detected in 30% (95% CI 24% to 37%) of the urinary cell samples from the patients that developed recurrent BC during the course of the study (Table 27). The most commonly altered arms were 8p, 8q, and 9p, as in the Early Detection cohort. Two percent of the 135 patients who did not develop recurrent BC during the course of the study exhibited aneuploidy in at least one of their urinary cell samples.

Markers in combination – Surveillance Cohort

[1087] As noted above, the ten-gene multiplex assay, the *TERT* singleplex assay, and the aneuploidy assays yielded 49%, 51%, and 30% sensitivities, respectively, when used separately (Table 25, Table 26, and Table 27). Thirty-two samples without *TERT* promoter mutations could be detected by mutations in one of the other ten genes (Fig. 28B and Table 25). Conversely, 41 samples without detectable mutations in the multiplex assay could be detected by virtue of *TERT* promoter mutations. Three of the urinary cell samples without any detectable mutations could be detected by the assay for aneuploidy. Thus, the sensitivity of UroSEEK was 66% (95% CI 59% to 73%). Fourteen percent of the 135 patients in this cohort who did not develop BC during the course of the study scored positive by the UroSEEK test, yielding a specificity of 86% (95% CI 77% to 91%). On average, UroSEEK positivity preceded the diagnosis of BC by 7 months, and in 47 cases by more than one year (Fig. 29B and Table 24).

[1088] There were 196 patients in the Surveillance cohort for whom cytology was available (Table 24). Among the 120 patients who developed recurrent BC in this cohort, 30 (25%) were positive by cytology. Conversely, no positive cytology results were observed in patients whose tumors did not recur. UroSEEK was positive in 90% of the recurrent BC patients whose urines were positive by cytology and in 61% of the 90 recurrent BC patients whose urines were negative by cytology. Thus in combination, UroSEEK plus cytology afforded 71% sensitivity (95% CI 61.84% to 78.77) (Fig. 28D and Table 22). Among the 76 patients who did not develop recurrent BC during the course of the study and in whom cytology was available, 18% scored as positive by either cytology or UroSEEK, affording a specificity of 82% (95% CI 71% to 90%;).

Low vs. high grade urothelial neoplasms in both Early Detection and Surveillance Cohorts

[1089] The advantage of UroSEEK over cytology was particularly evident in low-grade tumors (Papillary urothelial neoplasms of low malignant potential and non-invasive low

grade papillary urothelial carcinomas). There were a total of 49 low-grade tumors evaluated in this study in whom cytology was available (six from the Early Detection cohort and 43 from the Surveillance cohort). None of these low-grade tumors were detected by cytology (0% sensitivity; 95% CI 0.0% to 6.7%). In contrast, UroSEEK detected 67% (95% CI 51% to 81%) of the low-grade tumors (identical rate of 67% in both cohorts; Fig. 30). Analogously, there were a total of 102 high-grade tumors (in-situ urothelial carcinoma, non-invasive high grade papillary urothelial carcinoma or infiltrating high grade urothelial carcinoma) evaluated in this study in whom cytology was available (34 from the Early Detection cohort and 68 in the Surveillance cohort). Cytology was positive in 45% of these patients (50% and 41% in the Early Detection and Surveillance cohorts, respectively) while UroSEEK was positive in 80% of them (100% and 71% in the Early Detection and Surveillance cohorts, respectively; see below.

Summary of the performance of Cytology vs. UroSEEK.

Biopsy Outcome Diagnosis	n	Cytology				UroSEEK			
		Positive test	Negative test	Sensitivity	95% CI	Positive test	Negative test	Sensitivity	95% CI
PUNLMP/LGTCC	49	0	49	0%	0.00% to 6.06%	33	16	67%	54.36% to 79.38%
CIS/HGTCC/INTCC	102	46	56	45%	33.63% to 52.21%	82	20	80%	71.03% to 86.39%
Total	151								

UTUC Cohort characteristics

[1090] Thirty-two females and twenty-four males ranging in age from 39-85 years participated in the study (see below; individual data are in Table 28). This gender distribution, atypical of UTUC patients in Western countries where males predominate (Shariat et al., 2011 *World J Urol.* 29(4):481-6), is consistent with previous epidemiologic studies of Taiwanese individuals with known exposures to AA (see, e.g., Chen et al., 2012 *Proc Natl Acad Sci U S A*, 109(21):8241-8246). Tobacco use was reported by 18% of this cohort, all males. Based on estimated glomerular filtration rate (eGFR) values, renal function was unimpaired (chronic kidney disease (CKD) stage 0-2) in 45% of the subjects, while mild-to-moderate renal disease (CKD stage 3) or severe disease (CKD stages 4-5) was noted for 43% and 12% of the cohort, respectively.

Demographic, clinical and genetic features of the UTUC cohort stratified by UroSEEK results.

	n	%	Ten-gene multiplex positive	TERT positive	Aneuploidy positive	UroSEEK positive
All subjects	56	100%	64%	29%	39%	75%
Gender						
Males	24	43%	71%	33%	54%	83%
Females	32	57%	59%	25%	28%	69%
CKD stage						
0–2	25	45%	68%	36%	44%	76%
3A	14	25%	50%	21%	43%	71%
3B	10	18%	80%	20%	40%	80%
4	4	7%	25%	50%	0%	50%
5	3	5%	100%	0%	33%	100%
Tumor grade						
Low	6	11%	67%	50%	17%	67%
High	50	89%	64%	26%	42%	76%
Tumor stage						
Ta	11	20%	73%	55%	45%	82%
T1	8	14%	50%	0%	38%	75%
T2	10	18%	80%	20%	10%	80%
T3	24	43%	67%	33%	54%	79%

T4	3	5%	0%	0%	0%	0%
Upper urinary tract tumor site						
Lower ureter	17	30%	76%	18%	35%	76%
Upper ureter	1	2%	100%	0%	0%	100%
Ureterovesical junction	2	4%	0%	0%	0%	0%
Lower ureter and upper ureter	2	4%	100%	50%	50%	100%
Renal pelvis	21	38%	57%	38%	38%	76%
Renal pelvis and lower ureter	4	7%	75%	25%	50%	100%
Renal pelvis and upper ureter	5	9%	40%	40%	60%	60%
Renal pelvis, lower ureter, upper ureter	4	7%	75%	25%	50%	75%
Synchronous bladder cancer						
Present	21	38%	52%	29%	33%	62%
Absent	35	63%	71%	29%	43%	83%
UTUC risk factors						
Aristolactam-DNA adducts present	54	96%	65%	30%	39%	74%
Smoking history	10	18%	70%	30%	60%	70%

CKD, chronic kidney disease.

[1091] Tumors were confined to a single site along the upper urinary tract in the majority of cases (38% renal pelvis; 39% ureter), while multifocal tumors affecting both renal pelvis and ureter occurred in 23% of the patients. Synchronous bladder cancer (diagnosed within 3 months prior to nephroureterectomy) was present in 38%. Histologically, 89% of the tumors were classified as high grade, with the majority categorized as muscle- invasive (T2-T4, 66%).

Mutational analysis – UTUC Cohort

[1092] Three separate tests were performed for genetic abnormalities that might be found in urinary cells derived from UTUCs (Fig. 32, Table 29, Table 30, Table 31, and Fig. 33). First, mutations were evaluated in selected exomic regions of ten genes (CDKN2A, ERBB2, FGFR3, HRAS, KRAS, MET, MLL, PIK3CA, TP53, and VHL) that are frequently altered in urologic tumors (Sfakianos et al., 2015). For this purpose, a specific set of multiplex primers were designed that allowed detection of mutations in as few as 0.03% of urinary cells (Table 40). The capacity to detect such low mutant fractions was a result of the incorporation of molecular barcodes in each of the primers, thereby substantially reducing the artifacts associated with massively parallel sequencing. Second, *TERT* promoter mutations were evaluated, based on prior evidence that *TERT* promoter mutations are often found in UTUCs. A singleplex PCR was used for this analysis because the unusually high GC-content of the *TERT* promoter precluded its inclusion in the multiplex PCR design. Third, the extent of aneuploidy was evaluated using a technique in which a single PCR is used to co-amplify ~38,000 members of a subfamily of long interspersed nucleotide element-1 (L1 retrotransposons). L1 retrotransposons, like other human repeats, have spread throughout the genome via retrotransposition and are found on all 39 non-acrocentric autosomal arms.

[1093] The multiplex assay detected mutations in 36 of the 56 urinary cell samples from UTUC patients (64%, 95% CI 51 % to 76% (Table 29). A total of 57 mutations were detected in nine of the ten target genes (Fig. 34). The median mutant allele frequency (MAF) in the urinary cells was 5.6% and ranged from 0.3% to 80%. The most commonly altered genes were TP53 (58% of the 57 mutations) and FGFR3 (16% of the 57 mutations) (Table 18). None of the 188 urinary cell

samples from healthy individuals had a detectable mutation in any of the ten genes assayed (100% specificity, CI 97.5% to 100%).

[1094] Mutations in the *TERT* promoter were detected in 16 of the 56 urinary cell samples from UTUC patients (29%, 95% CI 18% to 42%) (Table 30). The median *TERT* MAF in the urinary cells was 2.22% and ranged from 0.59% to 46.3%. One of the 188 urinary samples from healthy individuals harbored a mutation (*TERT* g.1295250C>T with a MAF of 0.39%). In the UTUC urinary cell samples, mutations were detected in three positions: 94% of the mutations were at hg1295228 (67%) and hg1295250 (28%), which are 69 and 91 bp upstream of the transcription start site, respectively. These positions have been previously shown to be involved in the appropriate transcriptional regulation of *TERT*. In particular, the mutant alleles recruit the GABPA/B1 transcription factor, resulting in the H3K4me2/3 mark of active chromatin and reversing the epigenetic silencing present in normal cells.

Aristolochic acid exposure in the UTUC Cohort

[1095] The activated metabolites of aristolochic acid bind covalently to the exocyclic amino groups in purine bases, with a preference for dA, leading to characteristic A>T transversions. To determine whether the individuals in the cohort had been exposed to AA, renal cortical DNA adducts were qualified using mass spectrometry. All but two of the 56 patients had detectable aristolactam (AL)-DNA adducts with levels ranging from 0.4 to 68 dA-AL adducts per 108 nucleotides. Moreover, the A>T signature mutation associated with AA was highly represented in the mutational spectra of TP53 (18/32 A>T) and HRAS (2/2 A>T) found in urinary cells (Table 30).

Aneuploidy analysis in the UTUC Cohort

[1096] Aneuploidy was detected in 22 of the 56 urinary cell samples from UTUC patients (39%, 95% CI 28% to 52%, Table 31, and Fig. 33) but in none of the 188 urinary cell samples from healthy individuals. The most commonly altered arms were 1q, 7q, 8q, 17p, and 18q. Some of

these arms harbor well-known tumor oncogenes or suppressor genes that have been shown to undergo changes in copy numbers in many cancers (Vogelstein et al., 2013).

Comparison with primary tumors – the UTUC Cohort

[1097] Tumor samples from all 56 patients enrolled in this study were available for comparison and were studied with the same three assays used to analyze the urinary cell samples. This comparison served two purposes. First, it allowed determining if the mutations identified in the urinary cells were derived from the available tumor specimen from the same patient. There were a total of 39 UTUC cases in which a mutation could be identified in the urinary cells. In 35 (90%) of these 39 cases, at least one of the mutations identified in the urine sample (Table 29 and Table 30) was also identified in the corresponding tumor DNA sample (Table 32 and Table 33). When all 80 mutations identified in the urinary cells were considered, 63 (79%) were identified in the corresponding tumor sample (Table 32 and Table 33). In any of the three assays, the discrepancies between urine and tumor samples might be explained by the fact that only one tumor per patient was accessible, even though more than one anatomically distinct tumor was often evident clinically. Additionally, DNA was extracted from only one piece of tissue from each tumor, and intratumoral heterogeneity could have been responsible for some of the discrepancies.

[1098] The tumor data helped determine why 17 of the 56 urinary cell samples from UTUC patients did not contain detectable mutations. The reason could either have been that the primary tumors did not harbor a mutation present in the gene panel or that the primary tumor did contain such a mutation but the fraction of neoplastic cells in the urine sample was not high enough to allow its detection. From the evaluation of the primary tumor samples, it was found that four (24%) of the 17 urine samples without detectable mutations were from patients whose tumors did not contain any of the queried mutations (Table 32). The conclusion was that the main reason for failure of the mutation test was an insufficient number of cancer cells in the urine, and this accounted for 13 (76%) of the 17 failures.

[1099] There were 22 cases in which aneuploidy was observed in the urinary cell samples. Overall, 96% of the chromosome gains or losses observed in the urinary cells were also observed in the primary tumors (examples in Fig. 35). Conversely, there were 34 cases in which

aneuploidy was not observed in the urinary cell samples. Evaluation of the 56 tumors with the same assay showed that all but three were aneuploid, so as with mutations, the main reason for failure of the aneuploidy assay was insufficient amounts of neoplastic DNA in the urinary cells.

Biomarkers in combination – the UTUC Cohort

[1100] There are two factors that can limit sensitivity for genetically-based biomarkers. First, a sample can only be scored as positive for the biomarker if it contains DNA from a sufficient number of neoplastic cells to be detected by the assay. Second, the tumor from which the neoplastic cells were derived must harbor the genetic alteration that is queried. Combination assays can increase sensitivity by assessing more genetic alterations, and are thereby more likely to detect at least one genetic alteration present in the tumor. However, mutations in clinical samples often are present at low allele frequencies (Table 29 and Table 30), requiring high coverage of every base queried. It would be prohibitively expensive to perform whole exome sequencing at 10,000x coverage. In this study, the selected regions of 11 genes (including *TERT*) were carefully evaluated together with copy number analysis of 39 chromosome arms. Even if a tumor does not contain a genetic alteration in one of the 11 genes assessed, it might still be aneuploid and detectable by the urinary cell assay for aneuploidy. The sensitivity of aneuploidy detection is less than that of the mutation assays. Simulations showed that DNA containing a minimum of 1% neoplastic cells is required for reliable aneuploidy detection, while mutations present in as few as 0.03% of the DNA templates can be detected by the mutation assays used in this study. Nevertheless, urinary cell samples that had relatively high fractions of neoplastic cells but did not contain a detectable mutation in the 11 queried genes should still be detectable by virtue of their aneuploidy because, as noted above, 53/56 UTUCs studied here were aneuploid. Additionally, some of the mutations in the 11 genes queried, such as large insertions or deletions or complex changes, might be undetectable by mutation-based assays but a sample with such an undetectable mutation could still score positive in a test for aneuploidy.

[1101] To determine whether these theoretical arguments made a difference in practice, biomarker performance was evaluated with the combined approaches, collectively called UroSEEK. As noted above, the ten-gene multiplex assay, the *TERT* singleplex assay, and the aneuploidy assays yielded 64, 29%, and 39% sensitivities, respectively, when used separately.

Twenty-three samples without *TERT* promoter mutations tested positive for mutations in one of the other ten genes (Venn diagram in Fig. 32). Conversely, three samples without detectable mutations with the multiplex assay scored positive for *TERT* promoter mutations (Fig. 32). And, three of the urinary cell samples without any detectable mutations were positive for aneuploidy (Fig. 32). Thus, when the three assays were used together, and a positive result in any one assay was sufficient to score a sample as positive, the sensitivity rose to 75% (95% CI 62.2% to 84.6%). Only one of the 188 samples from healthy individuals scored positive in the UroSEEK test (specificity 99.5%, CI 97.5 to 100%).

[1102] To determine the basis for the increased sensitivity afforded by the combination assays, data from the primary tumors of the three patients whose urinary cell samples exhibited aneuploidy but did not harbor detectable mutations were evaluated. It was found that these three tumors did not contain any mutations in the 11 queried genes, explaining why these same assays were negative when applied to urinary cell DNA. As noted above, these three tumors were aneuploid, thus affording the opportunity to detect these copy number variations in the urinary cell samples.

Correlation with clinical features

[1103] A cancer biomarker should advantageously be able to detect tumors at an early stage, enabling surgical removal of the lesions prior to widespread metastasis. UroSEEK was sensitive in detecting both early and late tumors. It scored positive in 15 (79%) of 19 patients with stage Ta or T1 tumors and in 27 (73%) of 37 patients with stage T2-T4 tumors. Ten-year cancer specific survival rates show that 91% of UTUC patients with stage T1 malignancies are expected to be cured by surgery, compared to only 78%, 34% and 0% of patients with stage 2, 3, or 4 tumors, respectively.

[1104] UroSEEK sensitivity was independent of a variety of clinical parameters other than tumor stage, including gender, CKD stage, tumor grade, tumor location and risk factors for developing UTUC, indicating that the assay is suitable for evaluation of diverse patient populations. Furthermore, UroSEEK was considerably more sensitive than urine cytology in this cohort. Cytology was available in 42 cases, and of these only four (9.5%) were diagnosed as carcinoma cytologically. Even if samples scored as “suspicious for malignancy” by cytology were

considered as positive, the sensitivity was only 26% (including the four scored as positive and seven scored as suspicious). UroSEEK detected all four cases scored as positive by cytology, five of the seven cases scored as suspicious for malignancy, and 22 of the 31 samples scored by cytology as inconclusive or negative.

Example 6: Detection of aneuploidy in patients with cancer through amplification of long interspersed nucleotide elements (LINEs)

[1105] This Example describes a new approach for amplicon-based aneuploidy detection. This approach, called WALDO for **W**ithin-**S**ample-**A**neup**L**oidy-**D**etecti**O**n (WALDO), employs supervised machine learning to detect the small changes in multiple chromosome arms that are often present in cancers. It is shown herein that WALDO can be applied to identify chromosome arm gains or losses with improved sensitivity and equivalent specificity compared to previous approaches. Furthermore, machine learning can be incorporated to make genome-wide aneuploidy calls, in which samples are classified according to their aneuploidy status. This Example reports WALDO results on thousands of samples, including tissues of ten different tumor types as well as liquid biopsies of plasma from cancer patients. When two samples are available for comparison, WALDO can be used to assess genetic relatedness or to find somatic mutations within the LINEs. Thus, this approach can be used to provide an estimate of somatic mutation load, evaluate carcinogen signatures, and detect microsatellite instability (Fig. 1).

Materials and Methods

Samples

[1106] A total of 1,678 tumors were evaluated in this study (see below).

Sample Source	Sample Type	Number of Samples	Number of Samples Including Replicates	Matched Normal	Mutation Data
Peripheral white-blood-cell (WBC)	Normal	176	677	N/A	No

Tumor	Breast Invasive Carcinoma (BRCA)	45	45	No	No
Tumor	Colon Adenocarcinoma and Rectum Adenocarcinoma (COAD;COADREAD)	536	536	No	No
Tumor	Colorectal Adenoma	32	32	N/A	No
Tumor	Esophageal Carcinoma (ESCA)	42	42	No	No
Tumor	Head and Neck Squamous Cell Carcinoma (HNSC)	96	96	No	No
Tumor	Liver Heptaocellular Carcinoma (LIHC)	56	56	No	No
Tumor	Ovarian Serous Cystadenocarcinoma (OV)	157	157	No	No
Tumor	Pancreatic Adenocarcinoma (PAAD)	345	345	No	No
Tumor	Stomatic Adenocarcinoma (STAD)	28	28	No	No
Tumor	Uterine Corpus Endometrial Carcinoma (UCEC)	296	296	No	No
Tumor (Cell Line)	Mismatch Repair Deficient Colorectal Carcinoma	6	6	Yes	No
Plasma	Normal	402	566	N/A	No
Plasma	Pancreatic Adenocarcinoma (PAAD)	547	547	No	Yes
Plasma	Breast Invasive Carcinoma (BRCA)	28	28	No	Yes
Plasma	Colon Adenocarcinoma and Rectum Adenocarcinoma (COAD;COADREAD)	167	167	No	Yes
Plasma	Esophageal Carcinoma (ESCA)	17	17	No	Yes
Plasma	Liver Heptaocellular Carcinoma (LIHC)	54	54	No	Yes
Plasma	Stomatic Adenocarcinoma (STAD)	16	16	No	Yes
Plasma	Ovarian Serous Cystadenocarcionma (OV)	14	14	No	Yes
Plasma	Lung	113	113	No	Yes

[1107] The number of cancers of each histopathologic subtype are listed in the Appendices. The tumors were formalized fixed and paraffin-embedded (FFPE). In all cases, DNA was purified using QIAsymphony (cat # 937255). Peripheral white blood cells (WBCs) were purified from the blood of 176 healthy individuals. Plasma was purified from 566 healthy individuals and 982 patients with cancer. DNA was purified from WBCs and plasma using Qiagen kit numbers (cat # 1091063) and (cat # 937255) respectively. The majority of the plasma samples used in this study

has been independently evaluated for mutations in one of twelve commonly mutated genes. The fraction of mutant alleles in these plasma samples was used as an estimate of their neoplastic cell content. All individuals participating in the study provided written informed consent after approval by the institutional review boards of the hospitals at which they were collected.

Fast-SeqS

[1108] For each DNA sample evaluated, FAST-SeqS was used to amplify approximately 38,000 amplicons with a single primer pair (Kinde et al., 2012 *PloS ONE* 7:e41162). Massively parallel sequencing was performed on Illumina instruments (HiSeq 2500, HiSeq 4000, or MiSeq). During amplification, degenerate bases at the 5' end of the primer were used as molecular barcodes to uniquely label each DNA template molecule as described elsewhere (see, e.g., Kinde et al., 2011 *Proceedings of the National Academy of Sciences* 108:9530-9535). This ensured that each DNA template molecule was counted only once. In all instances in this paper, the term "reads" refers to uniquely identified reads. Depending on the experiment, each read was sequenced between 1 and 20 times. For each WBC and tumor DNA sample, 100,000 to 25 million reads were used for analysis. For each plasma DNA sample, 100,000 to 15 million reads were used. Replicates of normal DNA were included in every sequencing experiment and used to evaluate stochastic and experimental variability.

Sample alignment and genomic interval grouping

[1109] Bowtie2 was used to align reads to human reference genome assembly GRC37. 37,669 exact matches (33,844 excluding the sex chromosomes) to the reference genome were identified. These exact matches allowed inclusion of common polymorphisms. The polymorphisms included 24,720 single nucleotide polymorphisms (SNPs) and 1,500 insertion and deletion (indel) polymorphisms, with minor allele frequencies were >1% in the1000 Genomes database (Consortium 2012 *Nature* 491:56-65).

[1110] In light of experimental and stochastic variation, the number of reads that mapped to each genomic region of any euploid sample was expected to be variable. To minimize this variability,

clusters of 500-kb genomic intervals with similar read depth across all chromosomes in *multiple euploid samples* were identified. This step permitted estimation of the expected variability in read depth in a sample when no aneuploidy was present. Genomic intervals smaller and larger than 500 kb were tested, and it was found that 500 kb yielded reasonable performance in the assays described below at reasonable computational expense.

[1111] Clustering of the 500-kb genomic intervals was performed as follows. Each test sample was matched to euploid samples that had similar amplicon sizes. This was done because smaller amplicons will be over-represented in the amplicons generated from DNA that is of small size prior to amplification. The size of the amplicons generated by FastSeqS range from 100 to 140 bp (Kinde et al., 2012 *PloS ONE* 7:e41162). The size of plasma DNA is 140 to 180 bp (Diehl et al., 2005) *Proceedings of the National Academy of Sciences of the United States of America* 102:16368-16373; Chan et al., 2004 *Clinical chemistry* 50:88-92; Jahr et al., 2001 *Cancer research* 61:1659-1665; and Giacona et al., 1998 *Pancreas* 17:89-97), so the largest LINE amplicons will be substantially underrepresented in plasma DNA compared to WBC DNA, for example. It was found that seven euploid samples was sufficient for comparison to any test sample; using more than seven euploid samples did not substantially increase performance. The seven euploid samples were derived from a collection of 677 WBC or 566 plasma DNA from normal individuals, collectively termed the "euploid reference set". For each test sample p, the seven normal samples with the smallest Euclidean distance to p were selected, defined as $D(p,q)=\sqrt{\sum_n (q_n - p_n)^2}$ where, p_n and q_n are the fraction of amplicons of size n in samples p and q, and the sum is over all amplicon sizes in the two samples. Before calculating the Euclidian distances between the test samples from the samples in the euploid reference set, the following amplicons were excluded: (i) Using maximum likelihood estimates, the amplicons were ranked by variance among the seven euploid samples and the top 1% excluded. (ii), any amplicons with < 10 reads in one sample but > 50 reads in any of the other six samples were removed. In each sample, the 500-kb genomic intervals were scaled by subtracting the mean and dividing by the standard deviation of reads in each sample.

[1112] The scaled 500-kb genomic intervals were then clustered across the seven selected normal samples in the following way. First, each 500-kb genomic interval i was assigned to a primary cluster C_i. Next, the reads in genomic interval i across all samples was compared to the average number of read in the seven samples in all other genomic intervals i' that occurred on

the remaining 21 autosomal chromosomes. Insignificant results (paired t-test $p>0.05$, f-test $p>0.05$) were tested fro during the search for similarity. If the average number of reads in genomic interval *i'* was not significantly different from the number of reads in genomic interval *i*, it was added to cluster C_i. This process was repeated for each of the 4361 genomic intervals, yielding 4361 clusters. Every interval *i* belonged to its primary cluster but the same interval also belonged to an average of 176 other clusters (range of 100 to 252 clusters among 190 representative samples). The number of unique clusters was less than the 4361 because some clusters were composed of the same 500-kb genomic intervals. The number of unique clusters was typically 4310 to 4330 among 190 representative samples. Clusters contained an average of approximately two hundred 500-kb genomic intervals (see Fig. 45). Scaled reads were not randomly distributed (see Fig. 46A). However, the distribution of scaled reads within the ~200 genomic intervals in each cluster followed an approximately normal distribution (example in Fig. 46B-C).

Identifying chromosome arm gains or losses in a test sample

[1113] WALDO used the seven euploid samples described above *only* to define clusters of genomic intervals with similar amplification properties. The statistical tests for aneuploidy in WALDO were based on the read distributions *within* the test sample and independently of the read distributions in any euploid sample. For a test sample, maximum likelihood was used to estimate the means μ and variances σ^2 of the genomic intervals in each of the 4,361 clusters defined by the seven euploid samples that were chosen to match it on the basis of amplicon length. The robustness of these estimates was improved by iteratively removing outlying genomic intervals within the test sample from the clusters. Clusters containing fewer than 10 genomic intervals were not included in the analysis. For each cluster, any 500-kb genomic interval meeting the criteria $min(\ 2*\ CDF(\mu,\ \sigma_i^2),\ 2*(1-CDF(\mu,\ \sigma_i^2)\ ) < 0.01$ was removed from all clusters. Next, the μ and σ^2 parameters of each cluster were re-estimated by maximum likelihood. The two steps were repeated until no outlying genomic intervals remained. The statistical significance of the total reads was then estimated from all 500-kb genomic intervals on the arm. Because sums of normally distributed random variables are also normally distributed

random variables, the calculation was straightforward (see Fig 47). For each chromosome arm, $\sum_1^I R_i \sim N(\sum_1^I \mu_i, \sum_1^I \sigma_i^2)$ was calculated, where Ri is the scaled reads and I is the number of clusters on the arm. Z-scores were produced using the quantile function 1-CDF($\sum_1^I \mu_i, \sum_1^I \sigma_i^2$). Positive Z-scores > α represented gains and negative Z-scores < -α represented losses, where α was the selected significance threshold.

Arm level allelic imbalance

[1114] Common polymorphisms from 1000 Genomes (24,720 single nucleotide and 1,500 indels, MAF>1%) were used as candidate heterozygous sites. For each of the 677 normal samples, polymorphic sites were identified that could be confidently called as heterozygous and diploid. Polymorphisms were defined as those with variant-allele frequencies (VAF) (0.4<VAF<0.6), where VAF = #non-reference reads / total reads. VAFs were modeled at these sites as random variables taken from a normal distribution with μ=0.5; the variance σ^2 was estimated by maximum likelihood as a function of read depth (Fig. 48). To determine whether the alleles on a chromosome arm in a test sample were unbalanced, the subset of polymorphic sites was identified at which both alleles were present and in which the sum of the reads on both alleles was >25. The observed VAF was then compared with the normal distribution, using the expected variance for the observed read depth, yielding a two-sided P-value. All p-values on a chromosome arm were Z-transformed and combined with a weighted Stouffer's method, with the observed read depth at each site used as its weight. The formula used for this calculation was $Z \sim \frac{\sum_{i=1}^k w_i Z_i}{\sqrt{\sum_{i=1}^k w_i^2}}$, where w_i is UID depth at variant i, Z_i is the Z-score of variant i, and k is the number of variants observed on the chromosome arm. A chromosome arm was scored as having an allelic imbalance if the resulting Z score was greater than the selected statistical significance threshold α (one-sided test).

Generation of synthetic aneuploid samples

[1115] Data from 63 presumably euploid samples was selected, each containing at least 9 million reads, and each derived from the DNA of normal WBCs. Synthetic aneuploid samples were created by adding (or subtracting) reads from several chromosome arms to the reads from these normal DNA samples. Reads from 1, 5, 10, 15, 20, or 25 randomly selected chromosome arms were added to or subtracted from each sample. The additions and subtractions were designed to represent neoplastic cell fractions ranging from 0.5% to 10% and resulted in synthetic samples containing exactly nine million reads. The reads from each chromosome arm was added or subtracted uniformly. For example, when five chromosome arms that were lost were modeled, each was lost to the identical degree and we did not incorporate tumor heterogeneity into the model. Furthermore, synthetic samples containing two or more of the same extra chromosome arms were not created, such as synthetic cells containing 4 copies of chromosome 3p. This simplified approach did not comprehensively cover all biologically plausible aneuploidy events. However, limiting the possible combinations of altered arms made sample generation computationally tractable, and the resulting support vector machine worked well in practice.

[1116] The synthetically generated samples in which reads from only a single chromosome arm were added or subtracted enabled us to estimate the performance of WALDO when only a single chromosome arm of interest was gained or lost. The synthetic set in which 5-25 chromosome arms were altered permitted assessment of the performance of WALDO in typical samples derived from cancers. As shown in Fig. 37, most cancers have gains or losses of multiple chromosomes. The algorithms used to generate the synthetic samples are shown as pseudocode in Fig.49 and Fig. 50.

Genome-wide aneuploidy detection

[1117] A two-class support vector machine (SVM; Cortes 1995 *Machine learning* 20:273-297) was trained to discriminate between euploid samples and the synthetic samples in which the reads from 5 to 25 chromosome arms were added or subtracted. The training set contained 677

WBC negative samples (presumably euploid WBCs containing 3 million -15 million reads) and 3150 positive samples, all synthetic as described above. SVM training was done with the e1071 package in R, using radial basis kernel and default parameters (Meyer et al., 2015 *R package version*:1.6-3). Each sample had 39 Z-score features, representing chromosome arm gains and losses. 677 synthetic samples were randomly sampled so that the sizes of the negative and positive classes were equivalent, and this was repeated ten times. Each sample to be classified was scored by all ten SVMs, and the ten scores were averaged to yield a final score.

[1118] The number of reads from the data on experimental samples can vary widely, particularly when the samples are derived from sources with limited amounts of DNA such as plasma. Samples with low reads can generate artificially high SVM scores if read depth is not taken into account. Read depth was therefore controlled for by modeling the change in SVM scores as a function of read depth in the normal samples. In particular, each of the 63 WBC euploid samples was randomly down-sampled to yield ten replicates of lower read euploid samples of read depth ranging from 100,000 to 9 million. All down-sampled euploid samples were scored using the 10 SVMs were and the scores were averaged. This procedure yielded 630 SVM scores for the down-sampled euploid samples at each read depth. All scores were converted to ratios by finding the sample at each read depth with the minimum SVM score and dividing all scores at the same depth by that value. The average ratio r at each depth decreased monotonically as a function of increasing read depth (Fig. 51). The relation between read depth and SVM score was modeled using the following equation (A=-7.076*10^-7 and B = -1.946*10^-1). Raw SVM scores were corrected by dividing by the ratio r, using the formula $\log\left(1-\frac{1}{r}\right) = Ax + B$.

[1119] To score a sample as aneuploid, it was first determined whether any single chromosome arm in it was lost or gained in a statistically significant manner. A statistically significant gain of a single chromosome arm was defined as one whose Z-score was >4 $^{\sigma}$ above the maximum Z-score observed in the 677 normal WBC samples. Similarly, a statistically significant loss of a single chromosome arm was defined as one whose Z-score was <-4 $^{\sigma}$ below the minimum Z-score observed in the 677 normal WBC samples. Allelic imbalance based on SNPs was defined for a chromosome arm whose Z-score was Z-score was >4 $^{\sigma}$ above the maximum Z-score observed in the 677 normal WBC samples. Only samples in which no single chromosome arm was gained or lost when defined in this way were subjected to SVM analysis. The rationale for

this process was that the SVM was designed to identify samples with large numbers of chromosome arm gains or losses but relatively low neoplastic cell fractions. The SVM was not designed to detect aneuploidy in samples with neoplastic cell fractions >10%, which were easily identified through evaluation of their Z-scores and comparison to the 677 normal samples as described in the first part of this paragraph.

Somatic sequence mutations and microsatellite instability (MSI)

[1120] When matched normal samples were available, it was attempted to detect somatic single base substitution (SBS), insertion and deletion (indel) mutations based on LINE amplicon sequences and alignments. In such cases, the molecular barcoding approach for error reduction was used. For SBS, only amplicons that have at least 200 reads and 50 unique molecular barcodes were considered. For indels, reads that were observed in at least two clusters on the sequencing instrument were considered. The SBS mutations were identified by directly comparing amplicons from the test sample with amplicons from the matched normal, and did not require any alignment to the reference genome. Amplicons with fewer than 50 reads in the matched normal sample were excluded. A somatic SBS was defined as one in which at least five reads from the test sample differed from any normal read by exactly one nucleotide substitution.
[1121] Indels were called in a similar way. Amplicons from the test sample and matched normal sample to were first aligned the reference genome (GRc37) with Bowtie2 (Langmead 2012 *Nature Methods* 9:357-359). A somatic indel was defined as one in which at least ten reads from the test sample differed from any normal read by virtue of the same insertion or deletion.
[1122] Microsatellite instability in a test sample was determined by counting the number of somatic indels in mononucleotide tracts of > 3 nucleotides. There were 17,488 of these mononucleotide tracts in the LINE amplicons that were studied. It was expected that somatic indels in monotracts would be rare in a normal sample. Therefore, the null distribution of counts could be modeled as Poisson ($\lambda = 1$), where λ is the mean number of somatic indels in a monotract in a normal sample. A sample was called as harboring MSI if the number of somatic indels was statistically significant. To evaluate how often normal samples would be scored as MSI using this process, the total reads in normal samples was randomly split into two equal

partitions. The first partition was used as the reference sample and the second partition was used as a test sample.

Sample matching

[1123] To compare one sample to another, amplicons were first aligned to the reference genome GRC37 with Bowtie2. The 1000 Genomes common polymorphisms were used to identify the genotypes at 26,220 sites in each sample. Each polymorphic site was called as "0" (homozygous reference, >0.95 reads matching reference allele, minimum of ten reads), "1" (heterozygous, 0.05-0.95 UIDS matching either reference or alternate allele, minimum of ten reads of each allele), or "2" (homozygous alternate, >0.95 UIDs matching alternate allele, minimum of ten reads). Concordance was defined as the number of matched polymorphic sites that were identical in both samples (i.e., were both "0", both "1", or both "2") divided by the total number of genotypes that had adequate coverage in both samples. Two samples were considered a match if concordance was > 0.98 and at least 15,000 amplicons had adequate coverage.

TCGA somatic copy number alterations

[1124] The most recent Cancer Genome Atlas Level 4 somatic copy number alteration files from Firehose were downloaded (Aggregate_AnalysisFeatures.Level_4.2016 012800.0.0), from GISTIC analysis (Beroukhim et al., 2007 *Proceedings of the National Academy of Sciences* 104:20007-20012) of Affymetrix SNP6 arrays. 9 TCGA tumor types were selected that matched our cohorts of primary tumor samples (Breast invasive carcinoma (BRCA), colon adenocarcinoma (COAD), colon or rectal adenocarcinoma (COADREAD), esophageal carcinoma (ESCA), head and neck squamous cell carcinoma (HNSC), liver hepatocellular carcinoma (LIHC), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), stomach adenocarcinoma (STAD), and uterine corpus endometrial carcinoma (UCEC)). A total of 6276 samples were available (Breast invasive carcinoma (BRCA):1081, colon adenocarcinoma, colon or rectal adenocarcinoma (COAD;COADREAD): 2755, esophageal carcinoma (ESCA): 185, head and neck squamous cell carcinoma (HNSC): 523, liver

hepatocellular carcinoma (LIHC): 371, ovarian serous cystadenocarcinoma (OV): 580, pancreatic adenocarcinoma (PAAD): 185, stomach adenocarcinoma (STAD): 442, uterine corpus endometrial carcinoma (UCEC): 540). The data consisted of GISTIC $\log_2$ ratios representing gains or losses of each chromosome arm (Mermel et al., 2011 *Genome biology* 12:R41). Ratios > 0.2 or < 0.2 were considered gains or losses (Laddha et al., 2014 *Molecular cancer research* 12:485-490).

Comparison with a prior technique for detecting single chromosome arm alterations

[1125] The fraction of reads that mapped to each chromosome arm in each of the 677 WBC samples, and their averages and standard deviations, were calculated (Kinde et al., 2011 *Proceedings of the National Academy of Sciences* 108:9530-9535). The score for each arm was computed as: $z_{i,chrN} = (chrN_i - \mu_{chrN}) / \sigma_{chrN}$, where $chrN_i$ represents the normalized read counts for that chromosome arm and μ_{chrN} and σ_{chrN} represent the mean and standard deviation of the normalized reads counts.

Results

Statistical principles underlying WALDO

[1126] Unlike most conventional approaches for assessing copy number changes, WALDO does *not* compare normalized read counts from each chromosome arm in a test sample to the fraction of reads in each chromosome arm in other samples. Such conventional comparisons are subject to batch effects and other artifacts associated with variables that are difficult to control. To evaluate whole genome sequencing data, aneuploidy was detected by comparing the read counts of LINEs within 4361 genomic intervals each containing 500-kb of sequence. The read counts within the 500-kb genomic intervals within a sample were only compared to the read counts of other genomic intervals within the *same* sample - hence the "Within-Sample" designation in WALDO.

[1127] In euploid samples, the number of LINE reads within each 500-kb genomic interval should track with the number of reads in certain other genomic regions. Genomic intervals that

track together do so because the amplicons within them amplify to similar extents. Here, such genomic regions that track together are called "clusters". It is possible identify clusters from sequencing data on euploid samples. In a test sample, it is determined whether the number of reads in each genomic interval in each pre-defined cluster is within the expected bound of the other clusters from that same sample. If the reads within a genomic interval are outside the statistically expected bound, and there are many such outsiders on the same chromosome arm, then that chromosome arm is classified as aneuploid. The statistical basis of this test is described in the Materials and Methods. In brief, while the number of reads at each LINE is not randomly distributed across the genome, the distribution of scaled reads within each cluster is approximately Normal. A convenient property of Normal distributions is that the sum of multiple Normal distributions is also a Normal distribution. It is thus possible to compute the theoretical mean and variance of the summed reads on each chromosome arm simply by summing the means and variances of all the clusters represented on that chromosome arm.

[1128] WALDO also employs several other innovations that make it applicable to the analysis of PCR-generated amplicons from clinical samples. One of these innovations is controlling amplification bias stemming from the strong dependence of the data on the size of the initial template. Another is the use of a Support Vector Machine (SVM) to enable the detection of aneuploidy in samples containing low neoplastic fractions. The conceptual and statistical bases for WALDO are detailed in the Materials and Methods section herein.

Evaluation of chromosome arm gains and losses in primary tumor samples

[1129] WALDO was first used to study chromosome arm gains and losses in 1,677 primary tumor samples from ten cancer types. One of the outputs of WALDO is a z-score for each of the 39 non-acrocentric arms on the autosomal chromosomes. The z-scores for each of these chromosome arms in each of the primary tumor samples evaluated in this study are provided in Table 35. These results were compared with those obtained by The Cancer Genome Atlas (TCGA) on independent samples of the same tumor types (Zack et al., 2013 *Nature genetics* 45:1134-1140; and Beroukhim et al., 2007 *Proceedings of the National Academy of Sciences* 104:20007-20012). The fraction of tumor samples having a gain or a loss in each chromosome arm was identified in our data and in TCGA, considering all tumor types together and each

tumor type individually. As shown in the top half of Fig. 37, the fraction of samples in all cancer types scored as a gain by WALDO or as a gain by TCGA's algorithm (GISTIC) is shown for each chromosome arm, and the fraction of samples with a loss is shown in the bottom half. The correlations between arm-level gains scored in this study and those in TCGA are shown in Fig. 39A (R^2=0=45) and arm-level losses are shown in Fig. 39B (R^2=0.39). Considering that the samples were from completely different patients, the specific chromosome arms gained and lost in both datasets were remarkably similar. The chromosome arms with the most gains were 1q, 3q, 7p, 7q, 8q, and 20q and relatively few losses were observed on these arms. Those with the most losses were 4p, 4q, 8p, and 18q and relatively few gains were observed on these arms. The arms with fewest gains or losses were 10p, 16p, 19p, and 19q.

[1130] Similarly high correlations were observed for many of the specific tumor types in those cases in which a sufficient number of cancers were available for comparison (see below, and Fig. 40).

	Gain Correlation	Loss Correlation	WALDO Samples	GISTIC Samples
BRCA	0.629	0.436	89	181
COAD;COADREAD	0.582	0.428	536	2755
ESCA	0.043	0.07	42	185
HNSC	0.537	0.344	96	523
LIHC	0.64	0.287	56	371
OV	0.067	0.123	157	580
PAAD	0.384	0.702	345	185
STAD	0.552	0.555	28	442
UCEC	0.325	0.165	296	540

[1131] The highest correlations were for pancreatic adenocarcinomas and liver cancers (R^2=0.70 and R^2=0.64, respectively). An interesting outcome of this analysis was the large number of chromosome arms that were aneuploid in the great majority of cancer cases. The median number of chromosome arms that were lost or gained per cancer was 14, with interquartile range of 5 to 22. This large number was used for the development of the Support Vector Machine described below.

[1132] 32 benign tumors of the colon (colorectal adenomas) were also evaluated. It was found that 25 of them displayed gains or losses of chromosomes. The median number of chromosome arms that were lost or gained per benign tumor was 4, with interquartile range of 1 to 9.75. No benign tumors have yet been studied by TCGA, so comparison was not possible. However, comparison to colorectal cancers showed that the benign tumors had many fewer chromosome arm changes than observed in cancers. Additionally, the chromosome arms altered in the adenomas overlapped with those in the cancers, and the directionality of the changes (gains *vs.* losses) was preserved.

[1133] WALDO also allows determination of allelic imbalances based on the SNPs with the LINEs that are concomitantly sequenced. This provides a totally independent measure of chromosome arm changes than provided by the number of reads across the 500-kb genomic intervals. Note that measurements of allelic imbalance represent the ratios between the number of reads of the reference allele vs. those of the variant allele. This ratio will be the same whether the chromosome arm containing the reference allele is gained or the arm containing the variant allele is lost. Nevertheless, without wishing to be bound by theory, one would expect that there would be a strong relationship between the chromosomes exhibiting allelic imbalances and those exhibiting either gains or losses in the same tumor. It was found that 63% of chromosome arms with allelic imbalance also had a significant gain or loss at the same chromosome arm. Other uses of the SNPs within the LINEs are described herein.

[1134] Next, the sensitivity and specificity of WALDO to call single chromosome arm gains or losses was compared (see Materials and Methods). Both methods were applied to LINE amplicon sequencing data from 677 normal peripheral white blood cell (WBC) samples, with each WBC sample independently amplified and sequenced to an average depth of 9.5M reads. This experimental data was augmented by 24,570 synthetic samples with single chromosome alterations (see Materials and Methods). Sensitivity was computed as the total number of correctly identified altered arms divided by the total number of altered arms in the synthetic samples. Specificity was computed as 1 minus the total number of incorrectly called altered arms divided by the total number of normal arms in the experimental data from the normal WBC samples. For both WALDO and the previous method, three significance thresholds (± 1.96, ± 3.0, ± 5.0) and three neoplastic cell fractions (1%, 5%, 10%) were considered. For all thresholds

and neoplastic cell fractions, WALDO had higher specificity and sensitivity (see below, and Table 34).

Dilution	Threshold	WALDO Sensitivity	WALDO Specificity	Z Score Sensitivity	Z Score Specificity
0.010	1.96> or <-1.96	0.221	0.969	0.144	0.952
0.010	3> or <-3	0.031	0.999	0.020	0.995
0.010	5> or <-5	0.000	1.000	0.000	1.000
0.050	1.96> or <-1.96	0.969	0.969	0.899	0.952
0.050	3> or <-3	0.917	0.999	0.748	0.995
0.050	5> or <-5	0.671	1.000	0.443	1.000
0.100	1.96> or <-1.96	0.999	0.969	0.988	0.952
0.100	3> or <-3	0.995	0.999	0.957	0.995
0.100	5> or <-5	0.957	1.000	0.839	1.000

[1135] To further evaluate the ability of WALDO to detect single chromosome abnormalities, DNA from patients with trisomy 21 was also evaluated. The DNA from individuals with trisomies were physically mixed at a ratio of 2 ng of normal DNA and 0.2 ng of Trisomy 21 DNA. The mixtures were created to replicate typical fetal fractions in noninvasive prenatal testing (approximately 10%). Using polymorphisms in the LINE amplicons, the trisomy admixture rate of the samples (range 7.7%-10.4%) was estimated. Using a z threshold of 2.5, it was found that as few as 2M reads could detect trisomy 21 at fetal fractions typically observed (Sensitivity 95%). 16 normal WBC were then sampled at various read depths. At 2M reads using the same threshold, the specificity was 100 %. Sensitivities and specificities at other read depths and other admixtures of trisomy 21 samples are summarized in Fig. 41.

Aneuploidy detection in samples with low fractions of neoplastic cell DNA

[1136] Many potential applications of aneuploidy detection in cancer involve identifying a relatively small fraction of DNA from neoplastic cells within a large pool of DNA derived from normal cells. One notable application is liquid biopsy, i.e., the evaluation of bodily fluids such as urine, saliva, cyst fluid, or sputum for evidence of cancer. Given that aneuploidy is a general

feature of cancers of virtually all types (see Fig. 37), detecting aneuploidy could be used for this purpose.

[1137] To employ WALDO for liquid biopsies, a 2-stage approach was used. The first employed a search for individual chromosome arm gains or losses or allelic imbalance, as described above. Simulations with synthetic DNA showed that this approach could detect an individual chromosome arm gain or loss with sensitivities > 90% at specificities >99% when the fraction of DNA contributed by the neoplastic cells was >5% of the total DNA. To detect aneuploidy in samples with lower fractions of neoplastic cell DNA, that fact that the median number of chromosome arm gains or losses per tumor was high (Kinde et al., 2012 *PloS ONE* 7:e41162) was exploited. A variety of approaches to distinguish samples containing low fractions of neoplastic DNA with multiple chromosome abnormalities from euploid samples was therefore considered. These approaches included counting the number of significant arms, combining scores of the most significant arms, and summing squared window-based Z-scores. Based on synthetic samples, it was found that the optimum approach was obtained with a Support Vector Machine (among many machine learning algorithms tested). The Support Vector Machine training was designed to be generally applicable to any cancer type rather than based on patterns of gains and losses typical of specific cancer types. With synthetic samples, the Support Vector Machine could detect aneuploidy in 78% of samples with a neoplastic cell fraction of 1% at a specificity of 99% as determined by cross validation. This Support Vector Machine-based algorithm was therefore incorporated into WALDO for the evaluation of clinical samples with low neoplastic composition (see Fig. 38).

[1138] WALDO was then used to attempt to evaluate aneuploidy in plasma samples from 961 cancer patients and 566 healthy individuals (see Materials and Methods). Cancers of 8 different types were evaluated (see Table 36). The neoplastic cell fraction of each cancer sample was considered to be the mutant allele fractions determined from deep sequencing data. Samples were divided into those with neoplastic cell fractions >1% (122 samples), between 0.5% and 1% (96 samples) and <0.5% (738 samples). Sensitivity was defined as the proportion of cancer patient samples scored as aneuploid, while specificity was defined as 1 minus the fraction of healthy patient samples scored as aneuploid. Receiver operating curves (ROC) are shown in Fig. 38 for these three ranges of neoplastic fractions. At stringent specificity (99%), aneuploidy was identified in 42% of samples with neoplastic cell fractions >1% (see Fig. 38A). As expected,

sensitivity decreased with decreasing neoplastic cell fractions (see Fig. 38B, 38C). At 99% specificity, WALDO detected aneuploidy in 24% of samples with neoplastic cell fractions of 0.5 to 1% and in 19% of samples with neoplastic cell fractions of 0 to 0.5%. The specific cancer type of the patient was not highly correlated with positive aneuploidy calls. However, the number of template molecules that were assessed did correlate with sensitivity.

[1139] In plasma samples with higher neoplastic cell content, it was possible to determine which chromosome arms were gained or lost. Among 558 of the plasma samples that had a paired primary tumor, 188 samples had a significant chromosome arm gain or loss and 54% had a concordant gain or loss in the primary tumor. In samples with low neoplastic content, none of the individual arms were gained or lost at statistically significant levels but the Support Vector Machine component of WALDO was presumably able to pick out small deviations in multiple chromosome arms that distinguished them from euploid samples.

Sample matching

[1140] DNA profiling with short tandem repeats is a well-established forensic technique that is now routinely used. Carefully curated SNP panels have also been developed to ensure sample identity, such as between tumor and normal specimens from the same patients (Kidd et al., 2006 *Forensic science international* 164:20-32; and Pengelly et al., 2013 *Genome medicine* 5:89). The LINEs amplified in FAST-SeqS contain 26,220 common polymorphisms, including variants detected in >1% in 1000 Genomes (Consortium 2012 *Nature* 491:56-65). These polymorphisms theoretically provide a powerful way to profile DNA samples evaluated for aneuploidy without any additional work or cost. To determine whether such identification was possible in practice, a measure of concordance between any two samples was designed (see Materials and Methods). This to measure concordance was then used in replicates of 176 normal WBC samples to one another, using ~5 replicates per sample, for a total of 676 WBC samples. The input to WALDO was 676 samples, without specifying the sample name, so there were a total of 456,976 (676 x 676) possible matches. WALDO correctly matched all replicate samples with high concordance (>99.9%), without any false matching. Next, this protocol was performed on 970 plasma samples and 1,684 tumor samples. The 558 plasma samples should match the corresponding primary tumor samples and no other matches should be observed. This produced 7,038,409 ((970+1,683)

x (970+1,683)) possible matches. Nearly all the 2653 samples matched as expected, i.e., only to themselves or to the corresponding primary tumors, with concordance >99.8%. However, two plasma samples were found that did not match to the expected primary tumors and 12 plasma samples that matched to other plasma samples that were purportedly derived from different donors. In all these "mismatched cases", the FastSeqS data indicated high concordances (>99.8%). The mismatches were therefore most likely a result of mislabeling of the samples and illustrated the utility of sample identity check with WALDO.

Mutation load, carcinogenic signatures, microsatellite instability

[1141] When two samples, a normal and a cancer, are available from the same patient, LINE mutations that are in one sample but not the other can conceivably be discerned. For this application, molecular barcoding to reduce sequencing errors (see, e.g., Kinde et al., 2011 *Proceedings of the National Academy of Sciences* 108:9530-9535) can be used, as is achieved through the experimental and bioinformatics components of WALDO (see Materials and Methods).

[1142] To determine whether somatic mutation detection was feasible, ten urothelial carcinomas of the upper urinary tract (UTUCs) and normal tissues from the same patients were evaluated. These samples had previously been analyzed by exomic sequencing (Hoang et al., 2013 *Science translational medicine* 5:197ra102-197ra102). For each tumor sample, the number of somatic mutations were counted and the spectrum of single base substitutions (SBS) (A->T, A->C, etc.). It was found that the number of SBS in LINEs was highly correlated with the number of SBS in the exomes of these tumors (R^2=0.98, p <2.6*10^{-8}). The spectrum of mutations in the LINEs was similarly correlated with the spectrum of mutations in exonic sequences (R^2=0.95, p < 1.8*10^{-6}). Noticeably, six of these tumors were from patients exposed to aristolochic acid and the pathognomonic signature (A->T, T->A) of this mutagen was prominent in these six tumors (see Fig. 42, Fig. 43, and Fig. 44).

[1143] The LINEs assessed by WALDO harbor 17,488 mononucleotide tracts of >3 nucleotides. Because mononucleotide tracts are particularly sensitive to defects in mismatch repair, it was determined whether WALDO could be used to assess mismatch repair deficiency. For this purpose, the number of indels in the 17,488 LINE mononucleotide tracts were assessed. It was

found the number of indels in six mismatch repair-deficient colorectal cancers averaged 35 and ranged from 10 to 67. Normal tissues from these patients harbored only zero or one indel, and the difference between the cancers and normal tissues was highly significant ($p<7.2*10^{-4}$).

Example 7: Genome-wide quantification of rare mutations by Bottleneck Sequencing

[1144] The accumulation of random somatic mutations in the nuclear and mitochondrial genome over time underlies fundamental theories of carcinogenesis, neurodegeneration, and aging (see, e.g., Stratton et al., 2009 *Nature* 458:719-724; Kennedy et al., 2012 *Mech Ageing Dev* 133:118-126; and Vijg et al., 2014 *Current opinion in genetics & development* 26:141-149). Direct observation of these rare mutations in the human body with age therefore has the potential to enhance our understanding of human disease. Currently, no *simple* high-throughput method exists to directly and systematically quantify somatic mutational load in normal, non-diseased human tissues at a genome-wide level. Next-generation DNA sequencing (NGS) technologies address this issue, but their sequencing error rate limits the detection of rare mutations (see, e.g., Albertini et al., 1990 *Annu Rev Genet* 24:305-326; and Cole et al., 1994 *Mutat Res* 304:33-105).

[1145] This Example describes a *Bot*tleneck *Seq*uencing *S*ystem (BotSeqS) technology designed to accurately detect rare point mutations in any molecularly-barcoded library in a completely unbiased fashion. BotSeqS, a next-generation sequencing method that simultaneously quantifies rare somatic point mutations across the mitochondrial and nuclear genomes. BotSeqS combines molecular barcoding with a simple dilution step immediately prior to library amplification. In this Example, BotSeqS is used to show age and tissue-dependent accumulations of rare mutations and demonstrate that somatic mutational burden in *normal tissues* can vary by several orders of magnitude, depending on biologic and environmental factors. This Example also shows major differences between the mutational patterns of the mitochondrial and nuclear genomes in normal tissues. Lastly, the mutation spectra of normal tissues were different from each other, but similar to those of the cancers that arose in them. This technology can provide insights into the number and nature of genetic alterations in normal tissues and can be used to address a variety of fundamental questions about the genomes of diseased tissues.

Materials and Methods

Human tissue samples

[1146] Normal, non-diseased tissues for this study were acquired from five different sources (Table 43). For COL229 to COL237 and SIN230, colon or duodenum was obtained from consented patients at the Johns Hopkins Hospital with the approval of its Institutional Review Board. For COL373 to COL375 and BRA01 to BRA09, flash frozen, post-mortem colon and brain was requested from the NIH NeuroBioBank (neurobiobank.nih.gov), with the request being approved and fulfilled by University of Maryland Brain and Tissue Bank (Baltimore, Maryland) and University of Miami Brain Endowment Bank (Miami, Florida). For KID034 to KID038, flash frozen, post-mortem kidney cortex blocks (200 mg) were purchased from Windber Research Institute (Windber, Pennsylvania). COL238 and COL239 were as reported elsewhere (see, e.g., Parsons et al., 1995 *Science* 268:738-740; Hamilton et al., 1995 *The New England journal of medicine* 332:839-847; and De Vos et al., 2004 *American journal of human genetics* 74:954-964). SA_117, SA_118, SA_119, AA_105, AA_124, and AA_126 were as reported elsewhere (see, e.g., Hoang et al., 2013 *Science translational medicine* 5:197ra102). The initial rationale for the sample size for colon and brain was to acquire at least three individuals in each age group in order to understand the average trend of somatic mutational patterns for each age group. Age groups for colon and brain were selected based on human body growth and maintenance: early body development at < 10 years, fully grown young adult body at ~20-40 years, and old, maintained adult body at > 90 years. For colon, one tissue from the young child age group (SIN230) was later determined to be duodenum, leaving only two individuals representing the young child age group for colon epithelium. For normal kidney, criteria for kidney acquisition were an age-matched and non-smoking control group for the kidneys of smokers and aristolochic acid-exposed samples. All normal kidney controls were Caucasian and therefore less likely to originate from a high risk AA-exposed population (e.g. Asia). From the same kidney tissue source, three aliquots of flash frozen, post-mortem normal kidney from a five month old individual were available as technical replicates and to further test an age-trend for non-carcinogen exposed normal kidneys.

Preparation of Illumina Y-adapter-ligated molecules

[1147] Genomic DNA (34 ng to 1 μg) in 55 μL TE buffer was fragmented using BioRuptor (Diagenode) at high intensity for 15 s on and 90 s off, using 7 cycles at 3°C. After random fragmentation, Illumina Y-adapters were ligated to the DNA fragments using TruSeq DNA PCR-Free kit (Illumina) according to a standard low DNA input Illumina protocol with selection for 350 bp insert sizes. This resulted in adapter-ligated molecules in a total volume of 20 μL.

Dilution of Y-adapter-ligated molecules

[1148] Five ten-fold serial dilutions were performed in 96-well PCR plates starting with 2 μL of adapter-ligated molecules (prior to PCR) in 18 μL of dilution buffer (TE containing 1 ng/μL pBlueScript). Samples were mixed by gently pipetting with a multichannel pipette. Two μL of each sample was then transferred into 18 μL of fresh dilution buffer using a multichannel pipette. The mixing and transferring was repeated for a total of five serial dilutions. Only 2 μL of each dilution (1/10 total volume) was used as template for each PCR. A 10^3-fold dilution was accomplished as follows: (i) use of 2 μL of the total 20 μL of adapter-ligated molecules (10-fold dilution); (ii) mixing 2 μL of adapter-ligated molecules with dilution buffer in a total volume of 20 μL (10-fold dilution); and (iii) use of 2 μL of diluted adapter-ligated molecules from the total 20 μL volume in the PCR reaction (10-fold dilution, see below). The five serial dilutions resulted in final dilution factors of 10^3, 10^4, 10^5, 10^6, and 10^7.

PCR amplification of diluted Y-adapter-ligated molecules

[1149] Custom HPLC-purified PCR primers (IDT), TS-PCR Oligo1 (5'-AATGATACGGCGACCACCGAG*A; SEQ ID NO:808) and TS-PCR Oligo2 (5'-CAAGCAGAAGACGGCATACGA*G; SEQ ID NO:809), were designed with one phosphorothioated bond (*) at the 3' end. PCR was performed in 50 μL total volume with 0.5 μM TS-PCR Oligo1, 0.5 μM TS-PCR Oligo2, Q5 2X HotStart High-Fidelity Master Mix (NEB)

at 1X final concentration, and 2 μL of diluted adapter-ligated molecules as template. PCR was performed in Thermo HyBaid PCR Express HBPX Thermal Cycler. The following PCR program was used: 1) 98°C for 30 s 2) 98°C for 10 s, 69°C for 30 s, 72°C for 30 s for 18 cycles, and 3) 72° for 2 min. PCR reactions were purified with AMPure XP (Agilent) at 1.0X bead-to-sample ratio according to the manufacturer's protocol.

MiSeq run and analysis

[1150] A subset of amplified BotSeqS sequencing libraries was evaluated on an Illumina MiSeq instrument (~5 M clusters passed filter per library) to empirically deduce the optimal dilution. The "optimal dilution" was determined to result in 5 to 10 PCR duplicates per molecule when scaled to 1/2 lane of a HiSeq instrument (~70 M clusters passed filter per library in Rapid Run mode). For example, for an input of 500 ng gDNA into the TruSeq PCR-free library prep (selecting for 350 bp insert size), amplified libraries from the 10^4-, 10^5-, 10^6-fold dilutions were sequenced at 2 x 50 bp depth on MiSeq. Three different well-barcoded samples (which were also molecularly barcoded) were multiplexed in one MiSeq lane to test three dilutions of each sample. The .bam output files were uploaded into Galaxy, and Picard's Estimate Library Complexity Tool (Galaxy Tool Version 1.56.0) was executed using the default parameters. Optimal dilutions showed distributions ranging from one to four members per family with singletons comprising ~60-80% of total counts. In general, with an input of 500 ng of gDNA into the TruSeq PCR-free library prep, the 10^5-fold dilution yielded ~10 members per family on a subsequent HiSeq run used for BotSeqS. From our sequencing data, we estimate the average number of high quality clusters required to identify one rare mutation in colonic tissues was (1) 30 M in a normal child, (2) 12 M in a normal young adult, and (3) 5.8 M in a normal old adult.

Whole-genome sequencing

[1151] Thirty-two whole-genome sequencing (WGS) libraries were generated from the 34 individuals in this study. In the remaining two individuals without WGS, COL238 and COL239, Sanger sequence was performed to exclude clonal variants in the BotSeqS data. Of the final 20

μL of adapter-ligated molecules used to prepare BotSeqS libraries (prior to dilution), 10 μL was used to amplify a library for whole-genome sequencing using TruSeq PCR Primer Cocktail (Illumina) and TruSeq PCR Master Mix (Illumina) according to TruSeq PCR protocol. PCR reactions were purified with AMPure XP (Agilent) at 1.0X bead-to-sample ratio according to the manufacturer's instructions. The libraries were PE sequenced 2x100 bp on Illumina HiSeq at >30x coverage.

Spike-in sensitivity experiment

[1152] Two DNA mixtures were prepared from the DNA of normal spleen samples PEN93 and PEN95. Whole genome sequence data was available from these two samples (see, e.g., Jiao et al., 2011 *Science* 331:1199-1203) and SNPs in PEN93 that were not present in PEN95 could be identified. Both mixtures contained the same amount of PEN95 DNA, but the low spike-in mix contained only 10% of the PEN93 DNA contained in the high spike-in mix. BotSeqS libraries from these samples were first analyzed using the normal BotSeqS pipeline to minimize clonal and germline mutations. Indeed only a total of two mutations were detected among the two libraries; these two mutations likely represented rare mutations in the PEN95 sample, and suggest a mutation frequency of ~8 x 10^{-7} mutation/bp. Next, the data were processed through the BotSeqS pipeline *without* filtering out mutations that were present in dbSNP (build 130 and 142). Seven PEN93-specific SNPs in the low spike-in and 89 PEN93-specific SNPs in the high spike-in mixtures were identified. After normalizing for the number of sequenced bases, the "mutation frequency" (number of PEN93-specific SNPs/bp) was 2.71 x 10^{-6} for the low spike-in and 2.01 x 10^{-5} for the high spike-in samples. The difference between the low spike-in and the high spike-in was 7.4-fold, within the range expected from the 10-fold dilution given the relatively low number of mutations identified in the low spike-in sample.

Characterization of BotSeqS specificity

[1153] As one measure of specificity, we identified *rare* mutations as usual except that we used mutations that were present in only one strand rather than in both. Specifically, mutations were

present in ≥ 90% of the Watson family members and the reference sequence was present in ≥ 90% of the Crick family members, or vice versa, but satisfied our other criteria for being "rare". False Watson and Crick pairings were then created, where the Watson strand had overlapping but different coordinates than the Crick strand, and vice versa, to determine if they contained the same mutation by chance. BotSeqS works by having low coverage throughout the genome, generated through the bottleneck dilution step, and precluded this analysis in the nuclear DNA. Instead, mtDNA were used because of the multiple copies of mtDNA per cell. The coverage of mtDNA with BotSeqS is much higher than that of nuclear DNA and facilitated the identification of overlapping molecules. 30 BotSeqS control libraries were processed this way and a total of 146 mtDNA mutations were identified present in one strand only. Using this dataset, each sample was then searched for overlapping molecules and identified 27 examples. None of the 27 false Watson and Crick pairs shared the same artifactual mutation.

[1154] Non-random shearing could produce another type of artifact, falsely suggesting that the Watson and Crick strands of a family were actually derived from two different molecules that coincidentally had the same genomic coordinate. To test for such artifacts, Watson and Crick family pairs were identified that contained the variant in the Watson strand and the reference sequence in the Crick strand, or vice versa, but this time included heterozygous germline variants rather than just the rare variants, and in nuclear DNA rather than in mtDNA. There are many more heterozygous variants in nuclear DNA than in mtDNA because the mtDNA is derived only from the oocyte. The discordances of interest could arise as a result of mispairing of a Watson strand with a Crick strand derived from a different template molecule - i.e., non-random shearing. Alternatively, discordances could result from an amplification error in one of the two strands during an early PCR cycle. Using our WGS data, we first identified 8,535,891 nuclear heterozygous variants observed among the 30 DNA samples used for the control BotSeqS libraries (median of 268,180 variants per library with range 121,851 to 529,922, with the same common variants present in many libraries). From the 8,535,891 nuclear heterozygous variants, we identified a total of 3,960,818 families (median of 123,134 families per library with range 65,832 to 222,135) for which both strands could be evaluated. Of these, 3,960,807 families had the concordant sequence at the variant position in both strands; only 11 heterozygous variants were discordant (i.e., the variant was present in ≥ 90% of the Watson family members and the reference sequence was present in ≥ 90% of the Crick family members, or vice versa). The rate

of discordant germline heterozygous variants was thus 2.78×10^{-6} (11 out of 3,960,818) per bp. This rate is compatible with the known error rate of high fidelity DNA polymerases and could easily represent an amplification error that occurred in one of the two strands during the first PCR cycle, so represents an overestimate of shearing artifacts. Furthermore, it is important to note that BotSeqS eliminates such amplification errors by requiring mutations to be observed on both strands. Because BotSeqS requires mutations to be observed on both strands, the actual false positive rate can be estimated to be $\sim(1/3)(2.78 \times 10^{-6})(2.78 \times 10^{-6}) = 2.58 \times 10^{-12}$.

Generation of BotSeqS change and molecule tables

[1155] Sequence alignments and variant calling were performed with the Illumina secondary analysis package (CASAVA 1.8) using ELANDv2 matching to the GRCh37/hg19 human reference genome. High-quality reads were selected for further analysis only if they satisfied all of the following criteria: (i) passed chastity filter, (ii) read mapped in a proper pair, (iii) ≤ 5 mismatches to reference sequence, and (iv) perfect identity to reference sequence within the first and last five bases of each read. Sequencing reads were grouped into families based on identical paired-end endogenous barcodes. The members of a family were further subdivided into the two possible sequencing orientations to determine the number of Watson and Crick-derived family members. Watson and Crick families had identical genomic coordinates with each end sequenced in opposite reads. Quality scores of identical changes within a family were calculated as the average among the family members. The output for each BotSeqS library was two annotated tables of changes and template molecules (i.e., families).

Selection of high quality changes and molecules

[1156] Custom algorithms were written in Microsoft SQL Server Management Studio to query the changes and molecules tables for each BotSeqS library. Selection criteria are detailed in Table 44 – Table 48. In general, selection was based on quality, clonality, and mappability of single base pair substitutions. For example, it is known that one of the major sources of errors facing all short read alignment and variant callers are artifacts that arise when variants map to

repetitive regions in the genome, including low complexity regions and copy number variants (see, e.g., Li et al., 2014 *Bioinformatics* 30:2843-2851). The BotSeqS pipeline eliminates this universal error in a downstream step by filtering out the genomic noise from repetitive DNA and structural variants (detailed in Table 48). Indels were excluded because they are prone to alignment artifacts and are ~10 times less frequent than spontaneous point mutations. High quality single-base substitutions were defined as those with average quality scores (within the family) of ≥ Q30 and with ≥ 2 reads and ≥ 90% mutation fraction in both the Watson and Crick strands. Variants were considered to be clonal if the variant position was present in the WGS data from that sample or observed in > 1 template molecules (i.e., both strands of more than one UID). Any positions present in dbSNP130 or dbSNP142 were also excluded. It was noticed that the dbSNP filtering drastically minimized recurrent sequencing or mapping artifacts and highly mutable regions. For example, homopolymer tracts (≥8 bp) are mutation hotspots that flood the mutation list. It was observed that nearly all were filtered out with dbSNP142. Finally, families that harbored > 1 mutation were excluded as possible mapping artifacts.

Calculation of mutation frequency

[1157] Mutation frequencies were determined for each BotSeqS library (see Table 51) by dividing the total number of rare mutations by the total bp sequenced. The total bp sequenced was defined by number of families x 2 x read length of each family. The average length of the libraries was ~ 500 bp such that the 100 bp paired-end reads were unlikely to overlap. Only templates with perfect identity to the reference sequence in the first and last 5 bp of every read were considered. The reads were further trimmed by excluding cycle 6 and 7 to ensure quality. Therefore, the actual read length was 88 bases (100-7-5 = 88). For the samples from which technical replicate BotSeqS libraries were generated, the average mutation frequency of the technical replicates was considered the mutation frequency for the sample.

Validation of somatic mutations

[1158] All rare mutations from the nuclear and mtDNA genome passed visual inspection of the sequencing reads. For rare nuclear mutations, Sanger sequencing was performed on a representative set (514 out of 876 mutations). Of these, 514 of 514 (100%) were confirmed to be invisible by Sanger sequencing (excluding the COL238 and COL239 samples that did not have a matched WGS). This demonstrated that these mutations were neither present in the germline nor present in a highly clonal fashion. Mutations confirmed to be absent upon Sanger sequencing are indicated in Table 50.

Comparison to cancer genomes

[1159] Nineteen MAF files representing nuclear somatic mutations from 19 TCGA tumor types were downloaded at synapse.org/#!Synapse:syn1729383 (see, e.g., Kandoth et al., 2013 *Nature* 502:333-339). From the TCGA data, only single-base substitutions were considered and somatic mutations from ultra-mutated tumors were excluded. Mitochondrial DNA somatic mutations from colorectal and renal tumors were derived from supplementary file 2 of Ju et al. (2014 *eLife* 3).

Statistics

[1160] For study design, no prior power analysis or randomization was performed because the variance was initially unknown. The goal of the study was to find major, biologically meaningful differences between the cohorts. To find major differences, sample sizes can be small. Even with the small sample size, however, no violations of the assumptions of the tests were detected, including violations about the homogeneity of variances. T-test and ANOVA analyses were performed using GraphPad Prism 5.0f. Fisher's exact test was performed using R version 3.2.2. Principal component analysis was performed in R. All analyzed samples were reported in the manuscript.

Results

Principles underlying BotSeqS

[1161] The principal feature of BotSeqS is the dilution of any type of a sequencing library prior to PCR amplification. This dilution creates a bottleneck and permits an efficient, random sampling of double-stranded template molecules with a minimal amount of sequencing. Rare mutations, which would normally be masked by an abundance of wild-type sequences in conventional libraries, account for much more of the signal at the corresponding genomic position in a bottlenecked library. Dilution also increases the likelihood that both the "Watson" and "Crick" strands of a DNA molecule will be sequenced redundantly, a feature critical for the high accuracy of BotSeqS and the relatively small amount of sequencing required to implement it. The presence of the same rare mutation on both strands can substantially decrease artifacts and increase specificity (see, e.g., Schmitt et al., 2012 *PNAS U S A* 109:14508-14513). Finally, the random nature of dilution allows DNA molecules from both nuclear and mitochondrial genomes to be assessed from one library.

Generation of BotSeqS libraries

[1162] A standard Illumina TruSeq PCR-Free kit was used to generate 44 BotSeqS libraries from the normal tissues of 34 individuals (Table 43). This included nine individuals with one or two technical replicates. In addition, 10 of our 12 cohorts had more than one biological replicate, each containing two to six individuals.

[1163] The preparation of BotSeqS libraries starts with the random shearing of genomic DNA (Fig. 52). This fragments the genomes into variably-sized DNA molecules, each possessing unique end coordinates called endogenous barcodes (see, e.g., Kinde et al., 2011 *PNAS U S* A 108:9530-9535). Following ligation of standard sequencing adapters to the DNA molecules, the library is diluted to reduce the number of molecules in the population. To identify the correct dilution factor, a ten-fold dilution series was assessed on a MiSeq instrument (Fig. 53). After dilution, PCR amplification of the library generates multiple copies (duplicates) of each DNA

molecule. The endogenous barcodes enables the grouping of sequencing reads into families, also known as UIDs, for *u*nique *id*entifiers (see, e.g., Kinde et al., 2011 *PNAS U S* A 108:9530-9535); each family represents the PCR-derived progeny of a single-stranded template and each member of a family represents the sequence from a single cluster on the Illumina instrument. In the following, we consider the Watson strand to be the sequence derived from the first read of the sequencing instrument (Illumina adapter P5) and the Crick strand to be the sequence derived from the second read (Illumina adapter P7) of each member of the family (Fig. 52). To be considered a potential mutation, BotSeqS required that the identical sequence change be observed in $\geq$ 90% of the Watson and in $\geq$ 90% of the Crick family members and that each family be composed of at least two members. BotSeqS libraries were analyzed using an Illumina HiSeq 2500 instrument on rapid run mode with paired-end reads of 100 bases each. A median of 70 million (M) clusters per library passed the standard Illumina quality filters (range 37 to 188 M clusters per library; Table 43).

BotSeqS data processing pipeline

[1164] The goal of the BotSeqS pipeline was to accurately identify rare, somatic point mutations and to calculate the frequency of these mutations in the sample. To process the data for this purpose, raw sequencing data were input into Illumina's secondary analysis package (CASAVA 1.8) with ELANDv2 mapping to GRCh37/hg19 human reference genome. The BotSeqS pipeline begins by selecting high quality reads for analysis (see Materials and Methods). The data are then organized into two tables for each BotSeqS library: (i) a "change" table listing all differences from the reference sequence and (ii) a unique molecule table listing all families. Importantly, each table contains strand information; almost half (median 45%, range 8% to 62%) of the unique molecules from each BotSeqS library had both the Watson and Crick strands represented in the dataset, ensuring specificity in the subsequent mutation analysis. Moreover, most BotSeqS libraries (37 of 44) had a median number of family members between 5 and 20 (Fig. 56), further demonstrating that the libraries underwent successful bottlenecking.

[1165] To identify rare, somatic mutations, it was necessary to eliminate germline and clonal variants from the BotSeqS data (we defined clonal as those present in both strands of more than one template molecule). We performed whole genome sequencing (WGS) of the same DNA

sample or the same libraries that had been diluted for BotSeqS for 32 of the 34 individuals in this study (Table 43). For the remaining two individuals (COL238 and COL239), Sanger sequencing was performed to eliminate clonal variants, demonstrating that WGS was not necessary for BotSeqS. The vast majority (median 92%, range 88-94%) of variants were found to be germline, easily identifiable from the matched WGS dataset. In addition to clonality, we eliminated potential artifacts by considering only well-mapped positions and by using other filters (Table 44 – Table 48 and Materials and Methods). The requirement for mutations to be present on both strands was indeed necessary because, in the absence of this filter, there was a large number of G>T transversions (Fig. 57), known to represent artifacts in NGS library preparations (see, e.g., Costello et al., 2013 *Nucleic acids research* 41:e67). A "spike-in" validation experiment was further performed by mixing one individual's normal DNA (PEN93) into another individual's normal DNA (PEN95) at two different ratios. Using BotSeqS, it was possible to detect PEN93-specific SNPs in both samples with a 7.4-fold difference in frequency between the low and high spike-ins, within the expected error of the intended 10-fold difference (see Materials and Methods).

[1166] From the 44 BotSeqS libraries, a total of 666 and 876 rare somatic point mutations were identified in mtDNA and nuclear DNA, respectively (Table 49 and Table 50). All rare mutations passed visual inspection and a subset was Sanger-sequenced to confirm that the mutations were not germline or highly prevalent in the samples evaluated (see Materials and Methods). As expected from previous studies, point mutation frequencies of mtDNA ($1.40 \pm 1.29 \times 10^{-5}$ mutation/bp, mean ± s.d.) were significantly higher than those of nuclear DNA ($5.23 \pm 3.47 \times 10^{-7}$) in 25 control individuals (two-tailed t-test, $P < 0.0001$; Table 51). The specificity of BotSeqS was further determined using discordant germline heterozygous calls to estimate a false positive rate of 2.58×10^{-12} (see Materials and Methods).

Mutation frequencies vary with DNA repair capacity and carcinogen exposure

[1167] It was first asked if BotSeqS can detect the elevated levels of mutations in the normal tissues of mismatch repair deficient individuals. Individuals with biallelic inactivating germline mutations in mismatch repair machinery show higher levels of mutation in both normal and tumor tissues (see, e.g., Parsons et al., 1995 *Science* 268:738-740; and Shlien et al., 2015 *Nature*

genetics 47:257-262). Therefore, DNA was tested from normal colon epithelium of individuals (COL238 and COL239) with biallelic germline inactivating mutations in the *Post-Meiotic Segregation 2* (*PMS2*) gene. Using BotSeqS, it was found that the average mutation frequency of nuclear DNA in these two siblings ($6.63 \pm 3.47 \times 10^{-5}$ mutations/bp; ages 16 and 18) was significantly higher than that in similarly aged individuals ($5.13 \pm 1.73 \times 10^{-7}$ for COL235, COL236, COL237, COL374; average age 24) with proficient mismatch repair (two-tailed t-test, $P < 0.05$, Fig. 53a). This 129-fold increase in nuclear mutation frequency was associated with a significant difference in the nuclear mutational spectrum between $PMS2^{+/+}$ and $PMS2^{-/-}$ cohorts (Fisher's exact test, $P = 0.04$, Fig. 53b).

[1168] It was also tested if BotSeqS could identify a high number of mutations in the normal tissues of individuals exposed to environmental carcinogens. Genome-wide sequencing of upper tract urothelial carcinomas was previously performed, representing a cancer type associated with exposure to aristolochic acid (AA) or smoking (see, e.g., Hoang et al., 2013 *Science translational medicine* 5:197ra102). Mutagens in tobacco smoke as well as AA are metabolized to form DNA-adducts in the normal kidney cortrex (see, e.g., Hoang et al., 2013 *Science translational medicine* 5:197ra102; and Randerath et al., 1989 *Journal of the National Cancer Institute* 81:341-347). Four age-matched normal kidney cortices from individuals (KID034, KID035, KID036, KID037; average age 64 years) without known exposure to tobacco smoke or to AA were compared with the normal kidney cortex of three heavy smokers (SA_117, SA_118, SA_119; average age 65 years) as well as with three individuals who had been exposed to AA (AA_105, AA_124, AA_126; average age 79 years). The nuclear point mutation frequencies in smokers and AA-exposed kidneys were significantly higher, by 27- and 36-fold, respectively, than in the non-exposed controls (one-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.0001$ for AA and $P < 0.001$ for smoking) (Fig. 53a). This increased number of mutations in the nuclear genome was associated with a significantly altered nuclear mutational spectrum (Fisher's exact test with Bonferroni multiple comparison correction, $P = 2.58 \times 10^{-8}$ for AA and $P = 1.51 \times 10^{-15}$ for smoking) (Fig. 53b). Interestingly, the mtDNA point mutation frequencies and spectra between the non-exposed and exposed groups were not significantly different, despite the dramatic difference in their nuclear genomes (Fig. 53a, b).

Rare mutations accumulate with age

[1169] Many lines of evidence indicate that the human body accumulates random mutations with age. BotSeqS was designed to *directly* measure differences such as these and we tested whether rare point mutation frequencies in the DNA of three normal human tissues were dependent upon age. Normal colonic epithelium from 11 individuals showed mutation frequencies that significantly increased with age, by an average of 30-fold in mtDNA and 6.1-fold in nuclear DNA, over 91 years (see below and Fig. 54**;** one-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.001$ for both). Similarly, mutation frequencies increased by an average of 19-fold in mtDNA and 6.5-fold in nuclear DNA over 64 years in normal kidney cortices. The mutation frequencies in brain frontal cortex also significantly increased with age, albeit more slowly, by 7.3-fold in mtDNA and 5.7-fold in nuclear DNA over 90 years (one-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.001$ for mtDNA and $P < 0.05$ for nuclear).

Summary of rare mutation frequencies in normal human tissues

Genome	Normal Tissue	Number of Individuals	Mutation Frequency (x10^{-7} mutations/bp)			Average Lifespan (years)	Lifespan Fold-Difference
			Young Child	Young Adult	Old Adult		
mtDNA	Brain	9	18 ± 7	43 ± 6	131 ± 18	89.5	7.3
	Kidney	5	15	nd	277 ± 64	63.8	18.5
	Colon	11	12 ± 17	112 ± 43	365 ± 103	90.8	30.4
Nuclear	Brain	9	1.1 ± 0.3	2.2 ± 1.1	6.3 ± 2.3	89.5	5.7
	Kidney	5	1.2	nd	7.8 ± 1.5	63.8	6.5
	Colon	11	1.8 ± 0.5	5.5 ± 1.6	11 ± 1.5	90.8	6.1

nd, not determined

[1170] Within the dataset, point mutation frequencies in brain versus colonic tissues in three different age groups (children < 10 years; adults between 20 and 40 years; and old adults ≥ 90 years) could be directly comparec. Interestingly, the nuclear mutation frequency in colon was not significantly different from that of the brain in children ($1.81 \pm 0.45 \times 10^{-7}$ in colon vs. $1.06 \pm 0.27 \times 10^{-7}$ in brain, two-way ANOVA with Bonferroni multiple comparison post-test, $P > 0.05$).

However, the mutation frequency in the colon was significantly higher than that of the brain in young adults ($5.51 \pm 1.62 \times 10^{-7}$ in colon vs. $2.16 \pm 1.11 \times 10^{-7}$ in brain, two-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.05$) as well as in old adults ($1.10 \pm 0.15 \times 10^{-6}$ in colon vs. $6.29 \pm 2.31 \times 10^{-7}$ in brain, two-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.01$) (Fig. 58). No significant differences were found between the mtDNA mutation frequency of the colon versus that of brain in relatively young individuals (children or young adults). However, the mtDNA mutation frequency in the colon was significantly higher than that of the brain in old individuals ($3.65 \pm 1.03 \times 10^{-5}$ in colon vs. $1.31 \pm 0.18 \times 10^{-5}$ in brain, two-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.0001$) (Fig. 58).

The mutational patterns in mtDNA are very different from those of nuclear DNA

[1171] The spectra of the rare point mutations in each normal tissue studied were examined. Mutations in mtDNA were dominated by transitions (97% in colon, 89% in kidney, and 91% in brain) with a heavy strand bias, as expected from previous studies[12] (Fig. 54 and Table 49). The ratio of transitions to transversions was strikingly different in mtDNA (average of 15.3) compared to nuclear DNA (average of 1.1) in all three tissues.

[1172] To further assess the differences in mutation frequencies between the two genomes, we calculated the ratio between mtDNA-to-nuclear mutation frequencies for each individual (Table 51). Point mutation frequencies in the mtDNA were on average 24.5-fold higher than the nuclear genome in normal tissues (control cohort, Fig. 59). In patients with exposure histories or DNA repair defects, the ratios were significantly smaller due to the concomitantly greater number of nuclear (but not mitochondrial) DNA mutations in such individuals compared to those from the control cohort (one-way ANOVA with Bonferroni multiple comparison post-test, $P < 0.05$) (Fig. 59).

Mutational spectra are tissue-specific

[1173] Though rare mutations in mtDNA are dominated by transitions, there are still tissue-specific mtDNA differences that can be appreciated from the pie charts in Fig. 3. For example,

mitochondrial C:G to T:A transitions were more prominent, and A:T to G:C transitions less prominent, in normal colon (54% and 42%, respectively) and brain (51% and 40%, respectively) compared to normal kidney tissues (36% and 53%, respectively). The mutation spectra in the nuclear DNA of all three tissues were much more diverse. For example, C:G to T:A transitions predominated in normal colon (44% in colon compared to 22% in kidney and 29% in brain), while normal kidney and brain harbored a proportionately greater fraction of A:T to G:C transitions (25% in kidney and 19% in brain compared to 15% in colon) as well as A:T to C:G transversions (12% in kidney and 16% in brain compared to 5% in colon). Moreover, A:T to T:A transversions were more frequent in kidney (16%) compared to colon (6%) and brain (6%). Pairwise comparisons of the mutational spectra within each genome revealed significant differences between the substitution pattern of kidney and colon (Fisher's exact test with Bonferroni multiple comparison correction, $P = 0.0029$ in mtDNA and $P = 0.0312$ in nuclear DNA).

[1174] The spectra of the rare mutations found in normal kidney and colon tissues were compared to the *clonal* DNA mutations in cancers derived from the cells of these organs, using publically available data for the latter (see, e.g., Ju et al., 2014 *eLife* 3; and Kandoth et al., 2013 *Nature* 502:333-339). Brain frontal cortex was excluded in this analysis because it was not clear what tumor type should be used for comparison. To search for similarities and differences among normal and tumor mutational spectra, principal component analysis was performed on the nuclear and mtDNA spectra derived from the data on normal kidney cortex, normal colon epithelium, clear cell renal carcinoma, and colorectal carcinoma. It was found that the spectra of the rare mutations in normal colon and kidney tissues were very similar to those of the corresponding cancer type (Fig. 60).

Example 8: Safe sequencing system

[1175] Genetic mutations underlie many aspects of life and death including, for example, evolution and disease, respectively (see, e.g., Luria et al., 1943 *Genetics* 28:491-511; Roach et al., 2010 *Science* 328:636-639; Durbin et al., 2010 *Nature* 467:1061-1073; Shibata, 2011 *Carcinogenesis* 32:123-128; McMahon et al., 2007 *N Engl J Med* 356:2614-2621; Eastman et al., 1998 *J Infect Dis* 177:557-564; Chiu et al., 2008 *Proc Natl Acad Sci U S A* 105:20458-

20463; and Fan et al., 2008 *Proc Natl Acad Sci U S A* 105:16266-16271). Detection of such mutations, particularly at a stage prior to their becoming dominant in the population, will likely be essential to optimize diagnoses and/or therapy. For example, in neoplastic diseases, which are all driven by somatic mutations, the applications of rare mutant detection are manifold; they can be used to help identify residual disease at surgical margins or in lymph nodes, to follow the course of therapy when assessed in plasma, and perhaps to identify patients with early, surgically curable disease when evaluated in stool, sputum, plasma, and other bodily fluids (see, e.g., Hoque et al., 2003 *Cancer Res* 63:5723-5726; Thunnissen et al., 2003 *J Clin Pathol* 56:805-810; and Diehl et al., 2008 *Gastroenterology* 135:489-498).

[1176] This Example describes a "Safe-SeqS" (Safe-Sequencing System) to achieve a very high level of accuracy and sensitivity from sequence data. Safe-SeqS can be used to assess the fidelity of a polymerase, the accuracy of in vitro synthesized nucleic acid synthesis, and the prevalence of mutations in nuclear or mitochondrial nucleic acids of normal cells. Safe-SeqS can also be used to detect and/or quantify mosaicsm and somatic mutations. See, also, WO 2012/142213, incorporated herein by reference in its entirety.

Materials and Methods

Endogenous UIDs

[1177] Genomic DNA from human pancreas or cultured lymphoblastoid cells was prepared using Qiagen kits. The pancreas DNA was used for the capture experiment and the lymphoblastoid cells were used for the inverse PCR experiment. DNA was quantified by optical absorbance and with qPCR. DNA was fragmented to an average size of ~200 bp by acoustic shearing (Covaris), then end-repaired, A-tailed, and ligated to Y-shaped adapters according to standard Illumina protocols. The ends of each template molecule provide endogenous UIDs corresponding to their chromosomal positions. After PCR-mediated amplification of the libraries with primer sequences within the adapters, DNA was captured with a filter containing 2,594 nt corresponding to six cancer genes. After capture, 18 cycles of PCR were performed to ensure sufficient amounts of template for sequencing on an Illumina GA IIx instrument.

[1178] For the inverse PCR experiments (Fig. 65), we ligated custom adapters (IDT, Table 57) instead of standard Y-shaped Illumina adapters to sheared cellular DNA. These adapters retained the region complementary to the universal sequencing primer but lacked the grafting sequences required for hybridization to the Illumina GA IIx flow cell. The ligated DNA was diluted into 96 wells and the DNA in each column of 8 wells was amplified with a unique forward primer containing one of 12 index sequences at its 5' end plus a standard reverse primer (Table 57). Amplifications were performed using Phusion HotStart I (NEB) in 50 uL reactions containing 1X Phusion HF buffer, 0.5 mM dNTPs, 0.5 uM each forward and reverse primer (both 5'-phosphorylated), and 1U of Phusion polymerase. The following cycling conditions were used: one cycle of 98˚C for 30s; and 16 cycles of 98˚C for 10s, 65˚C for 30s, and 72˚C for 30s. All 96 reactions were pooled and then purified using a Qiagen MinElute PCR Purification Kit (cat. no. 28004) and a QIAquick Gel Extraction kit (cat. no. 28704). To prepare the circular templates necessary for inverse PCR, DNA was diluted to ~1 ng/uL and ligated with T4 DNA Ligase (Enzymatics) for 30 minutes at room temperature in a 600uL reaction containing 1X T4 DNA Ligation Buffer and 18,000U of T4 DNA Ligase. The ligation reaction was purified using a Qiagen MinElute kit. Inverse PCR was performed using Phusion Hot Start I on 90 ng of circular template distributed in twelve 50 uL reactions, each containing 1X Phusion HF Buffer, 0.25mM dNTPs, 0.5uM each of *KRAS* forward and reverse primers (Table 57) and 1U of Phusion polymerase. The *KRAS*-specific primers both contained grafting sequences for hybridization to the Illumina GA IIx flow cell (Table 57). The following cycling conditions were used: one cycle of 98˚C for 2 minutes; and 37 cycles of 98˚C for 10 seconds, 61˚C for 15 seconds, and 72˚C for 10 seconds. The final purification was performed with a NucleoSpin Extract II kit (Macherey-Nagel) and eluted in 20uL NE Buffer. The resulting DNA fragments contained UIDs composed of three sequences: two endogenous ones, represented by the two ends of the original sheared fragments plus the exogenous sequence introduced during the indexing amplification. As 12 exogenous sequences were used, this increased the number of distinct UIDs by 12-fold over that obtained without exogenous UIDs. This number could easily be increased by using a greater number of distinct primers.

Exogenous UIDs

[1179] Genomic DNA from normal human colonic mucosae or blood lymphocytes was prepared using Qiagen kits. The DNA from colonic mucosae was used for the experiments on *CTNNB1* and mitochondrial DNA, while the lymphocyte DNA was used for the experiments on *CTNNB1* and on polymerase fidelity. DNA was quantified with Digital PCR using primers that amplified single-copy genes from human cells (Analysis of Polymerase Fidelity and *CTNNB1*), qPCR (mitochondrial DNA), or by optical absorbance (oligonucleotides). Each strand of each template molecule was encoded with a 12 or 14 base UID using two cycles of amplicon-specific PCR, as described in the text and Fig. 63. The amplicon-specific primers both contained universal tag sequences at their 5' ends for a later amplification step. The UIDs constituted 12 or 14 random nucleotide sequences appended to the 5' end of the forward amplicon-specific primers (Table 57). These primers can generate 16.8 and 268 million distinct UIDs, respectively. It is important that the number of distinct UIDs greatly exceed the number of original template molecules to minimize the probability that two different original templates acquired the same UID. The UID assignment PCR cycles included Phusion Hot Start II (NEB) in a 45 uL reaction containing 1X Phusion HF buffer, 0.25mM dNTPs, 0.5 uM each forward (containing 12-14 Ns) and reverse primers, and 2U of Phusion polymerase. To keep the final template concentrations <1.5 ng/uL, multiple wells were used to create some libraries. The following cycling conditions were employed: one incubation of 98˚C for 30 seconds (to activate the Phusion Hot Start II); and two cycles of 98˚C for 10 seconds, 61˚C for 120 seconds, and 72˚C for 10 seconds. To ensure complete removal of the first round primers, each well was digested with 60 U of a single strand DNA specific nuclease (Exonuclease-I; Enzymatics) at 37˚C for 1 hour. After a 5 minute heat-inactivation at 98˚C, primers complementary to the introduced universal tags (Table 57) were added to a final concentration of 0.5uM each. These primers contained two terminal phosphorothioates to make them resistant to any residual Exonuclease-I activity. They also contained 5' grafting sequences necessary for hybridization to the Illumina GA IIx flow cell. Finally, they contained an index sequence between the grafting sequence and the universal tag sequence. This index sequence enables the PCR products from multiple different individuals to be simultaneously analyzed in the same flow cell compartment of the sequencer. The following cycling conditions were used for the subsequent 25 cycles of PCR: 98˚C for 10 seconds and 72˚C

for 15 seconds. No intermediate purification steps were performed in an effort to reduce the losses of template molecules.

[1180] After the second round of amplification, wells were consolidated and purified using a Qiagen QIAquick PCR Purification Kit (cat. no. 28104) and eluted in 50 uL EB Buffer (Qiagen). Fragments of the expected size were purified after agarose (mtDNA libraries) or polyacrylamide (all other libraries) gel electrophoresis. For agarose gel purification, the eight 6-uL aliquots were loaded into wells of a 2% Size Select Gel (Invitrogen) and bands of the expected size were collected in EB Buffer as specified by the manufacturer. For polyacrylamide gel purification, ten 5-uL aliquots were loaded into wells of a 10% TBE Polyacrylamide Gel (Invitrogen). Gel slices containing the fragments of interest were excised, crushed, and eluted as described elsewhere (see, e.g., Durbin et al., 2010 *Nature* 467:1061-1073).

Analysis of Phusion polymerase fidelity

[1181] Amplification of a fragment of human genomic DNA within the BMX (RefSeq Accession NM_203281.2) gene was first performed using the PCR conditions described above. The template was diluted so that an average of one template molecule was present in every 10 wells of a 96-well PCR plate. Fifty uL PCR reactions were then performed in 1X Phusion HF buffer, 0.25mM dNTPs, 0.5uM each forward and reverse primers (Table 57), and 2U of Phusion polymerase. The cycling conditions were one cycle of 98˚C for 30 seconds; and 19 cycles of 98˚C for 10 seconds, 61˚C for 120 seconds, and 72˚C for 10 seconds. The primers were removed by digestion with 60 U of Exonuclease-I at 37˚C for 1 hour followed by a 5 minute heat-inactivation at 98˚C. No purification of the PCR product was performed, either before or after Exonuclease-I digestion. The entire contents of each well were then used as templates for the exogenous UIDs strategy described above.

Sequencing

[1182] Sequencing of all the libraries described above was performed using an Illumina GA IIx instrument as specified by the manufacturer. The total length of the reads used for each experiment varied from 36 to 73 bases. Base-calling and sequence alignment was performed with

the Eland pipeline (Illumina). Only high quality reads meeting the following criteria were used for subsequent analysis: (i) the first 25 bases passed the standard Illumina chastity filter; (ii) every base in the read had a quality score ≥20; and (iii) ≤ 3 mismatches to expected sequences. For the exogenous UID libraries, we additionally required the UIDs to have a quality score ≥30. A relatively high frequency of errors was noticed at the ends of the reads in the endogenous UID libraries prepared with the standard Illumina protocol, presumably introduced during shearing or end-repair, so the first and last three bases of these tags were excluded from analysis.

Safe-SeqS analysis

[1183] High quality reads were grouped into UID-families based on their endogenous or exogenous UIDs. Only UID-families with two or more members were considered. Such UID-families included the vast majority (≥99%) of the sequencing reads. To ensure that the same data was used for both conventional and Safe-SeqS analysis, UID-families containing only one member were also excluded from conventional analysis. Furthermore, a base was only identified as "mutant" in conventional sequencing analysis if the same variant was identified in at least two members of at least one UID-family (i.e., two mutations) when comparing conventional analysis to that of Safe-SeqS with exogenous UIDs. For comparison with Safe-SeqS with endogenous UIDs, we required at least two members of each of two UID-families (i.e., four mutations) to identify a position as "mutant" in conventional analysis. With either endogenous or exogenous UIDs, a super-mutant was defined as a UID-family in which ≥95% of members shared the identical mutation. Thus, UID-families with <20 members had to be 100% identical at the mutant position, while a 5% combined replication and sequencing error rate was permitted in UID-families with more members. To determine polymerase fidelity using Safe-SeqS, and to compare the results with previous analyses of Phusion polymerase fidelity, it was necessary to realize that the previous analyses would only detect mutations present in both strands of the PCR products (see, e.g., Shibata, 2011 *Carcinogenesis* 32:123-128). This would be equivalent to analyzing PCR products generated with one less cycle with Safe-SeqS, and the appropriate correction was made in Table 53A. Unless otherwise specified, all values listed in the text and Tables represent means and standard deviations.

Results

Endogenous UIDs

[1184] UIDs, sometimes called barcodes or indexes, can be assigned to nucleic acid fragments in many ways. These include the introduction of exogenous sequences through PCR or ligation. Even more simply, randomly sheared genomic DNA inherently contains UIDs consisting of the sequences of the two ends of each sheared fragment (Fig. 62 and Fig. 65). Paired-end sequencing of these fragments yields UID-families that can be analyzed as described above. To employ such endogenous UIDs in Safe-SeqS, two separate approaches were used: one designed to evaluate many genes simultaneously and the other designed to evaluate a single gene fragment in depth (Fig. 62 and Fig. 65, respectively).

[1185] For the evaluation of multiple genes, standard Illumina sequencing adapters were ligated to the ends of sheared DNA fragments to produce a standard sequencing library, then captured genes of interest on a solid phase. In this experiment, a library made from the DNA of ~15,000 normal cells was used, and 2,594 bp from six genes were targeted for capture. After excluding known single nucleotide polymorphisms, 25,563 apparent mutations, corresponding to 2.4×10^{-4} ± mutations/bp, were also identified (Table 52). Based on previous analyses of mutation rates in human cells, at least 90% of these apparent mutations were likely to represent mutations introduced during template and library preparation or base-calling errors. Note that the error rate determined here (2.4×10^{-4} mutations/bp) is considerably lower than usually reported in experiments using the Illumina instrument because we used very stringent criteria for base calling.

[1186] With Safe-SeqS analysis of the same data, it was determined that 69,505 original template molecules were assessed in this experiment (*i.e.*, 69,505 UID-families, with an average of 40 members per family, were identified, Table 52). All of the polymorphic variants identified by conventional analysis were also identified by Safe-SeqS. However, only 8 super-mutants were observed among these families, corresponding to 3.5×10^{-6} mutations/bp. Thus Safe-SeqS decreased the presumptive sequencing errors by at least 70-fold.

[1187] Safe-SeqS analysis can also determine which strand of a template is mutated, thus an additional criteria for calling mutations could require that the mutation appears in only one or in both strands of the originally double stranded template. Massively parallel sequencers are able to

obtain sequence information from both ends of a template in two sequential reads. (This type of sequencing experiment is called a "paired end" run on the Illumina platform, but similar experiments can be done on other sequencing platforms where they may be called by another name.) The two strands of a double stranded template can be differentiated by the observed orientation of the sequences and the order in which they appear when sequence information is obtained from both ends. For example, a UID strand pair could consist of the following two groups of sequences when each end of a template is sequenced in sequential reads: 1) A sequence in the sense orientation that begins at position 100 of chromosome 2 in the first read followed by a sequence in the antisense orientation that begins at position 400 of chromosome 2 in the second read; and 2) A sequence in the antisense orientation that begins at position 400 of chromosome 2 in the first read followed by a sequence in the sense orientation that begins at position 100 of chromosome 2 in the second read. In the capture experiment described above, 42,222 of 69,505 UIDs (representing 21,111 original double stranded molecules) in the region of interest represented UID strand pairs. These 42,222 UIDs encompassed 1,417,838 bases in the region of interest. When allowing a mutation to only occur within UID strand pairs (whether in one or both strands), two super-mutants were observed, yielding a mutation rate of 1.4×10^{-6} super-mutants/bp. When requiring that a mutation occur in only one strand of a UID strand pair, only one super-mutant was observed, yielding a mutation rate of 7.1×10^{-7} super-mutants/bp. When requiring that a mutation occur in both strands of a UID strand pair, only one super-mutant was observed, yielding a mutation rate of 7.1×10^{-7} super-mutants/bp. Thus, requiring that mutations occur in only one or in both strands of templates can further increase the specificity of Safe-SeqS.

[1188] A strategy employing endogenous UIDs was also used to reduce false positive mutations upon deep sequencing of a single region of interest. In this case, a library prepared as described above from ~1,750 normal cells was used as template for inverse PCR employing primers complementary to a gene of interest, so the PCR products could be directly used for sequencing (Fig. 65). With conventional analysis, an average of 2.3×10^{-4} mutations/bp were observed, similar to that observed in the capture experiment (Table 52). Given that only 1,057 independent molecules from normal cells were assessed in this experiment, as determined through Safe-SeqS analysis, all mutations observed with conventional analysis likely represented false positives

(Table 52). With Safe-SeqS analysis of the same data, no super-mutants were identified at any position.

Exogenous UIDs

[1189] Though the results described above show that Safe-SeqS can increase the reliability of massively parallel sequencing, the number of different molecules that can be examined using endogenous UIDs is limited. For fragments sheared to an average size of 150 bp (range 125-175), 36 base paired-end sequencing can evaluate a maximum of ~7,200 different molecules containing a specific mutation (2 reads x 2 orientations x 36 bases/read x 50 base variation on either end of the fragment). In practice, the actual number of UIDs is smaller because the shearing process is not entirely random.

[1190] To make more efficient use of the original templates, a Safe-SeqS strategy was developed that employed a minimum number of enzymatic steps. This strategy also permitted the use of degraded or damaged DNA, such as found in clinical specimens or after bisulfite-treatment for the examination of cytosine methylation. As depicted in Fig. 63, this strategy employs two sets of PCR primers. The first set is synthesized with standard phosphoramidite precursors and contained sequences complementary to the gene of interest on the 3' end and different tails at the 5' ends of both the forward and reverse primers. The different tails allowed universal amplification in the next step. Finally, there was a stretch of 12 to 14 random nucleotides between the tail and the sequence-specific nucleotides in the forward primer. The random nucleotides form the UIDs. An equivalent way to assign UIDs to fragments, not used in this study, would employ 10,000 forward primers and 10,000 reverse primers synthesized on a microarray. Each of these 20,000 primers would have gene-specific primers at their 3'-ends and one of 10,000 specific, predetermined, non-overlapping UID sequences at their 5'-ends, allowing for 10^8 (i.e., $[10^4]^2$) possible UID combinations. In either case, two cycles of PCR are performed with the primers and a high-fidelity polymerase, producing a uniquely tagged, double-stranded DNA fragment from each of the two strands of each original template molecule (Fig. 63). The residual, unused UID assignment primers are removed by digestion with a single-strand specific exonuclease, without further purification, and two new primers are added. Alternatively or in addition to such digestion, one can use a silica column that selectively retains larger-sized

fragments or one can use solid phase reversible immobilization (SPRI) beads under conditions that selectively retain larger fragments to eliminate smaller, non-specific, amplification artifacts. This purification may potentially help in reducing primer-dimer accumulation in later steps. The new primers, complementary to the tails introduced in the UID assignment cycles, contain grafting sequences at their 5' ends, permitting solid-phase amplification on the Illumina instrument, and phosphorothioate residues at their 3' ends to make them resistant to any remaining exonuclease. Following 25 additional cycles of PCR, the products are loaded on the Illumina instrument. As shown below, this strategy allowed us to evaluate the majority of input fragments and was used for several illustrative experiments.

Analysis of DNA polymerase fidelity

[1191] Measurement of the error rates of DNA polymerases is essential for their characterization and dictates the situations in which these enzymes can be used. The error rate of Phusion polymerase was measured, as this polymerase has one of the lowest reported error frequencies of any commercially available enzyme and therefore poses a particular challenge for an in vitro-based approach. A single human DNA template molecule, comprising a segment of an arbitrarily chosen human gene, was first amplified through 19 rounds of PCR. The PCR products from these amplifications, in their entirety, were used as templates for Safe-SeqS as described in Fig. 63. In seven independent experiments of this type, the number of UID-families identified by sequencing was 624,678 ± 421,274, which is consistent with an amplification efficiency of 92 ± 9.6% per round of PCR.

[1192] The error rate of Phusion polymerase, estimated through cloning of PCR products encoding β-galactosidase in plasmid vectors and transformation into bacteria, is reported by the manufacturer to be 4.4×10^{-7} errors/bp/PCR cycle. Even with very high stringency base-calling, conventional analysis of the Illumina sequencing data revealed an apparent error rate of 9.1×10^{-6} errors/bp/PCR cycle, more than an order of magnitude higher than the reported Phusion polymerase error rate (Table 53A). In contrast, Safe-SeqS of the same data revealed an error rate of 4.5×10^{-7} errors/bp/PCR cycle, nearly identical to that measured for Phusion polymerase in biological assays (Table 53A). The vast majority (>99%) of these errors were single base substitutions (Table 54A), consistent with previous data on the mutation spectra created by other

prokaryotic DNA polymerases (Tindall et al. 1988 *Biochemistry* 27:6008-6013; de Boer et al., 1988 *Genetics* 118:181-191; Eckert et al., 1990 *Nucleic Acids Res* 18:3739-3744).

[1193] Safe-SeqS also allowed a determination of the total number of distinct mutational events and an estimation of PCR cycle in which the mutation occurred. There were 19 cycles of PCR performed in wells containing a single template molecule in these experiments. If a polymerase error occurred in cycle 19, there would be only one super-mutant produced (from the strand containing the mutation). If the error occurred in cycle 18 there should be two super-mutants (derived from the mutant strands produced in cycle 19), etc. Accordingly, the cycle in which the error occurred is related to the number of super-mutants containing that error. The data from seven independent experiments demonstrate a relatively consistent number of observed total polymerase errors ($2.2 \pm 1.1 \times 10^{-6}$ distinct mutations/bp), in good agreement with the expected number of observations from simulations ($1.5 \pm 0.21 \times 10^{-6}$ distinct mutations/bp). The data also show a highly variable timing of occurrence of polymerase errors among experiments (Table 55). This kind of information is difficult to derive using conventional analysis of the same next-generation sequencing data, in part because of the prohibitively high apparent mutation rate noted above.

Analysis of oligonucleotide composition

[1194] A small number of mistakes during the synthesis of oligonucleotides from phoshoramidite precursors are tolerable for most applications, such as routine PCR or cloning. However, for synthetic biology, wherein many oligonucleotides must be joined together, such mistakes present a major obstacle to success. Clever strategies for making the gene construction process more efficient have been devised (see, e.g., Kosuri et al., 2010 *Nat Biotechnol* 28:1295-129; and Matzas et al., 2010 *Nat Biotechnol* 28:1291-1294), but all such strategies would benefit from more accurate synthesis of the oligonucleotides themselves. Determining the number of errors in synthesized oligonucleotides is difficult because the fraction of oligonucleotides containing errors can be lower than the sensitivity of conventional next-generation sequencing analyses.

[1195] To determine whether Safe-SeqS could be used for this determination, standard phosphoramidite chemistry was used to synthesize an oligonucleotide containing 31 bases that

were designed to be identical to that analyzed in the polymerase fidelity experiment described above. In the synthetic oligonucleotide, the 31 bases were surrounded by sequences complementary to primers that could be used for the UID assignment steps of Safe-SeqS (Fig. 63). By performing Safe-SeqS on ~300,000 oligonucleotides, it was found that there were 8.9 ± 0.28 x 10^{-4} super-mutants/bp and that these errors occurred throughout the oligonucleotides (Fig. 66A). The oligonucleotides contained a large number of insertion and deletion errors, representing 8.2 ± 0.63% and 25 ± 1.5% of the total super-mutants, respectively. Importantly, both the position and nature of the errors were highly reproducible among seven independent replicates of this experiment performed on the same batch of oligonucleotides (Fig. 66A). This nature and distribution of errors had little in common with that of the errors produced by Phusion polymerase (Fig. 66B and Table 56), which were distributed in the expected stochastic pattern among replicate experiments. The number of errors in the oligonucleotides synthesized with phosphoramidites was ~60 times higher than in the equivalent products synthesized by Phusion polymerase. These data, *in toto*, indicate that the vast majority of errors in the former were generated during their synthesis rather than during the Safe-SeqS procedure.

[1196] Does Safe-SeqS preserve the ratio of mutant:normal sequences in the original templates? To address this question, two 31-base oligonucleotides of identical sequence with the exception of nt 15 (50:50 C/G instead of T) were synthesized and mixed them at nominal mutant/normal fractions of 3.3% and 0.33%. Through Safe-SeqS analysis of the oligonucleotide mixtures, it was found that the ratios were 2.8% and 0.27%, respectively. Thus, the UID assignment and amplification procedures used in Safe-SeqS do not greatly alter the proportion of variant sequences and thereby provide a reliable estimate of that proportion when unknown. This is also supported by the reproducibility of variant fractions when analyzed in independent Safe-SeqS experiments (Fig. 66A).

Analysis of DNA sequences from normal human cells

[1197] The exogenous UID strategy (Fig. 63) was then used to determine the prevalence of rare mutations in a small region of the *CTNNB1* gene from ~100,000 normal human cells from three unrelated individuals. Through comparison with the number of UID-families obtained in the Safe-SeqS experiments (Table 53B), it was calculated that the majority (78 ± 9.8 %) of the input

fragments were converted into UID-families. There was an average of 68 members/UID-family, easily fulfilling the required redundancy for Safe-SeqS (Fig. 67). Conventional analysis of the Illumina sequencing data revealed an average of 118,488 ± 11,357 mutations among the ~560 Mb of sequence analyzed per sample, corresponding to an apparent mutation prevalence of 2.1 ± 0.16 x 10^{-4} mutations/bp (Table 53B). Only an average of 99 ± 78 super-mutants were observed in the Safe-SeqS analysis. The vast majority (>99%) of super-mutants were single base substitutions and the calculated mutation rate was 9.0 ± 3.1 x 10^{-6} mutations/bp (Table 54B). Safe-SeqS thereby reduced the apparent frequency of mutations in genomic DNA by at least 24-fold (Fig. 64).

[1198] One possible strategy to increase the specificity of Safe-SeqS is to perform the library amplification (and possibly the UID assignment cycles) in multiple wells. This can be accomplished in as few as 2 or as many as 384 wells using standard PCR plates, or scaled up to many more wells when using a microfluidic device (thousands to millions). When performed this way, indexing sequences can be introduced into the templates that are unique to the wells in which the template is amplified. Rare mutations, thus, should give rise to two super-mutants (i.e., one from each strand), both with the same well index sequence. When performing Safe-SeqS with exogenous UIDs on the *CTNNB1* templates described above and diluted into 10 wells (each well yielding templates amplified with a different index sequence), the mutation rate was further reduced from 9.0 ± 3.1 x 10^{-6} to 3.7 ± 1.2 x 10^{-6} super-mutants/bp. Thus, analyzing templates in multiple compartments—in a manner that yields differentially encoded templates based on the compartment in which templates were amplified—may be an additional strategy to increase the specificity of Safe-SeqS.

Analysis of DNA sequences from mitochondrial DNA

[1199] The identical strategy was applied to a short segment of mitochondrial DNA in ~1,000 cells from each of seven unrelated individuals. Conventional analysis of the Illumina sequencing libraries produced with the Safe-SeqS procedure (Fig. 63) revealed an average of 30,599 ± 12,970 mutations among the ~150 Mb of sequence analyzed per sample, corresponding to an apparent mutation prevalence of 2.1 ± 0.94 x 10^{-4} mutations/bp (Table 53C). Only 135 ± 61 super-mutants were observed in the Safe-SeqS analysis. As with the *CTNNB1* gene, the vast majority of mutations were single base substitutions, though occasional single base deletions were also observed (Table 54C). The calculated mutation rate in the analyzed segment of

mtDNA was $1.4 \pm 0.68 \times 10^{-5}$ mutations/bp (Table 53C). Thus, Safe-SeqS thereby reduced the apparent frequency of mutations in genomic DNA by at least 15-fold.

Example 9: Detection of Genetic and Protein Biomarkers in Combination with Detection of Aneuploidy

[1200] Samples from a number of patients were tested for the presence of genetic biomarkers (NRAS, CTNNB1, PIK3CA, FBXW7, APC, EGFR, BRAF, CDKN2A, PTEN, FGFR2, HRAS, KRAS, AKT1, TP53, PPP2R1A, and/or GNAS) and protein biomarkers (CA19-9, CEA, HGF, OPN, CA125, prolactin, TIMP-1, and/or MPO). The same samples were also tested for the presence of aneuploidy using WALDO methods described herein. The results are shown in Table 59. As can be seen, the genetic and protein biomarker test can complement the aneuploidy test (e.g., some patients are negative for the genetic and protein biomarker test while being positive for aneuploidy, and vice versa), such that the presence of cancer can be more accurately and completely detected using both tests.

[1201] Once a subject, is identified as having cancer by the genetic and protein biomarker test, the aneuploidy test, or both, the subject can undergo further diagnostic testing and/or increased monitoring (e.g., any of the variety of further diagnostic testing and/or increased monitoring methods described herein) and/or be administered a therapeutic intervention (e.g., any of the variety of therapeutic interventions described herein).

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[1202] Certain of the following references are referred to herein. The contents of each of the following references is incorporated herein by reference in its entirety.

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Table1.txt

Table 1. Mutations identified in primary tumors.

Patient ID #	Sample ID #	Tumor type	AJCC Stage	Mutation identified in tumor tissue*	Mutant mean allele frequency (%)
CRC 456	CRC 456 PT1	Colorectum	I	KRAS p.G13D, c.38G>A	25.44
CRC 457	CRC 457 PT1	Colorectum	II	TP53 p.Q331Q, c.993G>A (Exon End)	28.97
CRC 457	CRC 457 PT1	Colorectum	II	BRAF p.V600E, c.1799T>A	22.63
CRC 458	CRC 458 PT1	Colorectum	II	TP53 p.R248Q, c.743G>A	51.94
CRC 459	CRC 459 PT1	Colorectum	II	TP53 p.A276G, c.827C>G	52.19
CRC 460	CRC 460 PT1	Colorectum	II	CTNNB1 p.S45F, c.134C>T	52.43
CRC 461	CRC 461 PT1	Colorectum	I	TP53 p.R248Q, c.743G>A	46.79
CRC 462	CRC 462 PT1	Colorectum	I	CTNNB1 p.S45P, c.133T>C	57.25
CRC 462	CRC 462 PT1	Colorectum	I	KRAS p.G13D, c.38G>A	28.49
CRC 462	CRC 462 PT1	Colorectum	I	FBXW7 p.R465C, c.1393C>T	9.85
CRC 463	CRC 463 PT1	Colorectum	I	TP53 p.G245S, c.733G>A	60.00
CRC 464	CRC 464 PT1	Colorectum	III	TP53 p.R306*, c.916C>T	47.56
CRC 465	CRC 465 PT1	Colorectum	II	TP53 p.L264fs, c.791delT	74.74
CRC 466	CRC 466 PT1	Colorectum	III	TP53 p.R175H, c.524G>A	53.98
CRC 466	CRC 466 PT1	Colorectum	III	KRAS p.G12V, c.35G>T	44.11
CRC 466	CRC 466 PT1	Colorectum	III	APC p.R1450*, c.4348C>T	31.96
CRC 468	CRC 468 PT1	Colorectum	III	TP53 p.E286G, c.857A>G	72.38
CRC 469	CRC 469 PT1	Colorectum	II	TP53 p.P151fs, c.451insC	38.68
CRC 469	CRC 469 PT1	Colorectum	II	PIK3CA p.Q546P, c.1637A>C	30.88
CRC 469	CRC 469 PT1	Colorectum	II	KRAS p.G12V, c.35G>T	28.15
CRC 469	CRC 469 PT1	Colorectum	II	FBXW7 p.R505G, c.1513C>G	26.84

Table1.txt

CRC 470	CRC 470 PT1	Colorectum	II	
TP53 p.R342*, c.1024C>T				71.09
CRC 470	CRC 470 PT1	Colorectum	II	
APC p.E1306*, c.3916G>T				55.22
CRC 470	CRC 470 PT1	Colorectum	II	
NRAS p.Q61L, c.182A>T				53.60
CRC 471	CRC 471 PT1	Colorectum	III	
TP53 p.R196*, c.586C>T				63.18
CRC 472	CRC 472 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				25.66
CRC 472	CRC 472 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				20.88
CRC 472	CRC 472 PT1	Colorectum	II	
APC p.R1450*, c.4348C>T				9.05
CRC 473	CRC 473 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				50.82
CRC 474	CRC 474 PT1	Colorectum	III	
TP53 p.P152L, c.455C>T				50.83
CRC 476	CRC 476 PT1	Colorectum	II	
TP53 p.R249G, c.745A>G				58.82
CRC 477	CRC 477 PT1	Colorectum	II	
TP53 p.K132Q, c.394A>C				28.19
CRC 479	CRC 479 PT1	Colorectum	II	
KRAS p.G12C, c.34G>T				41.60
CRC 480	CRC 480 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				48.72
CRC 480	CRC 480 PT1	Colorectum	III	
CTNNB1 p.T41A, c.121A>G				32.64
CRC 480	CRC 480 PT1	Colorectum	III	
TP53 p.H168R, c.503A>G				27.13
CRC 480	CRC 480 PT1	Colorectum	III	
TP53 p.R175C, c.523C>T				18.07
CRC 481	CRC 481 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				31.36
CRC 481	CRC 481 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				27.88
CRC 481	CRC 481 PT1	Colorectum	II	
FBXW7 p.E471fs, c.1412insA				15.62
CRC 482	CRC 482 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				81.49
CRC 483	CRC 483 PT1	Colorectum	I	
BRAF p.V600E, c.1799T>A				10.79
CRC 484	CRC 484 PT1	Colorectum	I	
KRAS p.G12C, c.34G>T				32.53
CRC 486	CRC 486 PT1	Colorectum	I	
KRAS p.G12D, c.35G>A				40.23
CRC 486	CRC 486 PT1	Colorectum	I	
APC p.R1450*, c.4348C>T				32.44

Table1.txt

CRC 486	CRC 486 PT1	Colorectum	I	TP53 p.W91fs, c.271delGGCCCCTGCACCAGCCCCCTCCT (SEQ ID NO:732) 27.77
CRC 487	CRC 487 PT1	Colorectum	I	KRAS p.G12D, c.35G>A 40.70
CRC 489	CRC 489 PT1	Colorectum	II	FBXW7 p.R465H, c.1394G>A 28.22
CRC 489	CRC 489 PT1	Colorectum	II	KRAS p.Q61K, c.181C>A 22.35
CRC 490	CRC 490 PT1	Colorectum	III	TP53 p.K132N, c.396G>T 58.62
CRC 491	CRC 491 PT1	Colorectum	III	TP53 p.R248Q, c.743G>A 57.78
CRC 491	CRC 491 PT1	Colorectum	III	FBXW7 p.R465H, c.1394G>A 23.25
CRC 492	CRC 492 PT1	Colorectum	III	TP53 p.R273H, c.818G>A 70.47
CRC 492	CRC 492 PT1	Colorectum	III	KRAS p.G12D, c.35G>A 30.62
CRC 492	CRC 492 PT1	Colorectum	III	APC p.E1309fs, c.3927delAAAGA 13.91
CRC 494	CRC 494 PT1	Colorectum	II	TP53 p.R248Q, c.743G>A 75.43
CRC 494	CRC 494 PT1	Colorectum	II	APC p.R1450*, c.4348C>T 25.96
CRC 496	CRC 496 PT1	Colorectum	I	TP53 p.R248W, c.742C>T 72.75
CRC 497	CRC 497 PT1	Colorectum	III	APC p.E1309*, c.3925G>T 28.67
CRC 497	CRC 497 PT1	Colorectum	III	FBXW7 p.R479Q, c.1436G>A 27.64
CRC 498	CRC 498 PT1	Colorectum	III	BRAF p.V600E, c.1799T>A 27.58
CRC 501	CRC 501 PT1	Colorectum	I	TP53 p.G266*, c.796G>T 13.63
CRC 502	CRC 502 PT1	Colorectum	I	TP53 p.G245S, c.733G>A 69.93
CRC 502	CRC 502 PT1	Colorectum	I	KRAS p.G12V, c.35G>T 61.39
CRC 503	CRC 503 PT1	Colorectum	I	TP53 p.Y163C, c.488A>G 55.68
CRC 504	CRC 504 PT1	Colorectum	III	APC p.E1309fs, c.3927delAAAGA 62.45
CRC 504	CRC 504 PT1	Colorectum	III	TP53 p.R273C, c.817C>T 60.01
CRC 505	CRC 505 PT1	Colorectum	III	TP53 p.R213*, c.637C>T 73.33
CRC 505	CRC 505 PT1	Colorectum	III	BRAF p.V600E, c.1799T>A 28.65

Table1.txt

CRC 506	CRC 506 PT1	Colorectum	III	APC p.I1311fs, c.3931insA	94.22
CRC 506	CRC 506 PT1	Colorectum	III	TP53 p.R273L, c.818G>T	84.33
CRC 507	CRC 507 PT1	Colorectum	I	CTNNB1 p.S45F, c.134C>T	69.17
CRC 507	CRC 507 PT1	Colorectum	I	PIK3CA p.Q546R, c.1637A>G	38.18
CRC 507	CRC 507 PT1	Colorectum	I	KRAS p.G12D, c.35G>A	35.85
CRC 508	CRC 508 PT1	Colorectum	I	FBXW7 p.R505C, c.1513C>T	15.83
CRC 508	CRC 508 PT1	Colorectum	I	BRAF p.V600E, c.1799T>A	9.57
CRC 511	CRC 511 PT1	Colorectum	II	KRAS p.G13D, c.38G>A	40.37
CRC 511	CRC 511 PT1	Colorectum	II	PIK3CA p.E545K, c.1633G>A	20.76
CRC 512	CRC 512 PT1	Colorectum	II	TP53 p.R342*, c.1024C>T	52.32
CRC 512	CRC 512 PT1	Colorectum	II	KRAS p.G12D, c.35G>A	37.37
CRC 513	CRC 513 PT1	Colorectum	II	TP53 p.C275Y, c.824G>A	50.25
CRC 513	CRC 513 PT1	Colorectum	II	APC p.E1306*, c.3916G>T	46.11
CRC 515	CRC 515 PT1	Colorectum	II	PPP2R1A p.R183Q, c.548G>A	13.52
CRC 515	CRC 515 PT1	Colorectum	II	TP53 p.K381fs, c.1141insA	12.33
CRC 516	CRC 516 PT1	Colorectum	II	CTNNB1 p.T41A, c.121A>G	70.87
CRC 516	CRC 516 PT1	Colorectum	II	TP53 p.Q104*, c.310C>T	58.43
CRC 517	CRC 517 PT1	Colorectum	II	TP53 p.G245S, c.733G>A	76.65
CRC 518	CRC 518 PT1	Colorectum	III	TP53 p.S215fs, c.644insGTG	75.00
CRC 520	CRC 520 PT1	Colorectum	III	KRAS p.G12V, c.35G>T	74.54
CRC 521	CRC 521 PT1	Colorectum	III	FBXW7 p.R367*, c.1099C>T	62.17
CRC 521	CRC 521 PT1	Colorectum	III	TP53 p.R248W, c.742C>T	50.29
CRC 521	CRC 521 PT1	Colorectum	III	KRAS p.A146V, c.437C>T	47.53
CRC 521	CRC 521 PT1	Colorectum	III	PIK3CA p.E545K, c.1633G>A	28.40

Table1.txt

CRC 522	CRC 522 PT1	Colorectum	II		
TP53 p.Y234N, c.700T>A				7.88	
CRC 523	CRC 523 PT1	Colorectum	III		
TP53 p.R175H, c.524G>A				67.94	
CRC 523	CRC 523 PT1	Colorectum	III		
APC p.E1309fs, c.3927delAAAGA				18.67	
CRC 523	CRC 523 PT1	Colorectum	III		
KRAS p.G12V, c.35G>T				17.84	
CRC 523	CRC 523 PT1	Colorectum	III		
TP53 p.D208N, c.622G>A				6.25	
CRC 524	CRC 524 PT1	Colorectum	II		
KRAS p.G12V, c.35G>T				40.85	
CRC 524	CRC 524 PT1	Colorectum	II		
PIK3CA p.H1047R, c.3140A>G				40.24	
CRC 524	CRC 524 PT1	Colorectum	II		
TP53 p.K120R, c.359A>G				25.47	
CRC 525	CRC 525 PT1	Colorectum	III		
TP53 p.R273H, c.818G>A				80.53	
CRC 525	CRC 525 PT1	Colorectum	III		
KRAS p.G13D, c.38G>A				58.33	
CRC 526	CRC 526 PT1	Colorectum	III		
AKT1 p.E17K, c.49G>A				41.99	
CRC 526	CRC 526 PT1	Colorectum	III		
BRAF p.V600E, c.1799T>A				12.07	
CRC 527	CRC 527 PT1	Colorectum	III		
KRAS p.A146T, c.436G>A				31.31	
CRC 528	CRC 528 PT1	Colorectum	II		
APC p.R1450*, c.4348C>T				62.82	
CRC 528	CRC 528 PT1	Colorectum	II		
KRAS p.G12D, c.35G>A				34.63	
CRC 529	CRC 529 PT1	Colorectum	II		
TP53 p.R306*, c.916C>T				66.44	
CRC 530	CRC 530 PT1	Colorectum	II		
KRAS p.A146T, c.436G>A				60.91	
CRC 531	CRC 531 PT1	Colorectum	III		
KRAS p.G12V, c.35G>T				37.04	
INDI 001	INDI 001 PT1	Lung	II		
TP53 p.Y236C, c.707A>G				49.07	
INDI 002	INDI 002 PT1	Lung	II		
TP53 p.S241F, c.722C>T				24.74	
INDI 002	INDI 002 PT1	Lung	II		
TP53 p.Y234*, c.702C>A				23.94	
INDI 004	INDI 004 PT1	Lung	I		
TP53 g.7576927C>A (Splice Site)				60.61	
INDI 005	INDI 005 PT1	Lung	I		
TP53 p.R156fs, c.467delG				53.41	
INDI 007	INDI 007 PT1	Lung	II	TP53 p.E180fs, c.540delCGCTGCCCCCACCATGAG (SEQ ID NO:733)	30.25

Table1.txt

INDI 009	INDI 009 PT1	Lung	II	
TP53 p.C176F, c.527G>T				72.87
INDI 012	INDI 012 PT1	Lung	I	
CDKN2A p.D84V, c.251A>T				57.62
INDI 012	INDI 012 PT1	Lung	I	
PIK3CA p.E545K, c.1633G>A				15.30
INDI 014	INDI 014 PT1	Lung	II	
TP53 p.E298*, c.892G>T				64.15
INDI 016	INDI 016 PT1	Lung	III	
TP53 p.R249M, c.746G>T				33.50
INDI 016	INDI 016 PT1	Lung	III	
PIK3CA p.E545D, c.1635G>T				14.39
INDI 017	INDI 017 PT1	Lung	I	
TP53 p.R249M, c.746G>T				47.03
INDI 017	INDI 017 PT1	Lung	I	
TP53 p.T125T, c.375G>A (Exon End)				34.15
INDI 023	INDI 023 PT1	Lung	II	
TP53 p.G266V, c.797G>T				19.59
INDI 024	INDI 024 PT1	Lung	II	
KRAS p.G12C, c.34G>T				46.56
INDI 026	INDI 026 PT1	Lung	I	
EGFR p.L858R, c.2573T>G				28.94
INDI 027	INDI 027 PT1	Colorectum	II	
TP53 p.R175H, c.524G>A				91.65
INDI 028	INDI 028 PT1	Colorectum	II	
TP53 p.G245S, c.733G>A				78.25
INDI 029	INDI 029 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				31.95
INDI 029	INDI 029 PT1	Colorectum	II	
TP53 p.R213Q, c.638G>A				30.20
INDI 030	INDI 030 PT1	Colorectum	II	
TP53 p.R273H, c.818G>A				74.02
INDI 031	INDI 031 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				39.15
INDI 031	INDI 031 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				31.10
INDI 032	INDI 032 PT1	Colorectum	III	
TP53 p.C135R, c.403T>C				38.56
INDI 032	INDI 032 PT1	Colorectum	III	
BRAF p.D594G, c.1781A>G				27.28
INDI 034	INDI 034 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				59.07
INDI 034	INDI 034 PT1	Colorectum	III	
TP53 p.W53*, c.159G>A				25.37
INDI 035	INDI 035 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				30.46
INDI 036	INDI 036 PT1	Colorectum	I	
KRAS p.G12V, c.35G>T				49.01

Table1.txt

INDI 036	INDI 036 PT1	Colorectum	I	
PIK3CA p.E542K, c.1624G>A				8.48
INDI 037	INDI 037 PT1	Colorectum	I	
PIK3CA p.E545A, c.1634A>C				42.60
INDI 037	INDI 037 PT1	Colorectum	I	
APC p.R1450*, c.4348C>T				32.65
INDI 038	INDI 038 PT1	Colorectum	II	
KRAS p.Q61K, c.181C>A				28.00
INDI 039	INDI 039 PT1	Colorectum	III	
BRAF p.D594G, c.1781A>G				34.56
INDI 040	INDI 040 PT1	Colorectum	I	
TP53 p.G266R, c.796G>A				49.71
INDI 042	INDI 042 PT1	Colorectum	I	
TP53 p.G245S, c.733G>A				35.25
INDI 042	INDI 042 PT1	Colorectum	I	
KRAS p.G12D, c.35G>A				30.73
INDI 043	INDI 043 PT1	Colorectum	II	
TP53 p.R273H, c.818G>A				54.45
INDI 044	INDI 044 PT1	Colorectum	II	
FBXW7 p.R505C, c.1513C>T				25.15
INDI 045	INDI 045 PT1	Colorectum	III	
FBXW7 p.R479Q, c.1436G>A				45.55
INDI 045	INDI 045 PT1	Colorectum	III	
PIK3CA p.E81K, c.241G>A				28.88
INDI 046	INDI 046 PT1	Colorectum	II	
TP53 p.R282W, c.844C>T				50.14
INDI 046	INDI 046 PT1	Colorectum	II	
TP53 p.T125T, c.375G>A (Exon End)				24.58
INDI 047	INDI 047 PT1	Colorectum	II	
TP53 p.R337L, c.1010G>T				41.14
INDI 048	INDI 048 PT1	Breast	II	
PIK3CA p.N345K, c.1035T>A				25.72
INDI 049	INDI 049 PT1	Breast	III	
PIK3CA p.H1047R, c.3140A>G				63.21
INDI 050	INDI 050 PT1	Breast	II	
TP53 p.Y220C, c.659A>G				34.63
INDI 050	INDI 050 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				20.26
INDI 053	INDI 053 PT1	Breast	II	
TP53 p.T211fs, c.633insT				42.86
INDI 054	INDI 054 PT1	Breast	II	
PIK3CA p.Q546R, c.1637A>G				29.90
INDI 059	INDI 059 PT1	Breast	II	
PIK3CA p.M1043V, c.3127A>G				46.12
INDI 060	INDI 060 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				59.88
INDI 061	INDI 061 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				36.04

Table1.txt

INDI 062	INDI 062 PT1	Breast	II	PIK3CA p.E545K, c.1633G>A	18.14
INDI 064	INDI 064 PT1	Breast	II	TP53 p.C242Y, c.725G>A	60.26
INDI 065	INDI 065 PT1	Breast	II	PIK3CA p.G1049R, c.3145G>C	22.50
INDI 066	INDI 066 PT1	Breast	III	TP53 p.V122fs, c.364delTG	38.46
INDI 066	INDI 066 PT1	Breast	III	PTEN p.P96L, c.287C>T	25.64
INDI 066	INDI 066 PT1	Breast	III	TP53 p.R175H, c.524G>A	10.53
INDI 068	INDI 068 PT1	Breast	II	TP53 p.C176Y, c.527G>A	66.60
INDI 068	INDI 068 PT1	Breast	II	PIK3CA p.N345K, c.1035T>A	56.31
INDI 070	INDI 070 PT1	Breast	III	PTEN p.C136R, c.406T>C	41.77
INDI 072	INDI 072 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	26.47
INDI 073	INDI 073 PT1	Breast	III	TP53 p.R196fs, c.587insT	82.26
INDI 073	INDI 073 PT1	Breast	III	AKT1 p.E17K, c.49G>A	79.55
INDI 074	INDI 074 PT1	Pancreas	II	TP53 p.R342*, c.1024C>T	15.38
INDI 074	INDI 074 PT1	Pancreas	II	KRAS p.G12V, c.35G>T	14.53
INDI 075	INDI 075 PT1	Ovary	III	TP53 p.Y220C, c.659A>G	71.43
INDI 076	INDI 076 PT1	Esophagus	II	TP53 p.N288fs, c.864insT	63.56
INDI 077	INDI 077 PT1	Liver	II	TP53 p.R249S, c.747G>T	42.83
INDI 077	INDI 077 PT1	Liver	II	CTNNB1 p.G34V, c.101G>T	28.82
INDI 078	INDI 078 PT1	Liver	II	TP53 g.7577498C>G (Splice Site)	75.35
INDI 079	INDI 079 PT1	Liver	II	TP53 p.C176F, c.527G>T	71.29
INDI 081	INDI 081 PT1	Colorectum	II	TP53 p.W53*, c.158G>A	21.11
INDI 082	INDI 082 PT1	Stomach	II	TP53 p.W53*, c.158G>A	23.87
INDI 083	INDI 083 PT1	Stomach	II	TP53 p.R196*, c.586C>T	21.77
INDI 085	INDI 085 PT1	Stomach	I	TP53 p.L130F, c.388C>T	6.39

Table1.txt

INDI 089	INDI 089 PT1	Colorectum	II		
TP53 p.R282W, c.844C>T				47.79	
INDI 089	INDI 089 PT1	Colorectum	II		
KRAS p.G12A, c.35G>C				33.42	
INDI 090	INDI 090 PT1	Colorectum	II		
TP53 p.G245A, c.734G>C				52.01	
INDI 092	INDI 092 PT1	Stomach	II		
TP53 p.C238R, c.712T>C				40.59	
INDI 093	INDI 093 PT1	Colorectum	I		
TP53 p.R175H, c.524G>A				78.24	
INDI 094	INDI 094 PT1	Colorectum	I		
TP53 p.R306*, c.916C>T				53.20	
INDI 094	INDI 094 PT1	Colorectum	I		
PPP2R1A p.R183W, c.547C>T				36.61	
INDI 095	INDI 095 PT1	Stomach	II		
PIK3CA p.E545K, c.1633G>A				23.48	
INDI 096	INDI 096 PT1	Colorectum	I		
KRAS p.G12D, c.35G>A				31.89	
INDI 096	INDI 096 PT1	Colorectum	I		
PIK3CA p.E545G, c.1634A>G				19.04	
INDI 097	INDI 097 PT1	Colorectum	III		
APC p.R1450*, c.4348C>T				21.00	
INDI 097	INDI 097 PT1	Colorectum	III		
TP53 p.K372fs, c.1114delA				20.79	
INDI 097	INDI 097 PT1	Colorectum	III		
BRAF p.V600E, c.1799T>A				18.14	
INDI 097	INDI 097 PT1	Colorectum	III		
TP53 p.S33fs, c.98insC				18.04	
INDI 097	INDI 097 PT1	Colorectum	III		
TP53 p.R175H, c.524G>A				16.31	
INDI 098	INDI 098 PT1	Colorectum	II		
TP53 p.R282W, c.844C>T				84.50	
INDI 098	INDI 098 PT1	Colorectum	II		
PIK3CA p.H1047R, c.3140A>G				58.68	
INDI 100	INDI 100 PT1	Colorectum	III		
KRAS p.G13D, c.38G>A				26.90	
INDI 100	INDI 100 PT1	Colorectum	III		
TP53 p.C141Y, c.422G>A				25.65	
INDI 101	INDI 101 PT1	Colorectum	III	TP53	p.P177fs,
c.531insCCACCATGAGCGCTGCTCAGATAGCGATG (SEQ ID NO:734)					40.96
INDI 101	INDI 101 PT1	Colorectum	III		
KRAS p.G12A, c.35G>C				12.88	
INDI 102	INDI 102 PT1	Colorectum	III		
APC p.R1450*, c.4348C>T				67.28	
INDI 104	INDI 104 PT1	Stomach	III		
TP53 p.V272M, c.814G>A				70.96	
INDI 107	INDI 107 PT1	Colorectum	II		
TP53 p.R175H, c.524G>A				51.22	

Table1.txt

INDI 107	INDI 107 PT1	Colorectum	II	
NRAS p.G13V, c.38G>T				23.77
INDI 108	INDI 108 PT1	Colorectum	II	
TP53 p.R267W, c.799C>T				44.88
INDI 108	INDI 108 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				38.27
INDI 109	INDI 109 PT1	Colorectum	III	
TP53 p.R248Q, c.743G>A				56.45
INDI 110	INDI 110 PT1	Stomach	I	
TP53 p.T211I, c.632C>T				46.16
INDI 111	INDI 111 PT1	Stomach	II	
TP53 p.Q192fs, c.574delC				15.93
INDI 112	INDI 112 PT1	Esophagus	II	
TP53 p.L194R, c.581T>G				46.74
INDI 112	INDI 112 PT1	Esophagus	II	
TP53 p.Q100*, c.298C>T				18.70
INDI 113	INDI 113 PT1	Colorectum	II	
TP53 g.7579310A>G (Splice Site)				28.53
INDI 113	INDI 113 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				24.69
INDI 116	INDI 116 PT1	Stomach	I	
TP53 p.S260Y, c.779C>A				60.35
INDI 116	INDI 116 PT1	Stomach	I	
TP53 p.Y327fs, c.981delT				39.13
INDI 119	INDI 119 PT1	Esophagus	I	
APC p.N1455fs, c.4364delA				34.88
INDI 119	INDI 119 PT1	Esophagus	I	
TP53 p.H179R, c.536A>G				33.33
INDI 120	INDI 120 PT1	Stomach	III	
TP53 g.7579310A>T (Splice Site)				49.86
INDI 121	INDI 121 PT1	Stomach	I	
TP53 p.G245S, c.733G>A				11.98
INDI 122	INDI 122 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				37.43
INDI 122	INDI 122 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				29.84
INDI 122	INDI 122 PT1	Colorectum	II	
APC p.R1450*, c.4348C>T				26.56
INDI 122	INDI 122 PT1	Colorectum	II	
TP53 p.Y236C, c.707A>G				10.85
INDI 122	INDI 122 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				5.46
INDI 123	INDI 123 PT1	Colorectum	II	
TP53 p.Y236C, c.707A>G				70.65
INDI 123	INDI 123 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				38.54
INDI 124	INDI 124 PT1	Colorectum	II	
TP53 p.A63V, c.188C>T				46.75

Table1.txt

INDI 124	INDI 124 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				11.34
INDI 125	INDI 125 PT1	Esophagus	II	
TP53 p.L194H, c.581T>A				43.43
INDI 126	INDI 126 PT1	Stomach	III	
TP53 p.K132R, c.395A>G				27.98
INDI 127	INDI 127 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				35.84
INDI 127	INDI 127 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				35.07
INDI 128	INDI 128 PT1	Colorectum	III	
CTNNB1 p.S45F, c.134C>T				86.54
INDI 128	INDI 128 PT1	Colorectum	III	
KRAS p.Q61R, c.182A>G				44.40
INDI 128	INDI 128 PT1	Colorectum	III	
TP53 p.S241F, c.722C>T				42.39
INDI 128	INDI 128 PT1	Colorectum	III	
TP53 p.R273C, c.817C>T				20.24
INDI 130	INDI 130 PT1	Stomach	II	
TP53 p.G245S, c.733G>A				13.96
INDI 131	INDI 131 PT1	Stomach	II	
PIK3CA p.H1047R, c.3140A>G				27.14
INDI 131	INDI 131 PT1	Stomach	II	
KRAS p.A59T, c.175G>A				23.60
INDI 134	INDI 134 PT1	Stomach	III	
TP53 p.R282W, c.844C>T				43.79
INDI 134	INDI 134 PT1	Stomach	III	
CTNNB1 p.S33C, c.98C>G				12.28
INDI 136	INDI 136 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				37.59
INDI 136	INDI 136 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				31.70
INDI 137	INDI 137 PT1	Stomach	II	
TP53 p.V272M, c.814G>A				22.66
INDI 140	INDI 140 PT1	Stomach	III	
CTNNB1 p.G34V, c.101G>T				36.58
INDI 141	INDI 141 PT1	Stomach	III	
TP53 p.L45fs, c.133insCTGT				24.94
INDI 143	INDI 143 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				31.29
INDI 143	INDI 143 PT1	Colorectum	II	
TP53 p.Y236C, c.707A>G				19.55
INDI 144	INDI 144 PT1	Colorectum	II	
TP53 p.Y234C, c.701A>G				50.28
INDI 144	INDI 144 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				39.23
INDI 145	INDI 145 PT1	Colorectum	II	
TP53 p.V272L, c.814G>T				50.99

Table1.txt

INDI 145	INDI 145 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				31.89
INDI 146	INDI 146 PT1	Colorectum	II	
TP53 p.V274F, c.820G>T				50.01
INDI 147	INDI 147 PT1	Stomach	II	
TP53 p.R175H, c.524G>A				38.03
INDI 148	INDI 148 PT1	Colorectum	II	
TP53 p.Y234S, c.701A>C				41.42
INDI 150	INDI 150 PT1	Colorectum	II	
TP53 g.7578176C>T (Splice Site)				49.20
INDI 150	INDI 150 PT1	Colorectum	II	
KRAS p.G12C, c.34G>T				46.81
INDI 151	INDI 151 PT1	Stomach	II	
TP53 p.Y220C, c.659A>G				19.12
INDI 152	INDI 152 PT1	Colorectum	I	
KRAS p.G13D, c.38G>A				78.56
INDI 152	INDI 152 PT1	Colorectum	I	
TP53 p.C176Y, c.527G>A				77.49
INDI 153	INDI 153 PT1	Stomach	II	
KRAS p.G12D, c.35G>A				25.95
INDI 155	INDI 155 PT1	Colorectum	II	
FBXW7 p.R505C, c.1513C>T				20.21
INDI 156	INDI 156 PT1	Colorectum	III	
TP53 p.P190fs, c.570delCCT				38.84
INDI 156	INDI 156 PT1	Colorectum	III	
KRAS p.G12V, c.35G>T				25.51
INDI 158	INDI 158 PT1	Colorectum	I	
TP53 p.V173G, c.518T>G				66.55
INDI 159	INDI 159 PT1	Colorectum	II	
KRAS p.G12S, c.34G>A				42.06
INDI 159	INDI 159 PT1	Colorectum	II	
FBXW7 p.R465C, c.1393C>T				34.17
INDI 160	INDI 160 PT1	Colorectum	II	
APC p.E1309*, c.3925G>T				28.50
INDI 161	INDI 161 PT1	Stomach	II	
TP53 p.M237K, c.710T>A				78.38
INDI 162	INDI 162 PT1	Stomach	III	
TP53 g.7578291T>G (Splice Site)				44.38
INDI 163	INDI 163 PT1	Colorectum	III	
BRAF p.V600E, c.1799T>A				26.51
INDI 163	INDI 163 PT1	Colorectum	III	
AKT1 p.E17K, c.49G>A				25.17
INDI 164	INDI 164 PT1	Colorectum	I	
TP53 p.R273C, c.817C>T				64.12
INDI 167	INDI 167 PT1	Stomach	II	
PIK3CA p.E545K, c.1633G>A				5.07
INDI 168	INDI 168 PT1	Stomach	II	
TP53 p.L257P, c.770T>C				39.48

Table1.txt

INDI 169	INDI 169 PT1	Colorectum	III	
TP53 p.G245S, c.733G>A				18.90
INDI 169	INDI 169 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				17.12
INDI 171	INDI 171 PT1	Stomach	III	
TP53 p.G199fs, c.597insA				50.55
INDI 172	INDI 172 PT1	Stomach	II	
TP53 p.R248Q, c.743G>A				9.30
INDI 173	INDI 173 PT1	Stomach	I	
TP53 p.R248W, c.742C>T				46.56
INDI 175	INDI 175 PT1	Colorectum	III	
TP53 p.L188fs, c.564delG				28.65
INDI 175	INDI 175 PT2	Colorectum	III	
TP53 p.L188fs, c.564delG				6.96
INDI 176	INDI 176 PT1	Stomach	II	
TP53 p.T125T, c.375G>C (Exon End)				21.93
INDI 178	INDI 178 PT1	Colorectum	III	
FBXW7 p.R465C, c.1393C>T				20.49
INDI 178	INDI 178 PT1	Colorectum	III	
TP53 p.Y234H, c.700T>C				18.92
INDI 179	INDI 179 PT1	Colorectum	III	
TP53 p.R273H, c.818G>A				19.58
INDI 182	INDI 182 PT1	Liver	III	
TP53 p.A159P, c.475G>C				50.10
INDI 182	INDI 182 PT1	Liver	III	
CTNNB1 p.S45P, c.133T>C				33.08
INDI 183	INDI 183 PT1	Stomach	I	
TP53 p.R175H, c.524G>A				22.88
INDI 184	INDI 184 PT1	Esophagus	II	
TP53 p.H193R, c.578A>G				74.76
INDI 185	INDI 185 PT1	Stomach	II	
TP53 p.S183fs, c.549insA				8.59
INDI 187	INDI 187 PT1	Stomach	I	
TP53 p.V31I, c.91G>A				46.72
INDI 187	INDI 187 PT1	Stomach	I	
PIK3CA p.H1047R, c.3140A>G				29.71
INDI 189	INDI 189 PT1	Esophagus	II	
TP53 p.V274F, c.820G>T				44.84
INDI 190	INDI 190 PT1	Liver	III	
TP53 p.P151fs, c.451insC				41.19
INDI 191	INDI 191 PT1	Colorectum	I	
TP53 p.L114*, c.341T>A				20.75
INDI 194	INDI 194 PT1	Colorectum	II	
CTNNB1 p.S45F, c.134C>T				62.15
INDI 194	INDI 194 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				20.09
INDI 195	INDI 195 PT1	Colorectum	III	
KRAS p.G12C, c.34G>T				14.89

Table1.txt

INDI 195	INDI 195 PT1	Colorectum	III	
TP53 p.L194P, c.581T>C				8.24
INDI 196	INDI 196 PT1	Colorectum	III	
PPP2R1A p.R183W, c.547C>T				34.87
INDI 196	INDI 196 PT1	Colorectum	III	
PIK3CA p.E545D, c.1635G>C				33.17
INDI 197	INDI 197 PT1	Colorectum	II	
TP53 p.V122fs, c.364delTG				65.23
INDI 198	INDI 198 PT1	Stomach	III	
TP53 p.V274F, c.820G>T				11.05
INDI 199	INDI 199 PT1	Stomach	II	
TP53 p.V272M, c.814G>A				36.77
INDI 199	INDI 199 PT1	Stomach	II	
APC p.R1450*, c.4348C>T				34.89
INDI 199	INDI 199 PT1	Stomach	II	
KRAS p.G12D, c.35G>A				33.60
INDI 200	INDI 200 PT1	Breast	III	
TP53 p.V272fs, c.816insG				69.74
INDI 202	INDI 202 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				28.89
INDI 202	INDI 202 PT1	Colorectum	II	
PIK3CA p.E545K, c.1633G>A				25.16
INDI 205	INDI 205 PT1	Liver	III	
TP53 p.E204*, c.610G>T				65.19
INDI 206	INDI 206 PT1	Stomach	III	
TP53 p.V272L, c.814G>C				58.79
INDI 209	INDI 209 PT1	Colorectum	II	
TP53 p.H179R, c.536A>G				43.29
INDI 210	INDI 210 PT1	Stomach	III	
TP53 p.C135*, c.405C>A				51.16
INDI 211	INDI 211 PT1	Colorectum	II	
TP53 p.R175H, c.524G>A				63.04
INDI 212	INDI 212 PT1	Colorectum	III	
BRAF p.V600E, c.1799T>A				26.54
INDI 213	INDI 213 PT1	Colorectum	III	
TP53 p.R282W, c.844C>T				67.18
INDI 213	INDI 213 PT1	Colorectum	III	
PIK3CA p.Q546R, c.1637A>G				25.64
INDI 214	INDI 214 PT1	Stomach	II	
PPP2R1A p.R183W, c.547C>T				40.57
INDI 215	INDI 215 PT1	Liver	II	
TP53 p.R196*, c.586C>T				62.24
INDI 216	INDI 216 PT1	Colorectum	III	
TP53 g.7577156C>T (Splice Site)				22.73
INDI 219	INDI 219 PT1	Liver	III	
KRAS p.G12C, c.34G>T				29.45
INDI 221	INDI 221 PT1	Colorectum	III	
KRAS p.G12V, c.35G>T				59.73

Table1.txt

INDI 221	INDI 221 PT1	Colorectum	III	
PIK3CA p.E542K, c.1624G>A				31.13
INDI 222	INDI 222 PT1	Colorectum	II	
TP53 p.G266E, c.797G>A				17.16
INDI 222	INDI 222 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				16.69
INDI 222	INDI 222 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				8.29
INDI 223	INDI 223 PT1	Colorectum	I	
TP53 p.R213*, c.637C>T				30.59
INDI 223	INDI 223 PT1	Colorectum	I	
APC p.R1450*, c.4348C>T				20.69
INDI 224	INDI 224 PT1	Lung	III	
TP53 p.R248W, c.742C>T				52.73
INDI 225	INDI 225 PT1	Colorectum	I	
KRAS p.G13D, c.38G>A				17.35
INDI 225	INDI 225 PT1	Colorectum	I	
APC p.R1450*, c.4348C>T				15.53
INDI 230	INDI 230 PT1	Colorectum	I	
KRAS p.G12D, c.35G>A				34.45
INDI 231	INDI 231 PT1	Lung	III	
KRAS p.G12D, c.35G>A				36.29
INDI 233	INDI 233 PT1	Colorectum	I	
TP53 p.R273H, c.818G>A				27.71
INDI 233	INDI 233 PT1	Colorectum	I	
TP53 p.R213*, c.637C>T				27.02
INDI 234	INDI 234 PT1	Colorectum	I	
TP53 p.L43fs, c.129delTG				70.17
INDI 236	INDI 236 PT1	Stomach	II	
PIK3CA p.E545K, c.1633G>A				11.86
INDI 239	INDI 239 PT1	Lung	III	
TP53 p.R282G, c.844C>G				48.44
INDI 239	INDI 239 PT1	Lung	III	
CDKN2A g.21971209T>A (Splice Site)				41.79
INDI 241	INDI 241 PT1	Stomach	III	
TP53 p.R209fs, c.626delAG				67.11
INDI 243	INDI 243 PT1	Colorectum	I	
TP53 p.R248W, c.742C>T				37.86
INDI 243	INDI 243 PT1	Colorectum	I	
FBXW7 p.R465H, c.1394G>A				31.07
INDI 243	INDI 243 PT1	Colorectum	I	
APC p.E1309fs, c.3927delAAAGA				22.22
INDI 244	INDI 244 PT1	Colorectum	III	
TP53 p.G245D, c.734G>A				39.80
INDI 244	INDI 244 PT1	Colorectum	III	
KRAS p.G12C, c.34G>T				35.75
INDI 244	INDI 244 PT1	Colorectum	III	
GNAS p.R201H, c.602G>A				33.89

Table1.txt

INDI 245	INDI 245 PT1	Colorectum	III	
KRAS p.Q61K, c.181C>A				48.05
INDI 246	INDI 246 PT1	Lung	II	
BRAF p.V600E, c.1799T>A				17.12
INDI 248	INDI 248 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				37.03
INDI 248	INDI 248 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				35.53
INDI 255	INDI 255 PT1	Colorectum	II	
TP53 p.R248W, c.742C>T				54.12
INDI 255	INDI 255 PT1	Colorectum	II	
KRAS p.G13V, c.38G>T				36.33
INDI 255	INDI 255 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				35.71
INDI 255	INDI 255 PT1	Colorectum	II	
APC p.E1309*, c.3925G>T				29.61
INDI 256	INDI 256 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				51.86
INDI 256	INDI 256 PT1	Colorectum	III	
KRAS p.G12S, c.34G>A				44.35
INDI 256	INDI 256 PT1	Colorectum	III	
FBXW7 p.R465H, c.1394G>A				28.81
INDI 257	INDI 257 PT1	Lung	III	
KRAS p.G12R, c.34G>C				56.11
INDI 259	INDI 259 PT1	Colorectum	II	
TP53 p.L348*, c.1043T>A				34.74
INDI 259	INDI 259 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				25.99
INDI 261	INDI 261 PT1	Breast	II	
PIK3CA p.E542K, c.1624G>A				38.73
INDI 262	INDI 262 PT1	Breast	III	
AKT1 p.E17K, c.49G>A				65.36
INDI 264	INDI 264 PT1	Lung	III	
TP53 p.C135F, c.404G>T				36.93
INDI 265	INDI 265 PT1	Breast	II	
PIK3CA p.N345K, c.1035T>A				45.85
INDI 268	INDI 268 PT1	Colorectum	III	
TP53 p.R196*, c.586C>T				35.33
INDI 268	INDI 268 PT1	Colorectum	III	
NRAS p.Q61R, c.182A>G				33.55
INDI 269	INDI 269 PT1	Lung	III	
TP53 p.G266*, c.796G>T				66.67
INDI 271	INDI 271 PT1	Colorectum	III	
KRAS p.G12C, c.34G>T				20.15
INDI 271	INDI 271 PT1	Colorectum	III	
FBXW7 p.R505C, c.1513C>T				15.27
INDI 279	INDI 279 PT1	Colorectum	II	
GNAS p.R201H, c.602G>A				25.95

Table1.txt

INDI 280	INDI 280 PT1	Breast	I	
TP53 p.N131fs, c.392delCAA				32.93
INDI 281	INDI 281 PT1	Colorectum	I	
BRAF p.V600E, c.1799T>A				5.97
INDI 283	INDI 283 PT1	Lung	I	
TP53 p.F134fs, c.400delT				34.20
INDI 283	INDI 283 PT1	Lung	I	
KRAS p.G12A, c.35G>C				26.40
INDI 283	INDI 283 PT1	Lung	I	
TP53 p.K132T, c.395A>C				24.56
INDI 284	INDI 284 PT1	Colorectum	II	
APC p.E1309fs, c.3927delAAAGA				52.77
INDI 284	INDI 284 PT1	Colorectum	II	
TP53 p.G245V, c.734G>T				51.05
INDI 284	INDI 284 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				38.29
INDI 285	INDI 285 PT1	Lung	II	
TP53 p.E339*, c.1015G>T				45.11
INDI 287	INDI 287 PT1	Breast	III	
TP53 p.S94*, c.281C>G				55.25
INDI 288	INDI 288 PT1	Lung	III	
TP53 p.T125T, c.375G>T (Exon End)				31.77
INDI 289	INDI 289 PT1	Breast	II	
PTEN p.A126S, c.376G>T				19.86
INDI 290	INDI 290 PT1	Colorectum	I	
TP53 p.R342*, c.1024C>T				71.01
INDI 290	INDI 290 PT1	Colorectum	I	
PIK3CA p.E545Q, c.1633G>C				28.69
INDI 291	INDI 291 PT1	Lung	I	
KRAS p.G12V, c.35G>T				50.47
INDI 292	INDI 292 PT1	Lung	III	
TP53 p.C124*, c.372C>A				38.73
INDI 295	INDI 295 PT1	Colorectum	II	
KRAS p.G12A, c.35G>C				61.99
INDI 296	INDI 296 PT1	Colorectum	II	
TP53 p.Q104*, c.310C>T				48.98
INDI 297	INDI 297 PT1	Breast	III	
TP53 p.R248Q, c.743G>A				37.66
INDI 298	INDI 298 PT1	Colorectum	I	
TP53 p.R175H, c.524G>A				76.12
INDI 298	INDI 298 PT1	Colorectum	I	
PIK3CA p.E542K, c.1624G>A				53.03
INDI 299	INDI 299 PT1	Colorectum	I	
TP53 p.R248Q, c.743G>A				80.67
INDI 301	INDI 301 PT1	Breast	II	
TP53 p.R273C, c.817C>T				40.63
INDI 303	INDI 303 PT1	Colorectum	I	
KRAS p.G12V, c.35G>T				27.93

Table1.txt

INDI 303	INDI 303 PT1	Colorectum	I	FBXW7 p.R505C, c.1513C>T	25.92
INDI 304	INDI 304 PT1	Colorectum	I	TP53 p.R282W, c.844C>T	66.36
INDI 305	INDI 305 PT1	Colorectum	II	NRAS p.G12D, c.35G>A	53.26
INDI 305	INDI 305 PT1	Colorectum	II	TP53 p.L130V, c.388C>G	49.04
INDI 306	INDI 306 PT1	Colorectum	III	TP53 p.R175H, c.524G>A	47.76
INDI 306	INDI 306 PT1	Colorectum	III	APC p.E1309fs, c.3927delAAAGA	13.97
INDI 307	INDI 307 PT1	Colorectum	III	TP53 p.R273H, c.818G>A	59.16
INDI 307	INDI 307 PT1	Colorectum	III	KRAS p.G13D, c.38G>A	36.89
INDI 308	INDI 308 PT1	Liver	II	PIK3CA p.H1047R, c.3140A>G	6.45
INDI 310	INDI 310 PT1	Colorectum	II	KRAS p.G13D, c.38G>A	34.65
INDI 310	INDI 310 PT1	Colorectum	II	PIK3CA p.E545A, c.1634A>C	34.06
INDI 311	INDI 311 PT1	Colorectum	III	PIK3CA p.E545K, c.1633G>A	61.54
INDI 311	INDI 311 PT1	Colorectum	III	TP53 p.R306*, c.916C>T	50.99
INDI 312	INDI 312 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	28.57
INDI 312	INDI 312 PT1	Breast	II	TP53 p.G226fs, c.677delG	12.50
INDI 313	INDI 313 PT1	Esophagus	II	TP53 p.Y126*, c.378C>G	38.44
INDI 315	INDI 315 PT1	Breast	II	TP53 p.H115fs, c.345insTTCTGGGACAGCCAAG (SEQ ID NO:735)	44.50
INDI 315	INDI 315 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	25.94
INDI 316	INDI 316 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	47.59
INDI 318	INDI 318 PT1	Stomach	III	KRAS p.G12D, c.35G>A	42.13
INDI 318	INDI 318 PT1	Stomach	III	TP53 p.G199V, c.596G>T	41.67
INDI 319	INDI 319 PT1	Stomach	I	TP53 p.M237K, c.710T>A	33.84
INDI 319	INDI 319 PT1	Stomach	I	TP53 p.P152L, c.455C>T	16.37
INDI 320	INDI 320 PT1	Colorectum	II	GNAS p.R201C, c.601C>T	39.45

Table1.txt

INDI 320	INDI 320 PT1	Colorectum	II		
TP53 p.R273C, c.817C>T				35.73	
INDI 320	INDI 320 PT1	Colorectum	II		
BRAF p.V600E, c.1799T>A				35.08	
INDI 322	INDI 322 PT1	Colorectum	III		
KRAS p.A146T, c.436G>A				52.34	
INDI 322	INDI 322 PT1	Colorectum	III		TP53
p.A88fs, c.263delCCCCTGCACCAGC (SEQ ID NO:736)					20.84
INDI 324	INDI 324 PT1	Lung	I		
KRAS p.G12C, c.34G>T				67.25	
INDI 324	INDI 324 PT1	Lung	I		
TP53 p.R273H, c.818G>A				44.54	
INDI 325	INDI 325 PT1	Colorectum	III		
TP53 p.F113V, c.337T>G				49.96	
INDI 325	INDI 325 PT1	Colorectum	III		
NRAS p.G12D, c.35G>A				27.65	
INDI 325	INDI 325 PT1	Colorectum	III		
APC p.E1309fs, c.3927delAAAGA				15.44	
INDI 326	INDI 326 PT1	Lung	I		
TP53 p.G245V, c.734G>T				23.09	
INDI 326	INDI 326 PT1	Lung	I		
TP53 p.G245C, c.733G>T				22.73	
INDI 327	INDI 327 PT1	Colorectum	II		
TP53 p.I195N, c.584T>A				66.08	
INDI 327	INDI 327 PT1	Colorectum	II		
NRAS p.Q61K, c.181C>A				13.89	
INDI 328	INDI 328 PT1	Colorectum	I		
TP53 p.R248W, c.742C>T				57.19	
INDI 328	INDI 328 PT1	Colorectum	I		
KRAS p.G12A, c.35G>C				33.93	
INDI 328	INDI 328 PT1	Colorectum	I		
PIK3CA p.E545K, c.1633G>A				30.62	
INDI 329	INDI 329 PT1	Colorectum	III		
BRAF p.V600E, c.1799T>A				11.24	
INDI 329	INDI 329 PT1	Colorectum	III		
PIK3CA p.E542K, c.1624G>A				5.12	
INDI 331	INDI 331 PT1	Lung	III		
KRAS p.G12C, c.34G>T				7.79	
INDI 333	INDI 333 PT1	Lung	II		
TP53 p.R248W, c.742C>T				41.49	
INDI 334	INDI 334 PT1	Breast	I		
TP53 p.N345fs, c.1035insT				23.34	
INDI 335	INDI 335 PT1	Lung	I		
KRAS p.G12V, c.35G>T				44.27	
INDI 337	INDI 337 PT1	Esophagus	III		
TP53 p.R273C, c.817C>T				56.00	
INDI 338	INDI 338 PT1	Colorectum	II		
PIK3CA p.H1047R, c.3140A>G				41.40	

Table1.txt

INDI 338	INDI 338 PT1	Colorectum	II	
FBXW7 p.R465H, c.1394G>A				36.03
INDI 338	INDI 338 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				35.55
INDI 339	INDI 339 PT1	Breast	II	
PIK3CA p.M1043I, c.3129G>A				8.19
INDI 340	INDI 340 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				64.19
INDI 340	INDI 340 PT1	Colorectum	III	
PIK3CA p.Q546K, c.1636C>A				41.63
INDI 340	INDI 340 PT1	Colorectum	III	
CTNNB1 p.S37F, c.110C>T				40.14
INDI 340	INDI 340 PT1	Colorectum	III	
FBXW7 p.R465L, c.1394G>T				9.60
INDI 343	INDI 343 PT1	Colorectum	III	
TP53 p.R306*, c.916C>T				14.91
INDI 343	INDI 343 PT1	Colorectum	III	
TP53 p.G244V, c.731G>T				13.32
INDI 344	INDI 344 PT1	Colorectum	II	
TP53 p.P278L, c.833C>T				59.52
INDI 344	INDI 344 PT1	Colorectum	II	
KRAS p.G12S, c.34G>A				37.22
INDI 346	INDI 346 PT1	Lung	I	
CDKN2A p.H83Y, c.247C>T				50.28
INDI 346	INDI 346 PT1	Lung	I	
TP53 p.C176F, c.527G>T				44.13
INDI 346	INDI 346 PT1	Lung	I	
TP53 p.S240C, c.718A>T				12.64
INDI 347	INDI 347 PT1	Esophagus	I	
TP53 p.V272M, c.814G>A				29.42
INDI 350	INDI 350 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				19.06
INDI 353	INDI 353 PT1	Lung	II	
TP53 p.K132N, c.396G>T				6.38
INDI 353	INDI 353 PT1	Lung	II	
TP53 p.M133L, c.397A>T				6.08
INDI 354	INDI 354 PT1	Colorectum	III	
NRAS p.G12D, c.35G>A				67.78
INDI 354	INDI 354 PT1	Colorectum	III	
TP53 p.P250L, c.749C>T				48.01
INDI 355	INDI 355 PT1	Lung	I	
KRAS p.G12C, c.34G>T				49.69
INDI 356	INDI 356 PT1	Colorectum	I	
BRAF p.V600E, c.1799T>A				20.30
INDI 357	INDI 357 PT1	Lung	I	
TP53 p.G154V, c.461G>T				59.03
INDI 358	INDI 358 PT1	Lung	II	
KRAS p.G12C, c.34G>T				17.78

Table1.txt

INDI 358	INDI 358 PT1	Lung	II	
KRAS p.G12V, c.35G>T				17.66
INDI 358	INDI 358 PT1	Lung	II	
TP53 p.G105C, c.313G>T				6.37
INDI 359	INDI 359 PT1	Breast	I	
TP53 p.R209fs, c.626delAG				46.53
INDI 359	INDI 359 PT1	Breast	I	
KRAS p.G12V, c.35G>T				27.27
INDI 362	INDI 362 PT1	Breast	II	
PIK3CA p.E542K, c.1624G>A				71.25
INDI 363	INDI 363 PT1	Breast	I	
TP53 p.H179R, c.536A>G				52.63
INDI 363	INDI 363 PT1	Breast	I	
PIK3CA p.H1047R, c.3140A>G				30.05
INDI 364	INDI 364 PT1	Lung	I	
KRAS p.G12C, c.34G>T				65.05
INDI 365	INDI 365 PT1	Colorectum	II	
TP53 p.C275F, c.824G>T				28.41
INDI 365	INDI 365 PT1	Colorectum	II	
APC p.E1309fs, c.3927delAAAGA				18.01
INDI 366	INDI 366 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				7.66
INDI 367	INDI 367 PT1	Liver	I	
CTNNB1 p.I35S, c.104T>G				43.40
INDI 368	INDI 368 PT1	Breast	II	
PIK3CA p.H1047L, c.3140A>T				30.03
INDI 369	INDI 369 PT1	Lung	I	
PIK3CA p.E545K, c.1633G>A				59.01
INDI 369	INDI 369 PT1	Lung	I	
TP53 g.7578556T>A (Splice Site)				44.24
INDI 371	INDI 371 PT1	Lung	III	
KRAS p.G12V, c.35G>T				36.49
INDI 371	INDI 371 PT1	Lung	III	
TP53 p.T125T, c.375G>T (Exon End)				6.88
INDI 372	INDI 372 PT1	Lung	II	
EGFR p.L858R, c.2573T>G				46.22
INDI 376	INDI 376 PT1	Colorectum	I	
TP53 g.7577156C>T (Splice Site)				37.05
INDI 376	INDI 376 PT1	Colorectum	I	
PIK3CA p.Q546R, c.1637A>G				9.99
INDI 377	INDI 377 PT1	Colorectum	II	
TP53 p.R248W, c.742C>T				60.16
INDI 377	INDI 377 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				42.91
INDI 377	INDI 377 PT1	Colorectum	II	
PIK3CA p.R88Q, c.263G>A				41.84
INDI 379	INDI 379 PT1	Colorectum	III	
TP53 p.G245S, c.733G>A				55.87

Table1.txt

INDI 379	INDI 379 PT1	Colorectum	III	
KRAS p.G13D, c.38G>A				34.63
INDI 379	INDI 379 PT1	Colorectum	III	
PIK3CA p.E542K, c.1624G>A				33.22
INDI 380	INDI 380 PT1	Colorectum	II	
TP53 p.N288fs, c.862delA				46.11
INDI 381	INDI 381 PT1	Lung	III	
PIK3CA p.H1047L, c.3140A>T				25.94
INDI 382	INDI 382 PT1	Breast	II	
TP53 p.N131I, c.392A>T				81.33
INDI 383	INDI 383 PT1	Lung	III	
TP53 p.Y205C, c.614A>G				18.84
INDI 383	INDI 383 PT1	Lung	III	
CDKN2A g.21971209T>A (Splice Site)				10.86
INDI 385	INDI 385 PT1	Colorectum	I	
TP53 p.G245S, c.733G>A				42.44
INDI 387	INDI 387 PT1	Liver	I	
TP53 p.R273L, c.818G>T				38.36
INDI 392	INDI 392 PT1	Lung	I	
TP53 p.R273L, c.818G>T				49.21
INDI 394	INDI 394 PT1	Lung	II	
KRAS p.G12C, c.34G>T				14.99
INDI 394	INDI 394 PT1	Lung	II	
PIK3CA p.E542K, c.1624G>A				9.76
INDI 395	INDI 395 PT1	Lung	I	
TP53 p.T125T, c.375G>T (Exon End)				29.94
INDI 396	INDI 396 PT1	Colorectum	I	
TP53 p.R175H, c.524G>A				84.89
INDI 397	INDI 397 PT1	Colorectum	III	
PIK3CA p.H1047Q, c.3141T>G				39.02
INDI 398	INDI 398 PT1	Colorectum	II	
TP53 p.A161T, c.481G>A				28.86
INDI 398	INDI 398 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				24.35
INDI 400	INDI 400 PT1	Colorectum	II	
TP53 p.R175H, c.524G>A				53.39
INDI 418	INDI 418 PT1	Colorectum	I	
TP53 p.R174W, c.520A>T				80.38
INDI 418	INDI 418 PT1	Colorectum	I	
TP53 p.R196*, c.586C>T				54.82
INDI 418	INDI 418 PT1	Colorectum	I	
APC p.K1308fs, c.3924insA				43.41
INDI 418	INDI 418 PT1	Colorectum	I	
KRAS p.G12V, c.35G>T				42.66
INDI 418	INDI 418 PT1	Colorectum	I	
PIK3CA p.E545K, c.1633G>A				39.63
INDI 419	INDI 419 PT1	Colorectum	I	
TP53 p.G245S, c.733G>A				60.08

Table1.txt

INDI 421	INDI 421 PT1	Colorectum	II	
APC p.E1306*, c.3916G>T				58.52
INDI 421	INDI 421 PT1	Colorectum	II	
TP53 p.R175H, c.524G>A				47.04
INDI 421	INDI 421 PT1	Colorectum	II	
NRAS p.Q61K, c.181C>A				39.37
INDI 422	INDI 422 PT1	Colorectum	II	
TP53 p.C176Y, c.527G>A				62.21
INDI 422	INDI 422 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				44.53
INDI 423	INDI 423 PT1	Colorectum	II	
TP53 p.E287*, c.859G>T				47.07
INDI 424	INDI 424 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				31.56
INDI 426	INDI 426 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				23.05
INDI 426	INDI 426 PT1	Breast	II	
PIK3CA p.E80K, c.238G>A				17.80
INDI 427	INDI 427 PT1	Colorectum	II	
KRAS p.G12C, c.34G>T				77.19
INDI 427	INDI 427 PT1	Colorectum	II	
PIK3CA p.E542K, c.1624G>A				51.38
INDI 428	INDI 428 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				41.38
INDI 428	INDI 428 PT1	Colorectum	III	
KRAS p.Q61H, c.183A>T				37.71
INDI 428	INDI 428 PT1	Colorectum	III	
PIK3CA p.R88Q, c.263G>A				14.65
INDI 431	INDI 431 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				16.21
INDI 431	INDI 431 PT1	Colorectum	II	
PIK3CA p.Q546P, c.1637A>C				6.63
INDI 433	INDI 433 PT1	Colorectum	II	
TP53 p.R282W, c.844C>T				62.19
INDI 434	INDI 434 PT1	Colorectum	II	
TP53 p.R273H, c.818G>A				71.80
INDI 436	INDI 436 PT1	Colorectum	III	
KRAS p.G12V, c.35G>T				36.68
INDI 436	INDI 436 PT1	Colorectum	III	
TP53 p.R290H, c.869G>A				20.71
INDI 437	INDI 437 PT1	Colorectum	I	
TP53 p.V157G, c.470T>G				70.94
INDI 437	INDI 437 PT1	Colorectum	I	
KRAS p.G12V, c.35G>T				47.10
INDI 438	INDI 438 PT1	Colorectum	II	
TP53 p.V216M, c.646G>A				51.26
INDI 438	INDI 438 PT1	Colorectum	II	
PIK3CA p.E545K, c.1633G>A				8.20

Table1.txt

INDI 439	INDI 439 PT1	Colorectum	III	TP53 p.R196*, c.586C>T 47.07
INDI 439	INDI 439 PT1	Colorectum	III	KRAS p.G12C, c.34G>T 30.48
INDI 439	INDI 439 PT1	Colorectum	III	BRAF p.F595L, c.1785T>G 30.26
INDI 440	INDI 440 PT1	Esophagus	II	TP53 p.H179L, c.536A>T 32.48
INDI 440	INDI 440 PT1	Esophagus	II	TP53 p.A39fs, c.117insA 31.32
INDI 441	INDI 441 PT1	Esophagus	II	TP53 p.H179L, c.536A>T 52.70
INDI 441	INDI 441 PT1	Esophagus	II	CDKN2A g.21971208C>G (Splice Site) 41.40
INDI 442	INDI 442 PT1	Breast	II	TP53 p.R196*, c.586C>T 33.35
INDI 442	INDI 442 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G 27.53
INDI 444	INDI 444 PT1	Colorectum	II	TP53 p.K132N, c.396G>C 63.26
INDI 444	INDI 444 PT1	Colorectum	II	KRAS p.G12D, c.35G>A 43.46
INDI 445	INDI 445 PT1	Breast	II	TP53 p.E171fs, c.513delGACGGAG 29.79
INDI 447	INDI 447 PT1	Breast	III	TP53 p.F113S, c.338T>C 36.13
INDI 447	INDI 447 PT1	Breast	III	PIK3CA p.G1049R, c.3145G>C 32.44
INDI 450	INDI 450 PT1	Esophagus	II	TP53 p.V31I, c.91G>A 39.80
INDI 450	INDI 450 PT1	Esophagus	II	TP53 p.T304fs, c.910delCTGCCCCCAGGGAGCA (SEQ ID NO:737) 34.17
INDI 450	INDI 450 PT1	Esophagus	II	TP53 p.I255F, c.763A>T 33.15
INDI 453	INDI 453 PT1	Breast	I	PIK3CA p.H1047R, c.3140A>G 77.85
INDI 454	INDI 454 PT1	Breast	III	TP53 p.L194R, c.581T>G 51.39
INDI 455	INDI 455 PT1	Breast	II	TP53 p.D259V, c.776A>T 31.15
INDI 456	INDI 456 PT1	Colorectum	II	KRAS p.G13D, c.38G>A 43.04
INDI 456	INDI 456 PT1	Colorectum	II	TP53 p.R282W, c.844C>T 30.07
INDI 456	INDI 456 PT1	Colorectum	II	PIK3CA p.H1047R, c.3140A>G 26.14
INDI 456	INDI 456 PT1	Colorectum	II	FBXW7 p.R505C, c.1513C>T 23.19

Table1.txt

INDI 457	INDI 457 PT1	Esophagus	II	
TP53 p.E221*, c.661G>T				38.49
INDI 457	INDI 457 PT1	Esophagus	II	
TP53 p.G266V, c.797G>T				37.68
INDI 459	INDI 459 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				53.76
INDI 459	INDI 459 PT1	Breast	II	
TP53 p.E285K, c.853G>A				53.50
INDI 461	INDI 461 PT1	Colorectum	III	
TP53 p.V172F, c.514G>T				39.80
INDI 462	INDI 462 PT1	Breast	III	
TP53 g.7578176C>A (Splice Site)				60.00
INDI 463	INDI 463 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				41.66
INDI 464	INDI 464 PT1	Liver	III	
TP53 p.K132*, c.394A>T				62.58
INDI 465	INDI 465 PT1	Esophagus	II	
TP53 p.Q38*, c.112C>T				66.98
INDI 466	INDI 466 PT1	Colorectum	II	
TP53 p.T155fs, c.463insA				56.34
INDI 466	INDI 466 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				56.21
INDI 467	INDI 467 PT1	Colorectum	II	
TP53 p.P151fs, c.451insC				66.21
INDI 468	INDI 468 PT1	Colorectum	II	
TP53 p.K132E, c.394A>G				48.93
INDI 468	INDI 468 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				48.84
INDI 470	INDI 470 PT1	Colorectum	III	
TP53 p.Q100*, c.298C>T				42.41
INDI 471	INDI 471 PT1	Breast	III	
TP53 p.R280I, c.839G>T				73.67
INDI 472	INDI 472 PT1	Colorectum	II	
TP53 p.L137fs, c.410insTGG				83.85
INDI 472	INDI 472 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				83.02
INDI 477	INDI 477 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				20.13
INDI 477	INDI 477 PT1	Colorectum	III	
BRAF p.V600E, c.1799T>A				14.98
INDI 478	INDI 478 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				62.74
INDI 479	INDI 479 PT1	Breast	III	
TP53 p.R175H, c.524G>A				61.05
INDI 480	INDI 480 PT1	Breast	III	
TP53 p.H179R, c.536A>G				48.24
INDI 483	INDI 483 PT1	Colorectum	II	
TP53 p.G266E, c.797G>A				35.19

Table1.txt

INDI 484	INDI 484 PT1	Colorectum	II	
TP53 p.R273H, c.818G>A				48.30
INDI 485	INDI 485 PT1	Esophagus	III	
TP53 p.Q331*, c.991C>T				62.58
INDI 490	INDI 490 PT1	Breast	III	
PIK3CA p.H1047R, c.3140A>G				36.52
INDI 491	INDI 491 PT1	Lung	I	
TP53 p.M44fs, c.130delA				24.25
INDI 494	INDI 494 PT1	Lung	III	
CDKN2A p.H83Y, c.247C>T				19.34
INDI 494	INDI 494 PT1	Lung	III	
TP53 p.G244A, c.731G>C				14.81
INDI 495	INDI 495 PT1	Lung	I	
KRAS p.G12C, c.34G>T				12.49
INDI 497	INDI 497 PT1	Lung	II	
TP53 p.C176R, c.526T>C				39.24
INDI 498	INDI 498 PT1	Colorectum	II	
TP53 p.Y234C, c.701A>G				52.89
INDI 501	INDI 501 PT1	Colorectum	III	
TP53 p.R342*, c.1024C>T				53.91
INDI 502	INDI 502 PT1	Colorectum	III	
TP53 p.I195T, c.584T>C				75.10
INDI 504	INDI 504 PT1	Breast	III	
TP53 p.G105V, c.314G>T				36.73
INDI 505	INDI 505 PT1	Lung	II	
TP53 p.R267P, c.800G>C				25.18
INDI 507	INDI 507 PT1	Lung	II	
TP53 p.R273C, c.817C>T				26.52
INDI 508	INDI 508 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				59.40
INDI 508	INDI 508 PT1	Colorectum	III	
KRAS p.A146V, c.437C>T				30.77
INDI 511	INDI 511 PT1	Colorectum	III	
TP53 p.S183fs, c.549insA				56.84
INDI 512	INDI 512 PT1	Breast	II	
AKT1 p.E17K, c.49G>A				34.63
INDI 513	INDI 513 PT1	Lung	I	
KRAS p.G12C, c.34G>T				50.62
INDI 514	INDI 514 PT1	Stomach	I	
TP53 p.R248Q, c.743G>A				60.06
INDI 515	INDI 515 PT1	Colorectum	III	
TP53 p.G262V, c.785G>T				61.40
INDI 516	INDI 516 PT1	Pancreas	II	
KRAS p.G12R, c.34G>C				17.16
INDI 516	INDI 516 PT1	Pancreas	II	
TP53 p.R248Q, c.743G>A				10.69
INDI 518	INDI 518 PT1	Colorectum	III	
TP53 p.N131fs, c.392delCAA				49.99

Table1.txt

INDI 519	INDI 519 PT1	Lung	I	
KRAS p.G13C, c.37G>T				36.23
INDI 521	INDI 521 PT1	Colorectum	II	
TP53 p.A159D, c.476C>A				29.57
INDI 522	INDI 522 PT1	Lung	I	
TP53 p.E298*, c.892G>T				22.77
INDI 523	INDI 523 PT1	Colorectum	I	
KRAS p.G12D, c.35G>A				27.63
INDI 524	INDI 524 PT1	Lung	III	
TP53 p.R175H, c.524G>A				51.01
INDI 524	INDI 524 PT1	Lung	III	
HRAS p.G13R, c.37G>C				51.01
INDI 525	INDI 525 PT1	Colorectum	I	
PIK3CA p.H1047R, c.3140A>G				37.98
INDI 525	INDI 525 PT1	Colorectum	I	
KRAS p.G13D, c.38G>A				33.70
INDI 526	INDI 526 PT1	Esophagus	III	
TP53 p.S241F, c.722C>T				35.86
INDI 527	INDI 527 PT1	Colorectum	III	
TP53 p.P152L, c.455C>T				59.88
INDI 527	INDI 527 PT1	Colorectum	III	
NRAS p.Q61K, c.181C>A				35.63
INDI 529	INDI 529 PT1	Colorectum	I	
TP53 p.R175H, c.524G>A				64.97
INDI 529	INDI 529 PT1	Colorectum	I	
KRAS p.A59E, c.176C>A				42.48
INDI 530	INDI 530 PT1	Breast	I	
TP53 p.R209fs, c.626delAG				61.39
INDI 532	INDI 532 PT1	Lung	I	
KRAS p.G12C, c.34G>T				23.14
INDI 532	INDI 532 PT1	Lung	I	
TP53 p.G105V, c.314G>T				18.58
INDI 533	INDI 533 PT1	Pancreas	II	
TP53 p.G266E, c.797G>A				36.92
INDI 533	INDI 533 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				17.82
INDI 533	INDI 533 PT1	Pancreas	II	
CDKN2A p.M54fs, c.161insTG				16.09
INDI 535	INDI 535 PT1	Lung	I	
TP53 p.V157F, c.469G>T				18.74
INDI 535	INDI 535 PT1	Lung	I	
PIK3CA p.E545K, c.1633G>A				7.51
INDI 537	INDI 537 PT1	Ovary	I	
CTNNB1 p.S33F, c.98C>T				29.33
INDI 538	INDI 538 PT1	Lung	III	
TP53 p.A161T, c.481G>A				19.04
INDI 539	INDI 539 PT1	Colorectum	II	
PTEN p.D92A, c.275A>C				45.51

Table1.txt

INDI 539	INDI 539 PT1	Colorectum	II	
TP53 p.K132N, c.396G>T				41.27
INDI 539	INDI 539 PT1	Colorectum	II	
TP53 p.K381fs, c.1141delA				40.24
INDI 539	INDI 539 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				32.95
INDI 544	INDI 544 PT1	Colorectum	III	
TP53 p.R213Q, c.638G>A				38.23
INDI 544	INDI 544 PT1	Colorectum	III	
TP53 p.G334R, c.1000G>C				31.36
INDI 545	INDI 545 PT1	Lung	I	
TP53 p.W91*, c.273G>A				33.63
INDI 545	INDI 545 PT1	Lung	I	
NRAS p.Q61L, c.182A>T				27.19
INDI 546	INDI 546 PT1	Lung	II	
KRAS p.G12C, c.34G>T				11.32
INDI 547	INDI 547 PT1	Stomach	III	
TP53 p.R342*, c.1024C>T				11.13
INDI 548	INDI 548 PT1	Breast	II	
PIK3CA p.E545K, c.1633G>A				34.66
INDI 549	INDI 549 PT1	Lung	III	
TP53 p.R196*, c.586C>T				50.29
INDI 551	INDI 551 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				29.86
INDI 555	INDI 555 PT1	Colorectum	II	
APC p.E1309fs, c.3927delAAAGA				48.67
INDI 555	INDI 555 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				40.71
INDI 555	INDI 555 PT1	Colorectum	II	
TP53 p.Q331Q, c.993G>A (Exon End)				7.43
INDI 558	INDI 558 PT1	Colorectum	I	
TP53 p.E285K, c.853G>A				39.99
INDI 558	INDI 558 PT1	Colorectum	I	
KRAS p.G12D, c.35G>A				35.03
INDI 558	INDI 558 PT1	Colorectum	I	
TP53 p.K132R, c.395A>G				30.55
INDI 560	INDI 560 PT1	Colorectum	I	
TP53 p.P278S, c.832C>T				43.81
INDI 560	INDI 560 PT1	Colorectum	I	
KRAS p.G13D, c.38G>A				33.51
INDI 562	INDI 562 PT1	Colorectum	I	
TP53 p.H179Y, c.535C>T				79.66
INDI 566	INDI 566 PT1	Breast	II	
TP53 p.R248W, c.742C>T				26.98
INDI 567	INDI 567 PT1	Colorectum	II	
KRAS p.G12A, c.35G>C				80.29
INDI 567	INDI 567 PT1	Colorectum	II	
TP53 p.R175H, c.524G>A				66.88

Table1.txt

INDI 567	INDI 567 PT1	Colorectum	II	
PIK3CA p.E545K, c.1633G>A				46.68
INDI 568	INDI 568 PT1	Breast	II	
TP53 p.E286fs, c.857delA				62.70
INDI 569	INDI 569 PT1	Breast	III	
PIK3CA p.H1047R, c.3140A>G				18.52
INDI 570	INDI 570 PT1	Colorectum	II	
CTNNB1 p.T41A, c.121A>G				72.65
INDI 570	INDI 570 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				34.40
INDI 570	INDI 570 PT1	Colorectum	II	
PIK3CA p.R88Q, c.263G>A				27.71
INDI 571	INDI 571 PT1	Breast	III	
PIK3CA p.E545K, c.1633G>A				36.17
INDI 572	INDI 572 PT1	Colorectum	II	
APC p.E1306*, c.3916G>T				30.43
INDI 572	INDI 572 PT1	Colorectum	II	
FBXW7 p.R479Q, c.1436G>A				29.76
INDI 572	INDI 572 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				28.22
INDI 573	INDI 573 PT1	Colorectum	I	
KRAS p.G12V, c.35G>T				60.50
INDI 573	INDI 573 PT1	Colorectum	I	
FBXW7 p.R505C, c.1513C>T				47.04
INDI 574	INDI 574 PT1	Colorectum	III	
PIK3CA p.R88Q, c.263G>A				23.51
INDI 574	INDI 574 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				18.46
INDI 575	INDI 575 PT1	Breast	II	
TP53 p.T125T, c.375G>C (Exon End)				20.71
INDI 578	INDI 578 PT1	Breast	I	
AKT1 p.E17K, c.49G>A				27.83
INDI 578	INDI 578 PT1	Breast	I	
PIK3CA p.E542K, c.1624G>A				26.63
INDI 581	INDI 581 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				50.24
INDI 581	INDI 581 PT1	Colorectum	II	
TP53 g.7579311C>A (Splice Site)				49.81
INDI 582	INDI 582 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				38.47
INDI 582	INDI 582 PT1	Colorectum	II	
TP53 p.V197G, c.590T>G				27.27
INDI 582	INDI 582 PT1	Colorectum	II	
FBXW7 p.R505C, c.1513C>T				21.31
INDI 583	INDI 583 PT1	Colorectum	II	
PPP2R1A p.R183W, c.547C>T				21.39
INDI 583	INDI 583 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				13.17

Table1.txt

INDI 584	INDI 584 PT1	Colorectum	II	TP53 p.P152fs, c.454insCCGCCCGGCA (SEQ ID NO:738)	45.97
INDI 585	INDI 585 PT1	Esophagus	III	TP53 p.E343*, c.1027G>T	31.31
INDI 586	INDI 586 PT1	Liver	III	TP53 p.G279E, c.836G>A	82.95
INDI 587	INDI 587 PT1	Colorectum	II	TP53 p.R175H, c.524G>A	49.31
INDI 588	INDI 588 PT1	Breast	III	TP53 p.H214R, c.641A>G	64.37
INDI 588	INDI 588 PT1	Breast	III	PIK3CA p.H1047R, c.3140A>G	52.48
INDI 589	INDI 589 PT1	Breast	II	TP53 p.R213*, c.637C>T	52.50
INDI 591	INDI 591 PT1	Colorectum	II	TP53 p.C242Y, c.725G>A	10.35
INDI 592	INDI 592 PT1	Breast	II	TP53 p.H179R, c.536A>G	26.87
INDI 593	INDI 593 PT1	Breast	II	AKT1 p.E17K, c.49G>A	35.72
INDI 594	INDI 594 PT1	Colorectum	III	CTNNB1 p.G34E, c.101G>A	50.15
INDI 594	INDI 594 PT1	Colorectum	III	TP53 p.Q167*, c.499C>T	37.58
INDI 595	INDI 595 PT1	Esophagus	II	TP53 g.7578555C>T (Splice Site)	15.39
INDI 596	INDI 596 PT1	Breast	III	TP53 p.H193R, c.578A>G	48.66
INDI 597	INDI 597 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	52.67
INDI 598	INDI 598 PT1	Colorectum	II	PTEN p.G132S, c.394G>A	66.23
INDI 598	INDI 598 PT1	Colorectum	II	KRAS p.G12V, c.35G>T	40.34
INDI 599	INDI 599 PT1	Colorectum	II	TP53 p.V203fs, c.609delATTTGCGTGTG (SEQ ID NO:739)	31.65
INDI 600	INDI 600 PT1	Colorectum	II	TP53 p.Q104*, c.310C>T	48.26
INDI 600	INDI 600 PT1	Colorectum	II	PIK3CA p.N345K, c.1035T>A	12.42
INDI 601	INDI 601 PT1	Breast	III	TP53 p.R213*, c.637C>T	57.70
INDI 602	INDI 602 PT1	Colorectum	II	TP53 p.E204*, c.610G>T	27.56
INDI 603	INDI 603 PT1	Breast	III	PIK3CA p.N345K, c.1035T>A	24.11
INDI 604	INDI 604 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G	60.24

Table1.txt

INDI 604	INDI 604 PT1	Breast	II	
TP53 p.Y220C, c.659A>G				56.88
INDI 605	INDI 605 PT1	Colorectum	II	
TP53 p.V122fs, c.364delTG				62.40
INDI 605	INDI 605 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				35.01
INDI 606	INDI 606 PT1	Breast	II	
TP53 p.R213*, c.637C>T				61.27
INDI 607	INDI 607 PT1	Breast	II	
TP53 p.C275F, c.824G>T				17.97
INDI 608	INDI 608 PT1	Colorectum	II	
TP53 p.V272E, c.815T>A				39.50
INDI 608	INDI 608 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				35.26
INDI 609	INDI 609 PT1	Colorectum	II	
TP53 p.T253P, c.757A>C				46.39
INDI 610	INDI 610 PT1	Colorectum	II	
TP53 p.H193Y, c.577C>T				24.53
INDI 611	INDI 611 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				16.69
INDI 612	INDI 612 PT1	Colorectum	II	
TP53 p.R213Q, c.638G>A				44.18
INDI 613	INDI 613 PT1	Breast	II	
TP53 p.R248Q, c.743G>A				37.44
INDI 613	INDI 613 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				31.70
INDI 614	INDI 614 PT1	Colorectum	II	
TP53 p.Q331Q, c.993G>A (Exon End)				79.45
INDI 614	INDI 614 PT1	Colorectum	II	
NRAS p.G12D, c.35G>A				54.67
INDI 615	INDI 615 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				66.51
INDI 618	INDI 618 PT1	Colorectum	III	
TP53 p.A63V, c.188C>T				62.39
INDI 618	INDI 618 PT1	Colorectum	III	
TP53 p.R342*, c.1024C>T				28.71
INDI 618	INDI 618 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				24.60
INDI 618	INDI 618 PT1	Colorectum	III	
PIK3CA p.E545K, c.1633G>A				17.18
INDI 620	INDI 620 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				43.98
INDI 621	INDI 621 PT1	Colorectum	II	
TP53 p.G266E, c.797G>A				59.05
INDI 623	INDI 623 PT1	Breast	III	
TP53 p.R273P, c.818G>C				63.07
INDI 624	INDI 624 PT1	Colorectum	II	
TP53 p.C176Y, c.527G>A				79.81

Table1.txt

INDI 625	INDI 625 PT1	Colorectum	II	
TP53 p.S127F, c.380C>T				49.25
INDI 625	INDI 625 PT1	Colorectum	II	
KRAS p.G12S, c.34G>A				38.10
INDI 626	INDI 626 PT1	Colorectum	II	
TP53 p.R280G, c.838A>G				72.20
INDI 626	INDI 626 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				36.41
INDI 627	INDI 627 PT1	Breast	II	
TP53 p.H214R, c.641A>G				47.36
INDI 628	INDI 628 PT1	Colorectum	II	
TP53 p.A63V, c.188C>T				44.69
INDI 628	INDI 628 PT1	Colorectum	II	
PIK3CA p.H1047L, c.3140A>T				33.46
INDI 628	INDI 628 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				31.58
INDI 628	INDI 628 PT1	Colorectum	II	
CTNNB1 p.T41A, c.121A>G				12.56
INDI 628	INDI 628 PT1	Colorectum	II	
TP53 p.S127P, c.379T>C				12.39
INDI 629	INDI 629 PT1	Breast	I	
TP53 p.I195T, c.584T>C				68.62
INDI 630	INDI 630 PT1	Breast	I	
PIK3CA p.E545K, c.1633G>A				23.88
INDI 631	INDI 631 PT1	Colorectum	II	
TP53 p.P278S, c.832C>T				62.21
INDI 631	INDI 631 PT1	Colorectum	II	
PIK3CA p.R88Q, c.263G>A				14.23
INDI 633	INDI 633 PT1	Colorectum	II	
TP53 p.I251fs, c.753delC				71.16
INDI 635	INDI 635 PT1	Colorectum	II	
PTEN p.R130Q, c.389G>A				30.74
INDI 635	INDI 635 PT1	Colorectum	II	
PIK3CA p.R88Q, c.263G>A				27.79
INDI 636	INDI 636 PT1	Liver	III	
CTNNB1 p.T41A, c.121A>G				71.84
INDI 637	INDI 637 PT1	Breast	III	
TP53 g.7578176C>G (Splice Site)				70.19
INDI 637	INDI 637 PT1	Breast	III	
PIK3CA p.H1047R, c.3140A>G				53.45
INDI 638	INDI 638 PT1	Breast	I	
TP53 p.R248W, c.742C>T				67.59
INDI 639	INDI 639 PT1	Liver	II	
TP53 p.R158L, c.473G>T				31.21
INDI 640	INDI 640 PT1	Colorectum	II	
TP53 p.C141Y, c.422G>A				78.92
INDI 641	INDI 641 PT1	Breast	III	
AKT1 p.E17K, c.49G>A				81.72

Table1.txt

INDI 643	INDI 643 PT1	Colorectum	II		
TP53 p.G245S, c.733G>A				88.25	
INDI 645	INDI 645 PT1	Liver	III		
TP53 p.R249S, c.747G>T				16.75	
INDI 646	INDI 646 PT1	Breast	II		
TP53 p.L194R, c.581T>G				34.67	
INDI 646	INDI 646 PT1	Breast	II		
PIK3CA p.H1047R, c.3140A>G				21.94	
INDI 647	INDI 647 PT1	Colorectum	III		
TP53 p.R248L, c.743G>T				72.87	
INDI 648	INDI 648 PT1	Colorectum	III		
TP53 p.E258G, c.773A>G				51.85	
INDI 648	INDI 648 PT1	Colorectum	III		
KRAS p.G12V, c.35G>T				43.84	
INDI 649	INDI 649 PT1	Colorectum	III		
TP53 p.P250L, c.749C>T				18.30	
INDI 650	INDI 650 PT1	Colorectum	III		
TP53 p.R213*, c.637C>T				31.51	
INDI 654	INDI 654 PT1	Colorectum	II		
PIK3CA p.H1047R, c.3140A>G				33.02	
INDI 654	INDI 654 PT1	Colorectum	II		
FBXW7 p.R465H, c.1394G>A				29.24	
INDI 655	INDI 655 PT1	Colorectum	II		
KRAS p.G12D, c.35G>A				29.16	
INDI 656	INDI 656 PT1	Breast	III		
AKT1 p.E17K, c.49G>A				36.55	
INDI 657	INDI 657 PT1	Colorectum	II		
TP53 p.R158H, c.473G>A				50.17	
INDI 657	INDI 657 PT1	Colorectum	II		
KRAS p.G12A, c.35G>C				46.79	
INDI 658	INDI 658 PT1	Colorectum	I	TP53 p.T125fs, c.375GTCTGTGACTTGCACG>LLUN (Exon End) (SEQ ID NO:740)	35.15
INDI 658	INDI 658 PT1	Colorectum	I		
KRAS p.G13D, c.38G>A				34.68	
INDI 658	INDI 658 PT1	Colorectum	I		
CDKN2A p.R80*, c.238C>T				31.71	
INDI 660	INDI 660 PT1	Colorectum	II		
KRAS p.G12D, c.35G>A				42.79	
INDI 662	INDI 662 PT1	Breast	I		
PIK3CA p.E545K, c.1633G>A				23.74	
INDI 663	INDI 663 PT1	Esophagus	II		
TP53 p.Q331*, c.991C>T				64.63	
INDI 665	INDI 665 PT1	Esophagus	III		
TP53 p.C135F, c.404G>T				71.61	
INDI 665	INDI 665 PT1	Esophagus	III		
FGFR2 p.P253R, c.758C>G				39.53	
INDI 666	INDI 666 PT1	Breast	II		
TP53 p.R306*, c.916C>T				66.76	

Table1.txt

INDI 667	INDI 667 PT1	Breast	II	
TP53 p.T125M, c.374C>T				38.93
INDI 669	INDI 669 PT1	Liver	III	
TP53 p.R249S, c.747G>T				39.61
INDI 670	INDI 670 PT1	Colorectum	III	
TP53 p.G117fs, c.350insGGAC				50.34
INDI 671	INDI 671 PT1	Lung	I	
EGFR p.L858R, c.2573T>G				23.18
INDI 673	INDI 673 PT1	Breast	II	
PIK3CA p.E542K, c.1624G>A				31.51
INDI 674	INDI 674 PT1	Lung	I	
TP53 p.R249G, c.745A>G				65.38
INDI 674	INDI 674 PT1	Lung	I	
KRAS p.G12C, c.34G>T				55.70
INDI 675	INDI 675 PT1	Colorectum	III	
BRAF p.I592V, c.1774A>G				53.02
INDI 675	INDI 675 PT1	Colorectum	III	
TP53 p.T125T, c.375G>A (Exon End)				50.24
INDI 675	INDI 675 PT1	Colorectum	III	
TP53 p.R181P, c.542G>C				24.50
INDI 675	INDI 675 PT1	Colorectum	III	
PIK3CA p.E542K, c.1624G>A				21.29
INDI 677	INDI 677 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				51.30
INDI 678	INDI 678 PT1	Colorectum	III	
TP53 p.E224fs, c.670insG				72.34
INDI 678	INDI 678 PT1	Colorectum	III	
KRAS p.Q61H, c.183A>T				39.77
INDI 679	INDI 679 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				24.24
INDI 683	INDI 683 PT1	Colorectum	II	
TP53 p.D281H, c.841G>C				70.69
INDI 683	INDI 683 PT1	Colorectum	II	
KRAS p.A146V, c.437C>T				68.91
INDI 685	INDI 685 PT1	Colorectum	III	
TP53 p.I195T, c.584T>C				38.87
INDI 686	INDI 686 PT1	Pancreas	II	
CDKN2A p.T77fs, c.231delCT				42.48
INDI 686	INDI 686 PT1	Pancreas	II	
KRAS p.G12V, c.35G>T				33.64
INDI 687	INDI 687 PT1	Lung	III	
KRAS p.G12V, c.35G>T				66.77
INDI 687	INDI 687 PT1	Lung	III	
TP53 p.R273L, c.818G>T				38.34
INDI 688	INDI 688 PT1	Colorectum	II	
TP53 p.R282W, c.844C>T				84.86
INDI 688	INDI 688 PT1	Colorectum	II	
KRAS p.A146T, c.436G>A				69.13

Table1.txt

INDI 691	INDI 691 PT1	Lung	I	
TP53 p.R248fs, c.742delC				41.49
INDI 692	INDI 692 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				40.63
INDI 692	INDI 692 PT1	Colorectum	III	
FBXW7 p.R505C, c.1513C>T				37.25
INDI 692	INDI 692 PT1	Colorectum	III	
PIK3CA p.E545K, c.1633G>A				34.15
INDI 693	INDI 693 PT1	Lung	III	
TP53 p.H193Y, c.577C>T				69.11
INDI 694	INDI 694 PT1	Lung	I	
TP53 g.7578290C>A (Splice Site)				38.74
INDI 694	INDI 694 PT1	Lung	I	
KRAS p.G12C, c.34G>T				30.67
INDI 695	INDI 695 PT1	Pancreas	II	
TP53 p.A138V, c.413C>T				31.96
INDI 695	INDI 695 PT1	Pancreas	II	
KRAS p.G12R, c.34G>C				22.83
INDI 696	INDI 696 PT1	Lung	II	
HRAS p.G13V, c.38G>T				63.25
INDI 697	INDI 697 PT1	Breast	II	
PIK3CA p.E542K, c.1624G>A				29.83
INDI 700	INDI 700 PT1	Lung	III	
TP53 p.E286*, c.856G>T				71.37
INDI 701	INDI 701 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				10.05
INDI 702	INDI 702 PT1	Lung	II	
TP53 p.E298*, c.892G>T				75.88
INDI 703	INDI 703 PT1	Lung	I	
TP53 p.K132N, c.396G>T				41.10
INDI 703	INDI 703 PT1	Lung	I	
CDKN2A p.D84H, c.250G>C				36.05
INDI 704	INDI 704 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				20.89
INDI 708	INDI 708 PT1	Colorectum	III	
KRAS p.G12C, c.34G>T				36.50
INDI 709	INDI 709 PT1	Colorectum	II	
FBXW7 p.R465C, c.1393C>T				29.51
INDI 709	INDI 709 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				21.44
INDI 710	INDI 710 PT1	Colorectum	III	
TP53 g.7578176C>G (Splice Site)				60.22
INDI 710	INDI 710 PT1	Colorectum	III	
PIK3CA p.Q546R, c.1637A>G				41.90
INDI 710	INDI 710 PT1	Colorectum	III	
KRAS p.G12D, c.35G>A				36.54
INDI 710	INDI 710 PT1	Colorectum	III	
APC p.R1450*, c.4348C>T				31.61

Table1.txt

INDI 711	INDI 711 PT1	Breast	III		
TP53 p.Y163C, c.488A>G				31.57	
INDI 711	INDI 711 PT1	Breast	III		
PIK3CA p.E545K, c.1633G>A				26.58	
INDI 712	INDI 712 PT1	Breast	I		
TP53 p.C141Y, c.422G>A				13.28	
INDI 714	INDI 714 PT1	Breast	III		
TP53 p.R175H, c.524G>A				56.98	
INDI 720	INDI 720 PT1	Colorectum	III		
KRAS p.G12D, c.35G>A				36.44	
INDI 723	INDI 723 PT1	Ovary	III		
TP53 p.S215I, c.644G>T				47.72	
INDI 724	INDI 724 PT1	Colorectum	II		
TP53 p.I254fs, c.761delCAT				59.80	
INDI 725	INDI 725 PT1	Colorectum	II		
APC p.E1309fs, c.3927delAAAGA				30.07	
INDI 726	INDI 726 PT1	Colorectum	I		
TP53 p.R248W, c.742C>T				81.19	
INDI 726	INDI 726 PT1	Colorectum	I		
KRAS p.A146T, c.436G>A				50.34	
INDI 729	INDI 729 PT1	Colorectum	II		
KRAS p.G13D, c.38G>A				9.59	
INDI 747	INDI 747 PT1	Colorectum	III		TP53 p.E180fs,
c.540delCGCTGCCCCCACCATGAG (SEQ ID NO:741)				12.34	
INDI 749	INDI 749 PT1	Colorectum	III		
KRAS p.G12D, c.35G>A				45.30	
INDI 749	INDI 749 PT1	Colorectum	III		
TP53 p.G105V, c.314G>T				26.38	
INDI 750	INDI 750 PT1	Colorectum	III		
TP53 p.R175H, c.524G>A				70.38	
INDI 751	INDI 751 PT1	Colorectum	III		
PIK3CA p.N345K, c.1035T>A				27.82	
INDI 752	INDI 752 PT1	Colorectum	III		
TP53 p.R175H, c.524G>A				69.65	
INDI 753	INDI 753 PT1	Esophagus	III		
TP53 p.Y220C, c.659A>G				79.67	
INDI 754	INDI 754 PT1	Breast	III		
TP53 p.Y220C, c.659A>G				51.92	
INDI 755	INDI 755 PT1	Esophagus	III		
TP53 p.I255F, c.763A>T				33.79	
INDI 755	INDI 755 PT1	Esophagus	III		
TP53 p.P151fs, c.451insC				23.65	
INDI 758	INDI 758 PT1	Colorectum	II		
KRAS p.G12V, c.35G>T				69.43	
INDI 758	INDI 758 PT1	Colorectum	II		
PIK3CA p.E545K, c.1633G>A				45.70	
INDI 759	INDI 759 PT1	Breast	III		
TP53 p.C135W, c.405C>G				54.74	

Table1.txt

INDI 761	INDI 761 PT1	Colorectum	II	TP53 p.E180fs, c.540delCGCTGCCCCCACCATGAG (SEQ ID NO:742) 54.92
INDI 763	INDI 763 PT1	Colorectum	I	TP53 p.R282W, c.844C>T 63.06
INDI 763	INDI 763 PT1	Colorectum	I	APC p.E1309fs, c.3927delAAAGA 56.26
INDI 764	INDI 764 PT1	Colorectum	II	TP53 p.E51fs, c.151delG 50.48
INDI 765	INDI 765 PT1	Colorectum	I	KRAS p.G12D, c.35G>A 56.37
INDI 766	INDI 766 PT1	Breast	II	PIK3CA p.E542K, c.1624G>A 27.69
INDI 767	INDI 767 PT1	Colorectum	II	KRAS p.G12D, c.35G>A 47.73
INDI 767	INDI 767 PT1	Colorectum	II	APC p.R1450*, c.4348C>T 25.97
INDI 768	INDI 768 PT1	Colorectum	II	KRAS p.G12V, c.35G>T 30.61
INDI 769	INDI 769 PT1	Colorectum	II	TP53 p.I251V, c.751A>G 91.14
INDI 769	INDI 769 PT1	Colorectum	II	TP53 p.Y163C, c.488A>G 85.92
INDI 769	INDI 769 PT1	Colorectum	II	KRAS p.G12D, c.35G>A 56.37
INDI 770	INDI 770 PT1	Colorectum	II	TP53 p.E285K, c.853G>A 63.00
INDI 770	INDI 770 PT1	Colorectum	II	PIK3CA p.E545K, c.1633G>A 59.73
INDI 770	INDI 770 PT1	Colorectum	II	APC p.E1306*, c.3916G>T 53.52
INDI 770	INDI 770 PT1	Colorectum	II	KRAS p.G13D, c.38G>A 42.01
INDI 771	INDI 771 PT1	Liver	II	CTNNB1 p.S45A, c.133T>G 5.44
INDI 772	INDI 772 PT1	Colorectum	II	TP53 p.E62*, c.184G>T 51.99
INDI 772	INDI 772 PT1	Colorectum	II	PIK3CA p.E545K, c.1633G>A 28.84
INDI 773	INDI 773 PT1	Colorectum	II	TP53 p.P152L, c.455C>T 77.86
INDI 774	INDI 774 PT1	Colorectum	I	KRAS p.G13D, c.38G>A 46.65
INDI 776	INDI 776 PT1	Esophagus	II	TP53 p.E346*, c.1036G>T 77.51
INDI 777	INDI 777 PT1	Colorectum	II	TP53 p.E258K, c.772G>A 66.10
INDI 778	INDI 778 PT1	Liver	II	CTNNB1 p.I35S, c.104T>G 31.67

Table1.txt

INDI 779	INDI 779 PT1	Colorectum	II	
TP53 p.E11Q, c.31G>C				79.59
INDI 779	INDI 779 PT1	Colorectum	II	
TP53 p.R248W, c.742C>T				61.49
INDI 779	INDI 779 PT1	Colorectum	II	
KRAS p.G12D, c.35G>A				38.85
INDI 780	INDI 780 PT1	Colorectum	II	
TP53 p.R273C, c.817C>T				47.55
INDI 782	INDI 782 PT1	Colorectum	III	
BRAF p.V600E, c.1799T>A				27.99
INDI 783	INDI 783 PT1	Colorectum	III	
TP53 p.V216L, c.646G>C				33.92
INDI 783	INDI 783 PT1	Colorectum	III	
KRAS p.G13D, c.38G>A				22.23
INDI 785	INDI 785 PT1	Colorectum	I	
KRAS p.G12R, c.34G>C				24.86
INDI 786	INDI 786 PT1	Liver	I	
TP53 p.C135F, c.404G>T				7.09
INDI 788	INDI 788 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				31.83
INDI 788	INDI 788 PT1	Colorectum	II	
FBXW7 p.R465C, c.1393C>T				28.38
INDI 788	INDI 788 PT1	Colorectum	II	
TP53 p.R273S, c.817C>A				27.87
INDI 798	INDI 798 PT1	Ovary	II	
TP53 p.Y163C, c.488A>G				84.11
INDI 800	INDI 800 PT1	Liver	II	
CTNNB1 p.T41A, c.121A>G				44.31
INDI 802	INDI 802 PT1	Pancreas	II	
CDKN2A p.E88*, c.262G>T				11.06
INDI 802	INDI 802 PT1	Pancreas	II	
PTEN p.P96S, c.286C>T				6.85
INDI 803	INDI 803 PT1	Esophagus	II	
TP53 p.R213*, c.637C>T				50.46
INDI 806	INDI 806 PT1	Colorectum	II	
TP53 p.I255S, c.764T>G				47.68
INDI 806	INDI 806 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				23.73
INDI 808	INDI 808 PT1	Colorectum	III	
TP53 p.R213*, c.637C>T				61.35
INDI 809	INDI 809 PT1	Colorectum	III	
APC p.I1304fs, c.3910delA				62.39
INDI 809	INDI 809 PT1	Colorectum	III	
TP53 p.R273H, c.818G>A				50.95
INDI 812	INDI 812 PT1	Ovary	II	
CTNNB1 p.T41A, c.121A>G				42.81
INDI 812	INDI 812 PT1	Ovary	II	
KRAS p.G12C, c.34G>T				40.86

Table1.txt

INDI 814	INDI 814 PT1	Stomach	I	
PIK3CA p.E545K, c.1633G>A				17.98
INDI 816	INDI 816 PT1	Colorectum	II	
TP53 p.L264fs, c.792delCTA				38.23
INDI 818	INDI 818 PT1	Ovary	III	
TP53 p.G154fs, c.460delG				79.96
INDI 819	INDI 819 PT1	Breast	III	
AKT1 p.E17K, c.49G>A				30.37
INDI 819	INDI 819 PT1	Breast	III	
TP53 p.R175H, c.524G>A				16.96
INDI 821	INDI 821 PT1	Colorectum	III	
TP53 p.E258*, c.772G>T				80.26
INDI 821	INDI 821 PT1	Colorectum	III	
BRAF p.V600E, c.1799T>A				37.74
INDI 822	INDI 822 PT1	Colorectum	II	
KRAS p.G12V, c.35G>T				45.41
INDI 822	INDI 822 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				27.95
INDI 823	INDI 823 PT1	Breast	II	
TP53 p.H193Y, c.577C>T				27.29
INDI 823	INDI 823 PT1	Breast	II	
TP53 p.Q192H, c.576G>T				27.29
INDI 823	INDI 823 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				26.32
INDI 825	INDI 825 PT1	Colorectum	III	
NRAS p.Q61K, c.181C>A				34.29
INDI 825	INDI 825 PT1	Colorectum	III	
FBXW7 p.R465C, c.1393C>T				25.77
INDI 826	INDI 826 PT1	Colorectum	II	
TP53 p.N239S, c.716A>G				66.64
INDI 826	INDI 826 PT1	Colorectum	II	
APC p.E1309fs, c.3927delAAAGA				32.30
INDI 827	INDI 827 PT1	Colorectum	III	
KRAS p.A146T, c.436G>A				46.32
INDI 827	INDI 827 PT1	Colorectum	III	
TP53 p.R175H, c.524G>A				32.32
INDI 827	INDI 827 PT1	Colorectum	III	
FBXW7 p.R505C, c.1513C>T				23.77
INDI 827	INDI 827 PT1	Colorectum	III	
PIK3CA p.E545G, c.1634A>G				22.20
INDI 829	INDI 829 PT1	Colorectum	III	
TP53 p.G266R, c.796G>A				39.08
INDI 829	INDI 829 PT1	Colorectum	III	
BRAF p.D594G, c.1781A>G				22.95
INDI 829	INDI 829 PT1	Colorectum	III	
NRAS p.Q61R, c.182A>G				20.90
INDI 829	INDI 829 PT1	Colorectum	III	
PIK3CA p.M1043I, c.3129G>A				19.84

Table1.txt

INDI 830	INDI 830 PT0	Breast	II	
TP53 p.R282W, c.844C>T				33.78
INDI 830	INDI 830 PT0	Breast	II	
PIK3CA p.N345K, c.1035T>A				22.35
INDI 831	INDI 831 PT1	Breast	I	
TP53 p.R175H, c.524G>A				24.73
INDI 832	INDI 832 PT1	Breast	II	
PIK3CA p.H1047R, c.3140A>G				25.65
INDI 833	INDI 833 PT1	Breast	I	
PTEN p.R130Q, c.389G>A				18.58
INDI 833	INDI 833 PT1	Breast	I	
PIK3CA p.M1043I, c.3129G>A				11.50
INDI 833	INDI 833 PT1	Breast	I	
PIK3CA p.N345K, c.1035T>A				5.90
INDI 835	INDI 835 PT1	Colorectum	III	
TP53 p.G245S, c.733G>A				38.90
INDI 837	INDI 837 PT1	Colorectum	II	
FBXW7 p.R465H, c.1394G>A				22.73
INDI 837	INDI 837 PT1	Colorectum	II	
BRAF p.V600E, c.1799T>A				19.54
INDI 838	INDI 838 PT1	Colorectum	III	
APC p.E1306*, c.3916G>T				53.28
INDI 838	INDI 838 PT1	Colorectum	III	
TP53 p.N131fs, c.392delCAA				51.96
INDI 841	INDI 841 PT1	Colorectum	III	
TP53 p.R248W, c.742C>T				50.91
INDI 843	INDI 843 PT1	Esophagus	I	
TP53 p.R280T, c.839G>C				34.42
INDI 843	INDI 843 PT1	Esophagus	I	
TP53 p.N131fs, c.392delCAA				14.68
INDI 846	INDI 846 PT1	Colorectum	II	
TP53 p.Y234C, c.701A>G				46.30
INDI 846	INDI 846 PT1	Colorectum	II	
APC p.E1309fs, c.3927delAAAGA				34.94
INDI 847	INDI 847 PT1	Liver	III	
KRAS p.G13D, c.38G>A				17.41
INDI 848	INDI 848 PT1	Colorectum	II	
PIK3CA p.H1047R, c.3140A>G				21.35
INDI 848	INDI 848 PT1	Colorectum	II	
TP53 p.K381fs, c.1141delA				18.55
INDI 849	INDI 849 PT1	Colorectum	II	
TP53 p.R248Q, c.743G>A				59.21
INDI 849	INDI 849 PT1	Colorectum	II	
KRAS p.G13D, c.38G>A				50.20
INDI 850	INDI 850 PT1	Esophagus	II	
TP53 p.H193P, c.578A>C				85.41
INDI 853	INDI 853 PT1	Esophagus	II	
TP53 g.7577018C>A (Splice Site)				22.00

Table1.txt

INDI 854	INDI 854 PT1	Colorectum	II	APC p.R1450*, c.4348C>T 15.44
INDI 855	INDI 855 PT1	Colorectum	II	TP53 p.Y205H, c.613T>C 58.93
INDI 856	INDI 856 PT1	Breast	III	TP53 p.G245D, c.734G>A 67.30
INDI 856	INDI 856 PT1	Breast	III	PIK3CA p.H1047R, c.3140A>G 40.28
INDI 857	INDI 857 PT1	Breast	III	TP53 p.C176G, c.526T>G 54.52
INDI 858	INDI 858 PT1	Breast	I	PIK3CA p.E542K, c.1624G>A 38.66
INDI 859	INDI 859 PT1	Esophagus	II	TP53 p.Y234N, c.700T>A 47.06
INDI 859	INDI 859 PT1	Esophagus	II	PIK3CA p.N1044K, c.3132T>A 5.34
INDI 860	INDI 860 PT1	Breast	I	PIK3CA p.E542K, c.1624G>A 38.31
INDI 860	INDI 860 PT1	Breast	I	TP53 g.7576927delC (Splice Site) 35.10
INDI 861	INDI 861 PT1	Liver	II	TP53 p.G334V, c.1001G>T 77.21
INDI 867	INDI 867 PT1	Esophagus	II	TP53 p.T125T, c.375G>T (Exon End) 40.23
INDI 867	INDI 867 PT1	Esophagus	II	TP53 p.R181P, c.542G>C 30.17
INDI 868	INDI 868 PT1	Liver	III	TP53 p.R280T, c.839G>C 63.26
INDI 870	INDI 870 PT1	Breast	II	PIK3CA p.N345K, c.1035T>A 39.76
INDI 872	INDI 872 PT1	Breast	III	TP53 p.H179Y, c.535C>T 86.26
INDI 872	INDI 872 PT1	Breast	III	PIK3CA p.H1047L, c.3140A>T 59.15
INDI 872	INDI 872 PT1	Breast	III	CTNNB1 p.S37C, c.110C>G 11.60
INDI 873	INDI 873 PT1	Breast	III	PIK3CA p.H1047R, c.3140A>G 24.40
INDI 878	INDI 878 PT1	Breast	III	TP53 p.R248W, c.742C>T 69.51
INDI 879	INDI 879 PT1	Breast	II	TP53 p.P142fs, c.424delATGTTTTGCCAACTGGCCAAGACCTGCC (SEQ ID NO:743) 6.01
INDI 881	INDI 881 PT1	Breast	II	PIK3CA p.H1047R, c.3140A>G 51.46
INDI 883	INDI 883 PT1	Breast	II	PIK3CA p.N345K, c.1035T>A 61.23
INDI 883	INDI 883 PT1	Breast	II	TP53 p.M237I, c.711G>A 51.69

Table1.txt

INDI 884	INDI 884 PT1	Breast	II		
TP53 p.Y220C, c.659A>G				75.48	
INDI 885	INDI 885 PT1	Breast	II		
TP53 p.H179R, c.536A>G				50.53	
INDI 886	INDI 886 PT1	Breast	II		
TP53 p.F109V, c.325T>G				19.67	
INDI 905	INDI 905 PT1	Esophagus	II		
TP53 p.S241F, c.722C>T				79.33	
INDI 907	INDI 907 PT1	Esophagus	II		
TP53 p.T256fs, c.767insCACT				48.23	
INDI 908	INDI 908 PT1	Esophagus	II		
TP53 p.G266V, c.797G>T				48.34	
INDI 909	INDI 909 PT1	Esophagus	II		
TP53 p.P152L, c.455C>T				54.23	
INDI 911	INDI 911 PT1	Esophagus	II		
TP53 p.Y220C, c.659A>G				24.18	
INDI 911	INDI 911 PT1	Esophagus	II		
TP53 p.R273L, c.818G>T				13.89	
INDI 913	INDI 913 PT1	Esophagus	III		
TP53 p.R248P, c.743G>C				62.23	
INDI 913	INDI 913 PT1	Esophagus	III		
TP53 p.V172F, c.514G>T				13.34	
INDI 915	INDI 915 PT1	Breast	II		
PIK3CA p.H1047R, c.3140A>G				23.70	
INDI 921	INDI 921 PT1	Breast	II		
PIK3CA p.N345K, c.1035T>A				35.42	
INDI 928	INDI 928 PT1	Stomach	II		
TP53 p.F338fs, c.1014delC				84.79	
INDI 929	INDI 929 PT1	Stomach	II		
TP53 p.V216L, c.646G>C				80.49	
INDI 930	INDI 930 PT1	Stomach	II		
TP53 p.R342*, c.1024C>T				30.55	
INDI 932	INDI 932PT1	Ovary	III		
TP53 p.L252fs, c.754delTCC				92.30	
INDI 933	INDI 933 PT1	Esophagus	III	TP53 p.I195fs, c.585insCCGAGTGGAAGGAT (SEQ ID NO:744)	50.81
INDI 933	INDI 933 PT1	Esophagus	III	TP53 p.I195fs, c.583insATCCGAGTGGAAGG (SEQ ID NO:745)	36.94
LCR 812	LCR 812 PT1	Pancreas	II		
KRAS p.G12D, c.35G>A				23.93	
LCR 812	LCR 812 PT1	Pancreas	II		
GNAS p.R201H, c.602G>A				11.85	
LCR 814	LCR 814 PT1	Pancreas	II		
TP53 p.E298*, c.892G>T				19.45	
LCR 814	LCR 814 PT1	Pancreas	II		
KRAS p.G12A, c.35G>C				11.15	
PANC 757	PANC 757 PT1	Pancreas	II		
KRAS p.G12D, c.35G>A				10.47	

Table1.txt

PANC 758	PANC 758 PT1	Pancreas	II	
TP53 p.R337L, c.1010G>T				37.50
PANC 758	PANC 758 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				15.38
PANC 759	PANC 759 PT1	Pancreas	II	
KRAS p.G12V, c.35G>T				28.07
PANC 760	PANC 760 PT1	Pancreas	II	
TP53 p.R175H, c.524G>A				10.65
PANC 760	PANC 760 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				6.75
PANC 761	PANC 761 PT1	Pancreas	II	
TP53 p.E286G, c.857A>G				25.19
PANC 761	PANC 761 PT1	Pancreas	II	
KRAS p.G12V, c.35G>T				22.14
PANC 762	PANC 762 PT1	Pancreas	II	
TP53 p.R175H, c.524G>A				36.11
PANC 762	PANC 762 PT1	Pancreas	II	
KRAS p.G12R, c.34G>C				18.13
PANC 765	PANC 765 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				24.19
PANC 765	PANC 765 PT1	Pancreas	II	TP53 p.S260fs,
c.778delCCATCATCACACTGGAAGACT (SEQ ID NO:746)				12.44
PANC 767	PANC 767 PT1	Pancreas	II	
TP53 p.R175H, c.524G>A				13.57
PANC 767	PANC 767 PT1	Pancreas	II	
KRAS p.G12R, c.34G>C				5.50
PANC 769	PANC 769 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				25.60
PANCA 1149	PANCA 1149 PT1	Pancreas	II	
TP53 p.R306*, c.916C>T				20.83
PANCA 1149	PANCA 1149 PT1	Pancreas	II	
KRAS p.G12V, c.35G>T				9.12
PANCA 1152	PANCA 1152 PT1	Pancreas	I	
TP53 p.R282W, c.844C>T				30.92
PANCA 1152	PANCA 1152 PT1	Pancreas	I	
KRAS p.G12D, c.35G>A				18.45
PANCA 1153	PANCA 1153 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				8.72
PANCA 1155	PANCA 1155 PT1	Pancreas	II	
KRAS p.G12D, c.35G>A				23.38

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

Table2.txt

Table 2. Histopathological and clinical characteristics of the cancer patients and healthy controls.

			Primary						
CancerSEEK		CancerSEEK							
		Plasma		tumor					
		Tumor		AJCC		Histopathology			
Logistic		Test							
Patient ID #		sample ID #		sample ID #		Age	Sex		
Race		type		Stage		Histopathology			
Regression Score		Result							
CRC 455	CRC 455 PLS 1		Not available		60	Male			
Caucasian	Colorectum		I		Adenocarcinoma				
0.681	Negative								
CRC 456	CRC 456 PLS 1		CRC 456 PT1		59	Female			
Caucasian	Colorectum		I		Adenocarcinoma				
0.986	Positive								
CRC 457	CRC 457 PLS 1		CRC 457 PT1		69	Female			
Caucasian	Colorectum		II		Adenocarcinoma				
0.978	Positive								
CRC 458	CRC 458 PLS 1		CRC 458 PT1		70	Female			
Caucasian	Colorectum		II		Adenocarcinoma				
0.693	Negative								
CRC 459	CRC 459 PLS 1		CRC 459 PT1		43	Female			
Caucasian	Colorectum		II		Adenocarcinoma				
0.515	Negative								
CRC 460	CRC 460 PLS 1		CRC 460 PT1		72	Male			
Caucasian	Colorectum		II		Adenocarcinoma				
0.707	Negative								
CRC 461	CRC 461 PLS 1		CRC 461 PT1		70	Male			
Caucasian	Colorectum		I		Adenocarcinoma				
0.117	Negative								
CRC 462	CRC 462 PLS 1		CRC 462 PT1		67	Female			
Caucasian	Colorectum		I		Adenocarcinoma				
0.381	Negative								
CRC 463	CRC 463 PLS 1		CRC 463 PT1		47	Female			
Caucasian	Colorectum		I		Adenocarcinoma				
0.892	Positive								
CRC 464	CRC 464 PLS 1		CRC 464 PT1		78	Male			
Caucasian	Colorectum		III		Adenocarcinoma				
0.557	Negative								
CRC 465	CRC 465 PLS 1		CRC 465 PT1		78	Male			
Caucasian	Colorectum		II		Adenocarcinoma				
0.698	Negative								
CRC 466	CRC 466 PLS 1		CRC 466 PT1		56	Female			
Caucasian	Colorectum		III		Adenocarcinoma				
0.356	Negative								

Table2.txt

CRC 467	CRC 467 PLS 1	CRC 467 PT1	51	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.878	Positive			
CRC 468	CRC 468 PLS 1	CRC 468 PT1	66	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.998	Positive			
CRC 469	CRC 469 PLS 1	CRC 469 PT1	80	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.117	Negative			
CRC 470	CRC 470 PLS 1	CRC 470 PT1	53	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.967	Positive			
CRC 471	CRC 471 PLS 1	CRC 471 PT1	72	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.915	Positive			
CRC 472	CRC 472 PLS 1	CRC 472 PT1	66	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.574	Negative			
CRC 473	CRC 473 PLS 1	CRC 473 PT1	81	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.934	Positive			
CRC 474	CRC 474 PLS 1	CRC 474 PT1	63	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.307	Negative			
CRC 475	CRC 475 PLS 1	CRC 475 PT1	72	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.750	Negative			
CRC 476	CRC 476 PLS 1	CRC 476 PT1	75	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.999	Positive			
CRC 477	CRC 477 PLS 1	CRC 477 PT1	78	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.981	Positive			
CRC 478	CRC 478 PLS 1	CRC 478 PT1	63	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.439	Negative			
CRC 479	CRC 479 PLS 1	CRC 479 PT1	47	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.969	Positive			
CRC 480	CRC 480 PLS 1	CRC 480 PT1	59	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.996	Positive			
CRC 481	CRC 481 PLS 1	CRC 481 PT1	83	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.951	Positive			
CRC 482	CRC 482 PLS 1	CRC 482 PT1	59	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.606	Negative			

Table2.txt

CRC 483	CRC 483 PLS 1	CRC 483 PT1	79	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.116	Negative			
CRC 484	CRC 484 PLS 1	CRC 484 PT1	73	Male	Black	Colorectum
I	Adenocarcinoma	0.904	Positive			
CRC 486	CRC 486 PLS 1	CRC 486 PT1	71	Female	Black	Colorectum
I	Adenocarcinoma	0.973	Positive			
CRC 487	CRC 487 PLS 1	CRC 487 PT1	57	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.117	Negative			
CRC 488	CRC 488 PLS 1	Not available	22	Female	Black	Colorectum
II	Adenocarcinoma	0.988	Positive			
CRC 489	CRC 489 PLS 1	CRC 489 PT1	67	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.991	Positive			
CRC 490	CRC 490 PLS 1	CRC 490 PT1	71	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.397	Negative			
CRC 491	CRC 491 PLS 1	CRC 491 PT1	67	Male	Black	Colorectum
III	Adenocarcinoma	0.840	Negative			
CRC 492	CRC 492 PLS 1	CRC 492 PT1	74	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.906	Positive			
CRC 493	CRC 493 PLS 1	CRC 493 PT1	74	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.739	Negative			
CRC 494	CRC 494 PLS 1	CRC 494 PT1	80	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.448	Negative			
CRC 495	CRC 495 PLS 1	Not available	81	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.116	Negative			
CRC 496	CRC 496 PLS 1	CRC 496 PT1	72	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.330	Negative			
CRC 497	CRC 497 PLS 1	CRC 497 PT1	62	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.990	Positive			
CRC 498	CRC 498 PLS 1	CRC 498 PT1	63	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.944	Positive			
CRC 499	CRC 499 PLS 1	Not available	61	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.543	Negative			

Table2.txt

CRC 500	CRC 500 PLS 1	Not available	64	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.308	Negative			
CRC 501	CRC 501 PLS 1	CRC 501 PT1	65	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.490	Negative			
CRC 502	CRC 502 PLS 1	CRC 502 PT1	68	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.121	Negative			
CRC 503	CRC 503 PLS 1	CRC 503 PT1	57	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.993	Positive			
CRC 504	CRC 504 PLS 1	CRC 504 PT1	75	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.999	Positive			
CRC 505	CRC 505 PLS 1	CRC 505 PT1	47	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.323	Negative			
CRC 506	CRC 506 PLS 1	CRC 506 PT1	66	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.680	Negative			
CRC 507	CRC 507 PLS 1	CRC 507 PT1	59	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.818	Negative			
CRC 508	CRC 508 PLS 1	CRC 508 PT1	80	Female	Caucasian	Colorectum
I	Adenocarcinoma	0.343	Negative			
CRC 509	CRC 509 PLS 1	Not available	61	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.480	Negative			
CRC 510	CRC 510 PLS 1	Not available	58	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.300	Negative			
CRC 511	CRC 511 PLS 1	CRC 511 PT1	50	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.125	Negative			
CRC 512	CRC 512 PLS 1	CRC 512 PT1	69	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.868	Positive			
CRC 513	CRC 513 PLS 1	CRC 513 PT1	72	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.994	Positive			
CRC 514	CRC 514 PLS 1	Not available	89	Male	Black	Colorectum
II	Adenocarcinoma	0.998	Positive			
CRC 515	CRC 515 PLS 1	CRC 515 PT1	38	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.640	Negative			

Table2.txt

CRC 516	CRC 516 PLS 1	CRC 516 PT1	78	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.664	Negative			
CRC 517	CRC 517 PLS 1	CRC 517 PT1	61	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.318	Negative			
CRC 518	CRC 518 PLS 1	CRC 518 PT1	54	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.999	Positive			
CRC 519	CRC 519 PLS 1	Not available	57	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.117	Negative			
CRC 520	CRC 520 PLS 1	CRC 520 PT1	86	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.974	Positive			
CRC 521	CRC 521 PLS 1	CRC 521 PT1	65	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.598	Negative			
CRC 522	CRC 522 PLS 1	CRC 522 PT1	52	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.868	Positive			
CRC 523	CRC 523 PLS 1	CRC 523 PT1	47	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.451	Negative			
CRC 524	CRC 524 PLS 1	CRC 524 PT1	59	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.983	Positive			
CRC 525	CRC 525 PLS 1	CRC 525 PT1	70	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.968	Positive			
CRC 526	CRC 526 PLS 1	CRC 526 PT1	69	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.521	Negative			
CRC 527	CRC 527 PLS 1	CRC 527 PT1	71	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.937	Positive			
CRC 528	CRC 528 PLS 1	CRC 528 PT1	47	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.338	Negative			
CRC 529	CRC 529 PLS 1	CRC 529 PT1	81	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.116	Negative			
CRC 530	CRC 530 PLS 1	CRC 530 PT1	91	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.956	Positive			
CRC 531	CRC 531 PLS 1	CRC 531 PT1	69	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.540	Negative			

Table2.txt

INDI 001	INDI 001 PLS 1	INDI 001 PT1	70	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.926	Positive
INDI 002	INDI 002 PLS 1	INDI 002 PT1	55	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.621	Negative
INDI 003	INDI 003 PLS 1	INDI 003 PT1	78	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.999	Positive
INDI 004	INDI 004 PLS 1	INDI 004 PT1	75	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.936	Positive
INDI 005	INDI 005 PLS 1	INDI 005 PT1	70	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.779	Negative
INDI 007	INDI 007 PLS 1	INDI 007 PT1	69	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.614	Negative
INDI 009	INDI 009 PLS 1	INDI 009 PT1	67	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.985	Positive
INDI 010	INDI 010 PLS 1	INDI 010 PT1	76	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.926	Positive
INDI 011	INDI 011 PLS 1	INDI 011 PT1	60	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.362	Negative
INDI 012	INDI 012 PLS 1	INDI 012 PT1	65	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.966	Positive
INDI 013	INDI 013 PLS 1	INDI 013 PT1	78	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.852	Negative
INDI 014	INDI 014 PLS 1	INDI 014 PT1	45	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.965	Positive
INDI 015	INDI 015 PLS 1	INDI 015 PT1	80	Female	Caucasian	Lung	I	Non-small cell lung cancer	0.121	Negative
INDI 016	INDI 016 PLS 1	INDI 016 PT1	63	Female	Caucasian	Lung	III	Non-small cell lung cancer	0.990	Positive
INDI 017	INDI 017 PLS 1	INDI 017 PT1	66	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.397	Negative
INDI 018	INDI 018 PLS 1	INDI 018 PT1	62	Female	Caucasian	Lung	III	Non-small cell lung cancer	0.824	Negative

Table2.txt

INDI 022	INDI 022 PLS 1	INDI 022 PT1	44	Female	Caucasian	Lung	III
Non-small cell lung cancer	0.996	Positive					
INDI 023	INDI 023 PLS 1	INDI 023 PT1	66	Male	Caucasian	Lung	II
Non-small cell lung cancer	0.998	Positive					
INDI 024	INDI 024 PLS 1	INDI 024 PT1	71	Female	Unknown	Lung	II
Non-small cell lung cancer	0.606	Negative					
INDI 025	INDI 025 PLS 1	INDI 025 PT1	86	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.972	Positive					
INDI 026	INDI 026 PLS 1	INDI 026 PT1	81	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.593	Negative					
INDI 027	INDI 027 PLS 1	INDI 027 PT1	89	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.981	Positive					
INDI 028	INDI 028 PLS 1	INDI 028 PT1	79	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.507	Negative					
INDI 029	INDI 029 PLS 1	INDI 029 PT1	53	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.328	Negative					
INDI 030	INDI 030 PLS 1	INDI 030 PT1	82	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.940	Positive					
INDI 031	INDI 031 PLS 1	INDI 031 PT1	66	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.371	Negative					
INDI 032	INDI 032 PLS 1	INDI 032 PT1	41	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.117	Negative					
INDI 034	INDI 034 PLS 1	INDI 034 PT1	88	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.997	Positive					
INDI 035	INDI 035 PLS 1	INDI 035 PT1	71	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.581	Negative					
INDI 036	INDI 036 PLS 1	INDI 036 PT1	66	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.801	Negative					
INDI 037	INDI 037 PLS 1	INDI 037 PT1	86	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.788	Negative					
INDI 038	INDI 038 PLS 1	INDI 038 PT1	65	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.449	Negative					

Table2.txt

INDI 039	INDI 039 PLS 1	INDI 039 PT1	43	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.993	Positive					
INDI 040	INDI 040 PLS 1	INDI 040 PT1	73	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.387	Negative					
INDI 042	INDI 042 PLS 1	INDI 042 PT1	84	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.368	Negative					
INDI 043	INDI 043 PLS 1	INDI 043 PT1	69	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.997	Positive					
INDI 044	INDI 044 PLS 1	INDI 044 PT1	44	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.979	Positive					
INDI 045	INDI 045 PLS 1	INDI 045 PT1	61	Female	Caucasian	Colorectum	III
Adenocarcinoma	1.000	Positive					
INDI 046	INDI 046 PLS 1	INDI 046 PT1	66	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.989	Positive					
INDI 047	INDI 047 PLS 1	INDI 047 PT1	36	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.977	Positive					
INDI 048	INDI 048 PLS 1	INDI 048 PT1	79	Female	Caucasian	Breast	II
Invasive lobular carcinoma	0.639	Negative					
INDI 049	INDI 049 PLS 1	INDI 049 PT1	58	Female	Caucasian	Breast	III
Invasive ductal adenocarcinoma	0.122	Negative					
INDI 050	INDI 050 PLS 1	INDI 050 PT1	44	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.123	Negative					
INDI 051	INDI 051 PLS 1	INDI 051 PT1	73	Female	Caucasian	Breast	III
Invasive ductal adenocarcinoma	0.877	Positive					
INDI 052	INDI 052 PLS 1	INDI 052 PT1	70	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.886	Positive					
INDI 053	INDI 053 PLS 1	INDI 053 PT1	74	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.121	Negative					
INDI 054	INDI 054 PLS 1	INDI 054 PT1	71	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.121	Negative					
INDI 055	INDI 055 PLS 1	INDI 055 PT1	69	Female	Asian	Breast	II
Invasive carcinoma (NOS)	0.404	Negative					

Table2.txt

INDI 056	INDI 056 PLS 1	INDI 056 PT1	50	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.332	Negative
INDI 057	INDI 057 PLS 1	INDI 057 PT1	84	Female	Asian	Breast	III	Invasive lobular carcinoma	0.803	Negative
INDI 058	INDI 058 PLS 1	INDI 058 PT1	46	Female	Asian	Breast	I	Invasive ductal adenocarcinoma	0.620	Negative
INDI 059	INDI 059 PLS 1	INDI 059 PT1	59	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.975	Positive
INDI 060	INDI 060 PLS 1	INDI 060 PT1	51	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.993	Positive
INDI 061	INDI 061 PLS 1	INDI 061 PT1	56	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.961	Positive
INDI 062	INDI 062 PLS 1	INDI 062 PT1	59	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.571	Negative
INDI 063	INDI 063 PLS 1	INDI 063 PT1	59	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.727	Negative
INDI 064	INDI 064 PLS 1	INDI 064 PT1	55	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.938	Positive
INDI 065	INDI 065 PLS 1	INDI 065 PT1	63	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.564	Negative
INDI 066	INDI 066 PLS 1	INDI 066 PT1	62	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.681	Negative
INDI 067	INDI 067 PLS 1	INDI 067 PT1	58	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.997	Positive
INDI 068	INDI 068 PLS 1	INDI 068 PT1	52	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.514	Negative
INDI 069	INDI 069 PLS 1	INDI 069 PT1	59	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.997	Positive
INDI 070	INDI 070 PLS 1	INDI 070 PT1	61	Female	Caucasian	Breast	III	Invasive lobular carcinoma	1.000	Positive
INDI 071	INDI 071 PLS 1	INDI 071 PT1	63	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.972	Positive

Table2.txt

INDI 072	INDI 072 PLS 1	INDI 072 PT1	63	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.986	Positive
INDI 073	INDI 073 PLS 1	INDI 073 PT1	55	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.861	Negative
INDI 074	INDI 074 PLS 1	INDI 074 PT1	78	Male	Caucasian	Pancreas	II	Adenocarcinoma	1.000	Positive
INDI 075	INDI 075 PLS 1	INDI 075 PT1	58	Female	Asian	Ovary	III	Epithelial carcinoma	0.955	Positive
INDI 076	INDI 076 PLS 1	INDI 076 PT1	49	Male	Black	Esophagus	II	Squamous cell carcinoma	0.990	Positive
INDI 077	INDI 077 PLS 1	INDI 077 PT1	77	Male	Caucasian	Liver	II	Hepatocellular carcinoma	1.000	Positive
INDI 078	INDI 078 PLS 1	INDI 078 PT1	56	Male	Caucasian	Liver	II	Hepatocellular carcinoma	0.992	Positive
INDI 079	INDI 079 PLS 1	INDI 079 PT1	42	Male	Asian	Liver	II	Hepatocellular carcinoma	0.999	Positive
INDI 080	INDI 080 PLS 1	INDI 080 PT1	70	Male	Asian	Liver	I	Hepatocellular carcinoma	0.984	Positive
INDI 081	INDI 081 PLS 1	INDI 081 PT1	70	Male	Asian	Colorectum	II	Adenocarcinoma	0.997	Positive
INDI 082	INDI 082 PLS 1	INDI 082 PT1	80	Male	Asian	Stomach	II	Adenocarcinoma	0.117	Negative
INDI 083	INDI 083 PLS 1	INDI 083 PT1	50	Male	Asian	Stomach	II	Adenocarcinoma	0.993	Positive
INDI 084	INDI 084 PLS 1	INDI 084 PT1	78	Female	Asian	Stomach	II	Adenocarcinoma	0.997	Positive
INDI 085	INDI 085 PLS 1	INDI 085 PT1	61	Male	Asian	Stomach	I	Adenocarcinoma	0.940	Positive
INDI 086	INDI 086 PLS 1	INDI 086 PT1	50	Male	Asian	Stomach	I	Adenocarcinoma	0.997	Positive
INDI 087	INDI 087 PLS 1	INDI 087 PT1	39	Female	Asian	Stomach	I	Adenocarcinoma	0.999	Positive

Table2.txt

INDI 089	INDI 089 PLS 1	INDI 089 PT1	59	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.999	Positive			
INDI 090	INDI 090 PLS 1	INDI 090 PT1	72	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.967	Positive			
INDI 092	INDI 092 PLS 1	INDI 092 PT1	64	Male	Caucasian	Stomach
II	Adenocarcinoma	0.848	Negative			
INDI 093	INDI 093 PLS 1	INDI 093 PT1	75	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.997	Positive			
INDI 094	INDI 094 PLS 1	INDI 094 PT1	72	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.993	Positive			
INDI 095	INDI 095 PLS 1	INDI 095 PT1	73	Male	Caucasian	Stomach
II	Adenocarcinoma	0.792	Negative			
INDI 096	INDI 096 PLS 1	INDI 096 PT1	68	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.652	Negative			
INDI 097	INDI 097 PLS 1	INDI 097 PT1	80	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.997	Positive			
INDI 098	INDI 098 PLS 1	INDI 098 PT1	61	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.308	Negative			
INDI 100	INDI 100 PLS 1	INDI 100 PT1	71	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.992	Positive			
INDI 101	INDI 101 PLS 1	INDI 101 PT1	55	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.793	Negative			
INDI 102	INDI 102 PLS 1	INDI 102 PT1	38	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.977	Positive			
INDI 103	INDI 103 PLS 1	INDI 103 PT1	54	Male	Caucasian	Stomach
II	Adenocarcinoma	0.583	Negative			
INDI 104	INDI 104 PLS 1	INDI 104 PT1	63	Male	Caucasian	Stomach
III	Adenocarcinoma	0.983	Positive			
INDI 107	INDI 107 PLS 1	INDI 107 PT1	66	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.975	Positive			
INDI 108	INDI 108 PLS 1	INDI 108 PT1	61	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.984	Positive			

Table2.txt

INDI 109	INDI 109 PLS 1	INDI 109 PT1	68	Female	Asian	Colorectum
III	Adenocarcinoma	0.997	Positive			
INDI 110	INDI 110 PLS 1	INDI 110 PT1	64	Male	Asian	Stomach
I	Adenocarcinoma	0.972	Positive			
INDI 111	INDI 111 PLS 1	INDI 111 PT1	54	Male	Asian	Stomach
II	Adenocarcinoma	0.938	Positive			
INDI 112	INDI 112 PLS 1	INDI 112 PT1	66	Male	Asian	Esophagus
II	Squamous cell carcinoma	1.000	Positive			
INDI 113	INDI 113 PLS 1	INDI 113 PT1	82	Male	Asian	Colorectum
II	Adenocarcinoma	0.998	Positive			
INDI 116	INDI 116 PLS 1	INDI 116 PT1	37	Male	Asian	Stomach
I	Adenocarcinoma	1.000	Positive			
INDI 119	INDI 119 PLS 1	INDI 119 PT1	46	Male	Asian	Esophagus
I	Adenocarcinoma	1.000	Positive			
INDI 120	INDI 120 PLS 1	INDI 120 PT1	74	Female	Asian	Stomach
III	Adenocarcinoma	0.983	Positive			
INDI 121	INDI 121 PLS 1	INDI 121 PT1	41	Male	Asian	Stomach
I	Adenocarcinoma	0.919	Positive			
INDI 122	INDI 122 PLS 1	INDI 122 PT1	24	Female	Asian	Colorectum
II	Adenocarcinoma	0.998	Positive			
INDI 123	INDI 123 PLS 1	INDI 123 PT1	70	Female	Asian	Colorectum
II	Adenocarcinoma	0.996	Positive			
INDI 124	INDI 124 PLS 1	INDI 124 PT1	70	Male	Asian	Colorectum
II	Adenocarcinoma	1.000	Positive			
INDI 125	INDI 125 PLS 1	INDI 125 PT1	55	Male	Asian	Esophagus
II	Squamous cell carcinoma	0.999	Positive			
INDI 126	INDI 126 PLS 1	INDI 126 PT1	60	Male	Asian	Stomach
III	Adenocarcinoma	0.999	Positive			
INDI 127	INDI 127 PLS 1	INDI 127 PT1	62	Male	Asian	Colorectum
II	Adenocarcinoma	1.000	Positive			
INDI 128	INDI 128 PLS 1	INDI 128 PT1	48	Female	Asian	Colorectum
III	Adenocarcinoma	1.000	Positive			

Table2.txt

INDI 129 INDI 129 PLS 1 INDI 129 PT1 63 Female
Asian Liver II Hepatocellular carcinoma
0.999 Positive
INDI 130 INDI 130 PLS 1 INDI 130 PT1 67 Male
Asian Stomach II Adenocarcinoma
0.982 Positive
INDI 131 INDI 131 PLS 1 INDI 131 PT1 79 Male
Asian Stomach II Adenocarcinoma
0.993 Positive
INDI 132 INDI 132 PLS 1 INDI 132 PT1 64 Male
Asian Esophagus III Squamous cell carcinoma
0.918 Positive
INDI 133 INDI 133 PLS 1 INDI 133 PT1 48 Male
Asian Stomach I Adenocarcinoma
0.990 Positive
INDI 134 INDI 134 PLS 1 INDI 134 PT1 49 Male
Asian Stomach III Adenocarcinoma
0.993 Positive
INDI 135 INDI 135 PLS 1 INDI 135 PT1 70 Male
Asian Stomach III Adenocarcinoma
0.999 Positive
INDI 136 INDI 136 PLS 1 INDI 136 PT1 60 Female
Asian Colorectum II Adenocarcinoma
0.984 Positive
INDI 137 INDI 137 PLS 1 INDI 137 PT1 58 Male
Asian Stomach II Adenocarcinoma
0.998 Positive
INDI 139 INDI 139 PLS 1 INDI 139 PT1 65 Female
Asian Stomach III Adenocarcinoma
1.000 Positive
INDI 140 INDI 140 PLS 1 INDI 140 PT1 48 Male
Asian Stomach III Adenocarcinoma
0.992 Positive
INDI 141 INDI 141 PLS 1 INDI 141 PT1 67 Male
Asian Stomach III Adenocarcinoma
0.965 Positive
INDI 143 INDI 143 PLS 1 INDI 143 PT1 35 Male
Asian Colorectum II Adenocarcinoma
0.998 Positive
INDI 144 INDI 144 PLS 1 INDI 144 PT1 51 Female
Asian Colorectum II Adenocarcinoma
1.000 Positive
INDI 145 INDI 145 PLS 1 INDI 145 PT1 70 Male
Asian Colorectum II Adenocarcinoma
0.999 Positive
INDI 146 INDI 146 PLS 1 INDI 146 PT1 65 Male
Asian Colorectum II Adenocarcinoma
0.934 Positive

Table2.txt

INDI 147	INDI 147 PLS 1	INDI 147 PT1	62	Female	Asian	Stomach	II	Adenocarcinoma	0.953	Positive
INDI 148	INDI 148 PLS 1	INDI 148 PT1	72	Male	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 150	INDI 150 PLS 1	INDI 150 PT1	47	Female	Asian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 151	INDI 151 PLS 1	INDI 151 PT1	59	Female	Asian	Stomach	II	Adenocarcinoma	1.000	Positive
INDI 152	INDI 152 PLS 1	INDI 152 PT1	53	Female	Asian	Colorectum	I	Adenocarcinoma	0.988	Positive
INDI 153	INDI 153 PLS 1	INDI 153 PT1	42	Female	Asian	Stomach	II	Adenocarcinoma	0.369	Negative
INDI 155	INDI 155 PLS 1	INDI 155 PT1	60	Male	Asian	Colorectum	II	Adenocarcinoma	0.836	Negative
INDI 156	INDI 156 PLS 1	INDI 156 PT1	56	Male	Asian	Colorectum	III	Adenocarcinoma	1.000	Positive
INDI 158	INDI 158 PLS 1	INDI 158 PT1	70	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.980	Positive
INDI 159	INDI 159 PLS 1	INDI 159 PT1	80	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.852	Negative
INDI 160	INDI 160 PLS 1	INDI 160 PT1	76	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.890	Positive
INDI 161	INDI 161 PLS 1	INDI 161 PT1	57	Male	Caucasian	Stomach	II	Adenocarcinoma	0.920	Positive
INDI 162	INDI 162 PLS 1	INDI 162 PT1	68	Male	Caucasian	Stomach	III	Adenocarcinoma	0.998	Positive
INDI 163	INDI 163 PLS 1	INDI 163 PT1	64	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.934	Positive
INDI 164	INDI 164 PLS 1	INDI 164 PT1	64	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.467	Negative
INDI 165	INDI 165 PLS 1	INDI 165 PT1	69	Male	Caucasian	Colorectum	I	Adenocarcinoma	0.995	Positive

Table2.txt

INDI 167	INDI 167 PLS 1	INDI 167 PT1	45	Male	Asian	Stomach	II
Adenocarcinoma	0.962	Positive					
INDI 168	INDI 168 PLS 1	INDI 168 PT1	51	Male	Asian	Stomach	II
Adenocarcinoma	1.000	Positive					
INDI 169	INDI 169 PLS 1	INDI 169 PT1	41	Female	Asian	Colorectum	III
Adenocarcinoma	0.965	Positive					
INDI 170	INDI 170 PLS 1	INDI 170 PT1	57	Female	Asian	Colorectum	I
Adenocarcinoma	0.992	Positive					
INDI 171	INDI 171 PLS 1	INDI 171 PT1	64	Male	Asian	Stomach	III
Adenocarcinoma	1.000	Positive					
INDI 172	INDI 172 PLS 1	INDI 172 PT1	44	Female	Asian	Stomach	II
Adenocarcinoma	1.000	Positive					
INDI 173	INDI 173 PLS 1	INDI 173 PT1	76	Male	Asian	Stomach	I
Adenocarcinoma	0.999	Positive					
INDI 175	INDI 175 PLS 1	INDI 175 PT1	68	Male	Asian	Colorectum	III
Adenocarcinoma	1.000	Positive					
INDI 176	INDI 176 PLS 1	INDI 176 PT1	61	Male	Asian	Stomach	II
Adenocarcinoma	0.997	Positive					
INDI 177	INDI 177 PLS 1	INDI 177 PT1	42	Female	Asian	Liver	III
Hepatocellular carcinoma	1.000	Positive					
INDI 178	INDI 178 PLS 1	INDI 178 PT1	44	Male	Asian	Colorectum	III
Adenocarcinoma	0.967	Positive					
INDI 179	INDI 179 PLS 1	INDI 179 PT1	57	Male	Asian	Colorectum	III
Adenocarcinoma	0.998	Positive					
INDI 180	INDI 180 PLS 1	INDI 180 PT1	58	Male	Asian	Colorectum	III
Adenocarcinoma	0.921	Positive					
INDI 182	INDI 182 PLS 1	INDI 182 PT1	69	Male	Asian	Liver	III
Hepatocellular carcinoma	1.000	Positive					
INDI 183	INDI 183 PLS 1	INDI 183 PT1	51	Female	Asian	Stomach	I
Adenocarcinoma	0.999	Positive					
INDI 184	INDI 184 PLS 1	INDI 184 PT1	60	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.983	Positive					

Table2.txt

INDI 185 INDI 185 PLS 1 INDI 185 PT1 62 Male
Asian Stomach II Adenocarcinoma
1.000 Positive
INDI 186 INDI 186 PLS 1 INDI 186 PT1 65 Male
Asian Stomach II Adenocarcinoma
1.000 Positive
INDI 187 INDI 187 PLS 1 INDI 187 PT1 74 Female
Asian Stomach I Adenocarcinoma
0.994 Positive
INDI 188 INDI 188 PLS 1 INDI 188 PT1 68 Female
Asian Stomach I Adenocarcinoma
0.983 Positive
INDI 189 INDI 189 PLS 1 INDI 189 PT1 57 Female
Asian Esophagus II Squamous cell carcinoma
1.000 Positive
INDI 190 INDI 190 PLS 1 INDI 190 PT1 52 Male
Asian Liver III Hepatocellular carcinoma
0.988 Positive
INDI 191 INDI 191 PLS 1 INDI 191 PT1 68 Female
Asian Colorectum I Adenocarcinoma
0.947 Positive
INDI 192 INDI 192 PLS 1 INDI 192 PT1 58 Male
Asian Colorectum II Adenocarcinoma
0.992 Positive
INDI 194 INDI 194 PLS 1 INDI 194 PT1 60 Female
Asian Colorectum II Adenocarcinoma
0.968 Positive
INDI 195 INDI 195 PLS 1 INDI 195 PT1 51 Female
Asian Colorectum III Adenocarcinoma
0.966 Positive
INDI 196 INDI 196 PLS 1 INDI 196 PT1 68 Male
Asian Colorectum III Adenocarcinoma
0.955 Positive
INDI 197 INDI 197 PLS 1 INDI 197 PT1 35 Female
Asian Colorectum II Adenocarcinoma
0.998 Positive
INDI 198 INDI 198 PLS 1 INDI 198 PT1 49 Male
Asian Stomach III Adenocarcinoma
1.000 Positive
INDI 199 INDI 199 PLS 1 INDI 199 PT1 82 Male
Asian Stomach II Adenocarcinoma
0.992 Positive
INDI 200 INDI 200 PLS 1 INDI 200 PT1 43 Female
Asian Breast III Invasive ductal adenocarcinoma
0.936 Positive
INDI 202 INDI 202 PLS 1 INDI 202 PT1 52 Male
Asian Colorectum II Adenocarcinoma
0.984 Positive

Table2.txt

INDI 203	INDI 203 PLS 1	INDI 203 PT1	73	Male	Asian	0.995	
Stomach	II	Adenocarcinoma	Positive				
INDI 205	INDI 205 PLS 1	INDI 205 PT1	59	Male	Asian	0.997	
Liver	III	Hepatocellular carcinoma	Positive				
INDI 206	INDI 206 PLS 1	INDI 206 PT1	72	Male	Asian	0.957	
Stomach	III	Adenocarcinoma	Positive				
INDI 207	INDI 207 PLS 1	INDI 207 PT1	52	Female	Asian	1.000	
Colorectum	II	Adenocarcinoma	Positive				
INDI 208	INDI 208 PLS 1	INDI 208 PT1	52	Male	Asian	0.997	
Liver	II	Hepatocellular carcinoma	Positive				
INDI 209	INDI 209 PLS 1	INDI 209 PT1	65	Female	Asian	0.992	
Colorectum	II	Adenocarcinoma	Positive				
INDI 210	INDI 210 PLS 1	INDI 210 PT1	60	Male	Asian	0.991	
Stomach	III	Adenocarcinoma	Positive				
INDI 211	INDI 211 PLS 1	INDI 211 PT1	77	Male	Asian	0.993	
Colorectum	II	Adenocarcinoma	Positive				
INDI 212	INDI 212 PLS 1	INDI 212 PT1	36	Female	Asian	1.000	
Colorectum	III	Adenocarcinoma	Positive				
INDI 213	INDI 213 PLS 1	INDI 213 PT1	44	Female	Asian	0.982	
Colorectum	III	Adenocarcinoma	Positive				
INDI 214	INDI 214 PLS 1	INDI 214 PT1	77	Male	Asian	0.935	
Stomach	II	Adenocarcinoma	Positive				
INDI 215	INDI 215 PLS 1	INDI 215 PT1	65	Female	Asian	0.903	
Liver	II	Hepatocellular carcinoma	Positive				
INDI 216	INDI 216 PLS 1	INDI 216 PT1	58	Male	Caucasian	0.981	
Colorectum	III	Adenocarcinoma	Positive				
INDI 218	INDI 218 PLS 1	INDI 218 PT1	41	Male	Caucasian	0.900	
Colorectum	III	Adenocarcinoma	Positive				
INDI 219	INDI 219 PLS 1	INDI 219 PT1	54	Male	Caucasian	0.994	
Liver	III	Hepatocellular carcinoma	Positive				
INDI 220	INDI 220 PLS 1	Not available	51	Female	Caucasian	0.982	
Lung	I	Non-small cell lung cancer	Positive				

Table2.txt

INDI 221	INDI 221 PLS 1	INDI 221 PT1	77	Male	Caucasian	Colorectum	III	Adenocarcinoma	1.000	Positive
INDI 222	INDI 222 PLS 1	INDI 222 PT1	67	Female	Caucasian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 223	INDI 223 PLS 1	INDI 223 PT1	72	Male	Caucasian	Colorectum	I	Adenocarcinoma	0.501	Negative
INDI 224	INDI 224 PLS 1	INDI 224 PT1	67	Male	Caucasian	Lung	III	Non-small cell lung cancer	1.000	Positive
INDI 225	INDI 225 PLS 1	INDI 225 PT1	70	Male	Caucasian	Colorectum	I	Adenocarcinoma	0.997	Positive
INDI 226	INDI 226 PLS 1	Not available	47	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.117	Negative
INDI 227	INDI 227 PLS 1	INDI 227 PT1	55	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.919	Positive
INDI 228	INDI 228 PLS 1	INDI 228 PT1	68	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.293	Negative
INDI 229	INDI 229 PLS 1	INDI 229 PT1	64	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.968	Positive
INDI 230	INDI 230 PLS 1	INDI 230 PT1	74	Male	Caucasian	Colorectum	I	Adenocarcinoma	0.984	Positive
INDI 231	INDI 231 PLS 1	INDI 231 PT1	54	Female	Caucasian	Lung	III	Non-small cell lung cancer	0.999	Positive
INDI 233	INDI 233 PLS 1	INDI 233 PT1	73	Female	Caucasian	Colorectum	I	Adenocarcinoma	1.000	Positive
INDI 234	INDI 234 PLS 1	INDI 234 PT1	66	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.125	Negative
INDI 236	INDI 236 PLS 1	INDI 236 PT1	72	Male	Caucasian	Stomach	II	Adenocarcinoma	0.117	Negative
INDI 237	INDI 237 PLS 1	Not available	51	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.434	Negative
INDI 238	INDI 238 PLS 1	Not available	67	Female	Caucasian	Liver	II	Hepatocellular carcinoma	0.999	Positive

Table2.txt

INDI 239	INDI 239 PLS 1	INDI 239 PT1	70	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.987	Positive
INDI 241	INDI 241 PLS 1	INDI 241 PT1	79	Male	Caucasian	Stomach	III	Adenocarcinoma	0.370	Negative
INDI 243	INDI 243 PLS 1	INDI 243 PT1	71	Male	Caucasian	Colorectum	I	Adenocarcinoma	0.982	Positive
INDI 244	INDI 244 PLS 1	INDI 244 PT1	85	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.908	Positive
INDI 245	INDI 245 PLS 1	INDI 245 PT1	87	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.998	Positive
INDI 246	INDI 246 PLS 1	INDI 246 PT1	80	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.314	Negative
INDI 247	INDI 247 PLS 1	Not available	72	Female	Caucasian	Lung	I	Non-small cell lung cancer	0.972	Positive
INDI 248	INDI 248 PLS 1	INDI 248 PT1	55	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.453	Negative
INDI 250	INDI 250 PLS 1	Not available	81	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.985	Positive
INDI 251	INDI 251 PLS 1	Not available	81	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.983	Positive
INDI 252	INDI 252 PLS 1	Not available	75	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.994	Positive
INDI 253	INDI 253 PLS 1	Not available	72	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.218	Negative
INDI 255	INDI 255 PLS 1	INDI 255 PT1	64	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.950	Positive
INDI 256	INDI 256 PLS 1	INDI 256 PT1	73	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.991	Positive
INDI 257	INDI 257 PLS 1	INDI 257 PT1	69	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.991	Positive
INDI 258	INDI 258 PLS 1	INDI 258 PT1	64	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.503	Negative

Table2.txt

INDI 259	INDI 259 PLS 1	INDI 259 PT1	78	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.942	Positive			
INDI 260	INDI 260 PLS 1	Not available	73	Female	Caucasian	Stomach
I	Adenocarcinoma	0.256	Negative			
INDI 261	INDI 261 PLS 1	INDI 261 PT1	49	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.123	Negative			
INDI 262	INDI 262 PLS 1	INDI 262 PT1	63	Female	Caucasian	Breast
III	Invasive lobular carcinoma	0.705	Negative			
INDI 264	INDI 264 PLS 1	INDI 264 PT1	54	Female	Caucasian	Lung
III	Non-small cell lung cancer	0.672	Negative			
INDI 265	INDI 265 PLS 1	INDI 265 PT1	50	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.117	Negative			
INDI 266	INDI 266 PLS 1	Not available	69	Male	Caucasian	Lung
I	Non-small cell lung cancer	0.930	Positive			
INDI 267	INDI 267 PLS 1	Not available	74	Male	Caucasian	Esophagus
II	Squamous cell carcinoma	0.767	Negative			
INDI 268	INDI 268 PLS 1	INDI 268 PT1	60	Female	Caucasian	Colorectum
III	Adenocarcinoma	0.995	Positive			
INDI 269	INDI 269 PLS 1	INDI 269 PT1	66	Male	Caucasian	Lung
III	Non-small cell lung cancer	0.618	Negative			
INDI 270	INDI 270 PLS 1	Not available	53	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.125	Negative			
INDI 271	INDI 271 PLS 1	INDI 271 PT1	93	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.609	Negative			
INDI 273	INDI 273 PLS 1	Not available	71	Female	Caucasian	Lung
I	Non-small cell lung cancer	0.998	Positive			
INDI 274	INDI 274 PLS 1	Not available	78	Female	Caucasian	Breast
II	Invasive lobular carcinoma	0.125	Negative			
INDI 275	INDI 275 PLS 1	Not available	46	Female	Caucasian	Breast
II	Invasive lobular carcinoma	0.335	Negative			
INDI 276	INDI 276 PLS 1	Not available	63	Male	Caucasian	Liver
II	Cholangiocarcinoma	1.000	Positive			

Table2.txt

INDI 277	INDI 277 PLS 1	Not available	72	Male	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.116	Negative					
INDI 278	INDI 278 PLS 1	Not available	57	Female	Caucasian	Ovary	III
Epithelial carcinoma	0.984	Positive					
INDI 279	INDI 279 PLS 1	INDI 279 PT1	87	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.967	Positive					
INDI 280	INDI 280 PLS 1	INDI 280 PT1	72	Female	Unknown	Breast	I
Invasive ductal adenocarcinoma	0.347	Negative					
INDI 281	INDI 281 PLS 1	INDI 281 PT1	78	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.724	Negative					
INDI 283	INDI 283 PLS 1	INDI 283 PT1	73	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.593	Negative					
INDI 284	INDI 284 PLS 1	INDI 284 PT1	75	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.918	Positive					
INDI 285	INDI 285 PLS 1	INDI 285 PT1	57	Female	Caucasian	Lung	II
Non-small cell lung cancer	0.998	Positive					
INDI 286	INDI 286 PLS 1	Not available	49	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.620	Negative					
INDI 287	INDI 287 PLS 1	INDI 287 PT1	52	Female	Caucasian	Breast	III
Invasive ductal adenocarcinoma	0.996	Positive					
INDI 288	INDI 288 PLS 1	INDI 288 PT1	75	Female	Caucasian	Lung	III
Non-small cell lung cancer	1.000	Positive					
INDI 289	INDI 289 PLS 1	INDI 289 PT1	55	Female	Caucasian	Breast	II
Invasive lobular carcinoma	0.521	Negative					
INDI 290	INDI 290 PLS 1	INDI 290 PT1	70	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.896	Positive					
INDI 291	INDI 291 PLS 1	INDI 291 PT1	71	Male	Asian	Lung	I
Non-small cell lung cancer	0.804	Negative					
INDI 292	INDI 292 PLS 1	INDI 292 PT1	73	Female	Asian	Lung	III
Non-small cell lung cancer	0.772	Negative					
INDI 293	INDI 293 PLS 1	Not available	81	Female	Asian	Colorectum	II
Adenocarcinoma	0.996	Positive					

Table2.txt

INDI 295	INDI 295 PLS 1	INDI 295 PT1	59	Female	Caucasian	Colorectum	Positive
II	Adenocarcinoma	0.939					
INDI 296	INDI 296 PLS 1	INDI 296 PT1	43	Female	Caucasian	Colorectum	Positive
II	Adenocarcinoma	0.940					
INDI 297	INDI 297 PLS 1	INDI 297 PT1	42	Female	Caucasian	Breast	Positive
III	Invasive ductal adenocarcinoma	0.896					
INDI 298	INDI 298 PLS 1	INDI 298 PT1	42	Female	Caucasian	Colorectum	Positive
I	Adenocarcinoma	0.886					
INDI 299	INDI 299 PLS 1	INDI 299 PT1	73	Male	Caucasian	Colorectum	Positive
I	Adenocarcinoma	0.924					
INDI 300	INDI 300 PLS 1	INDI 300 PT1	47	Female	Caucasian	Breast	Positive
III	Invasive ductal adenocarcinoma	0.917					
INDI 301	INDI 301 PLS 1	INDI 301 PT1	47	Female	Caucasian	Breast	Positive
II	Invasive ductal adenocarcinoma	0.989					
INDI 302	INDI 302 PLS 1	INDI 302 PT1	69	Male	Caucasian	Colorectum	Positive
I	Adenocarcinoma	0.960					
INDI 303	INDI 303 PLS 1	INDI 303 PT1	66	Male	Caucasian	Colorectum	Positive
I	Adenocarcinoma	0.955					
INDI 304	INDI 304 PLS 1	INDI 304 PT1	53	Male	Caucasian	Colorectum	Positive
I	Adenocarcinoma	0.997					
INDI 305	INDI 305 PLS 1	INDI 305 PT1	55	Male	Caucasian	Colorectum	Positive
II	Adenocarcinoma	1.000					
INDI 306	INDI 306 PLS 1	INDI 306 PT1	66	Male	Caucasian	Colorectum	Positive
III	Adenocarcinoma	1.000					
INDI 307	INDI 307 PLS 1	INDI 307 PT1	64	Male	Caucasian	Colorectum	Positive
III	Adenocarcinoma	0.944					
INDI 308	INDI 308 PLS 1	INDI 308 PT1	39	Male	Asian	Liver	Positive
II	Hepatocellular carcinoma	0.974					
INDI 309	INDI 309 PLS 1	INDI 309 PT1	39	Male	Asian	Colorectum	Positive
II	Adenocarcinoma	0.913					
INDI 310	INDI 310 PLS 1	INDI 310 PT1	78	Male	Asian	Colorectum	Positive
II	Adenocarcinoma	0.999					

Table2.txt

INDI 311	INDI 311 PLS 1	INDI 311 PT1	52	Female	Asian	Colorectum	III
Adenocarcinoma	0.977	Positive					
INDI 312	INDI 312 PLS 1	INDI 312 PT1	56	Female	Asian	Breast	II
Invasive ductal adenocarcinoma	0.751	Negative					
INDI 313	INDI 313 PLS 1	INDI 313 PT1	43	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.939	Positive					
INDI 314	INDI 314 PLS 1	INDI 314 PT1	46	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.982	Positive					
INDI 315	INDI 315 PLS 1	INDI 315 PT1	64	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.123	Negative					
INDI 316	INDI 316 PLS 1	INDI 316 PT1	43	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.123	Negative					
INDI 317	INDI 317 PLS 1	INDI 317 PT1	37	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.116	Negative					
INDI 318	INDI 318 PLS 1	INDI 318 PT1	76	Male	Caucasian	Stomach	III
Adenocarcinoma	0.997	Positive					
INDI 319	INDI 319 PLS 1	INDI 319 PT1	76	Male	Caucasian	Stomach	I
Adenocarcinoma	0.374	Negative					
INDI 320	INDI 320 PLS 1	INDI 320 PT1	51	Male	Caucasian	Colorectum	II
Adenocarcinoma	1.000	Positive					
INDI 321	INDI 321 PLS 1	INDI 321 PT1	64	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.836	Negative					
INDI 322	INDI 322 PLS 1	INDI 322 PT1	61	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.930	Positive					
INDI 323	INDI 323 PLS 1	INDI 323 PT1	44	Female	Caucasian	Breast	I
Invasive ductal adenocarcinoma	0.125	Negative					
INDI 324	INDI 324 PLS 1	INDI 324 PT1	58	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.877	Positive					
INDI 325	INDI 325 PLS 1	INDI 325 PT1	58	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.933	Positive					
INDI 326	INDI 326 PLS 1	INDI 326 PT1	54	Male	Caucasian	Lung	I
Non-small cell lung cancer	0.992	Positive					

Table2.txt

INDI 327	INDI 327 PLS 1	INDI 327 PT1	71	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.954	Positive
INDI 328	INDI 328 PLS 1	INDI 328 PT1	71	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.993	Positive
INDI 329	INDI 329 PLS 1	INDI 329 PT1	87	Female	Caucasian	Colorectum	III	Adenocarcinoma	1.000	Positive
INDI 331	INDI 331 PLS 1A	INDI 331 PT1	55	Female	Caucasian	Lung	III	Non-small cell lung cancer	1.000	Positive
INDI 332	INDI 332 PLS 1	INDI 332 PT1	65	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.369	Negative
INDI 333	INDI 333 PLS 1A	INDI 333 PT1	72	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.473	Negative
INDI 334	INDI 334 PLS 1	INDI 334 PT1	85	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.622	Negative
INDI 335	INDI 335 PLS 1A	INDI 335 PT1	55	Female	Caucasian	Lung	I	Non-small cell lung cancer	0.929	Positive
INDI 336	INDI 336 PLS 1A	INDI 336 PT1	71	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.995	Positive
INDI 337	INDI 337 PLS 1	INDI 337 PT1	44	Male	Caucasian	Esophagus	III	Adenocarcinoma	0.235	Negative
INDI 338	INDI 338 PLS 1	INDI 338 PT1	90	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.971	Positive
INDI 339	INDI 339 PLS 1	INDI 339 PT1	52	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.121	Negative
INDI 340	INDI 340 PLS 1	INDI 340 PT1	83	Male	Caucasian	Colorectum	III	Adenocarcinoma	1.000	Positive
INDI 341	INDI 341 PLS 1	INDI 341 PT1	74	Female	Caucasian	Liver	II	Cholangiocarcinoma	0.998	Positive
INDI 342	INDI 342 PLS 1A	INDI 342 PT1	82	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.125	Negative
INDI 343	INDI 343 PLS 1	INDI 343 PT1	54	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.573	Negative

Table2.txt

INDI 344	INDI 344 PLS 1	INDI 344 PT1	73	Male	Caucasian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 346	INDI 346 PLS 1A	INDI 346 PT1	57	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.916	Positive
INDI 347	INDI 347 PLS 1	INDI 347 PT1	57	Male	Caucasian	Esophagus	I	Squamous cell carcinoma	0.650	Negative
INDI 348	INDI 348 PLS 1	INDI 348 PT1	44	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.242	Negative
INDI 350	INDI 350 PLS 1	INDI 350 PT1	50	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.610	Negative
INDI 352	INDI 352 PLS 1	INDI 352 PT1	51	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.122	Negative
INDI 353	INDI 353 PLS 1A	INDI 353 PT1	66	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.998	Positive
INDI 354	INDI 354 PLS 1	INDI 354 PT1	69	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.989	Positive
INDI 355	INDI 355 PLS 1A	INDI 355 PT1	73	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.863	Positive
INDI 356	INDI 356 PLS 1	INDI 356 PT1	84	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.883	Positive
INDI 357	INDI 357 PLS 1A	INDI 357 PT1	73	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.580	Negative
INDI 358	INDI 358 PLS 1A	INDI 358 PT1	64	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.686	Negative
INDI 359	INDI 359 PLS 1	INDI 359 PT1	67	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.850	Negative
INDI 360	INDI 360 PLS 1A	INDI 360 PT1	59	Female	Caucasian	Lung	II	Non-small cell lung cancer	0.985	Positive
INDI 361	INDI 361 PLS 1	INDI 361 PT1	74	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.324	Negative
INDI 362	INDI 362 PLS 1	INDI 362 PT1	46	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.304	Negative

Table2.txt

INDI 363	INDI 363 PLS 1	INDI 363 PT1	74	Female	Caucasian	Breast	I
Invasive ductal adenocarcinoma	0.121	Negative					
INDI 364	INDI 364 PLS 1A	INDI 364 PT1	72	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.856	Negative					
INDI 365	INDI 365 PLS 1	INDI 365 PT1	69	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.995	Positive					
INDI 366	INDI 366 PLS 1	INDI 366 PT1	74	Female	Caucasian	Pancreas	II
Adenocarcinoma	0.998	Positive					
INDI 367	INDI 367 PLS 1	INDI 367 PT1	72	Male	Caucasian	Liver	I
Hepatocellular carcinoma	0.965	Positive					
INDI 368	INDI 368 PLS 1	INDI 368 PT1	66	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	1.000	Positive					
INDI 369	INDI 369 PLS 1A	INDI 369 PT1	81	Male	Caucasian	Lung	I
Non-small cell lung cancer	0.553	Negative					
INDI 371	INDI 371 PLS 1A	INDI 371 PT1	63	Male	Caucasian	Lung	III
Non-small cell lung cancer	0.998	Positive					
INDI 372	INDI 372 PLS 1A	INDI 372 PT1	67	Female	Caucasian	Lung	II
Non-small cell lung cancer	0.995	Positive					
INDI 373	INDI 373 PLS 1A	INDI 373 PT1	72	Male	Caucasian	Lung	I
Non-small cell lung cancer	0.842	Negative					
INDI 374	INDI 374 PLS 1	INDI 374 PT1	51	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.956	Positive					
INDI 375	INDI 375 PLS 1	INDI 375 PT1	51	Male	Caucasian	Liver	I
Hepatocellular carcinoma	0.970	Positive					
INDI 376	INDI 376 PLS 1	INDI 376 PT1	59	Male	Unknown	Colorectum	I
Adenocarcinoma	0.298	Negative					
INDI 377	INDI 377 PLS 1	INDI 377 PT1	64	Female	Caucasian	Colorectum	II
Adenocarcinoma	1.000	Positive					
INDI 378	INDI 378 PLS 1	INDI 378 PT1	87	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.155	Negative					
INDI 379	INDI 379 PLS 1	INDI 379 PT1	69	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.312	Negative					

Table2.txt

INDI 380	INDI 380 PLS 1	INDI 380 PT1	92	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.997	Positive					
INDI 381	INDI 381 PLS 1A	INDI 381 PT1	54	Male	Caucasian	Lung	III
Non-small cell lung cancer	0.640	Negative					
INDI 382	INDI 382 PLS 1	INDI 382 PT1	73	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.498	Negative					
INDI 383	INDI 383 PLS 1A	INDI 383 PT1	54	Male	Caucasian	Lung	III
Non-small cell lung cancer	0.976	Positive					
INDI 384	INDI 384 PLS 1	INDI 384 PT1	54	Male	Caucasian	Pancreas	II
Adenocarcinoma	0.596	Negative					
INDI 385	INDI 385 PLS 1	INDI 385 PT1	87	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.629	Negative					
INDI 386	INDI 386 PLS 1	INDI 386 PT1	42	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.121	Negative					
INDI 387	INDI 387 PLS 1	INDI 387 PT1	62	Male	Caucasian	Liver	I
Hepatocellular carcinoma	0.955	Positive					
INDI 388	INDI 388 PLS 1	INDI 388 PT1	77	Male	Caucasian	Pancreas	II
Adenocarcinoma	0.992	Positive					
INDI 389	INDI 389 PLS 1A	INDI 389 PT1	57	Female	Caucasian	Lung	III
Non-small cell lung cancer	0.992	Positive					
INDI 390	INDI 390 PLS 1	INDI 390 PT1	79	Male	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.578	Negative					
INDI 391	INDI 391 PLS 1	INDI 391 PT1	46	Female	Caucasian	Liver	II
Cholangiocarcinoma	1.000	Positive					
INDI 392	INDI 392 PLS 1A	INDI 392 PT1	57	Male	Caucasian	Lung	I
Non-small cell lung cancer	0.326	Negative					
INDI 393	INDI 393 PLS 1	INDI 393 PT1	66	Male	Unknown	Liver	II
Hepatocellular carcinoma	0.911	Positive					
INDI 394	INDI 394 PLS 1A	INDI 394 PT1	77	Male	Unknown	Lung	II
Non-small cell lung cancer	0.960	Positive					
INDI 395	INDI 395 PLS 1A	INDI 395 PT1	79	Female	Caucasian	Lung	I
Non-small cell lung cancer	0.855	Negative					

Table2.txt

INDI 396	INDI 396 PLS 1	INDI 396 PT1	59	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.965	Positive			
INDI 397	INDI 397 PLS 1	INDI 397 PT1	55	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.987	Positive			
INDI 398	INDI 398 PLS 1	INDI 398 PT1	91	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.495	Negative			
INDI 400	INDI 400 PLS 1	INDI 400 PT1	80	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.980	Positive			
INDI 402	INDI 402 PLS 1	Not available	47	Female	Caucasian	Breast
I	Invasive lobular carcinoma	0.322	Negative			
INDI 403	INDI 403 PLS 1A	Not available	63	Male	Caucasian	Lung
III	Non-small cell lung cancer	0.569	Negative			
INDI 404	INDI 404 PLS 1	Not available	58	Female	Caucasian	Breast
III	Invasive lobular carcinoma	0.121	Negative			
INDI 405	INDI 405 PLS 1A	Not available	64	Male	Caucasian	Lung
I	Non-small cell lung cancer	0.829	Negative			
INDI 407	INDI 407 PLS 1	Not available	47	Female	Caucasian	Breast
I	Invasive ductal adenocarcinoma	0.300	Negative			
INDI 408	INDI 408 PLS 1	Not available	47	Female	Caucasian	Breast
II	Invasive carcinoma (NOS)	0.117	Negative			
INDI 409	INDI 409 PLS 1	Not available	65	Female	Caucasian	Breast
II	Invasive lobular carcinoma	0.238	Negative			
INDI 411	INDI 411 PLS 1	Not available	63	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.312	Negative			
INDI 412	INDI 412 PLS 1	Not available	50	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.945	Positive			
INDI 413	INDI 413 PLS 1	Not available	65	Female	Caucasian	Lung
I	Non-small cell lung cancer	0.877	Positive			
INDI 414	INDI 414 PLS 1	Not available	71	Male	Asian	Lung
II	Non-small cell lung cancer	0.620	Negative			
INDI 415	INDI 415 PLS 1	Not available	63	Male	Asian	Lung
II	Non-small cell lung cancer	0.979	Positive			

Table2.txt

INDI 417	INDI 417 PLS 1	Not available	68	Male	Asian	Lung	I
Non-small cell lung cancer	0.883	Positive					
INDI 418	INDI 418 PLS 1	INDI 418 PT1	63	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.953	Positive					
INDI 419	INDI 419 PLS 1	INDI 419 PT1	56	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.813	Negative					
INDI 421	INDI 421 PLS 1	INDI 421 PT1	67	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.683	Negative					
INDI 422	INDI 422 PLS 1	INDI 422 PT1	79	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.994	Positive					
INDI 423	INDI 423 PLS 1	INDI 423 PT1	65	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.991	Positive					
INDI 424	INDI 424 PLS 1	INDI 424 PT1	68	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.413	Negative					
INDI 425	INDI 425 PLS 1	Not available	45	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.690	Negative					
INDI 426	INDI 426 PLS 1	INDI 426 PT1	57	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.666	Negative					
INDI 427	INDI 427 PLS 1	INDI 427 PT1	73	Female	Caucasian	Colorectum	II
Adenocarcinoma	1.000	Positive					
INDI 428	INDI 428 PLS 1	INDI 428 PT1	65	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.774	Negative					
INDI 429	INDI 429 PLS 1	Not available	65	Female	Caucasian	Colorectum	II
Adenocarcinoma	1.000	Positive					
INDI 431	INDI 431 PLS 1	INDI 431 PT1	57	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.711	Negative					
INDI 433	INDI 433 PLS 1	INDI 433 PT1	62	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.985	Positive					
INDI 434	INDI 434 PLS 1	INDI 434 PT1	73	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.817	Negative					
INDI 436	INDI 436 PLS 1	INDI 436 PT1	59	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.697	Negative					

Table2.txt

INDI 437	INDI 437 PLS 1	INDI 437 PT1	74	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.950	Positive					
INDI 438	INDI 438 PLS 1	INDI 438 PT1	59	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.777	Negative					
INDI 439	INDI 439 PLS 1	INDI 439 PT1	72	Male	Asian	Colorectum	III
Adenocarcinoma	1.000	Positive					
INDI 440	INDI 440 PLS 1	INDI 440 PT1	48	Male	Asian	Esophagus	II
Adenocarcinoma	0.996	Positive					
INDI 441	INDI 441 PLS 1	INDI 441 PT1	61	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.980	Positive					
INDI 442	INDI 442 PLS 1	INDI 442 PT1	41	Female	Asian	Breast	II
Invasive ductal adenocarcinoma	0.956	Positive					
INDI 443	INDI 443 PLS 1	INDI 443 PT1	62	Female	Asian	Breast	II
Invasive carcinoma (NOS)	0.878	Positive					
INDI 444	INDI 444 PLS 1	INDI 444 PT1	64	Male	Asian	Colorectum	II
Adenocarcinoma	0.993	Positive					
INDI 445	INDI 445 PLS 1	INDI 445 PT1	47	Female	Asian	Breast	II
Invasive ductal adenocarcinoma	1.000	Positive					
INDI 446	INDI 446 PLS 1	Not available	52	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.999	Positive					
INDI 447	INDI 447 PLS 1	INDI 447 PT1	33	Female	Asian	Breast	III
Invasive ductal adenocarcinoma	1.000	Positive					
INDI 449	INDI 449 PLS 1	INDI 449 PT1	46	Female	Asian	Breast	III
Invasive ductal adenocarcinoma	0.985	Positive					
INDI 450	INDI 450 PLS 1	INDI 450 PT1	60	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.993	Positive					
INDI 452	INDI 452 PLS 1	Not available	72	Male	Asian	Colorectum	II
Adenocarcinoma	0.999	Positive					
INDI 453	INDI 453 PLS 1	INDI 453 PT1	69	Female	Asian	Breast	I
Invasive ductal adenocarcinoma	0.900	Positive					
INDI 454	INDI 454 PLS 1	INDI 454 PT1	54	Female	Asian	Breast	III
Invasive ductal adenocarcinoma	0.901	Positive					

Table2.txt

INDI 455	INDI 455 PLS 1	INDI 455 PT1	52	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.855	Negative
INDI 456	INDI 456 PLS 1	INDI 456 PT1	59	Female	Asian	Colorectum	II	Adenocarcinoma	0.994	Positive
INDI 457	INDI 457 PLS 1	INDI 457 PT1	59	Male	Asian	Esophagus	II	Squamous cell carcinoma	1.000	Positive
INDI 458	INDI 458 PLS 1	INDI 458 PT1	46	Female	Asian	Breast	III	Invasive carcinoma (NOS)	0.999	Positive
INDI 459	INDI 459 PLS 1	INDI 459 PT1	45	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	1.000	Positive
INDI 460	INDI 460 PLS 1	INDI 460 PT1	39	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.380	Negative
INDI 461	INDI 461 PLS 1	INDI 461 PT1	49	Male	Asian	Colorectum	III	Adenocarcinoma	0.989	Positive
INDI 462	INDI 462 PLS 1	INDI 462 PT1	54	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	1.000	Positive
INDI 463	INDI 463 PLS 1	INDI 463 PT1	33	Female	Asian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 464	INDI 464 PLS 1	INDI 464 PT1	67	Male	Asian	Liver	III	Cholangiocarcinoma	1.000	Positive
INDI 465	INDI 465 PLS 1	INDI 465 PT1	45	Male	Asian	Esophagus	II	Squamous cell carcinoma	1.000	Positive
INDI 466	INDI 466 PLS 1	INDI 466 PT1	60	Female	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 467	INDI 467 PLS 1	INDI 467 PT1	82	Female	Asian	Colorectum	II	Adenocarcinoma	0.972	Positive
INDI 468	INDI 468 PLS 1	INDI 468 PT1	62	Female	Asian	Colorectum	II	Adenocarcinoma	0.971	Positive
INDI 469	INDI 469 PLS 1	INDI 469 PT1	37	Female	Asian	Breast	III	Invasive lobular carcinoma	0.695	Negative
INDI 470	INDI 470 PLS 1	INDI 470 PT1	60	Female	Asian	Colorectum	III	Adenocarcinoma	0.988	Positive

Table2.txt

INDI 471	INDI 471 PLS 1	INDI 471 PT1	46	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.123	Negative
INDI 472	INDI 472 PLS 1	INDI 472 PT1	51	Female	Asian	Colorectum	II	Adenocarcinoma	0.991	Positive
INDI 473	INDI 473 PLS 1	INDI 473 PT1	30	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.880	Positive
INDI 474	INDI 474 PLS 1	INDI 474 PT1	72	Female	Asian	Breast	II	Invasive carcinoma (NOS)	0.989	Positive
INDI 475	INDI 475 PLS 1	INDI 475 PT1	62	Male	Asian	Liver	III	Hepatocellular carcinoma	0.993	Positive
INDI 476	INDI 476 PLS 1	INDI 476 PT1	30	Male	Asian	Esophagus	II	Squamous cell carcinoma	0.996	Positive
INDI 477	INDI 477 PLS 1	INDI 477 PT1	30	Male	Asian	Colorectum	III	Adenocarcinoma	0.928	Positive
INDI 478	INDI 478 PLS 1	INDI 478 PT1	54	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.982	Positive
INDI 479	INDI 479 PLS 1	INDI 479 PT1	29	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.824	Negative
INDI 480	INDI 480 PLS 1	INDI 480 PT1	60	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.932	Positive
INDI 482	INDI 482 PLS 1	INDI 482 PT1	74	Female	Caucasian	Liver	II	Hepatocellular carcinoma	0.999	Positive
INDI 483	INDI 483 PLS 1	INDI 483 PT1	54	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.552	Negative
INDI 484	INDI 484 PLS 1	INDI 484 PT1	86	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.528	Negative
INDI 485	INDI 485 PLS 1	INDI 485 PT1	53	Male	Caucasian	Esophagus	III	Adenocarcinoma	0.448	Negative
INDI 487	INDI 487 PLS 1	INDI 487 PT1	72	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.117	Negative
INDI 488	INDI 488 PLS 1	Not available	48	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.848	Negative

Table2.txt

INDI 489	INDI 489 PLS 1	INDI 489 PT1	60	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.943	Positive
INDI 490	INDI 490 PLS 1	INDI 490 PT1	70	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	1.000	Positive
INDI 491	INDI 491 PLS 1	INDI 491 PT1	70	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.615	Negative
INDI 492	INDI 492 PLS 1	INDI 492 PT1	65	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.572	Negative
INDI 493	INDI 493 PLS 1	INDI 493 PT1	41	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.116	Negative
INDI 494	INDI 494 PLS 1	INDI 494 PT1	83	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.997	Positive
INDI 495	INDI 495 PLS 1	INDI 495 PT1	60	Female	Caucasian	Lung	I	Non-small cell lung cancer	0.122	Negative
INDI 497	INDI 497 PLS 1	INDI 497 PT1	68	Male	Caucasian	Lung	II	Small cell	0.509	Negative
INDI 498	INDI 498 PLS 1	INDI 498 PT1	62	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.524	Negative
INDI 499	INDI 499 PLS 1	Not available	60	Female	Caucasian	Lung	I	Non-small cell lung cancer	0.642	Negative
INDI 501	INDI 501 PLS 1	INDI 501 PT1	56	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.125	Negative
INDI 502	INDI 502 PLS 1	INDI 502 PT1	61	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.858	Negative
INDI 503	INDI 503 PLS 1	Not available	67	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.923	Positive
INDI 504	INDI 504 PLS 1	INDI 504 PT1	44	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.122	Negative
INDI 505	INDI 505 PLS 1	INDI 505 PT1	77	Male	Caucasian	Lung	II	Non-small cell lung cancer	1.000	Positive
INDI 506	INDI 506 PLS 1	INDI 506 PT1	80	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.947	Positive

Table2.txt

INDI 507	INDI 507 PLS 1	INDI 507 PT1	57	Male	Caucasian	Lung	II	Non-small cell lung cancer
0.991	Positive							
INDI 508	INDI 508 PLS 1	INDI 508 PT1	46	Male	Caucasian	Colorectum	III	Adenocarcinoma
0.122	Negative							
INDI 511	INDI 511 PLS 1	INDI 511 PT1	52	Male	Caucasian	Colorectum	III	Adenocarcinoma
0.637	Negative							
INDI 512	INDI 512 PLS 1	INDI 512 PT1	47	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma
0.761	Negative							
INDI 513	INDI 513 PLS 1	INDI 513 PT1	55	Female	Caucasian	Lung	I	Non-small cell lung cancer
0.502	Negative							
INDI 514	INDI 514 PLS 1	INDI 514 PT1	73	Male	Caucasian	Stomach	I	Adenocarcinoma
0.991	Positive							
INDI 515	INDI 515 PLS 1	INDI 515 PT1	85	Male	Caucasian	Colorectum	III	Adenocarcinoma
0.983	Positive							
INDI 516	INDI 516 PLS 1	INDI 516 PT1	75	Male	Caucasian	Pancreas	II	Adenocarcinoma
0.999	Positive							
INDI 517	INDI 517 PLS 1	INDI 517 PT1	75	Male	Caucasian	Breast	III	Invasive ductal adenocarcinoma
0.588	Negative							
INDI 518	INDI 518 PLS 1	INDI 518 PT1	60	Male	Caucasian	Colorectum	III	Adenocarcinoma
0.898	Positive							
INDI 519	INDI 519 PLS 1	INDI 519 PT1	80	Male	Caucasian	Lung	I	Non-small cell lung cancer
0.852	Negative							
INDI 521	INDI 521 PLS 1	INDI 521 PT1	75	Female	Caucasian	Colorectum	II	Adenocarcinoma
0.933	Positive							
INDI 522	INDI 522 PLS 1	INDI 522 PT1	76	Male	Caucasian	Lung	I	Non-small cell lung cancer
0.208	Negative							
INDI 523	INDI 523 PLS 1	INDI 523 PT1	84	Male	Caucasian	Colorectum	I	Adenocarcinoma
0.997	Positive							
INDI 524	INDI 524 PLS 1	INDI 524 PT1	73	Male	Caucasian	Lung	III	Non-small cell lung cancer
0.982	Positive							
INDI 525	INDI 525 PLS 1	INDI 525 PT1	75	Male	Unknown	Colorectum	I	Adenocarcinoma
0.978	Positive							

Table2.txt

INDI 526	INDI 526 PLS 1	INDI 526 PT1	79	Male	Caucasian	Esophagus	Positive
0.975							
INDI 527	INDI 527 PLS 1	INDI 527 PT1	72	Female	Caucasian	Colorectum	Positive
0.932							
INDI 528	INDI 528 PLS 1	Not available	48	Male	Caucasian	Colorectum	Positive
0.950							
INDI 529	INDI 529 PLS 1	INDI 529 PT1	71	Male	Caucasian	Colorectum	Negative
0.505							
INDI 530	INDI 530 PLS 1	INDI 530 PT1	53	Female	Caucasian	Breast	Negative
0.421							
INDI 532	INDI 532 PLS 1	INDI 532 PT1	71	Male	Unknown	Lung	Negative
0.813							
INDI 533	INDI 533 PLS 1	INDI 533 PT1	77	Male	Caucasian	Pancreas	Positive
0.909							
INDI 534	INDI 534 PLS 1	INDI 534 PT1	47	Female	Caucasian	Stomach	Negative
0.421							
INDI 535	INDI 535 PLS 1	INDI 535 PT1	78	Male	Caucasian	Lung	Positive
0.966							
INDI 537	INDI 537 PLS 1	INDI 537 PT1	52	Female	Caucasian	Ovary	Negative
0.644							
INDI 538	INDI 538 PLS 1	INDI 538 PT1	43	Male	Caucasian	Lung	Positive
0.959							
INDI 539	INDI 539 PLS 1	INDI 539 PT1	73	Female	Caucasian	Colorectum	Positive
0.991							
INDI 540	INDI 540 PLS 1	INDI 540 PT1	83	Female	Caucasian	Breast	Negative
0.630							
INDI 541	INDI 541 PLS 1	Not available	44	Female	Caucasian	Breast	Negative
0.571							
INDI 544	INDI 544 PLS 1	INDI 544 PT1	44	Male	Caucasian	Colorectum	Positive
1.000							
INDI 545	INDI 545 PLS 1	INDI 545 PT1	71	Female	Caucasian	Lung	Positive
0.950							

INDI 526	INDI 526 PLS 1	INDI 526 PT1	79	Male
Caucasian	Esophagus	III	Adenocarcinoma	
0.975	Positive			
INDI 527	INDI 527 PLS 1	INDI 527 PT1	72	Female
Caucasian	Colorectum	III	Adenocarcinoma	
0.932	Positive			
INDI 528	INDI 528 PLS 1	Not available	48	Male
Caucasian	Colorectum	II	Adenocarcinoma	
0.950	Positive			
INDI 529	INDI 529 PLS 1	INDI 529 PT1	71	Male
Caucasian	Colorectum	I	Adenocarcinoma	
0.505	Negative			
INDI 530	INDI 530 PLS 1	INDI 530 PT1	53	Female
Caucasian	Breast	I	Invasive ductal adenocarcinoma	
0.421	Negative			
INDI 532	INDI 532 PLS 1	INDI 532 PT1	71	Male
Unknown	Lung	I	Non-small cell lung cancer	
0.813	Negative			
INDI 533	INDI 533 PLS 1	INDI 533 PT1	77	Male
Caucasian	Pancreas	II	Adenocarcinoma	
0.909	Positive			
INDI 534	INDI 534 PLS 1	INDI 534 PT1	47	Female
Caucasian	Stomach	III	Adenocarcinoma	
0.421	Negative			
INDI 535	INDI 535 PLS 1	INDI 535 PT1	78	Male
Caucasian	Lung	I	Non-small cell lung cancer	
0.966	Positive			
INDI 537	INDI 537 PLS 1	INDI 537 PT1	52	Female
Caucasian	Ovary	I	Epithelial carcinoma	
0.644	Negative			
INDI 538	INDI 538 PLS 1	INDI 538 PT1	43	Male
Caucasian	Lung	III	Non-small cell lung cancer	
0.959	Positive			
INDI 539	INDI 539 PLS 1	INDI 539 PT1	73	Female
Caucasian	Colorectum	II	Adenocarcinoma	
0.991	Positive			
INDI 540	INDI 540 PLS 1	INDI 540 PT1	83	Female
Caucasian	Breast	II	Invasive ductal adenocarcinoma	
0.630	Negative			
INDI 541	INDI 541 PLS 1	Not available	44	Female
Caucasian	Breast	II	Invasive ductal adenocarcinoma	
0.571	Negative			
INDI 544	INDI 544 PLS 1	INDI 544 PT1	44	Male
Caucasian	Colorectum	III	Adenocarcinoma	
1.000	Positive			
INDI 545	INDI 545 PLS 1	INDI 545 PT1	71	Female
Caucasian	Lung	I	Non-small cell lung cancer	
0.950	Positive			

Table2.txt

INDI 546	INDI 546 PLS 1	INDI 546 PT1	76	Female	Caucasian	Lung	II
Non-small cell lung cancer	0.837	Negative					
INDI 547	INDI 547 PLS 1	INDI 547 PT1	55	Male	Caucasian	Stomach	III
Adenocarcinoma	0.125	Negative					
INDI 548	INDI 548 PLS 1	INDI 548 PT1	82	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.951	Positive					
INDI 549	INDI 549 PLS 1	INDI 549 PT1	74	Female	Caucasian	Lung	III
Non-small cell lung cancer	0.898	Positive					
INDI 550	INDI 550 PLS 1	INDI 550 PT1	52	Male	Caucasian	Lung	III
Non-small cell lung cancer	0.568	Negative					
INDI 551	INDI 551 PLS 1	INDI 551 PT1	68	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.866	Positive					
INDI 555	INDI 555 PLS 1	INDI 555 PT1	74	Male	Asian	Colorectum	II
Adenocarcinoma	0.950	Positive					
INDI 558	INDI 558 PLS 1	INDI 558 PT1	57	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.966	Positive					
INDI 559	INDI 559 PLS 1	INDI 559 PT1	54	Female	Caucasian	Breast	III
Invasive lobular carcinoma	0.847	Negative					
INDI 560	INDI 560 PLS 1	INDI 560 PT1	72	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.379	Negative					
INDI 561	INDI 561 PLS 1	INDI 561 PT1	56	Female	Caucasian	Breast	III
Invasive ductal adenocarcinoma	0.828	Negative					
INDI 562	INDI 562 PLS 1	INDI 562 PT1	78	Female	Caucasian	Colorectum	I
Adenocarcinoma	0.999	Positive					
INDI 564	INDI 564 PLS 1	INDI 564 PT1	66	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.955	Positive					
INDI 565	INDI 565 PLS 1	INDI 565 PT1	54	Female	Caucasian	Breast	III
Invasive ductal adenocarcinoma	0.640	Negative					
INDI 566	INDI 566 PLS 1	INDI 566 PT1	36	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.412	Negative					
INDI 567	INDI 567 PLS 1	INDI 567 PT1	64	Male	Caucasian	Colorectum	II
Adenocarcinoma	1.000	Positive					

Table2.txt

INDI 568	INDI 568 PLS 1	INDI 568 PT1	55	Female	Caucasian	Breast	II	Invasive carcinoma (NOS)	0.342	Negative
INDI 569	INDI 569 PLS 1	INDI 569 PT1	64	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.339	Negative
INDI 570	INDI 570 PLS 1	INDI 570 PT1	46	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.986	Positive
INDI 571	INDI 571 PLS 1	INDI 571 PT1	61	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.121	Negative
INDI 572	INDI 572 PLS 1	INDI 572 PT1	59	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.834	Negative
INDI 573	INDI 573 PLS 1	INDI 573 PT1	51	Female	Caucasian	Colorectum	I	Adenocarcinoma	0.372	Negative
INDI 574	INDI 574 PLS 1	INDI 574 PT1	60	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.966	Positive
INDI 575	INDI 575 PLS 1	INDI 575 PT1	58	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.974	Positive
INDI 577	INDI 577 PLS 1	INDI 577 PT1	65	Female	Asian	Breast	I	Invasive ductal adenocarcinoma	0.351	Negative
INDI 578	INDI 578 PLS 1	INDI 578 PT1	50	Female	Asian	Breast	I	Invasive ductal adenocarcinoma	0.811	Negative
INDI 579	INDI 579 PLS 1	INDI 579 PT1	33	Female	Asian	Breast	I	Invasive ductal adenocarcinoma	0.698	Negative
INDI 581	INDI 581 PLS 1	INDI 581 PT1	79	Female	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 582	INDI 582 PLS 1	INDI 582 PT1	72	Male	Asian	Colorectum	II	Adenocarcinoma	0.999	Positive
INDI 583	INDI 583 PLS 1	INDI 583 PT1	67	Female	Asian	Colorectum	II	Adenocarcinoma	0.979	Positive
INDI 584	INDI 584 PLS 1	INDI 584 PT1	80	Male	Asian	Colorectum	II	Adenocarcinoma	0.974	Positive
INDI 585	INDI 585 PLS 1	INDI 585 PT1	59	Male	Asian	Esophagus	III	Squamous cell carcinoma	0.999	Positive

Table2.txt

INDI 586 INDI 586 PLS 1 INDI 586 PT1 59 Female
Asian Liver III Hepatocellular carcinoma
1.000 Positive
INDI 587 INDI 587 PLS 1 INDI 587 PT1 64 Male
Asian Colorectum II Adenocarcinoma
0.980 Positive
INDI 588 INDI 588 PLS 1 INDI 588 PT1 33 Female
Asian Breast III Invasive ductal adenocarcinoma
0.125 Negative
INDI 589 INDI 589 PLS 1 INDI 589 PT1 43 Female
Asian Breast II Invasive ductal adenocarcinoma
0.117 Negative
INDI 591 INDI 591 PLS 1 INDI 591 PT1 81 Male
Asian Colorectum II Adenocarcinoma
0.999 Positive
INDI 592 INDI 592 PLS 1 INDI 592 PT1 49 Female
Asian Breast II Invasive ductal adenocarcinoma
0.291 Negative
INDI 593 INDI 593 PLS 1 INDI 593 PT1 82 Female
Asian Breast II Invasive ductal adenocarcinoma
0.988 Positive
INDI 594 INDI 594 PLS 1 INDI 594 PT1 56 Female
Asian Colorectum III Adenocarcinoma
0.992 Positive
INDI 595 INDI 595 PLS 1 INDI 595 PT1 64 Male
Asian Esophagus II Squamous cell carcinoma
0.999 Positive
INDI 596 INDI 596 PLS 1 INDI 596 PT1 56 Female
Asian Breast III Invasive ductal adenocarcinoma
0.539 Negative
INDI 597 INDI 597 PLS 1 INDI 597 PT1 56 Female
Asian Breast II Invasive ductal adenocarcinoma
0.591 Negative
INDI 598 INDI 598 PLS 1 INDI 598 PT1 84 Male
Asian Colorectum II Adenocarcinoma
0.974 Positive
INDI 599 INDI 599 PLS 1 INDI 599 PT1 50 Female
Asian Colorectum II Adenocarcinoma
0.897 Positive
INDI 600 INDI 600 PLS 1 INDI 600 PT1 85 Male
Asian Colorectum II Adenocarcinoma
0.813 Negative
INDI 601 INDI 601 PLS 1 INDI 601 PT1 52 Female
Asian Breast III Invasive ductal adenocarcinoma
1.000 Positive
INDI 602 INDI 602 PLS 1 INDI 602 PT1 47 Female
Asian Colorectum II Adenocarcinoma
0.998 Positive

Table2.txt

INDI 603	INDI 603 PLS 1	INDI 603 PT1	58	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.548	Negative
INDI 604	INDI 604 PLS 1	INDI 604 PT1	48	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.948	Positive
INDI 605	INDI 605 PLS 1	INDI 605 PT1	58	Female	Asian	Colorectum	II	Adenocarcinoma	0.986	Positive
INDI 606	INDI 606 PLS 1	INDI 606 PT1	71	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.681	Negative
INDI 607	INDI 607 PLS 1	INDI 607 PT1	46	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.667	Negative
INDI 608	INDI 608 PLS 1	INDI 608 PT1	51	Female	Asian	Colorectum	II	Adenocarcinoma	0.964	Positive
INDI 609	INDI 609 PLS 1	INDI 609 PT1	60	Male	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 610	INDI 610 PLS 1	INDI 610 PT1	50	Female	Asian	Colorectum	II	Adenocarcinoma	0.965	Positive
INDI 611	INDI 611 PLS 1	INDI 611 PT1	59	Male	Asian	Colorectum	II	Adenocarcinoma	0.932	Positive
INDI 612	INDI 612 PLS 1	INDI 612 PT1	55	Female	Asian	Colorectum	II	Adenocarcinoma	0.774	Negative
INDI 613	INDI 613 PLS 1	INDI 613 PT1	52	Female	Asian	Breast	II	Invasive lobular carcinoma	0.931	Positive
INDI 614	INDI 614 PLS 1	INDI 614 PT1	64	Female	Asian	Colorectum	II	Adenocarcinoma	0.999	Positive
INDI 615	INDI 615 PLS 1	INDI 615 PT1	67	Male	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 617	INDI 617 PLS 1	INDI 617 PT1	22	Male	Asian	Colorectum	III	Adenocarcinoma	0.923	Positive
INDI 618	INDI 618 PLS 1	INDI 618 PT1	54	Male	Asian	Colorectum	III	Adenocarcinoma	0.977	Positive
INDI 619	INDI 619 PLS 1	INDI 619 PT1	52	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.125	Negative

Table2.txt

INDI 620	INDI 620 PLS 1	INDI 620 PT1	55	Male	Asian	Colorectum	II	Adenocarcinoma
0.998	Positive							
INDI 621	INDI 621 PLS 1	INDI 621 PT1	58	Male	Asian	Colorectum	II	Adenocarcinoma
0.910	Positive							
INDI 622	INDI 622 PLS 1	INDI 622 PT1	65	Male	Asian	Liver	III	Hepatocellular carcinoma
1.000	Positive							
INDI 623	INDI 623 PLS 1	INDI 623 PT1	48	Female	Asian	Breast	III	Invasive ductal adenocarcinoma
0.998	Positive							
INDI 624	INDI 624 PLS 1	INDI 624 PT1	55	Female	Asian	Colorectum	II	Adenocarcinoma
0.986	Positive							
INDI 625	INDI 625 PLS 1	INDI 625 PT1	60	Female	Asian	Colorectum	II	Adenocarcinoma
0.961	Positive							
INDI 626	INDI 626 PLS 1	INDI 626 PT1	79	Male	Asian	Colorectum	II	Adenocarcinoma
1.000	Positive							
INDI 627	INDI 627 PLS 1	INDI 627 PT1	52	Female	Asian	Breast	II	Invasive ductal adenocarcinoma
0.927	Positive							
INDI 628	INDI 628 PLS 1	INDI 628 PT1	51	Female	Asian	Colorectum	II	Adenocarcinoma
0.923	Positive							
INDI 629	INDI 629 PLS 1	INDI 629 PT1	53	Female	Asian	Breast	I	Invasive ductal adenocarcinoma
0.762	Negative							
INDI 630	INDI 630 PLS 1	INDI 630 PT1	55	Female	Asian	Breast	I	Invasive ductal adenocarcinoma
0.714	Negative							
INDI 631	INDI 631 PLS 1	INDI 631 PT1	39	Female	Asian	Colorectum	II	Adenocarcinoma
0.998	Positive							
INDI 632	INDI 632 PLS 1	INDI 632 PT1	72	Female	Asian	Colorectum	II	Adenocarcinoma
0.998	Positive							
INDI 633	INDI 633 PLS 1	INDI 633 PT1	52	Female	Asian	Colorectum	II	Adenocarcinoma
0.993	Positive							
INDI 635	INDI 635 PLS 1	INDI 635 PT1	50	Male	Asian	Colorectum	II	Adenocarcinoma
0.991	Positive							
INDI 636	INDI 636 PLS 1	INDI 636 PT1	63	Male	Asian	Liver	III	Hepatocellular carcinoma
1.000	Positive							

Table2.txt

INDI 637	INDI 637 PLS 1	INDI 637 PT1	52	Female	Asian	Breast	III	Invasive ductal adenocarcinoma	0.877	Positive
INDI 638	INDI 638 PLS 1	INDI 638 PT1	52	Female	Asian	Breast	I	Invasive ductal adenocarcinoma	0.888	Positive
INDI 639	INDI 639 PLS 1	INDI 639 PT1	53	Male	Asian	Liver	II	Hepatocellular carcinoma	1.000	Positive
INDI 640	INDI 640 PLS 1	INDI 640 PT1	65	Male	Asian	Colorectum	II	Adenocarcinoma	0.998	Positive
INDI 641	INDI 641 PLS 1	INDI 641 PT1	65	Female	Asian	Breast	III	Invasive lobular carcinoma	0.838	Negative
INDI 643	INDI 643 PLS 1	INDI 643 PT1	67	Female	Asian	Colorectum	II	Adenocarcinoma	0.999	Positive
INDI 644	INDI 644 PLS 1	INDI 644 PT1	67	Male	Asian	Colorectum	I	Adenocarcinoma	0.925	Positive
INDI 645	INDI 645 PLS 1	INDI 645 PT1	54	Male	Asian	Liver	III	Hepatocellular carcinoma	1.000	Positive
INDI 646	INDI 646 PLS 1	INDI 646 PT1	60	Female	Asian	Breast	II	Invasive lobular carcinoma	0.432	Negative
INDI 647	INDI 647 PLS 1	INDI 647 PT1	61	Male	Asian	Colorectum	III	Adenocarcinoma	0.999	Positive
INDI 648	INDI 648 PLS 1	INDI 648 PT1	63	Male	Asian	Colorectum	III	Adenocarcinoma	1.000	Positive
INDI 649	INDI 649 PLS 1	INDI 649 PT1	51	Male	Asian	Colorectum	III	Adenocarcinoma	0.999	Positive
INDI 650	INDI 650 PLS 1	INDI 650 PT1	34	Male	Asian	Colorectum	III	Adenocarcinoma	0.857	Negative
INDI 651	INDI 651 PLS 1	INDI 651 PT1	74	Male	Asian	Colorectum	III	Adenocarcinoma	0.881	Positive
INDI 654	INDI 654 PLS 1	INDI 654 PT1	69	Male	Asian	Colorectum	II	Adenocarcinoma	0.932	Positive
INDI 655	INDI 655 PLS 1	INDI 655 PT1	46	Female	Asian	Colorectum	II	Adenocarcinoma	0.854	Negative

Table2.txt

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   INDI 656      INDI 656 PLS 1       INDI 656 PT1       48    Female
Asian               Breast       III    Invasive ductal adenocarcinoma
0.207               Negative
   INDI 657      INDI 657 PLS 1       INDI 657 PT1       49    Female
Asian              Colorectum      II            Adenocarcinoma
1.000               Positive
   INDI 658      INDI 658 PLS 1       INDI 658 PT1       37    Female
Asian              Colorectum      I             Adenocarcinoma
0.997               Positive
   INDI 659      INDI 659 PLS 1       INDI 659 PT1       42    Female
Asian               Breast        II    Invasive ductal adenocarcinoma
0.310               Negative
   INDI 660      INDI 660 PLS 1       INDI 660 PT1       79    Female
Asian              Colorectum      II            Adenocarcinoma
0.955               Positive
   INDI 661      INDI 661 PLS 1       INDI 661 PT1       58    Female
Asian               Liver        III          Cholangiocarcinoma
0.989               Positive
   INDI 662      INDI 662 PLS 1       INDI 662 PT1       57    Female
Asian               Breast        I     Invasive ductal adenocarcinoma
0.614               Negative
   INDI 663      INDI 663 PLS 1       INDI 663 PT1       52     Male
Asian              Esophagus       II       Squamous cell carcinoma
1.000               Positive
   INDI 664      INDI 664 PLS 1       INDI 664 PT1       61    Female
Asian               Breast        I     Invasive ductal adenocarcinoma
0.641               Negative
   INDI 665      INDI 665 PLS 1       INDI 665 PT1       64     Male
Asian              Esophagus      III            Adenocarcinoma
1.000               Positive
   INDI 666      INDI 666 PLS 1       INDI 666 PT1       45    Female
Asian               Breast        II    Invasive ductal adenocarcinoma
0.831               Negative
   INDI 667      INDI 667 PLS 1       INDI 667 PT1       70    Female
Asian               Breast        II    Invasive ductal adenocarcinoma
0.326               Negative
   INDI 668      INDI 668 PLS 1       INDI 668 PT1       76    Female
Asian               Breast       III      Invasive lobular carcinoma
0.382               Negative
   INDI 669      INDI 669 PLS 1       INDI 669 PT1       61     Male
Caucasian             Liver        III       Hepatocellular carcinoma
 0.996              Positive
   INDI 670      INDI 670 PLS 1       INDI 670 PT1       74     Male
Caucasian           Colorectum     III            Adenocarcinoma
 0.999              Positive
   INDI 671      INDI 671 PLS 1       INDI 671 PT1       61    Female
Caucasian              Lung         I       Non-small cell lung cancer
 0.877              Positive
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Table2.txt

INDI 672	INDI 672 PLS 1	INDI 672 PT1	63	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.117	Negative
INDI 673	INDI 673 PLS 1	INDI 673 PT1	58	Female	Caucasian	Breast	II	Invasive lobular carcinoma	0.943	Positive
INDI 674	INDI 674 PLS 1	INDI 674 PT1	70	Male	Caucasian	Lung	I	Non-small cell lung cancer	0.626	Negative
INDI 675	INDI 675 PLS 1	INDI 675 PT1	92	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.991	Positive
INDI 677	INDI 677 PLS 1	INDI 677 PT1	60	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.559	Negative
INDI 678	INDI 678 PLS 1	INDI 678 PT1	46	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.977	Positive
INDI 679	INDI 679 PLS 1	INDI 679 PT1	51	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.116	Negative
INDI 681	INDI 681 PLS 1	INDI 681 PT1	73	Male	Caucasian	Lung	II	Non-small cell lung cancer	0.758	Negative
INDI 682	INDI 682 PLS 1	Not available	66	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.778	Negative
INDI 683	INDI 683 PLS 1	INDI 683 PT1	75	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.589	Negative
INDI 684	INDI 684 PLS 1	Not available	66	Male	Caucasian	Liver	III	Hepatocellular carcinoma	0.806	Negative
INDI 685	INDI 685 PLS 1	INDI 685 PT1	79	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.239	Negative
INDI 686	INDI 686 PLS 1	INDI 686 PT1	66	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.984	Positive
INDI 687	INDI 687 PLS 1	INDI 687 PT1	56	Male	Caucasian	Lung	III	Non-small cell lung cancer	1.000	Positive
INDI 688	INDI 688 PLS 1	INDI 688 PT1	75	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.908	Positive
INDI 690	INDI 690 PLS 1	Not available	80	Male	Caucasian	Lung	III	Non-small cell lung cancer	0.583	Negative

Table2.txt

INDI 691	INDI 691 PLS 1	INDI 691 PT1	74	Female	Caucasian	Lung	Positive
I	Non-small cell lung cancer	0.914					
INDI 692	INDI 692 PLS 1	INDI 692 PT1	85	Female	Caucasian	Colorectum	Positive
III	Adenocarcinoma	0.955					
INDI 693	INDI 693 PLS 1	INDI 693 PT1	70	Male	Caucasian	Lung	Positive
III	Non-small cell lung cancer	0.998					
INDI 694	INDI 694 PLS 1	INDI 694 PT1	55	Female	Caucasian	Lung	Positive
I	Non-small cell lung cancer	0.958					
INDI 695	INDI 695 PLS 1	INDI 695 PT1	74	Female	Caucasian	Pancreas	Negative
II	Adenocarcinoma	0.378					
INDI 696	INDI 696 PLS 1	INDI 696 PT1	76	Male	Caucasian	Lung	Positive
II	Non-small cell lung cancer	0.948					
INDI 697	INDI 697 PLS 1	INDI 697 PT1	70	Female	Caucasian	Breast	Positive
II	Invasive ductal adenocarcinoma	0.974					
INDI 698	INDI 698 PLS 1	Not available	58	Female	Caucasian	Ovary	Positive
III	Epithelial carcinoma	0.947					
INDI 699	INDI 699 PLS 1	Not available	74	Female	Caucasian	Pancreas	Positive
II	Adenocarcinoma	0.997					
INDI 700	INDI 700 PLS 1	INDI 700 PT1	67	Male	Caucasian	Lung	Positive
III	Non-small cell lung cancer	0.986					
INDI 701	INDI 701 PLS 1	INDI 701 PT1	71	Female	Caucasian	Colorectum	Positive
II	Adenocarcinoma	0.874					
INDI 702	INDI 702 PLS 1	INDI 702 PT1	74	Male	Caucasian	Lung	Positive
II	Non-small cell lung cancer	0.997					
INDI 703	INDI 703 PLS 1	INDI 703 PT1	79	Male	Caucasian	Lung	Negative
I	Non-small cell lung cancer	0.656					
INDI 704	INDI 704 PLS 1	INDI 704 PT1	35	Female	Caucasian	Breast	Negative
II	Invasive ductal adenocarcinoma	0.395					
INDI 706	INDI 706 PLS 1	INDI 706 PT1	65	Female	Caucasian	Lung	Positive
I	Non-small cell lung cancer	0.993					
INDI 708	INDI 708 PLS 1	INDI 708 PT1	58	Male	Caucasian	Colorectum	Positive
III	Adenocarcinoma	0.995					

Table2.txt

INDI 709	INDI 709 PLS 1	INDI 709 PT1	92	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.842	Negative
INDI 710	INDI 710 PLS 1	INDI 710 PT1	74	Female	Caucasian	Colorectum	III	Adenocarcinoma	0.977	Positive
INDI 711	INDI 711 PLS 1	INDI 711 PT1	47	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.979	Positive
INDI 712	INDI 712 PLS 1	INDI 712 PT1	76	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.354	Negative
INDI 713	INDI 713 PLS 1	INDI 713 PT1	71	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.342	Negative
INDI 714	INDI 714 PLS 1	INDI 714 PT1	78	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.956	Positive
INDI 715	INDI 715 PLS 1	INDI 715 PT1	83	Female	Caucasian	Breast	III	Invasive ductal adenocarcinoma	0.987	Positive
INDI 716	INDI 716 PLS 1	INDI 716 PT1	78	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.975	Positive
INDI 717	INDI 717 PLS 1	INDI 717 PT1	65	Female	Caucasian	Breast	I	Invasive lobular carcinoma	0.812	Negative
INDI 718	INDI 718 PLS 1	Not available	61	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.829	Negative
INDI 720	INDI 720 PLS 1	INDI 720 PT1	52	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.654	Negative
INDI 721	INDI 721 PLS 1	INDI 721 PT1	56	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma	0.598	Negative
INDI 722	INDI 722 PLS 1	INDI 722 PT1	75	Female	Caucasian	Breast	I	Invasive ductal adenocarcinoma	0.201	Negative
INDI 723	INDI 723 PLS 1	INDI 723 PT1	74	Female	Caucasian	Ovary	III	Epithelial carcinoma	0.993	Positive
INDI 724	INDI 724 PLS 1	INDI 724 PT1	67	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.230	Negative
INDI 725	INDI 725 PLS 1	INDI 725 PT1	61	Male	Caucasian	Colorectum	II	Adenocarcinoma	0.636	Negative

Table2.txt

INDI 726	INDI 726 PLS 1	INDI 726 PT1	60	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.315	Negative			
INDI 729	INDI 729 PLS 1	INDI 729 PT1	63	Male	Caucasian	Colorectum
II	Adenocarcinoma	0.465	Negative			
INDI 731	INDI 731 PLS 1	Not available	65	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.469	Negative			
INDI 732	INDI 732 PLS 1	Not available	56	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.756	Negative			
INDI 734	INDI 734 PLS 1	Not available	71	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.938	Positive			
INDI 735	INDI 735 PLS 1	Not available	66	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.997	Positive			
INDI 736	INDI 736 PLS 1	Not available	66	Male	Caucasian	Lung
III	Non-small cell lung cancer	0.958	Positive			
INDI 737	INDI 737 PLS 1	Not available	58	Male	Caucasian	Stomach
I	Adenocarcinoma	0.944	Positive			
INDI 740	INDI 740 PLS 1	Not available	86	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.991	Positive			
INDI 741	INDI 741 PLS 1	Not available	67	Female	Caucasian	Pancreas
III	Adenocarcinoma	0.995	Positive			
INDI 742	INDI 742 PLS 1	Not available	72	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.826	Negative			
INDI 743	INDI 743 PLS 1	Not available	35	Male	Caucasian	Stomach
II	Adenocarcinoma	0.117	Negative			
INDI 745	INDI 745 PLS 1	Not available	65	Male	Asian	Pancreas
II	Adenocarcinoma	0.953	Positive			
INDI 746	INDI 746 PLS 1	INDI 746 PT1	51	Male	Asian	Colorectum
III	Adenocarcinoma	0.993	Positive			
INDI 747	INDI 747 PLS 1	INDI 747 PT1	24	Female	Asian	Colorectum
III	Adenocarcinoma	0.988	Positive			
INDI 749	INDI 749 PLS 1	INDI 749 PT1	50	Female	Asian	Colorectum
III	Adenocarcinoma	0.900	Positive			

Table2.txt

INDI 750	INDI 750 PLS 1	INDI 750 PT1	49	Male	Asian	Colorectum
III	Adenocarcinoma	0.973	Positive			
INDI 751	INDI 751 PLS 1	INDI 751 PT1	44	Male	Asian	Colorectum
III	Adenocarcinoma	0.982	Positive			
INDI 752	INDI 752 PLS 1	INDI 752 PT1	58	Male	Asian	Colorectum
III	Adenocarcinoma	0.975	Positive			
INDI 753	INDI 753 PLS 1	INDI 753 PT1	59	Male	Asian	Esophagus
III	Squamous cell carcinoma	0.999	Positive			
INDI 754	INDI 754 PLS 1	INDI 754 PT1	63	Female	Asian	Breast
III	Invasive ductal adenocarcinoma	0.125	Negative			
INDI 755	INDI 755 PLS 1	INDI 755 PT1	70	Male	Asian	Esophagus
III	Squamous cell carcinoma	0.996	Positive			
INDI 756	INDI 756 PLS 1	INDI 756 PT1	63	Female	Asian	Breast
II	Invasive ductal adenocarcinoma	0.543	Negative			
INDI 757	INDI 757 PLS 1	INDI 757 PT1	58	Female	Asian	Breast
II	Invasive ductal adenocarcinoma	0.117	Negative			
INDI 758	INDI 758 PLS 1	INDI 758 PT1	82	Female	Asian	Colorectum
II	Adenocarcinoma	0.987	Positive			
INDI 759	INDI 759 PLS 1	INDI 759 PT1	62	Female	Asian	Breast
III	Invasive ductal adenocarcinoma	0.117	Negative			
INDI 760	INDI 760 PLS 1	INDI 760 PT1	65	Male	Asian	Liver
III	Hepatocellular carcinoma	0.997	Positive			
INDI 761	INDI 761 PLS 1	INDI 761 PT1	63	Female	Asian	Colorectum
II	Adenocarcinoma	0.995	Positive			
INDI 762	INDI 762 PLS 1	INDI 762 PT1	69	Male	Asian	Esophagus
II	Adenocarcinoma	0.690	Negative			
INDI 763	INDI 763 PLS 1	INDI 763 PT1	59	Female	Asian	Colorectum
I	Adenocarcinoma	0.824	Negative			
INDI 764	INDI 764 PLS 1	INDI 764 PT1	61	Male	Asian	Colorectum
II	Adenocarcinoma	0.993	Positive			
INDI 765	INDI 765 PLS 1	INDI 765 PT1	68	Male	Asian	Colorectum
I	Adenocarcinoma	1.000	Positive			

Table2.txt

INDI 766	INDI 766 PLS 1	INDI 766 PT1	38	Female	Asian	Breast	II	Invasive ductal adenocarcinoma	0.125	Negative
INDI 767	INDI 767 PLS 1	INDI 767 PT1	62	Male	Asian	Colorectum	II	Adenocarcinoma	0.996	Positive
INDI 768	INDI 768 PLS 1	INDI 768 PT1	49	Male	Asian	Colorectum	II	Adenocarcinoma	0.735	Negative
INDI 769	INDI 769 PLS 1	INDI 769 PT1	46	Male	Asian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 770	INDI 770 PLS 1	INDI 770 PT1	61	Female	Asian	Colorectum	II	Adenocarcinoma	0.970	Positive
INDI 771	INDI 771 PLS 1	INDI 771 PT1	60	Male	Asian	Liver	II	Hepatocellular carcinoma	0.994	Positive
INDI 772	INDI 772 PLS 1	INDI 772 PT1	52	Female	Asian	Colorectum	II	Adenocarcinoma	0.819	Negative
INDI 773	INDI 773 PLS 1	INDI 773 PT1	77	Male	Asian	Colorectum	II	Adenocarcinoma	0.841	Negative
INDI 774	INDI 774 PLS 1	INDI 774 PT1	67	Female	Asian	Colorectum	I	Adenocarcinoma	0.984	Positive
INDI 775	INDI 775 PLS 1	INDI 775 PT1	76	Male	Asian	Liver	II	Hepatocellular carcinoma	0.999	Positive
INDI 776	INDI 776 PLS 1	INDI 776 PT1	61	Male	Asian	Esophagus	II	Squamous cell carcinoma	0.998	Positive
INDI 777	INDI 777 PLS 1	INDI 777 PT1	67	Female	Asian	Colorectum	II	Adenocarcinoma	0.994	Positive
INDI 778	INDI 778 PLS 1	INDI 778 PT1	57	Male	Asian	Liver	II	Hepatocellular carcinoma	0.999	Positive
INDI 779	INDI 779 PLS 1	INDI 779 PT1	61	Female	Asian	Colorectum	II	Adenocarcinoma	1.000	Positive
INDI 780	INDI 780 PLS 1	INDI 780 PT1	52	Female	Asian	Colorectum	II	Adenocarcinoma	0.946	Positive
INDI 781	INDI 781 PLS 1	INDI 781 PT1	57	Male	Asian	Colorectum	II	Adenocarcinoma	0.965	Positive

Table2.txt

INDI 782	INDI 782 PLS 1	INDI 782 PT1	92	Female	Caucasian	Colorectum
III	Adenocarcinoma	1.000	Positive			
INDI 783	INDI 783 PLS 1	INDI 783 PT1	55	Male	Caucasian	Colorectum
III	Adenocarcinoma	0.680	Negative			
INDI 784	INDI 784 PLS 1	Not available	76	Male	Caucasian	Stomach
I	Adenocarcinoma	0.985	Positive			
INDI 785	INDI 785 PLS 1	INDI 785 PT1	77	Male	Caucasian	Colorectum
I	Adenocarcinoma	0.302	Negative			
INDI 786	INDI 786 PLS 1	INDI 786 PT1	76	Male	Caucasian	Liver
I	Hepatocellular carcinoma	0.978	Positive			
INDI 787	INDI 787 PLS 1	INDI 787 PT1	89	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.121	Negative			
INDI 788	INDI 788 PLS 1	INDI 788 PT1	77	Female	Caucasian	Colorectum
II	Adenocarcinoma	0.688	Negative			
INDI 789	INDI 789 PLS 1	INDI 789 PT1	70	Male	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.117	Negative			
INDI 790	INDI 790 PLS 1	INDI 790 PT1	53	Female	Caucasian	Breast
II	Invasive lobular carcinoma	0.771	Negative			
INDI 791	INDI 791 PLS 1	INDI 791 PT0	52	Female	Caucasian	Breast
III	Invasive ductal adenocarcinoma	0.320	Negative			
INDI 792	INDI 792 PLS 1	Not available	58	Male	Caucasian	Stomach
I	Adenocarcinoma	0.377	Negative			
INDI 793	INDI 793 PLS 1	Not available	83	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.836	Negative			
INDI 794	INDI 794 PLS 1	Not available	43	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.571	Negative			
INDI 795	INDI 795 PLS 1	Not available	68	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.595	Negative			
INDI 797	INDI 797 PLS 1	INDI 797 PT1	69	Male	Caucasian	Stomach
II	Adenocarcinoma	0.955	Positive			
INDI 798	INDI 798 PLS 1	INDI 798 PT1	75	Female	Caucasian	Ovary
II	Epithelial carcinoma	1.000	Positive			

Table2.txt

INDI 799	INDI 799 PLS 1	Not available	74	Male	Unknown	Stomach	II	Adenocarcinoma	0.239	Negative
INDI 800	INDI 800 PLS 1	INDI 800 PT1	75	Male	Caucasian	Liver	II	Hepatocellular carcinoma	0.997	Positive
INDI 801	INDI 801 PLS 1	INDI 801 PT1	77	Male	Caucasian	Stomach	I	Adenocarcinoma	0.293	Negative
INDI 802	INDI 802 PLS 1	INDI 802 PT1	60	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.987	Positive
INDI 803	INDI 803 PLS 1	INDI 803 PT1	65	Female	Caucasian	Esophagus	II	Adenocarcinoma	0.385	Negative
INDI 805	INDI 805 PLS 1	Not available	61	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.632	Negative
INDI 806	INDI 806 PLS 1	INDI 806 PT1	65	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.661	Negative
INDI 808	INDI 808 PLS 1	INDI 808 PT1	73	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.601	Negative
INDI 809	INDI 809 PLS 1	INDI 809 PT1	67	Male	Caucasian	Colorectum	III	Adenocarcinoma	0.213	Negative
INDI 812	INDI 812 PLS 1	INDI 812 PT1	56	Female	Caucasian	Ovary	II	Epithelial carcinoma	1.000	Positive
INDI 814	INDI 814 PLS 1	INDI 814 PT1	65	Male	Caucasian	Stomach	I	Adenocarcinoma	0.386	Negative
INDI 815	INDI 815 PLS 1	INDI 815 PT1	77	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.997	Positive
INDI 816	INDI 816 PLS 1	INDI 816 PT1	58	Female	Caucasian	Colorectum	II	Adenocarcinoma	0.336	Negative
INDI 817	INDI 817 PLS 1	INDI 817 PT1	79	Male	Caucasian	Liver	III	Hepatocellular carcinoma	0.990	Positive
INDI 818	INDI 818 PLS 1	INDI 818 PT1	73	Female	Caucasian	Ovary	III	Epithelial carcinoma	1.000	Positive
INDI 819	INDI 819 PLS 1	INDI 819 PT1	63	Female	Caucasian	Breast	III	Invasive lobular carcinoma	0.979	Positive

Table2.txt

INDI 821	INDI 821 PLS 1	INDI 821 PT1	67	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.776	Negative					
INDI 822	INDI 822 PLS 1	INDI 822 PT1	77	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.123	Negative					
INDI 823	INDI 823 PLS 1	INDI 823 PT1	73	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.121	Negative					
INDI 824	INDI 824 PLS 1	Not available	75	Male	Caucasian	Esophagus	II
Adenocarcinoma	0.998	Positive					
INDI 825	INDI 825 PLS 1	INDI 825 PT1	68	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.511	Negative					
INDI 826	INDI 826 PLS 1	INDI 826 PT1	60	Male	Caucasian	Colorectum	II
Adenocarcinoma	0.925	Positive					
INDI 827	INDI 827 PLS 1	INDI 827 PT1	74	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.956	Positive					
INDI 828	INDI 828 PLS 1	INDI 828 PT1	78	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.117	Negative					
INDI 829	INDI 829 PLS 1	INDI 829 PT1	47	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.122	Negative					
INDI 830	INDI 830 PLS 0	INDI 830 PT0	61	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.954	Positive					
INDI 831	INDI 831 PLS 1	INDI 831 PT1	79	Female	Caucasian	Breast	I
Invasive ductal adenocarcinoma	0.175	Negative					
INDI 832	INDI 832 PLS 1	INDI 832 PT1	84	Female	Caucasian	Breast	II
Invasive lobular carcinoma	0.831	Negative					
INDI 833	INDI 833 PLS 1	INDI 833 PT1	78	Female	Caucasian	Breast	I
Invasive ductal adenocarcinoma	0.876	Positive					
INDI 835	INDI 835 PLS 1	INDI 835 PT1	66	Male	Caucasian	Colorectum	III
Adenocarcinoma	0.856	Negative					
INDI 837	INDI 837 PLS 1	INDI 837 PT1	67	Female	Caucasian	Colorectum	II
Adenocarcinoma	0.609	Negative					
INDI 838	INDI 838 PLS 1	INDI 838 PT1	62	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.603	Negative					

Table2.txt

INDI 839	INDI 839 PLS 1	Not available	74	Female	Caucasian	Breast	II
Invasive lobular carcinoma	0.125	Negative					
INDI 840	INDI 840 PLS 0	Not available	71	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.125	Negative					
INDI 841	INDI 841 PLS 1	INDI 841 PT1	84	Female	Caucasian	Colorectum	III
Adenocarcinoma	0.994	Positive					
INDI 842	INDI 842 PLS 1	Not available	52	Female	Caucasian	Breast	I
Invasive ductal adenocarcinoma	0.826	Negative					
INDI 843	INDI 843 PLS 1	INDI 843 PT1	79	Female	Caucasian	Esophagus	I
Squamous cell carcinoma	0.122	Negative					
INDI 844	INDI 844 PLS 1	Not available	71	Female	Caucasian	Stomach	I
Adenocarcinoma	0.876	Positive					
INDI 846	INDI 846 PLS 1	INDI 846 PT1	44	Male	Asian	Colorectum	II
Adenocarcinoma	0.991	Positive					
INDI 847	INDI 847 PLS 1	INDI 847 PT1	51	Female	Asian	Liver	III
Hepatocellular carcinoma	0.976	Positive					
INDI 848	INDI 848 PLS 1	INDI 848 PT1	47	Male	Asian	Colorectum	II
Adenocarcinoma	0.876	Positive					
INDI 849	INDI 849 PLS 1	INDI 849 PT1	80	Male	Asian	Colorectum	II
Adenocarcinoma	0.841	Negative					
INDI 850	INDI 850 PLS 1	INDI 850 PT1	45	Male	Asian	Esophagus	II
Squamous cell carcinoma	1.000	Positive					
INDI 853	INDI 853 PLS 1	INDI 853 PT1	82	Male	Asian	Esophagus	II
Squamous cell carcinoma	0.998	Positive					
INDI 854	INDI 854 PLS 1	INDI 854 PT1	59	Male	Asian	Colorectum	II
Adenocarcinoma	0.991	Positive					
INDI 855	INDI 855 PLS 1	INDI 855 PT1	71	Male	Asian	Colorectum	II
Adenocarcinoma	0.999	Positive					
INDI 856	INDI 856 PLS 1	INDI 856 PT1	85	Female	Asian	Breast	III
Invasive ductal adenocarcinoma	0.116	Negative					
INDI 857	INDI 857 PLS 1	INDI 857 PT1	42	Female	Asian	Breast	III
Invasive ductal adenocarcinoma	0.356	Negative					

Table2.txt

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   INDI 858      INDI 858 PLS 1       INDI 858 PT1       46    Female
Asian                Breast        I     Invasive ductal adenocarcinoma
0.480               Negative
   INDI 859      INDI 859 PLS 1       INDI 859 PT1       55     Male
Asian               Esophagus       II       Squamous cell carcinoma
0.992                Positive
   INDI 860      INDI 860 PLS 1       INDI 860 PT1       56    Female
Asian                Breast        I     Invasive ductal adenocarcinoma
0.121               Negative
   INDI 861      INDI 861 PLS 1       INDI 861 PT1       69     Male
Asian                Liver         II       Hepatocellular carcinoma
0.997               Positive
   INDI 862      INDI 862 PLS 1       INDI 862 PT1       67     Male
Asian               Pancreas       II            Adenocarcinoma
0.910               Positive
   INDI 864      INDI 864 PLS 1       INDI 864 PT1       28     Male
Asian                Liver        III       Hepatocellular carcinoma
0.999               Positive
   INDI 865      INDI 865 PLS 1       INDI 865 PT1       65    Female
Asian                Breast       III    Invasive ductal adenocarcinoma
0.392               Negative
   INDI 867      INDI 867 PLS 1       INDI 867 PT1       46     Male
Asian               Esophagus       II       Squamous cell carcinoma
0.995                Positive
   INDI 868      INDI 868 PLS 1       INDI 868 PT1       58     Male
Asian                Liver        III       Hepatocellular carcinoma
0.993               Positive
   INDI 870      INDI 870 PLS 1       INDI 870 PT1       58    Female
Caucasian              Breast        II    Invasive ductal adenocarcinoma
 0.947              Positive
   INDI 872      INDI 872 PLS 1       INDI 872 PT1       74    Female
Caucasian              Breast       III    Invasive ductal adenocarcinoma
 0.986              Positive
   INDI 873      INDI 873 PLS 1       INDI 873 PT1       65    Female
Caucasian              Breast       III    Invasive ductal adenocarcinoma
 0.527              Negative
   INDI 875      INDI 875 PLS 1       INDI 875 PT1       48     Male
Caucasian              Breast        II      Invasive lobular carcinoma
 0.252              Negative
   INDI 876      INDI 876 PLS 1       INDI 876 PT1       65    Female
Caucasian              Breast        II    Invasive ductal adenocarcinoma
 0.331              Negative
   INDI 877      INDI 877 PLS 1       INDI 877 PT1       55    Female
Caucasian              Breast        I     Invasive ductal adenocarcinoma
 0.999              Positive
   INDI 878      INDI 878 PLS 1       INDI 878 PT1       59    Female
Caucasian              Breast       III    Invasive ductal adenocarcinoma
 0.992              Positive
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Table2.txt

INDI 879	INDI 879 PLS 1	INDI 879 PT1	63	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma
0.340	Negative							
INDI 880	INDI 880 PLS 1	INDI 880 PT1	56	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma
0.675	Negative							
INDI 881	INDI 881 PLS 1	INDI 881 PT1	62	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma
0.835	Negative							
INDI 882	INDI 882 PLS 1	INDI 882 PT1	56	Female	Caucasian	Breast	II	Invasive ductal adenocarcinoma
0.779	Negative							
INDI 883	INDI 883 PLS 1	INDI 883 PT1	67	Female	Caucasian	Breast	II	Invasive lobular carcinoma
0.602	Negative							
INDI 884	INDI 884 PLS 1	INDI 884 PT1	38	Female	Asian	Breast	II	Invasive ductal adenocarcinoma
0.999	Positive							
INDI 885	INDI 885 PLS 1	INDI 885 PT1	41	Female	Asian	Breast	II	Invasive ductal adenocarcinoma
0.547	Negative							
INDI 886	INDI 886 PLS 1	INDI 886 PT1	52	Female	Asian	Breast	II	Invasive ductal adenocarcinoma
0.123	Negative							
INDI 887	INDI 887 PLS 1	INDI 887 PT1	41	Female	Asian	Breast	III	Metaplastic carcinoma
0.987	Positive							
INDI 888	INDI 888 PLS 1	Not available	70	Male	Caucasian	Pancreas	II	Adenocarcinoma
0.976	Positive							
INDI 889	INDI 889 PLS 1	Not available	63	Female	Caucasian	Colorectum	II	Adenocarcinoma
0.999	Positive							
INDI 892	INDI 892 PLS 1	Not available	74	Female	Caucasian	Stomach	I	Adenocarcinoma
0.561	Negative							
INDI 893	INDI 893 PLS 1	Not available	75	Male	Caucasian	Pancreas	II	Adenocarcinoma
0.972	Positive							
INDI 896	INDI 896 PLS 1	Not available	65	Male	Caucasian	Lung	I	Non-small cell lung cancer
0.864	Positive							
INDI 897	INDI 897 PLS 1	Not available	65	Female	Caucasian	Breast	III	Invasive lobular carcinoma
0.993	Positive							
INDI 898	INDI 898 PLS 1	Not available	79	Female	Caucasian	Breast	I	Invasive lobular carcinoma
0.967	Positive							

Table2.txt

INDI 899	INDI 899 PLS 1	Not available	75	Female	Caucasian	Breast
I	Invasive ductal adenocarcinoma	0.154	Negative			
INDI 902	INDI 902 PLS 1	Not available	78	Female	Caucasian	Breast
III	Invasive ductal adenocarcinoma	0.997	Positive			
INDI 903	INDI 903 PLS 1	Not available	54	Female	Caucasian	Breast
I	Invasive lobular carcinoma	0.651	Negative			
INDI 905	INDI 905 PLS 1	INDI 905 PT1	67	Male	Asian	Esophagus
II	Squamous cell carcinoma	1.000	Positive			
INDI 907	INDI 907 PLS 1	INDI 907 PT1	63	Male	Asian	Esophagus
II	Squamous cell carcinoma	0.971	Positive			
INDI 908	INDI 908 PLS 1	INDI 908 PT1	46	Male	Asian	Esophagus
II	Squamous cell carcinoma	0.999	Positive			
INDI 909	INDI 909 PLS 1	INDI 909 PT1	60	Female	Asian	Esophagus
II	Squamous cell carcinoma	0.987	Positive			
INDI 911	INDI 911 PLS 1	INDI 911 PT1	49	Male	Asian	Esophagus
II	Squamous cell carcinoma	0.887	Positive			
INDI 913	INDI 913 PLS 1	INDI 913 PT1	77	Female	Asian	Esophagus
III	Squamous cell carcinoma	0.835	Negative			
INDI 915	INDI 915 PLS 1	INDI 915 PT1	71	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.328	Negative			
INDI 917	INDI 917 PLS 1	Not available	66	Male	Caucasian	Liver
III	Hepatocellular carcinoma	0.997	Positive			
INDI 919	INDI 919 PLS 1	Not available	67	Female	Caucasian	Breast
II	Invasive lobular carcinoma	0.458	Negative			
INDI 920	INDI 920 PLS 1	Not available	59	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.944	Positive			
INDI 921	INDI 921 PLS 1	INDI 921 PT1	67	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.458	Negative			
INDI 922	INDI 922 PLS 1	Not available	49	Female	Caucasian	Breast
II	Invasive ductal adenocarcinoma	0.125	Negative			
INDI 923	INDI 923 PLS 1	Not available	72	Male	Caucasian	Esophagus
I	Adenocarcinoma	0.306	Negative			

Table2.txt

INDI 924	INDI 924 PLS 1	Not available	73	Female	Caucasian	Breast	III
Invasive lobular carcinoma	0.395	Negative					
INDI 926	INDI 926 PLS 1	Not available	51	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.343	Negative					
INDI 927	INDI 927 PLS 1	Not available	59	Female	Caucasian	Breast	II
Invasive ductal adenocarcinoma	0.304	Negative					
INDI 928	INDI 928 PLS 1	INDI 928 PT1	75	Male	Caucasian	Stomach	II
Adenocarcinoma	0.998	Positive					
INDI 929	INDI 929 PLS 1	INDI 929 PT1	75	Male	Caucasian	Stomach	II
Adenocarcinoma	0.719	Negative					
INDI 930	INDI 930 PLS 1	INDI 930 PT1	75	Male	Caucasian	Stomach	II
Adenocarcinoma	0.672	Negative					
INDI 931	INDI 931 PLS 1	Not available	50	Female	Caucasian	Ovary	III
Epithelial carcinoma	0.955	Positive					
INDI 932	INDI 932 PLS 1	INDI 932PT1	71	Female	Caucasian	Ovary	III
Epithelial carcinoma	0.999	Positive					
INDI 933	INDI 933 PLS 1	INDI 933 PT1	67	Male	Caucasian	Esophagus	III
Adenocarcinoma	0.527	Negative					
INDI 935	INDI 935 PLS 1	Not available	75	Male	Caucasian	Esophagus	I
Adenocarcinoma	0.810	Negative					
INDI 936	INDI 936 PLS 1	Not available	72	Female	Caucasian	Ovary	I
Epithelial carcinoma	0.363	Negative					
INDI 937	INDI 937 PLS 1	INDI 937 PT1	60	Male	Caucasian	Esophagus	III
Adenocarcinoma	0.541	Negative					
LCR 588	LCR 588 PLS1	Not applicable	63	Female	Caucasian	Normal	NA
NA	0.260	Negative					
LCR 589	LCR 589 PLS1	Not applicable	45	Male	Caucasian	Normal	NA
NA	0.186	Negative					
LCR 590	LCR 590 PLS1	Not applicable	54	Male	Caucasian	Normal	NA
NA	0.235	Negative					
LCR 591	LCR 591 PLS1	Not applicable	44	Male	Caucasian	Normal	NA
NA	0.125	Negative					

Table2.txt

LCR 592	LCR 592 PLS1	Not applicable	53	Female	Caucasian	Normal	NA
NA	0.117	Negative					
LCR 593	LCR 593 PLS1	Not applicable	65	Male	Caucasian	Normal	NA
NA	0.175	Negative					
LCR 594	LCR 594 PLS1	Not applicable	57	Male	Caucasian	Normal	NA
NA	0.121	Negative					
LCR 595	LCR 595 PLS1	Not applicable	65	Male	Caucasian	Normal	NA
NA	0.296	Negative					
LCR 596	LCR 596 PLS1	Not available	78	Male	Caucasian	Colorectum	I
Adenocarcinoma	0.181	Negative					
LCR 597	LCR 597 PLS1	Not applicable	51	Male	Caucasian	Normal	NA
NA	0.435	Negative					
LCR 599	LCR 599 PLS1	Not applicable	51	Male	Asian	Normal	NA
NA	0.339	Negative					
LCR 600	LCR 600 PLS1	Not applicable	66	Female	Caucasian	Normal	NA
NA	0.121	Negative					
LCR 601	LCR 601 PLS1	Not applicable	61	Male	Caucasian	Normal	NA
NA	0.307	Negative					
LCR 602	LCR 602 PLS1	Not applicable	69	Male	Caucasian	Normal	NA
NA	0.315	Negative					
LCR 603	LCR 603 PLS1	Not applicable	60	Female	Caucasian	Normal	NA
NA	0.125	Negative					
LCR 604	LCR 604 PLS1	Not applicable	63	Female	Caucasian	Normal	NA
NA	0.121	Negative					
LCR 605	LCR 605 PLS1	Not applicable	67	Male	Caucasian	Normal	NA
NA	0.326	Negative					
LCR 606	LCR 606 PLS1	Not applicable	55	Male	Caucasian	Normal	NA
NA	0.779	Negative					
LCR 607	LCR 607 PLS1	Not applicable	43	Female	Caucasian	Normal	NA
NA	0.585	Negative					
LCR 608	LCR 608 PLS1	Not applicable	66	Female	Caucasian	Normal	NA
NA	0.593	Negative					

Table2.txt

LCR 610	LCR 610 PLS1	Not applicable	51	Male	
Caucasian	Normal	NA	NA		
0.125	Negative				
LCR 611	LCR 611 PLS1	Not applicable	66	Female	
Caucasian	Normal	NA	NA		
0.196	Negative				
LCR 612	LCR 612 PLS1	Not applicable	62	Female	
Caucasian	Normal	NA	NA		
0.116	Negative				
LCR 613	LCR 613 PLS1	Not applicable	48	Female	
Caucasian	Normal	NA	NA		
0.117	Negative				
LCR 614	LCR 614 PLS1	Not applicable	56	Female	
Asian	Normal	NA	NA		
0.239	Negative				
LCR 616	LCR 616 PLS1	Not applicable	81	Female	
Caucasian	Normal	NA	NA		
0.125	Negative				
LCR 617	LCR 617 PLS1	Not applicable	61	Female	
Caucasian	Normal	NA	NA		
0.122	Negative				
LCR 618	LCR 618 PLS1	Not applicable	60	Female	
Caucasian	Normal	NA	NA		
0.293	Negative				
LCR 619	LCR 619 PLS1	Not applicable	55	Female	
Caucasian	Normal	NA	NA		
0.122	Negative				
LCR 620	LCR 620 PLS1	Not applicable	59	Female	
Caucasian	Normal	NA	NA		
0.494	Negative				
LCR 621	LCR 621 PLS1	Not applicable	79	Female	
Caucasian	Normal	NA	NA		
0.117	Negative				
LCR 622	LCR 622 PLS1	Not applicable	57	Female	
Caucasian	Normal	NA	NA		
0.125	Negative				
LCR 623	LCR 623 PLS1	Not applicable	45	Female	
Caucasian	Normal	NA	NA		
0.835	Negative				
LCR 624	LCR 624 PLS1	Not applicable	71	Female	
Caucasian	Normal	NA	NA		
0.116	Negative				
LCR 625	LCR 625 PLS1	Not applicable	76	Male	
Caucasian	Normal	NA	NA		
0.486	Negative				
LCR 626	LCR 626 PLS1	Not applicable	60	Female	
Caucasian	Normal	NA	NA		
0.603	Negative				

Table2.txt

LCR 627	LCR 627 PLS1	Not applicable	69	Female	Caucasian	Normal
NA	NA	0.861	Negative			
LCR 628	LCR 628 PLS1	Not applicable	54	Female	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 629	LCR 629 PLS1	Not applicable	54	Male	Caucasian	Normal
NA	NA	0.639	Negative			
LCR 630	LCR 630 PLS1	Not applicable	79	Female	Caucasian	Normal
NA	NA	0.298	Negative			
LCR 631	LCR 631 PLS1	Not applicable	59	Female	Caucasian	Normal
NA	NA	0.220	Negative			
LCR 632	LCR 632 PLS1	Not applicable	66	Female	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 633	LCR 633 PLS1	Not applicable	60	Male	Asian	Normal
NA	NA	0.547	Negative			
LCR 634	LCR 634 PLS1	Not applicable	62	Male	Caucasian	Normal
NA	NA	0.121	Negative			
LCR 635	LCR 635 PLS1	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 636	LCR 636 PLS1	Not applicable	72	Female	Caucasian	Normal
NA	NA	0.345	Negative			
LCR 637	LCR 637 PLS1	Not applicable	47	Female	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 638	LCR 638 PLS1	Not applicable	78	Female	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 639	LCR 639 PLS1	Not applicable	71	Male	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 640	LCR 640 PLS1	Not applicable	73	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 641	LCR 641 PLS1	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.705	Negative			
LCR 642	LCR 642 PLS1	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.229	Negative			

Table2.txt

LCR 643	LCR 643 PLS1	Not applicable	61	Male	Caucasian	Normal
NA	NA	0.116	Negative			
LCR 644	LCR 644 PLS1	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 645	LCR 645 PLS1	Not applicable	62	Female	Caucasian	Normal
NA	NA	0.510	Negative			
LCR 646	LCR 646 PLS1	Not applicable	77	Male	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 647	LCR 647 PLS1	Not applicable	76	Female	Caucasian	Normal
NA	NA	0.168	Negative			
LCR 648	LCR 648 PLS1	Not applicable	55	Male	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 649	LCR 649 PLS1	Not applicable	61	Female	Asian	Normal
NA	NA	0.125	Negative			
LCR 650	LCR 650 PLS1	Not applicable	51	Female	Asian	Normal
NA	NA	0.747	Negative			
LCR 652	LCR 652 PLS1	Not applicable	58	Female	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 653	LCR 653 PLS1	Not applicable	75	Female	Caucasian	Normal
NA	NA	0.329	Negative			
LCR 654	LCR 654 PLS1	Not applicable	51	Female	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 655	LCR 655 PLS1	Not applicable	60	Male	Asian	Normal
NA	NA	0.122	Negative			
LCR 658	LCR 658 PLS1	Not applicable	57	Female	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 659	LCR 659 PLS1	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 660	LCR 660 PLS1	Not applicable	61	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 661	LCR 661 PLS1	Not applicable	69	Male	Caucasian	Normal
NA	NA	0.117	Negative			

Table2.txt

LCR 662	LCR 662 PLS1	Not applicable	59	Male	Caucasian	Normal
NA	NA	0.193	Negative			
LCR 663	LCR 663 PLS1	Not applicable	81	Male	Caucasian	Normal
NA	NA	0.317	Negative			
LCR 665	LCR 665 PLS1	Not applicable	68	Male	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 666	LCR 666 PLS1	Not applicable	72	Male	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 667	LCR 667 PLS1	Not applicable	50	Female	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 668	LCR 668 PLS1	Not applicable	80	Female	Caucasian	Normal
NA	NA	0.121	Negative			
LCR 670	LCR 670 PLS1	Not applicable	63	Female	Asian	Normal
NA	NA	0.125	Negative			
LCR 671	LCR 671 PLS1	Not applicable	52	Female	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 672	LCR 672 PLS1	Not applicable	66	Male	Asian	Normal
NA	NA	0.601	Negative			
LCR 673	LCR 673 PLS1	Not applicable	58	Female	Caucasian	Normal
NA	NA	0.116	Negative			
LCR 674	LCR 674 PLS1	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.179	Negative			
LCR 675	LCR 675 PLS1	Not applicable	55	Male	Caucasian	Normal
NA	NA	0.187	Negative			
LCR 676	LCR 676 PLS1	Not applicable	63	Male	Caucasian	Normal
NA	NA	0.245	Negative			
LCR 677	LCR 677 PLS1	Not applicable	73	Male	Caucasian	Normal
NA	NA	0.156	Negative			
LCR 678	LCR 678 PLS1	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.186	Negative			
LCR 679	LCR 679 PLS1	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.125	Negative			

Table2.txt

LCR 680	LCR 680 PLS1	Not applicable	64	Female	Caucasian	Normal
NA	NA	0.699	Negative			
LCR 681	LCR 681 PLS1	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.597	Negative			
LCR 682	LCR 682 PLS1	Not applicable	65	Female	Caucasian	Normal
NA	NA	0.631	Negative			
LCR 683	LCR 683 PLS1	Not applicable	82	Male	Caucasian	Normal
NA	NA	0.322	Negative			
LCR 684	LCR 684 PLS1	Not applicable	56	Female	Asian	Normal
NA	NA	0.121	Negative			
LCR 685	LCR 685 PLS1	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.845	Negative			
LCR 686	LCR 686 PLS1	Not applicable	58	Female	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 687	LCR 687 PLS1	Not applicable	51	Female	Caucasian	Normal
NA	NA	0.121	Negative			
LCR 688	LCR 688 PLS1	Not applicable	80	Male	Caucasian	Normal
NA	NA	0.419	Negative			
LCR 689	LCR 689 PLS1	Not applicable	57	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 690	LCR 690 PLS1	Not applicable	81	Male	Asian	Normal
NA	NA	0.123	Negative			
LCR 691	LCR 691 PLS1	Not applicable	53	Male	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 692	LCR 692 PLS1	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.770	Negative			
LCR 693	LCR 693 PLS1	Not applicable	61	Male	Caucasian	Normal
NA	NA	0.116	Negative			
LCR 694	LCR 694 PLS1	Not applicable	59	Female	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 697	LCR 697 PLS1	Not applicable	61	Male	Caucasian	Normal
NA	NA	0.308	Negative			

Table2.txt

LCR 698	LCR 698 PLS1	Not applicable	74	Male	Caucasian	Normal
NA	NA	0.328	Negative			
LCR 699	LCR 699 PLS1	Not applicable	71	Female	Caucasian	Normal
NA	NA	0.123	Negative			
LCR 700	LCR 700 PLS1	Not applicable	78	Female	Caucasian	Normal
NA	NA	0.755	Negative			
LCR 701	LCR 701 PLS1	Not applicable	52	Male	Caucasian	Normal
NA	NA	0.630	Negative			
LCR 702	LCR 702 PLS1	Not applicable	85	Female	Caucasian	Normal
NA	NA	0.968	Positive			
LCR 703	LCR 703 PLS1	Not applicable	85	Male	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 704	LCR 704 PLS1	Not applicable	81	Male	Caucasian	Normal
NA	NA	1.000	Positive			
LCR 705	LCR 705 PLS1	Not applicable	54	Female	Caucasian	Normal
NA	NA	0.485	Negative			
LCR 706	LCR 706 PLS1	Not applicable	66	Male	Unknown	Normal
NA	NA	0.192	Negative			
LCR 707	LCR 707 PLS1	Not applicable	82	Male	Caucasian	Normal
NA	NA	0.216	Negative			
LCR 709	LCR 709 PLS1	Not applicable	67	Female	Caucasian	Normal
NA	NA	0.400	Negative			
LCR 710	LCR 710 PLS1	Not applicable	71	Male	Caucasian	Normal
NA	NA	0.758	Negative			
LCR 711	LCR 711 PLS1	Not applicable	66	Male	Unknown	Normal
NA	NA	0.123	Negative			
LCR 712	LCR 712 PLS1	Not applicable	61	Male	Unknown	Normal
NA	NA	0.121	Negative			
LCR 713	LCR 713 PLS1	Not applicable	79	Male	Caucasian	Normal
NA	NA	0.861	Negative			
LCR 714	LCR 714 PLS1	Not applicable	72	Female	Caucasian	Normal
NA	NA	0.123	Negative			

Table2.txt

LCR 715	LCR 715 PLS1	Not applicable	52	Male	Caucasian	Normal
NA	NA	0.122	Negative			
LCR 716	LCR 716 PLS1	Not applicable	69	Male	Caucasian	Normal
NA	NA	0.538	Negative			
LCR 717	LCR 717 PLS1	Not applicable	75	Female	Caucasian	Normal
NA	NA	0.507	Negative			
LCR 718	LCR 718 PLS1	Not applicable	52	Male	Asian	Normal
NA	NA	0.523	Negative			
LCR 719	LCR 719 PLS1	Not applicable	60	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 720	LCR 720 PLS1	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.116	Negative			
LCR 721	LCR 721 PLS1	Not applicable	75	Male	Caucasian	Normal
NA	NA	0.517	Negative			
LCR 722	LCR 722 PLS1	Not applicable	80	Male	Caucasian	Normal
NA	NA	0.377	Negative			
LCR 723	LCR 723 PLS1	Not applicable	61	Female	Asian	Normal
NA	NA	0.117	Negative			
LCR 724	LCR 724 PLS1	Not applicable	52	Female	Asian	Normal
NA	NA	0.122	Negative			
LCR 725	LCR 725 PLS1	Not applicable	65	Female	Caucasian	Normal
NA	NA	0.184	Negative			
LCR 726	LCR 726 PLS1	Not applicable	60	Female	Unknown	Normal
NA	NA	0.564	Negative			
LCR 727	LCR 727 PLS1	Not applicable	65	Male	Unknown	Normal
NA	NA	0.125	Negative			
LCR 728	LCR 728 PLS1	Not applicable	51	Male	Unknown	Normal
NA	NA	0.303	Negative			
LCR 729	LCR 729 PLS1	Not applicable	67	Male	Unknown	Normal
NA	NA	0.122	Negative			
LCR 730	LCR 730 PLS1	Not applicable	71	Male	Caucasian	Normal
NA	NA	0.117	Negative			

Table2.txt

LCR 731	LCR 731 PLS1	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.294	Negative			
LCR 732	LCR 732 PLS1	Not applicable	50	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 733	LCR 733 PLS1	Not applicable	80	Male	Caucasian	Normal
NA	NA	0.305	Negative			
LCR 734	LCR 734 PLS1	Not applicable	77	Female	Unknown	Normal
NA	NA	0.377	Negative			
LCR 736	LCR 736 PLS1	Not applicable	59	Male	Caucasian	Normal
NA	NA	0.404	Negative			
LCR 737	LCR 737 PLS1	Not applicable	81	Male	Caucasian	Normal
NA	NA	0.863	Negative			
LCR 738	LCR 738 PLS1	Not applicable	84	Female	Caucasian	Normal
NA	NA	0.591	Negative			
LCR 739	LCR 739 PLS1	Not applicable	36	Male	Caucasian	Normal
NA	NA	0.390	Negative			
LCR 740	LCR 740 PLS1	Not applicable	81	Male	Caucasian	Normal
NA	NA	0.411	Negative			
LCR 741	LCR 741 PLS1	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.374	Negative			
LCR 742	LCR 742 PLS1	Not applicable	50	Male	Caucasian	Normal
NA	NA	0.860	Negative			
LCR 743	LCR 743 PLS1	Not applicable	77	Male	Caucasian	Normal
NA	NA	0.603	Negative			
LCR 745	LCR 745 PLS1	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.680	Negative			
LCR 746	LCR 746 PLS1	Not applicable	53	Male	Caucasian	Normal
NA	NA	0.553	Negative			
LCR 747	LCR 747 PLS1	Not applicable	80	Male	Caucasian	Normal
NA	NA	0.327	Negative			
LCR 749	LCR 749 PLS1	Not applicable	70	Female	Caucasian	Normal
NA	NA	0.221	Negative			

Table2.txt

LCR 750	LCR 750 PLS1	Not applicable	78	Male	Caucasian	Normal
NA	NA	0.851	Negative			
LCR 751	LCR 751 PLS1	Not applicable	76	Male	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 752	LCR 752 PLS1	Not applicable	88	Male	Caucasian	Normal
NA	NA	0.855	Negative			
LCR 753	LCR 753 PLS1	Not applicable	80	Male	Caucasian	Normal
NA	NA	0.193	Negative			
LCR 754	LCR 754 PLS1	Not applicable	40	Male	Caucasian	Normal
NA	NA	0.121	Negative			
LCR 755	LCR 755 PLS1	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.125	Negative			
LCR 757	LCR 757 PLS1	Not applicable	75	Female	Caucasian	Normal
NA	NA	0.387	Negative			
LCR 758	LCR 758 PLS1	Not applicable	73	Male	Caucasian	Normal
NA	NA	0.473	Negative			
LCR 759	LCR 759 PLS1	Not applicable	55	Male	Caucasian	Normal
NA	NA	0.736	Negative			
LCR 760	LCR 760 PLS1	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.401	Negative			
LCR 761	LCR 761 PLS1	Not applicable	62	Male	Asian	Normal
NA	NA	0.117	Negative			
LCR 762	LCR 762 PLS1	Not applicable	73	Male	Caucasian	Normal
NA	NA	0.117	Negative			
LCR 763	LCR 763 PLS1	Not applicable	60	Male	Caucasian	Normal
NA	NA	0.121	Negative			
LCR 764	LCR 764 PLS1	Not applicable	72	Female	Caucasian	Normal
NA	NA	0.184	Negative			
LCR 765	LCR 765 PLS1	Not applicable	51	Male	Caucasian	Normal
NA	NA	0.339	Negative			
LCR 766	LCR 766 PLS1	Not applicable	76	Female	Caucasian	Normal
NA	NA	0.116	Negative			

Table2.txt

LCR 768	LCR 768 PLS1	Not applicable	56	Male
Unknown	Normal	NA	NA	
0.886	Positive			
LCR 769	LCR 769 PLS1	Not applicable	51	Male
Caucasian	Normal	NA	NA	
0.338	Negative			
LCR 770	LCR 770 PLS1	Not applicable	34	Male
Asian	Normal	NA	NA	
0.121	Negative			
LCR 771	LCR 771 PLS1	Not applicable	70	Male
Caucasian	Normal	NA	NA	
0.388	Negative			
LCR 772	LCR 772 PLS1	Not applicable	73	Male
Caucasian	Normal	NA	NA	
0.121	Negative			
LCR 773	LCR 773 PLS1	Not applicable	44	Male
Caucasian	Normal	NA	NA	
0.156	Negative			
LCR 774	LCR 774 PLS1	Not applicable	67	Female
Caucasian	Normal	NA	NA	
0.600	Negative			
LCR 775	LCR 775 PLS1	Not applicable	51	Female
Caucasian	Normal	NA	NA	
0.935	Positive			
LCR 776	LCR 776 PLS1	Not applicable	50	Male
Caucasian	Normal	NA	NA	
0.117	Negative			
LCR 777	LCR 777 PLS1	Not applicable	86	Female
Caucasian	Normal	NA	NA	
0.511	Negative			
LCR 778	LCR 778 PLS1	Not applicable	57	Male
Unknown	Normal	NA	NA	
0.209	Negative			
LCR 779	LCR 779 PLS1	Not applicable	65	Female
Unknown	Normal	NA	NA	
0.721	Negative			
LCR 780	LCR 780 PLS1	Not applicable	65	Female
Unknown	Normal	NA	NA	
0.122	Negative			
LCR 781	LCR 781 PLS1	Not applicable	71	Female
Unknown	Normal	NA	NA	
0.125	Negative			
LCR 782	LCR 782 PLS1	Not applicable	56	Female
Caucasian	Normal	NA	NA	
0.220	Negative			
LCR 783	LCR 783 PLS1	Not applicable	68	Male
Caucasian	Normal	NA	NA	
0.703	Negative			

Table2.txt

LCR 784	LCR 784 PLS1	Not applicable	62	Female	Caucasian	Normal
NA	NA	0.638	Negative			
LCR 785	LCR 785 PLS1	Not applicable	55	Male	Caucasian	Normal
NA	NA	0.827	Negative			
LCR 786	LCR 786 PLS1	Not applicable	75	Female	Caucasian	Normal
NA	NA	0.333	Negative			
LCR 812	LCR 812 PLS1	LCR 812 PT1	77	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.999	Positive			
LCR 814	LCR 814 PLS1	LCR 814 PT1	61	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.711	Negative			
NL 918	NL PLS 918	Not applicable	24	Male	Hispanic	Normal
NA	NA	0.117	Negative			
NL 919	NL PLS 919	Not applicable	18	Male	Hispanic	Normal
NA	NA	0.875	Positive			
NL 920	NL PLS 920	Not applicable	23	Male	Caucasian	Normal
NA	NA	0.122	Negative			
NL 921	NL PLS 921	Not applicable	23	Male	Hispanic	Normal
NA	NA	0.125	Negative			
NL 922	NL PLS 922	Not applicable	30	Male	Hispanic	Normal
NA	NA	0.116	Negative			
NL 923	NL PLS 923	Not applicable	27	Male	Hispanic	Normal
NA	NA	0.610	Negative			
NL 924	NL PLS 924	Not applicable	25	Male	Black	Normal
NA	NA	0.335	Negative			
NL 925	NL PLS 925	Not applicable	29	Male	Black	Normal
NA	NA	0.121	Negative			
NL 930	NL PLS 930	Not applicable	25	Male	Black	Normal
NA	NA	0.192	Negative			
NL 931	NL PLS 931	Not applicable	29	Male	Black	Normal
NA	NA	0.300	Negative			
NL 932	NL PLS 932	Not applicable	25	Male	Black	Normal
NA	NA	0.116	Negative			

Table2.txt

NL 938	NL PLS 938	Not applicable	29	Male
Black	Normal	NA	NA	
0.117	Negative			
NL 939	NL PLS 939	Not applicable	28	Male
Black	Normal	NA	NA	
0.599	Negative			
NL 940	NL PLS 940	Not applicable	29	Male
Hispanic	Normal	NA	NA	
0.117	Negative			
NL 941	NL PLS 941	Not applicable	30	Male
Black	Normal	NA	NA	
0.116	Negative			
NL 942	NL PLS 942	Not applicable	30	Male
Black	Normal	NA	NA	
0.660	Negative			
NL 943	NL PLS 943	Not applicable	28	Male
Hispanic	Normal	NA	NA	
0.122	Negative			
NL 944	NL PLS 944	Not applicable	23	Male
Hispanic	Normal	NA	NA	
0.341	Negative			
NL 945	NL PLS 945	Not applicable	29	Male
Caucasian	Normal	NA	NA	
0.843	Negative			
NL 946	NL PLS 946	Not applicable	26	Male
Hispanic	Normal	NA	NA	
0.382	Negative			
NL 947	NL PLS 947	Not applicable	25	Female
Hispanic	Normal	NA	NA	
0.558	Negative			
NL 948	NL PLS 948	Not applicable	24	Male
Black	Normal	NA	NA	
0.125	Negative			
NL 949	NL PLS 949	Not applicable	22	Male
Caucasian	Normal	NA	NA	
0.117	Negative			
NL 950	NL PLS 950	Not applicable	28	Male
Black	Normal	NA	NA	
0.320	Negative			
NL 951	NL PLS 951	Not applicable	18	Male
Caucasian	Normal	NA	NA	
0.116	Negative			
NL 952	NL PLS 952	Not applicable	24	Male
Caucasian	Normal	NA	NA	
0.230	Negative			
NL 964	NL PLS 964	Not applicable	27	Male
Hispanic	Normal	NA	NA	
0.125	Negative			

Table2.txt

NL 965	NL PLS 965	Not applicable	28	Male
Black	Normal	NA	NA	
0.612	Negative			
NL 1160	NL PLSA 1160	Not applicable	19	Male
Black	Normal	NA	NA	
0.677	Negative			
NL 1163	NL PLSA 1163	Not applicable	29	Male
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1164	NL PLSA 1164	Not applicable	28	Male
Hispanic	Normal	NA	NA	
0.319	Negative			
NL 1165	NL PLSA 1165	Not applicable	19	Male
Hispanic	Normal	NA	NA	
0.303	Negative			
NL 1166	NL PLSA 1166	Not applicable	30	Female
Black	Normal	NA	NA	
0.117	Negative			
NL 1167	NL PLSA 1167	Not applicable	29	Male
Black	Normal	NA	NA	
0.329	Negative			
NL 1168	NL PLSA 1168	Not applicable	29	Male
Black	Normal	NA	NA	
0.121	Negative			
NL 1169	NL PLSA 1169	Not applicable	24	Female
Black	Normal	NA	NA	
0.125	Negative			
NL 1170	NL PLSA 1170	Not applicable	26	Male
Hispanic	Normal	NA	NA	
0.125	Negative			
NL 1171	NL PLSA 1171	Not applicable	29	Male
Hispanic	Normal	NA	NA	
0.122	Negative			
NL 1172	NL PLSA 1172	Not applicable	27	Male
Hispanic	Normal	NA	NA	
0.334	Negative			
NL 1173	NL PLSA 1173	Not applicable	26	Male
Hispanic	Normal	NA	NA	
0.125	Negative			
NL 1174	NL PLSA 1174	Not applicable	30	Male
Black	Normal	NA	NA	
0.122	Negative			
NL 1175	NL PLSA 1175	Not applicable	28	Male
Hispanic	Normal	NA	NA	
0.121	Negative			
NL 1176	NL PLSA 1176	Not applicable	29	Male
Hispanic	Normal	NA	NA	
0.125	Negative			

Table2.txt

NL 1177	NL PLSA 1177	Not applicable	23	Female
Hispanic	Normal	NA	NA	
0.338	Negative			
NL 1178	NL PLSA 1178	Not applicable	26	Male
Hispanic	Normal	NA	NA	
0.123	Negative			
NL 1179	NL PLSA 1179	Not applicable	29	Female
Hispanic	Normal	NA	NA	
0.316	Negative			
NL 1180	NL PLSA 1180	Not applicable	25	Male
Hispanic	Normal	NA	NA	
0.121	Negative			
NL 1181	NL PLSA 1181	Not applicable	26	Male
Hispanic	Normal	NA	NA	
0.633	Negative			
NL 1182	NL PLSA 1182	Not applicable	26	Male
Black	Normal	NA	NA	
0.322	Negative			
NL 1183	NL PLSA 1183	Not applicable	20	Male
Black	Normal	NA	NA	
0.297	Negative			
NL 1184	NL PLSA 1184	Not applicable	24	Male
Black	Normal	NA	NA	
0.357	Negative			
NL 1185	NL PLSA 1185	Not applicable	28	Female
Hispanic	Normal	NA	NA	
0.125	Negative			
NL 1186	NL PLSA 1186	Not applicable	30	Male
Black	Normal	NA	NA	
0.117	Negative			
NL 1187	NL PLSA 1187	Not applicable	30	Male
Hispanic	Normal	NA	NA	
0.117	Negative			
NL 1188	NL PLSA 1188	Not applicable	28	Female
Hispanic	Normal	NA	NA	
0.316	Negative			
NL 1189	NL PLSA 1189	Not applicable	24	Male
Black	Normal	NA	NA	
0.317	Negative			
NL 1190	NL PLSA 1190	Not applicable	25	Male
Black	Normal	NA	NA	
0.121	Negative			
NL 1191	NL PLSA 1191	Not applicable	29	Female
Hispanic	Normal	NA	NA	
0.320	Negative			
NL 1192	NL PLSA 1192	Not applicable	27	Male
Hispanic	Normal	NA	NA	
0.125	Negative			

Table2.txt

NL 1193	NL PLSA 1193	Not applicable	28	Female	Hispanic	Normal
NA	NA	0.125	Negative			
NL 1194	NL PLSA 1194	Not applicable	26	Male	Caucasian	Normal
NA	NA	0.334	Negative			
NL 1195	NL PLSA 1195	Not applicable	27	Male	Black	Normal
NA	NA	0.311	Negative			
NL 1196	NL PLSA 1196	Not applicable	22	Male	Hispanic	Normal
NA	NA	0.309	Negative			
NL 1197	NL PLSA 1197	Not applicable	21	Male	Hispanic	Normal
NA	NA	0.489	Negative			
NL 1198	NL PLSA 1198	Not applicable	26	Female	Black	Normal
NA	NA	0.125	Negative			
NL 1199	NL PLSA 1199	Not applicable	28	Female	Hispanic	Normal
NA	NA	0.125	Negative			
NL 1200	NL PLSA 1200	Not applicable	19	Male	Hispanic	Normal
NA	NA	0.316	Negative			
NL 1201	NL PLSA 1201	Not applicable	30	Male	Hispanic	Normal
NA	NA	0.125	Negative			
NL 1202	NL PLSA 1202	Not applicable	27	Male	Hispanic	Normal
NA	NA	0.117	Negative			
NL 1203	NL PLSA 1203	Not applicable	24	Male	Black	Normal
NA	NA	0.322	Negative			
NL 1204	NL PLSA 1204	Not applicable	25	Male	Black	Normal
NA	NA	0.125	Negative			
NL 1205	NL PLSA 1205	Not applicable	27	Male	Black	Normal
NA	NA	0.125	Negative			
NL 1206	NL PLSA 1206	Not applicable	28	Male	Black	Normal
NA	NA	0.323	Negative			
NL 1207	NL PLSA 1207	Not applicable	21	Male	Hispanic	Normal
NA	NA	0.125	Negative			
NL 1208	NL PLSA 1208	Not applicable	30	Male	Black	Normal
NA	NA	0.125	Negative			

Table2.txt

NL 1209	NL PLSA 1209	Not applicable	29	Male	Black	Normal
NA	NA	0.302	Negative			
NL 1210	NL PLSA 1210	Not applicable	21	Male	Black	Normal
NA	NA	0.123	Negative			
NL 1211	NL PLSA 1211	Not applicable	29	Male	Hispanic	Normal
NA	NA	0.310	Negative			
NL 1212	NL PLSA 1212	Not applicable	27	Female	Hispanic	Normal
NA	NA	0.121	Negative			
NL 1213	NL PLSA 1213	Not applicable	26	Male	Black	Normal
NA	NA	0.122	Negative			
NL 1214	NL PLSA 1214	Not applicable	24	Male	Hispanic	Normal
NA	NA	0.121	Negative			
NL 1215	NL PLSA 1215	Not applicable	25	Male	Hispanic	Normal
NA	NA	0.122	Negative			
NL 1216	NL PLSA 1216	Not applicable	29	Male	Black	Normal
NA	NA	0.565	Negative			
NL 1217	NL PLSA 1217	Not applicable	24	Male	Hispanic	Normal
NA	NA	0.121	Negative			
NL 1218	NL PLSA 1218	Not applicable	28	Male	Black	Normal
NA	NA	0.320	Negative			
NL 1219	NL PLSA 1219	Not applicable	25	Male	Black	Normal
NA	NA	0.117	Negative			
NL 1220	NL PLSA 1220	Not applicable	30	Male	Hispanic	Normal
NA	NA	0.117	Negative			
NL 1221	NL PLSA 1221	Not applicable	28	Male	Black	Normal
NA	NA	0.125	Negative			
NL 1222	NL PLSA 1222	Not applicable	24	Male	Hispanic	Normal
NA	NA	0.121	Negative			
NL 1223	NL PLSA 1223	Not applicable	28	Male	Hispanic	Normal
NA	NA	0.121	Negative			
NL 1224	NL PLSA 1224	Not applicable	27	Female	Black	Normal
NA	NA	0.116	Negative			

Table2.txt

NL 1225	NL PLSA 1225	Not applicable	28	Male	Hispanic	Normal	NA
NA	0.123	Negative					
NL 1226	NL PLSA 1226	Not applicable	26	Female	Black	Normal	NA
NA	0.117	Negative					
NL 1227	NL PLSA 1227	Not applicable	27	Male	Black	Normal	NA
NA	0.125	Negative					
NL 1228	NL PLSA 1228	Not applicable	30	Male	Black	Normal	NA
NA	0.117	Negative					
NL 1229	NL PLSA 1229	Not applicable	29	Male	Hispanic	Normal	NA
NA	0.125	Negative					
NL 1230	NL PLSA 1230	Not applicable	28	Male	Hispanic	Normal	NA
NA	0.125	Negative					
NL 1231	NL PLSA 1231	Not applicable	28	Female	Hispanic	Normal	NA
NA	0.121	Negative					
NL 1232	NL PLSA 1232	Not applicable	29	Male	Hispanic	Normal	NA
NA	0.117	Negative					
NL 1233	NL PLSA 1233	Not applicable	26	Male	Hispanic	Normal	NA
NA	0.355	Negative					
NL 1234	NL PLSA 1234	Not applicable	22	Male	Hispanic	Normal	NA
NA	0.121	Negative					
NL 1235	NL PLSA 1235	Not applicable	27	Male	Caucasian	Normal	NA
NA	0.575	Negative					
NL 1236	NL PLSA 1236	Not applicable	28	Male	Hispanic	Normal	NA
NA	0.122	Negative					
NL 1237	NL PLSA 1237	Not applicable	21	Male	Black	Normal	NA
NA	0.121	Negative					
NL 1238	NL PLSA 1238	Not applicable	22	Male	Black	Normal	NA
NA	0.320	Negative					
NL 1239	NL PLSA 1239	Not applicable	25	Male	Black	Normal	NA
NA	0.121	Negative					
NL 1240	NL PLSA 1240	Not applicable	27	Male	Black	Normal	NA
NA	0.258	Negative					

Table2.txt

NL 1241	NL PLSA 1241	Not applicable	26	Male	Black
Normal	NA	NA	0.532	Negative	
NL 1242	NL PLSA 1242	Not applicable	29	Male	Black
Normal	NA	NA	0.123	Negative	
NL 1243	NL PLSA 1243	Not applicable	26	Male	Black
Normal	NA	NA	0.121	Negative	
NL 1244	NL PLSA 1244	Not applicable	19	Male	Black
Normal	NA	NA	0.321	Negative	
NL 1245	NL PLSA 1245	Not applicable	29	Male	Hispanic
Normal	NA	NA	0.309	Negative	
NL 1246	NL PLSA 1246	Not applicable	24	Male	Black
Normal	NA	NA	0.123	Negative	
NL 1247	NL PLSA 1247	Not applicable	26	Male	Hispanic
Normal	NA	NA	0.727	Negative	
NL 1248	NL PLSA 1248	Not applicable	24	Male	Hispanic
Normal	NA	NA	0.121	Negative	
NL 1249	NL PLSA 1249	Not applicable	27	Female	Black
Normal	NA	NA	0.123	Negative	
NL 1250	NL PLSA 1250	Not applicable	28	Female	Hispanic
Normal	NA	NA	0.248	Negative	
NL 1251	NL PLSA 1251	Not applicable	23	Female	Black
Normal	NA	NA	0.121	Negative	
NL 1252	NL PLSA 1252	Not applicable	21	Female	Caucasian
Normal	NA	NA	0.374	Negative	
NL 1253	NL PLSA 1253	Not applicable	29	Female	Black
Normal	NA	NA	0.121	Negative	
NL 1254	NL PLSA 1254	Not applicable	25	Female	Black
Normal	NA	NA	0.584	Negative	
NL 1255	NL PLSA 1255	Not applicable	30	Female	Black
Normal	NA	NA	0.297	Negative	
NL 1256	NL PLSA 1256	Not applicable	24	Female	Black
Normal	NA	NA	0.117	Negative	

Table2.txt

NL 1257	NL PLSA 1257	Not applicable	30	Female	Black	Normal
NA	NA	0.341	Negative			
NL 1258	NL PLSA 1258	Not applicable	30	Female	Black	Normal
NA	NA	0.324	Negative			
NL 1259	NL PLSA 1259	Not applicable	29	Female	Black	Normal
NA	NA	0.604	Negative			
NL 1260	NL PLSA 1260	Not applicable	30	Female	Hispanic	Normal
NA	NA	0.116	Negative			
NL 1291	NL PLSA 1291	Not applicable	28	Female	Hispanic	Normal
NA	NA	0.117	Negative			
NL 1292	NL PLSA 1292	Not applicable	26	Female	Black	Normal
NA	NA	0.376	Negative			
NL 1293	NL PLSA 1293	Not applicable	27	Female	Hispanic	Normal
NA	NA	0.514	Negative			
NL 1294	NL PLSA 1294	Not applicable	28	Female	Hispanic	Normal
NA	NA	0.416	Negative			
NL 1295	NL PLSA 1295	Not applicable	30	Female	Hispanic	Normal
NA	NA	0.117	Negative			
NL 1296	NL PLSA 1296	Not applicable	25	Female	Hispanic	Normal
NA	NA	0.116	Negative			
NL 1297	NL PLSA 1297	Not applicable	25	Female	Hispanic	Normal
NA	NA	0.117	Negative			
NL 1298	NL PLSA 1298	Not applicable	30	Female	Hispanic	Normal
NA	NA	0.122	Negative			
NL 1299	NL PLSA 1299	Not applicable	21	Female	Black	Normal
NA	NA	0.125	Negative			
NL 1300	NL PLSA 1300	Not applicable	30	Female	Black	Normal
NA	NA	0.242	Negative			
NL 1301	NL PLSA 1301	Not applicable	28	Female	Caucasian	Normal
NA	NA	0.573	Negative			
NL 1302	NL PLSA 1302	Not applicable	23	Female	Black	Normal
NA	NA	0.833	Negative			

Table2.txt

NL 1303	NL PLSA 1303	Not applicable	27	Female	Black
Normal	NA	NA	0.122	Negative	
NL 1304	NL PLSA 1304	Not applicable	26	Female	Black
Normal	NA	NA	0.117	Negative	
NL 1305	NL PLSA 1305	Not applicable	28	Female	Black
Normal	NA	NA	0.192	Negative	
NL 1306	NL PLSA 1306	Not applicable	26	Female	Hispanic
Normal	NA	NA	0.409	Negative	
NL 1307	NL PLSA 1307	Not applicable	30	Female	Caucasian
Normal	NA	NA	0.125	Negative	
NL 1308	NL PLSA 1308	Not applicable	26	Female	Black
Normal	NA	NA	0.121	Negative	
NL 1309	NL PLSA 1309	Not applicable	21	Female	Black
Normal	NA	NA	0.125	Negative	
NL 1310	NL PLSA 1310	Not applicable	23	Female	Black
Normal	NA	NA	0.414	Negative	
NL 1311	NL PLSA 1311	Not applicable	23	Female	Black
Normal	NA	NA	0.553	Negative	
NL 1312	NL PLSA 1312	Not applicable	23	Female	Black
Normal	NA	NA	0.121	Negative	
NL 1313	NL PLSA 1313	Not applicable	27	Female	Black
Normal	NA	NA	0.117	Negative	
NL 1314	NL PLSA 1314	Not applicable	18	Female	Hispanic
Normal	NA	NA	0.125	Negative	
NL 1315	NL PLSA 1315	Not applicable	27	Female	Black
Normal	NA	NA	0.576	Negative	
NL 1316	NL PLSA 1316	Not applicable	25	Female	Black
Normal	NA	NA	0.117	Negative	
NL 1317	NL PLSA 1317	Not applicable	30	Female	Black
Normal	NA	NA	0.362	Negative	
NL 1318	NL PLSA 1318	Not applicable	21	Female	Black
Normal	NA	NA	0.121	Negative	

Table2.txt

NL 1319 NL PLSA 1319 Not applicable 28 Female
Hispanic Normal NA NA
0.116 Negative
NL 1320 NL PLSA 1320 Not applicable 28 Female
Black Normal NA NA
0.125 Negative
NL 1321 NL PLSA 1321 Not applicable 26 Female
Hispanic Normal NA NA
0.121 Negative
NL 1322 NL PLSA 1322 Not applicable 19 Female
Hispanic Normal NA NA
0.125 Negative
NL 1323 NL PLSA 1323 Not applicable 27 Female
Hispanic Normal NA NA
0.121 Negative
NL 1324 NL PLSA 1324 Not applicable 21 Female
Hispanic Normal NA NA
0.123 Negative
NL 1325 NL PLSA 1325 Not applicable 23 Female
Black Normal NA NA
0.331 Negative
NL 1326 NL PLSA 1326 Not applicable 29 Female
Hispanic Normal NA NA
0.356 Negative
NL 1327 NL PLSA 1327 Not applicable 24 Female
Hispanic Normal NA NA
0.122 Negative
NL 1328 NL PLSA 1328 Not applicable 21 Male
Black/Hispanic Normal NA NA
0.125 Negative
NL 1329 NL PLSA 1329 Not applicable 22 Male
Black Normal NA NA
0.125 Negative
NL 1330 NL PLSA 1330 Not applicable 29 Male
Black Normal NA NA
0.121 Negative
NL 1331 NL PLSA 1331 Not applicable 18 Female
Caucasian/Hispanic Normal NA NA
0.122 Negative
NL 1332 NL PLSA 1332 Not applicable 30 Male
Black Normal NA NA
0.117 Negative
NL 1333 NL PLSA 1333 Not applicable 25 Male
Black Normal NA NA
0.123 Negative
NL 1334 NL PLSA 1334 Not applicable 23 Male
Black Normal NA NA
0.489 Negative

Table2.txt

```
   NL 1335        NL PLSA 1335       Not applicable      30     Male
Black                 Normal        NA                  NA
0.849                Negative
   NL 1336        NL PLSA 1336       Not applicable      21     Male
Caucasian/Hispanic           Normal        NA                NA
      0.325               Negative
   NL 1337        NL PLSA 1337       Not applicable      30    Female
Black                 Normal        NA                  NA
0.122                Negative
   NL 1338        NL PLSA 1338       Not applicable      27     Male
Black                 Normal        NA                  NA
0.188                Negative
   NL 1339        NL PLSA 1339       Not applicable      21     Male
Black                 Normal        NA                  NA
0.117                Negative
   NL 1340        NL PLSA 1340       Not applicable      21     Male
Black                 Normal        NA                  NA
0.125                Negative
   NL 1341        NL PLSA 1341       Not applicable      17    Female
Caucasian/Hispanic           Normal        NA                NA
      0.125               Negative
   NL 1342        NL PLSA 1342       Not applicable      20     Male
Black/Hispanic             Normal        NA                NA
    0.205               Negative
   NL 1343        NL PLSA 1343       Not applicable      19     Male
Black                 Normal        NA                  NA
0.122                Negative
   NL 1344        NL PLSA 1344       Not applicable      22     Male
Black/Hispanic             Normal        NA                NA
    0.125               Negative
   NL 1345        NL PLSA 1345       Not applicable      20     Male
Caucasian/Hispanic           Normal        NA                NA
      0.125               Negative
   NL 1346        NL PLSA 1346       Not applicable      30     Male
Black                 Normal        NA                  NA
0.346                Negative
   NL 1347        NL PLSA 1347       Not applicable      26     Male
Caucasian/Hispanic           Normal        NA                NA
      0.343               Negative
   NL 1348        NL PLSA 1348       Not applicable      23     Male
Black                 Normal        NA                  NA
0.125                Negative
   NL 1349        NL PLSA 1349       Not applicable      28     Male
Black                 Normal        NA                  NA
0.117                Negative
   NL 1350        NL PLSA 1350       Not applicable      23    Female
Black                 Normal        NA                  NA
0.397                Negative
```

Table2.txt

NL 1351 NL PLSA 1351 Not applicable 29 Female
Black/Hispanic Normal NA NA
0.317 Negative
NL 1352 NL PLSA 1352 Not applicable 21 Male
Caucasian/Hispanic Normal NA NA
0.125 Negative
NL 1353 NL PLSA 1353 Not applicable 23 Male
Black Normal NA NA
0.593 Negative
NL 1354 NL PLSA 1354 Not applicable 26 Male
Black Normal NA NA
0.299 Negative
NL 1355 NL PLSA 1355 Not applicable 29 Male
Black Normal NA NA
0.116 Negative
NL 1356 NL PLSA 1356 Not applicable 25 Female
Caucasian/Hispanic Normal NA NA
0.327 Negative
NL 1357 NL PLSA 1357 Not applicable 24 Male
Caucasian/Hispanic Normal NA NA
0.121 Negative
NL 1358 NL PLSA 1358 Not applicable 25 Female
Black Normal NA NA
0.553 Negative
NL 1359 NL PLSA 1359 Not applicable 29 Female
Caucasian/Hispanic Normal NA NA
0.570 Negative
NL 1360 NL PLSA 1360 Not applicable 28 Male
Black Normal NA NA
0.125 Negative
NL 1361 NL PLSA 1361 Not applicable 30 Male
Black Normal NA NA
0.123 Negative
NL 1362 NL PLSA 1362 Not applicable 30 Male
Black Normal NA NA
0.122 Negative
NL 1363 NL PLSA 1363 Not applicable 29 Male
Caucasian Normal NA NA
0.125 Negative
NL 1364 NL PLSA 1364 Not applicable 22 Male
Black/Hispanic Normal NA NA
0.441 Negative
NL 1365 NL PLSA 1365 Not applicable 23 Male
Caucasian/Hispanic Normal NA NA
0.325 Negative
NL 1366 NL PLSA 1366 Not applicable 24 Male
Black Normal NA NA
0.125 Negative

Table2.txt

NL 1367 NL PLSA 1367 Not applicable 21 Male
Black Normal NA NA
0.383 Negative
NL 1368 NL PLSA 1368 Not applicable 25 Male
Black Normal NA NA
0.121 Negative
NL 1369 NL PLSA 1369 Not applicable 21 Male
Caucasian/Hispanic Normal NA NA
0.618 Negative
NL 1370 NL PLSA 1370 Not applicable 28 Male
Black Normal NA NA
0.304 Negative
NL 1371 NL PLSA 1371 Not applicable 28 Male
Black Normal NA NA
0.116 Negative
NL 1372 NL PLSA 1372 Not applicable 22 Male
Black/Hispanic Normal NA NA
0.125 Negative
NL 1373 NL PLSA 1373 Not applicable 26 Male
Black Normal NA NA
0.311 Negative
NL 1374 NL PLSA 1374 Not applicable 26 Male
Black Normal NA NA
0.117 Negative
NL 1375 NL PLSA 1375 Not applicable 30 Male
Caucasian/Hispanic Normal NA NA
0.117 Negative
NL 1376 NL PLSA 1376 Not applicable 24 Male
Black Normal NA NA
0.121 Negative
NL 1377 NL PLSA 1377 Not applicable 24 Female
Caucasian/Hispanic Normal NA NA
0.319 Negative
NL 1378 NL PLSA 1378 Not applicable 27 Male
Black Normal NA NA
0.122 Negative
NL 1379 NL PLSA 1379 Not applicable 28 Male
Caucasian/Hispanic Normal NA NA
0.125 Negative
NL 1380 NL PLSA 1380 Not applicable 21 Male
Black Normal NA NA
0.125 Negative
NL 1381 NL PLSA 1381 Not applicable 24 Male
Caucasian/Hispanic Normal NA NA
0.123 Negative
NL 1382 NL PLSA 1382 Not applicable 27 Female
Black Normal NA NA
0.305 Negative

Table2.txt

NL 1383	NL PLSA 1383	Not applicable	28	Male	Black	Normal
NA	NA	0.337	Negative			
NL 1384	NL PLSA 1384	Not applicable	25	Male	Black	Normal
NA	NA	0.301	Negative			
NL 1385	NL PLSA 1385	Not applicable	26	Female	Caucasian/Hispanic	Normal
NA	NA	0.366	Negative			
NL 1386	NL PLSA 1386	Not applicable	20	Male	Caucasian/Hispanic	Normal
NA	NA	0.122	Negative			
NL 1387	NL PLSA 1387	Not applicable	23	Female	Caucasian/Hispanic	Normal
NA	NA	0.489	Negative			
NL 1388	NL PLSA 1388	Not applicable	19	Female	Black/Hispanic	Normal
NA	NA	0.303	Negative			
NL 1389	NL PLSA 1389	Not applicable	28	Female	Caucasian/Hispanic	Normal
NA	NA	0.388	Negative			
NL 1390	NL PLSA 1390	Not applicable	29	Male	Black/Hispanic	Normal
NA	NA	0.403	Negative			
NL 1391	NL PLSA 1391	Not applicable	29	Male	Black	Normal
NA	NA	0.590	Negative			
NL 1392	NL PLSA 1392	Not applicable	29	Male	Black	Normal
NA	NA	0.123	Negative			
NL 1393	NL PLSA 1393	Not applicable	28	Male	Black	Normal
NA	NA	0.481	Negative			
NL 1394	NL PLSA 1394	Not applicable	27	Male	Black/Hispanic	Normal
NA	NA	0.191	Negative			
NL 1395	NL PLSA 1395	Not applicable	29	Female	Caucasian/Hispanic	Normal
NA	NA	0.117	Negative			
NL 1396	NL PLSA 1396	Not applicable	27	Male	Black/Hispanic	Normal
NA	NA	0.117	Negative			
NL 1397	NL PLSA 1397	Not applicable	22	Male	Caucasian/Hispanic	Normal
NA	NA	0.320	Negative			
NL 1398	NL PLSA 1398	Not applicable	22	Male	Black	Normal
NA	NA	0.123	Negative			

Table2.txt

NL 1399	NL PLSA 1399	Not applicable	25	Male	Black/Hispanic	Normal
NA	NA	0.121	Negative			
NL 1400	NL PLSA 1400	Not applicable	28	Male	Caucasian/Hispanic	Normal
NA	NA	0.307	Negative			
NL 1401	NL PLSA 1401	Not applicable	20	Female	Black	Normal
NA	NA	0.116	Negative			
NL 1402	NL PLSA 1402	Not applicable	23	Female	Black	Normal
NA	NA	0.125	Negative			
NL 1403	NL PLSA 1403	Not applicable	19	Female	Black	Normal
NA	NA	0.311	Negative			
NL 1404	NL PLSA 1404	Not applicable	26	Female	Hispanic	Normal
NA	NA	0.125	Negative			
NL 1405	NL PLSA 1405	Not applicable	29	Female	Black	Normal
NA	NA	0.123	Negative			
NL 1406	NL PLSA 1406	Not applicable	26	Female	Black	Normal
NA	NA	0.841	Negative			
NL 1407	NL PLSA 1407	Not applicable	22	Female	Black	Normal
NA	NA	0.125	Negative			
NL 1408	NL PLSA 1408	Not applicable	30	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1409	NL PLSA 1409	Not applicable	22	Female	Black	Normal
NA	NA	0.390	Negative			
NL 1410	NL PLSA 1410	Not applicable	25	Female	Caucasian	Normal
NA	NA	0.219	Negative			
NL 1411	NL PLSA 1411	Not applicable	25	Female	Black	Normal
NA	NA	0.116	Negative			
NL 1412	NL PLSA 1412	Not applicable	27	Female	Black	Normal
NA	NA	0.299	Negative			
NL 1413	NL PLSA 1413	Not applicable	23	Female	Black	Normal
NA	NA	0.123	Negative			
NL 1414	NL PLSA 1414	Not applicable	20	Female	Hispanic	Normal
NA	NA	0.345	Negative			

Table2.txt

NL 1425 NL PLSA 1425 Not applicable 25 Male
Black Normal NA NA
0.121 Negative
NL 1426 NL PLSA 1426 Not applicable 24 Female
Black Normal NA NA
0.123 Negative
NL 1427 NL PLSA 1427 Not applicable 27 Male
Caucasian/Hispanic Normal NA NA
0.125 Negative
NL 1428 NL PLSA 1428 Not applicable 27 Male
Caucasian/Hispanic Normal NA NA
0.553 Negative
NL 1429 NL PLSA 1429 Not applicable 27 Male
Black/Hispanic Normal NA NA
0.121 Negative
NL 1430 NL PLSA 1430 Not applicable 30 Male
Black/Hispanic Normal NA NA
0.307 Negative
NL 1431 NL PLSA 1431 Not applicable 28 Male
Caucasian/Hispanic Normal NA NA
0.219 Negative
NL 1432 NL PLSA 1432 Not applicable 25 Male
Caucasian/Hispanic Normal NA NA
0.122 Negative
NL 1433 NL PLSA 1433 Not applicable 21 Male
Black Normal NA NA
0.125 Negative
NL 1434 NL PLSA 1434 Not applicable 27 Male
Black Normal NA NA
0.125 Negative
NL 1435 NL PLSA 1435 Not applicable 29 Male
Black Normal NA NA
0.125 Negative
NL 1436 NL PLSA 1436 Not applicable 24 Female
Caucasian/Hispanic Normal NA NA
0.237 Negative
NL 1437 NL PLSA 1437 Not applicable 30 Female
Caucasian/Hispanic Normal NA NA
0.117 Negative
NL 1438 NL PLSA 1438 Not applicable 28 Male
Black Normal NA NA
0.122 Negative
NL 1439 NL PLSA 1439 Not applicable 28 Male
Black Normal NA NA
0.117 Negative
NL 1440 NL PLSA 1440 Not applicable 20 Male
Black Normal NA NA
0.117 Negative

Table2.txt

NL 1441	NL PLSA 1441	Not applicable	27	Male	Black	Normal
NA	NA	0.125	Negative			
NL 1442	NL PLSA 1442	Not applicable	28	Male	Black	Normal
NA	NA	0.117	Negative			
NL 1443	NL PLSA 1443	Not applicable	23	Female	Caucasian/Hispanic	Normal
NA	NA	0.317	Negative			
NL 1444	NL PLSA 1444	Not applicable	23	Male	Caucasian/Hispanic	Normal
NA	NA	0.816	Negative			
NL 1445	NL PLSA 1445	Not applicable	20	Female	Black/Hispanic	Normal
NA	NA	0.117	Negative			
NL 1482	NL PLSA 1482	Not applicable	55	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1483	NL PLSA 1483	Not applicable	79	Male	Caucasian	Normal
NA	NA	0.575	Negative			
NL 1484	NL PLSA 1484	Not applicable	69	Female	Caucasian	Normal
NA	NA	0.357	Negative			
NL 1485	NL PLSA 1485	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1486	NL PLSA 1486	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1487	NL PLSA 1487	Not applicable	60	Male	Caucasian	Normal
NA	NA	0.338	Negative			
NL 1488	NL PLSA 1488	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.116	Negative			
NL 1489	NL PLSA 1489	Not applicable	57	Male	Caucasian	Normal
NA	NA	0.818	Negative			
NL 1490	NL PLSA 1490	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1491	NL PLSA 1491	Not applicable	62	Male	Caucasian	Normal
NA	NA	0.325	Negative			
NL 1492	NL PLSA 1492	Not applicable	62	Male	Caucasian	Normal
NA	NA	0.123	Negative			

Table2.txt

NL 1493	NL PLSA 1493	Not applicable	76	Male	Caucasian	Normal
NA	NA	0.297	Negative			
NL 1494	NL PLSA 1494	Not applicable	58	Female	Caucasian	Normal
NA	NA	0.116	Negative			
NL 1495	NL PLSA 1495	Not applicable	78	Female	Caucasian	Normal
NA	NA	0.355	Negative			
NL 1496	NL PLSA 1496	Not applicable	77	Female	Caucasian	Normal
NA	NA	0.413	Negative			
NL 1497	NL PLSA 1497	Not applicable	84	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1498	NL PLSA 1498	Not applicable	76	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1499	NL PLSA 1499	Not applicable	58	Male	Black	Normal
NA	NA	0.308	Negative			
NL 1500	NL PLSA 1500	Not applicable	80	Female	Caucasian	Normal
NA	NA	0.193	Negative			
NL 1501	NL PLSA 1501	Not applicable	59	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1502	NL PLSA 1502	Not applicable	59	Female	Caucasian	Normal
NA	NA	0.123	Negative			
NL 1503	NL PLSA 1503	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1504	NL PLSA 1504	Not applicable	57	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1505	NL PLSA 1505	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.457	Negative			
NL 1506	NL PLSA 1506	Not applicable	66	Male	Black	Normal
NA	NA	0.509	Negative			
NL 1507	NL PLSA 1507	Not applicable	72	Male	Caucasian	Normal
NA	NA	0.731	Negative			
NL 1508	NL PLSA 1508	Not applicable	64	Female	Caucasian	Normal
NA	NA	0.125	Negative			

Table2.txt

NL 1509	NL PLSA 1509	Not applicable	67	Male
Caucasian	Normal	NA	NA	
0.328	Negative			
NL 1510	NL PLSA 1510	Not applicable	71	Female
Caucasian	Normal	NA	NA	
0.300	Negative			
NL 1511	NL PLSA 1511	Not applicable	57	Male
Caucasian	Normal	NA	NA	
0.514	Negative			
NL 1512	NL PLSA 1512	Not applicable	56	Male
Caucasian	Normal	NA	NA	
0.121	Negative			
NL 1513	NL PLSA 1513	Not applicable	60	Female
Caucasian	Normal	NA	NA	
0.185	Negative			
NL 1514	NL PLSA 1514	Not applicable	56	Male
Caucasian	Normal	NA	NA	
0.329	Negative			
NL 1515	NL PLSA 1515	Not applicable	55	Male
Caucasian	Normal	NA	NA	
0.238	Negative			
NL 1516	NL PLSA 1516	Not applicable	73	Female
Caucasian	Normal	NA	NA	
0.117	Negative			
NL 1517	NL PLSA 1517	Not applicable	66	Male
Caucasian	Normal	NA	NA	
0.305	Negative			
NL 1518	NL PLSA 1518	Not applicable	70	Male
Caucasian	Normal	NA	NA	
0.443	Negative			
NL 1519	NL PLSA 1519	Not applicable	61	Female
Caucasian	Normal	NA	NA	
0.122	Negative			
NL 1520	NL PLSA 1520	Not applicable	69	Female
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1521	NL PLSA 1521	Not applicable	69	Female
Caucasian	Normal	NA	NA	
0.314	Negative			
NL 1522	NL PLSA 1522	Not applicable	59	Male
Caucasian	Normal	NA	NA	
0.116	Negative			
NL 1523	NL PLSA 1523	Not applicable	64	Female
Caucasian	Normal	NA	NA	
0.314	Negative			
NL 1524	NL PLSA 1524	Not applicable	62	Female
Caucasian	Normal	NA	NA	
0.600	Negative			

Table2.txt

NL 1525	NL PLSA 1525	Not applicable	65	Female	Black	Normal
NA	NA	0.550	Negative			
NL 1526	NL PLSA 1526	Not applicable	79	Female	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1527	NL PLSA 1527	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.296	Negative			
NL 1528	NL PLSA 1528	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.301	Negative			
NL 1529	NL PLSA 1529	Not applicable	74	Male	Caucasian	Normal
NA	NA	0.814	Negative			
NL 1530	NL PLSA 1530	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.421	Negative			
NL 1531	NL PLSA 1531	Not applicable	58	Male	Caucasian	Normal
NA	NA	0.116	Negative			
NL 1532	NL PLSA 1532	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.409	Negative			
NL 1533	NL PLSA 1533	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.295	Negative			
NL 1534	NL PLSA 1534	Not applicable	67	Male	Caucasian	Normal
NA	NA	0.490	Negative			
NL 1535	NL PLSA 1535	Not applicable	61	Male	Caucasian	Normal
NA	NA	0.229	Negative			
NL 1536	NL PLSA 1536	Not applicable	68	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1537	NL PLSA 1537	Not applicable	75	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1538	NL PLSA 1538	Not applicable	69	Male	Caucasian	Normal
NA	NA	0.297	Negative			
NL 1539	NL PLSA 1539	Not applicable	70	Male	Caucasian	Normal
NA	NA	0.425	Negative			
NL 1540	NL PLSA 1540	Not applicable	68	Female	Other	Normal
NA	NA	0.123	Negative			

Table2.txt

NL 1541	NL PLSA 1541	Not applicable	78	Male	Caucasian	Normal	NA
NA	0.617	Negative					
NL 1542	NL PLSA 1542	Not applicable	63	Female	Black	Normal	NA
NA	0.213	Negative					
NL 1543	NL PLSA 1543	Not applicable	60	Male	Caucasian	Normal	NA
NA	0.338	Negative					
NL 1544	NL PLSA 1544	Not applicable	63	Male	Caucasian	Normal	NA
NA	0.117	Negative					
NL 1545	NL PLSA 1545	Not applicable	61	Female	Black	Normal	NA
NA	0.451	Negative					
NL 1546	NL PLSA 1546	Not applicable	78	Male	Caucasian	Normal	NA
NA	0.338	Negative					
NL 1547	NL PLSA 1547	Not applicable	70	Female	Black	Normal	NA
NA	0.246	Negative					
NL 1548	NL PLSA 1548	Not applicable	61	Female	Caucasian	Normal	NA
NA	0.125	Negative					
NL 1549	NL PLSA 1549	Not applicable	57	Male	Black	Normal	NA
NA	0.731	Negative					
NL 1550	NL PLSA 1550	Not applicable	76	Male	Caucasian	Normal	NA
NA	0.542	Negative					
NL 1551	NL PLSA 1551	Not applicable	64	Male	Asian	Normal	NA
NA	0.123	Negative					
NL 1552	NL PLSA 1552	Not applicable	72	Male	Caucasian	Normal	NA
NA	0.415	Negative					
NL 1553	NL PLSA 1553	Not applicable	76	Female	Asian	Normal	NA
NA	0.307	Negative					
NL 1554	NL PLSA 1554	Not applicable	79	Female	Caucasian	Normal	NA
NA	0.117	Negative					
NL 1555	NL PLSA 1555	Not applicable	58	Male	Caucasian	Normal	NA
NA	0.435	Negative					
NL 1556	NL PLSA 1556	Not applicable	57	Female	Black	Normal	NA
NA	0.305	Negative					

Table2.txt

NL 1557	NL PLSA 1557	Not applicable	67	Female
Caucasian	Normal	NA	NA	
0.673	Negative			
NL 1558	NL PLSA 1558	Not applicable	67	Female
Caucasian	Normal	NA	NA	
0.465	Negative			
NL 1559	NL PLSA 1559	Not applicable	71	Male
Caucasian	Normal	NA	NA	
0.518	Negative			
NL 1560	NL PLSA 1560	Not applicable	60	Male
Caucasian	Normal	NA	NA	
0.847	Negative			
NL 1561	NL PLSA 1561	Not applicable	62	Male
Caucasian	Normal	NA	NA	
0.472	Negative			
NL 1562	NL PLSA 1562	Not applicable	64	Female
Caucasian	Normal	NA	NA	
0.976	Positive			
NL 1563	NL PLSA 1563	Not applicable	64	Male
Caucasian	Normal	NA	NA	
0.399	Negative			
NL 1564	NL PLSA 1564	Not applicable	60	Male
Caucasian	Normal	NA	NA	
0.485	Negative			
NL 1565	NL PLSA 1565	Not applicable	59	Female
Caucasian	Normal	NA	NA	
0.121	Negative			
NL 1566	NL PLSA 1566	Not applicable	59	Female
Caucasian	Normal	NA	NA	
0.305	Negative			
NL 1567	NL PLSA 1567	Not applicable	60	Female
Caucasian	Normal	NA	NA	
0.116	Negative			
NL 1568	NL PLSA 1568	Not applicable	57	Female
Caucasian	Normal	NA	NA	
0.207	Negative			
NL 1569	NL PLSA 1569	Not applicable	70	Male
Caucasian	Normal	NA	NA	
0.616	Negative			
NL 1570	NL PLSA 1570	Not applicable	56	Female
Caucasian	Normal	NA	NA	
0.295	Negative			
NL 1571	NL PLSA 1571	Not applicable	64	Male
Caucasian	Normal	NA	NA	
0.303	Negative			
NL 1572	NL PLSA 1572	Not applicable	68	Female
Caucasian	Normal	NA	NA	
0.125	Negative			

Table2.txt

NL 1573	NL PLSA 1573	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.195	Negative			
NL 1574	NL PLSA 1574	Not applicable	65	Female	Caucasian	Normal
NA	NA	0.554	Negative			
NL 1575	NL PLSA 1575	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.333	Negative			
NL 1576	NL PLSA 1576	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.121	Negative			
NL 1577	NL PLSA 1577	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.543	Negative			
NL 1578	NL PLSA 1578	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1579	NL PLSA 1579	Not applicable	66	Female	Caucasian	Normal
NA	NA	0.256	Negative			
NL 1580	NL PLSA 1580	Not applicable	59	Male	Caucasian	Normal
NA	NA	0.242	Negative			
NL 1581	NL PLSA 1581	Not applicable	81	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1582	NL PLSA 1582	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.197	Negative			
NL 1583	NL PLSA 1583	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.334	Negative			
NL 1584	NL PLSA 1584	Not applicable	64	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1585	NL PLSA 1585	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1586	NL PLSA 1586	Not applicable	64	Female	Caucasian	Normal
NA	NA	0.382	Negative			
NL 1587	NL PLSA 1587	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.719	Negative			
NL 1588	NL PLSA 1588	Not applicable	62	Female	Caucasian	Normal
NA	NA	0.508	Negative			

Table2.txt

NL 1589	NL PLSA 1589	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.666	Negative			
NL 1590	NL PLSA 1590	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.123	Negative			
NL 1591	NL PLSA 1591	Not applicable	71	Female	Caucasian	Normal
NA	NA	0.188	Negative			
NL 1592	NL PLSA 1592	Not applicable	68	Female	Caucasian	Normal
NA	NA	0.320	Negative			
NL 1593	NL PLSA 1593	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.122	Negative			
NL 1594	NL PLSA 1594	Not applicable	60	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1595	NL PLSA 1595	Not applicable	75	Male	Caucasian	Normal
NA	NA	0.396	Negative			
NL 1596	NL PLSA 1596	Not applicable	67	Male	Caucasian	Normal
NA	NA	0.321	Negative			
NL 1597	NL PLSA 1597	Not applicable	59	Female	Asian	Normal
NA	NA	0.125	Negative			
NL 1598	NL PLSA 1598	Not applicable	63	Male	Caucasian	Normal
NA	NA	0.238	Negative			
NL 1599	NL PLSA 1599	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.116	Negative			
NL 1600	NL PLSA 1600	Not applicable	64	Male	Caucasian	Normal
NA	NA	0.338	Negative			
NL 1601	NL PLSA 1601	Not applicable	69	Female	Caucasian	Normal
NA	NA	0.318	Negative			
NL 1602	NL PLSA 1602	Not applicable	78	Female	Caucasian	Normal
NA	NA	0.242	Negative			
NL 1603	NL PLSA 1603	Not applicable	60	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1604	NL PLSA 1604	Not applicable	55	Female	Caucasian	Normal
NA	NA	0.331	Negative			

Table2.txt

NL 1605	NL PLSA 1605	Not applicable	65	Female
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1606	NL PLSA 1606	Not applicable	61	Male
Caucasian	Normal	NA	NA	
0.121	Negative			
NL 1607	NL PLSA 1607	Not applicable	57	Male
Caucasian	Normal	NA	NA	
0.381	Negative			
NL 1608	NL PLSA 1608	Not applicable	59	Female
Caucasian	Normal	NA	NA	
0.121	Negative			
NL 1609	NL PLSA 1609	Not applicable	57	Female
Caucasian	Normal	NA	NA	
0.301	Negative			
NL 1610	NL PLSA 1610	Not applicable	63	Female
Black	Normal	NA	NA	
0.121	Negative			
NL 1611	NL PLSA 1611	Not applicable	63	Male
Caucasian	Normal	NA	NA	
0.538	Negative			
NL 1612	NL PLSA 1612	Not applicable	68	Male
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1613	NL PLSA 1613	Not applicable	71	Male
Caucasian	Normal	NA	NA	
0.117	Negative			
NL 1614	NL PLSA 1614	Not applicable	63	Female
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1615	NL PLSA 1615	Not applicable	56	Male
Caucasian	Normal	NA	NA	
0.125	Negative			
NL 1616	NL PLSA 1616	Not applicable	62	Male
Black	Normal	NA	NA	
0.815	Negative			
NL 1617	NL PLSA 1617	Not applicable	73	Female
Caucasian	Normal	NA	NA	
0.121	Negative			
NL 1618	NL PLSA 1618	Not applicable	71	Female
Caucasian	Normal	NA	NA	
0.116	Negative			
NL 1619	NL PLSA 1619	Not applicable	72	Female
Caucasian	Normal	NA	NA	
0.200	Negative			
NL 1620	NL PLSA 1620	Not applicable	68	Female
Caucasian	Normal	NA	NA	
0.301	Negative			

Table2.txt

NL 1621	NL PLSA 1621	Not applicable	55	Female	Black	Normal
NA	NA	0.117	Negative			
NL 1622	NL PLSA 1622	Not applicable	56	Female	Black	Normal
NA	NA	0.480	Negative			
NL 1623	NL PLSA 1623	Not applicable	72	Male	Caucasian	Normal
NA	NA	0.122	Negative			
NL 1624	NL PLSA 1624	Not applicable	75	Male	Caucasian	Normal
NA	NA	0.121	Negative			
NL 1625	NL PLSA 1625	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1626	NL PLSA 1626	Not applicable	73	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1627	NL PLSA 1627	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.192	Negative			
NL 1628	NL PLSA 1628	Not applicable	76	Female	Caucasian	Normal
NA	NA	0.116	Negative			
NL 1629	NL PLSA 1629	Not applicable	60	Female	Black	Normal
NA	NA	0.187	Negative			
NL 1630	NL PLSA 1630	Not applicable	71	Male	Asian	Normal
NA	NA	0.121	Negative			
NL 1631	NL PLSA 1631	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.123	Negative			
NL 1632	NL PLSA 1632	Not applicable	64	Male	Asian	Normal
NA	NA	0.117	Negative			
NL 1633	NL PLSA 1633	Not applicable	63	Male	Caucasian	Normal
NA	NA	0.122	Negative			
NL 1634	NL PLSA 1634	Not applicable	67	Female	Caucasian	Normal
NA	NA	0.180	Negative			
NL 1635	NL PLSA 1635	Not applicable	62	Male	Caucasian	Normal
NA	NA	0.335	Negative			
NL 1636	NL PLSA 1636	Not applicable	58	Female	Caucasian	Normal
NA	NA	0.125	Negative			

Table2.txt

NL 1637	NL PLSA 1637	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1638	NL PLSA 1638	Not applicable	70	Female	Caucasian	Normal
NA	NA	0.310	Negative			
NL 1639	NL PLSA 1639	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.187	Negative			
NL 1640	NL PLSA 1640	Not applicable	56	Male	Caucasian	Normal
NA	NA	0.121	Negative			
NL 1641	NL PLSA 1641	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.123	Negative			
NL 1642	NL PLSA 1642	Not applicable	64	Male	Caucasian	Normal
NA	NA	0.175	Negative			
NL 1643	NL PLSA 1643	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.122	Negative			
NL 1644	NL PLSA 1644	Not applicable	56	Female	Caucasian	Normal
NA	NA	0.222	Negative			
NL 1645	NL PLSA 1645	Not applicable	66	Male	Caucasian	Normal
NA	NA	0.117	Negative			
NL 1646	NL PLSA 1646	Not applicable	64	Male	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1647	NL PLSA 1647	Not applicable	62	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1648	NL PLSA 1648	Not applicable	59	Male	Caucasian	Normal
NA	NA	0.306	Negative			
NL 1649	NL PLSA 1649	Not applicable	59	Male	Asian	Normal
NA	NA	0.747	Negative			
NL 1650	NL PLSA 1650	Not applicable	60	Female	Caucasian	Normal
NA	NA	0.125	Negative			
NL 1651	NL PLSA 1651	Not applicable	84	Male	Caucasian	Normal
NA	NA	0.311	Negative			
NL 1652	NL PLSA 1652	Not applicable	67	Female	Caucasian	Normal
NA	NA	0.317	Negative			

Table2.txt

NL 1653	NL PLSA 1653	Not applicable	70	Male	Black	Normal
NA	NA	0.568	Negative			
NL 1654	NL PLSA 1654	Not applicable	67	Female	Caucasian	Normal
NA	NA	0.121	Negative			
NL 1655	NL PLSA 1655	Not applicable	71	Female	Caucasian	Normal
NA	NA	0.720	Negative			
NL 1656	NL PLSA 1656	Not applicable	68	Male	Caucasian	Normal
NA	NA	0.522	Negative			
NL 1657	NL PLSA 1657	Not applicable	63	Female	Caucasian	Normal
NA	NA	0.320	Negative			
NL 1658	NL PLSA 1658	Not applicable	71	Male	Caucasian	Normal
NA	NA	0.324	Negative			
NL 1659	NL PLSA 1659	Not applicable	59	Male	Black	Normal
NA	NA	0.300	Negative			
NL 1660	NL PLSA 1660	Not applicable	61	Female	Caucasian	Normal
NA	NA	0.333	Negative			
NL 1661	NL PLSA 1661	Not applicable	65	Male	Caucasian	Normal
NA	NA	0.334	Negative			
NL 1662	NL PLSA 1662	Not applicable	58	Male	Caucasian	Normal
NA	NA	0.121	Negative			
NL 1663	NL PLSA 1663	Not applicable	55	Male	Asian	Normal
NA	NA	0.116	Negative			
NL 1664	NL PLSA 1664	Not applicable	59	Male	Caucasian	Normal
NA	NA	0.308	Negative			
NL 1665	NL PLSA 1665	Not applicable	75	Female	Caucasian	Normal
NA	NA	0.471	Negative			
NL 1666	NL PLSA 1666	Not applicable	74	Female	Caucasian	Normal
NA	NA	0.304	Negative			
NL 1667	NL PLSA 1667	Not applicable	72	Female	Black	Normal
NA	NA	0.313	Negative			
NL 1668	NL PLSA 1668	Not applicable	66	Female	Caucasian	Normal
NA	NA	0.309	Negative			

Table2.txt

NL 1669	NL PLSA 1669	Not applicable	56	Female	Caucasian	Normal	NA
NA	0.577	Negative					
NL 1701	NL PLSA 1701	Not applicable	87	Male	Unknown	Normal	NA
NA	0.528	Negative					
NL 1702	NL PLSA 1702	Not applicable	82	Female	Unknown	Normal	NA
NA	0.214	Negative					
NL 1703	NL PLSA 1703	Not applicable	82	Female	Unknown	Normal	NA
NA	0.713	Negative					
NL 1704	NL PLSA 1704	Not applicable	66	Female	Unknown	Normal	NA
NA	0.338	Negative					
NL 1705	NL PLSA 1705	Not applicable	77	Female	Unknown	Normal	NA
NA	0.117	Negative					
NL 1706	NL PLSA 1706	Not applicable	56	Male	Unknown	Normal	NA
NA	0.308	Negative					
NL 1707	NL PLSA 1707	Not applicable	62	Male	Unknown	Normal	NA
NA	0.314	Negative					
NL 1708	NL PLSA 1708	Not applicable	76	Male	Unknown	Normal	NA
NA	0.576	Negative					
NL 1709	NL PLSA 1709	Not applicable	68	Male	Unknown	Normal	NA
NA	0.566	Negative					
NL 1710	NL PLSA 1710	Not applicable	77	Female	Unknown	Normal	NA
NA	0.323	Negative					
NL 1711	NL PLSA 1711	Not applicable	46	Female	Unknown	Normal	NA
NA	0.123	Negative					
NL 1712	NL PLSA 1712	Not applicable	76	Male	Unknown	Normal	NA
NA	0.305	Negative					
NL 1713	NL PLSA 1713	Not applicable	37	Male	Unknown	Normal	NA
NA	0.178	Negative					
NL 1714	NL PLSA 1714	Not applicable	62	Female	Unknown	Normal	NA
NA	0.121	Negative					
NL 1715	NL PLSA 1715	Not applicable	67	Female	Unknown	Normal	NA
NA	0.187	Negative					

Table2.txt

NL 1716	NL PLSA 1716	Not applicable	55	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1717	NL PLSA 1717	Not applicable	58	Male
Unknown	Normal	NA	NA	
0.353	Negative			
NL 1718	NL PLSA 1718	Not applicable	44	Female
Unknown	Normal	NA	NA	
0.349	Negative			
NL 1719	NL PLSA 1719	Not applicable	66	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1720	NL PLSA 1720	Not applicable	72	Female
Unknown	Normal	NA	NA	
0.444	Negative			
NL 1721	NL PLSA 1721	Not applicable	64	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1722	NL PLSA 1722	Not applicable	55	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1723	NL PLSA 1723	Not applicable	74	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1724	NL PLSA 1724	Not applicable	71	Female
Unknown	Normal	NA	NA	
0.599	Negative			
NL 1725	NL PLSA 1725	Not applicable	28	Female
Unknown	Normal	NA	NA	
0.624	Negative			
NL 1726	NL PLSA 1726	Not applicable	67	Male
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1727	NL PLSA 1727	Not applicable	53	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1728	NL PLSA 1728	Not applicable	64	Female
Unknown	Normal	NA	NA	
0.735	Negative			
NL 1729	NL PLSA 1729	Not applicable	64	Female
Unknown	Normal	NA	NA	
0.322	Negative			
NL 1730	NL PLSA 1730	Not applicable	33	Female
Unknown	Normal	NA	NA	
0.599	Negative			
NL 1731	NL PLSA 1731	Not applicable	54	Female
Unknown	Normal	NA	NA	
0.236	Negative			

Table2.txt

NL 1732	NL PLSA 1732	Not applicable	24	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1733	NL PLSA 1733	Not applicable	27	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1734	NL PLSA 1734	Not applicable	53	Male
Unknown	Normal	NA	NA	
0.155	Negative			
NL 1735	NL PLSA 1735	Not applicable	74	Female
Unknown	Normal	NA	NA	
0.187	Negative			
NL 1736	NL PLSA 1736	Not applicable	53	Female
Unknown	Normal	NA	NA	
0.564	Negative			
NL 1737	NL PLSA 1737	Not applicable	63	Male
Unknown	Normal	NA	NA	
0.183	Negative			
NL 1738	NL PLSA 1738	Not applicable	68	Male
Unknown	Normal	NA	NA	
0.175	Negative			
NL 1739	NL PLSA 1739	Not applicable	52	Male
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1740	NL PLSA 1740	Not applicable	73	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1741	NL PLSA 1741	Not applicable	66	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1742	NL PLSA 1742	Not applicable	52	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1743	NL PLSA 1743	Not applicable	64	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1744	NL PLSA 1744	Not applicable	72	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1745	NL PLSA 1745	Not applicable	63	Male
Unknown	Normal	NA	NA	
0.154	Negative			
NL 1746	NL PLSA 1746	Not applicable	47	Female
Unknown	Normal	NA	NA	
0.344	Negative			
NL 1747	NL PLSA 1747	Not applicable	37	Male
Unknown	Normal	NA	NA	
0.121	Negative			

Table2.txt

NL 1748	NL PLSA 1748	Not applicable	47	Male
Unknown	Normal	NA	NA	
0.182	Negative			
NL 1749	NL PLSA 1749	Not applicable	48	Male
Unknown	Normal	NA	NA	
0.323	Negative			
NL 1750	NL PLSA 1750	Not applicable	53	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1751	NL PLSA 1751	Not applicable	43	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1752	NL PLSA 1752	Not applicable	23	Female
Unknown	Normal	NA	NA	
0.303	Negative			
NL 1753	NL PLSA 1753	Not applicable	33	Male
Unknown	Normal	NA	NA	
0.810	Negative			
NL 1754	NL PLSA 1754	Not applicable	57	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1755	NL PLSA 1755	Not applicable	57	Female
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1756	NL PLSA 1756	Not applicable	46	Male
Unknown	Normal	NA	NA	
0.332	Negative			
NL 1757	NL PLSA 1757	Not applicable	73	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1758	NL PLSA 1758	Not applicable	42	Female
Unknown	Normal	NA	NA	
0.554	Negative			
NL 1759	NL PLSA 1759	Not applicable	61	Male
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1760	NL PLSA 1760	Not applicable	35	Female
Unknown	Normal	NA	NA	
0.337	Negative			
NL 1761	NL PLSA 1761	Not applicable	47	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1762	NL PLSA 1762	Not applicable	52	Female
Unknown	Normal	NA	NA	
0.297	Negative			
NL 1763	NL PLSA 1763	Not applicable	55	Female
Unknown	Normal	NA	NA	
0.237	Negative			

Table2.txt

NL 1764	NL PLSA 1764	Not applicable	21	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1765	NL PLSA 1765	Not applicable	63	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1766	NL PLSA 1766	Not applicable	61	Male
Unknown	Normal	NA	NA	
0.327	Negative			
NL 1767	NL PLSA 1767	Not applicable	43	Male
Unknown	Normal	NA	NA	
0.226	Negative			
NL 1768	NL PLSA 1768	Not applicable	68	Male
Unknown	Normal	NA	NA	
0.332	Negative			
NL 1769	NL PLSA 1769	Not applicable	53	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1770	NL PLSA 1770	Not applicable	55	Male
Unknown	Normal	NA	NA	
0.428	Negative			
NL 1771	NL PLSA 1771	Not applicable	26	Female
Unknown	Normal	NA	NA	
0.245	Negative			
NL 1772	NL PLSA 1772	Not applicable	64	Male
Unknown	Normal	NA	NA	
0.178	Negative			
NL 1773	NL PLSA 1773	Not applicable	67	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1774	NL PLSA 1774	Not applicable	61	Female
Unknown	Normal	NA	NA	
0.319	Negative			
NL 1775	NL PLSA 1775	Not applicable	34	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1776	NL PLSA 1776	Not applicable	46	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1777	NL PLSA 1777	Not applicable	57	Male
Unknown	Normal	NA	NA	
0.240	Negative			
NL 1778	NL PLSA 1778	Not applicable	45	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1779	NL PLSA 1779	Not applicable	56	Female
Unknown	Normal	NA	NA	
0.198	Negative			

Table2.txt

NL 1780	NL PLSA 1780	Not applicable	63	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1781	NL PLSA 1781	Not applicable	66	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1782	NL PLSA 1782	Not applicable	58	Female
Unknown	Normal	NA	NA	
0.405	Negative			
NL 1783	NL PLSA 1783	Not applicable	43	Male
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1784	NL PLSA 1784	Not applicable	65	Female
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1785	NL PLSA 1785	Not applicable	35	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1786	NL PLSA 1786	Not applicable	65	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1787	NL PLSA 1787	Not applicable	32	Female
Unknown	Normal	NA	NA	
0.236	Negative			
NL 1788	NL PLSA 1788	Not applicable	73	Female
Unknown	Normal	NA	NA	
0.436	Negative			
NL 1789	NL PLSA 1789	Not applicable	62	Female
Unknown	Normal	NA	NA	
0.670	Negative			
NL 1790	NL PLSA 1790	Not applicable	54	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1791	NL PLSA 1791	Not applicable	55	Female
Unknown	Normal	NA	NA	
0.313	Negative			
NL 1792	NL PLSA 1792	Not applicable	52	Male
Unknown	Normal	NA	NA	
0.338	Negative			
NL 1793	NL PLSA 1793	Not applicable	68	Female
Unknown	Normal	NA	NA	
0.345	Negative			
NL 1794	NL PLSA 1794	Not applicable	62	Male
Unknown	Normal	NA	NA	
0.354	Negative			
NL 1795	NL PLSA 1795	Not applicable	24	Female
Unknown	Normal	NA	NA	
0.240	Negative			

Table2.txt

NL 1796	NL PLSA 1796	Not applicable	23	Female
Unknown	Normal	NA	NA	
0.248	Negative			
NL 1797	NL PLSA 1797	Not applicable	52	Female
Unknown	Normal	NA	NA	
0.221	Negative			
NL 1798	NL PLSA 1798	Not applicable	52	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1799	NL PLSA 1799	Not applicable	63	Male
Unknown	Normal	NA	NA	
0.234	Negative			
NL 1800	NL PLSA 1800	Not applicable	52	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1801	NL PLSA 1801	Not applicable	47	Male
Unknown	Normal	NA	NA	
0.331	Negative			
NL 1802	NL PLSA 1802	Not applicable	46	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1803	NL PLSA 1803	Not applicable	44	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1804	NL PLSA 1804	Not applicable	83	Male
Unknown	Normal	NA	NA	
0.322	Negative			
NL 1805	NL PLSA 1805	Not applicable	60	Female
Unknown	Normal	NA	NA	
0.176	Negative			
NL 1806	NL PLSA 1806	Not applicable	72	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1807	NL PLSA 1807	Not applicable	41	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1808	NL PLSA 1808	Not applicable	26	Male
Unknown	Normal	NA	NA	
0.306	Negative			
NL 1809	NL PLSA 1809	Not applicable	57	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1810	NL PLSA 1810	Not applicable	47	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1811	NL PLSA 1811	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.121	Negative			

Table2.txt

NL 1812	NL PLSA 1812	Not applicable	63	Female
Unknown	Normal	NA	NA	
0.596	Negative			
NL 1813	NL PLSA 1813	Not applicable	57	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1814	NL PLSA 1814	Not applicable	42	Female
Unknown	Normal	NA	NA	
0.322	Negative			
NL 1815	NL PLSA 1815	Not applicable	41	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1816	NL PLSA 1816	Not applicable	36	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1817	NL PLSA 1817	Not applicable	57	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1818	NL PLSA 1818	Not applicable	67	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1819	NL PLSA 1819	Not applicable	82	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1820	NL PLSA 1820	Not applicable	28	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1821	NL PLSA 1821	Not applicable	67	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1822	NL PLSA 1822	Not applicable	35	Male
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1823	NL PLSA 1823	Not applicable	67	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1824	NL PLSA 1824	Not applicable	45	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1825	NL PLSA 1825	Not applicable	24	Female
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1826	NL PLSA 1826	Not applicable	58	Male
Unknown	Normal	NA	NA	
0.805	Negative			
NL 1827	NL PLSA 1827	Not applicable	65	Female
Unknown	Normal	NA	NA	
0.125	Negative			

Table2.txt

NL 1828	NL PLSA 1828	Not applicable	64	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1829	NL PLSA 1829	Not applicable	67	Male
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1830	NL PLSA 1830	Not applicable	73	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1831	NL PLSA 1831	Not applicable	64	Female
Unknown	Normal	NA	NA	
0.710	Negative			
NL 1832	NL PLSA 1832	Not applicable	62	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1833	NL PLSA 1833	Not applicable	52	Male
Unknown	Normal	NA	NA	
0.587	Negative			
NL 1834	NL PLSA 1834	Not applicable	47	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1835	NL PLSA 1835	Not applicable	47	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1836	NL PLSA 1836	Not applicable	57	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1837	NL PLSA 1837	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.253	Negative			
NL 1838	NL PLSA 1838	Not applicable	52	Female
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1839	NL PLSA 1839	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.309	Negative			
NL 1840	NL PLSA 1840	Not applicable	32	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1841	NL PLSA 1841	Not applicable	32	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1842	NL PLSA 1842	Not applicable	72	Male
Unknown	Normal	NA	NA	
0.305	Negative			
NL 1843	NL PLSA 1843	Not applicable	61	Male
Unknown	Normal	NA	NA	
0.122	Negative			

Table2.txt

NL 1844	NL PLSA 1844	Not applicable	61	Male
Unknown	Normal	NA	NA	
0.184	Negative			
NL 1845	NL PLSA 1845	Not applicable	77	Male
Unknown	Normal	NA	NA	
0.515	Negative			
NL 1846	NL PLSA 1846	Not applicable	71	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1847	NL PLSA 1847	Not applicable	28	Female
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1848	NL PLSA 1848	Not applicable	44	Female
Unknown	Normal	NA	NA	
0.123	Negative			
NL 1849	NL PLSA 1849	Not applicable	61	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1850	NL PLSA 1850	Not applicable	58	Male
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1851	NL PLSA 1851	Not applicable	51	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1852	NL PLSA 1852	Not applicable	28	Male
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1853	NL PLSA 1853	Not applicable	62	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1854	NL PLSA 1854	Not applicable	64	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1855	NL PLSA 1855	Not applicable	61	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1856	NL PLSA 1856	Not applicable	61	Female
Unknown	Normal	NA	NA	
0.191	Negative			
NL 1857	NL PLSA 1857	Not applicable	64	Male
Unknown	Normal	NA	NA	
0.117	Negative			
NL 1858	NL PLSA 1858	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.234	Negative			
NL 1859	NL PLSA 1859	Not applicable	62	Female
Unknown	Normal	NA	NA	
0.325	Negative			

Table2.txt

NL 1860	NL PLSA 1860	Not applicable	58	Female
Unknown	Normal	NA	NA	
0.803	Negative			
NL 1861	NL PLSA 1861	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1862	NL PLSA 1862	Not applicable	51	Female
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1863	NL PLSA 1863	Not applicable	63	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1864	NL PLSA 1864	Not applicable	25	Female
Unknown	Normal	NA	NA	
0.317	Negative			
NL 1865	NL PLSA 1865	Not applicable	62	Female
Unknown	Normal	NA	NA	
0.116	Negative			
NL 1866	NL PLSA 1866	Not applicable	55	Female
Unknown	Normal	NA	NA	
0.324	Negative			
NL 1867	NL PLSA 1867	Not applicable	73	Female
Unknown	Normal	NA	NA	
0.122	Negative			
NL 1868	NL PLSA 1868	Not applicable	38	Male
Unknown	Normal	NA	NA	
0.125	Negative			
NL 1869	NL PLSA 1869	Not applicable	52	Female
Unknown	Normal	NA	NA	
0.121	Negative			
NL 1870	NL PLSA 1870	Not applicable	34	Female
Unknown	Normal	NA	NA	
0.123	Negative			
PANC 669	PANC 669 PLS 1	Not available	82	Male
Caucasian	Pancreas	II	Adenocarcinoma	
0.982	Positive			
PANC 670	PANC 670 PLS 1	Not available	44	Female
Caucasian	Pancreas	II	Adenocarcinoma	
0.560	Negative			
PANC 671	PANC 671 PLS 1	Not available	64	Male
Caucasian	Pancreas	II	Adenocarcinoma	
0.994	Positive			
PANC 672	PANC 672 PLS 1	Not available	69	Male
Caucasian	Pancreas	II	Adenocarcinoma	
0.982	Positive			
PANC 673	PANC 673 PLS 1	Not available	61	Female
Caucasian	Pancreas	II	Adenocarcinoma	
0.423	Negative			

Table2.txt

PANC 674	PANC 674 PLS 1	Not available	56	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.993	Positive
PANC 675	PANC 675 PLS 1	Not available	77	Female	Caucasian	Pancreas	II	Adenocarcinoma	1.000	Positive
PANC 676	PANC 676 PLS 1	Not available	65	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.977	Positive
PANC 677	PANC 677 PLS 1	Not available	73	Male	Caucasian	Pancreas	II	Adenocarcinoma	1.000	Positive
PANC 678	PANC 678 PLS 1	Not available	48	Male	Black	Pancreas	II	Adenocarcinoma	0.463	Negative
PANC 679	PANC 679 PLS 1	Not available	53	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.605	Negative
PANC 680	PANC 680 PLS 1	Not available	57	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.822	Negative
PANC 757	PANC 757 PLS 1	PANC 757 PT1	70	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.231	Negative
PANC 758	PANC 758 PLS 1	PANC 758 PT1	56	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.679	Negative
PANC 759	PANC 759 PLS 1	PANC 759 PT1	56	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.832	Negative
PANC 760	PANC 760 PLS 1	PANC 760 PT1	48	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.872	Positive
PANC 761	PANC 761 PLS 1	PANC 761 PT1	53	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.904	Positive
PANC 762	PANC 762 PLS 1	PANC 762 PT1	70	Female	Caucasian	Pancreas	II	Adenocarcinoma	1.000	Positive
PANC 764	PANC 764 PLS 1	PANC 764 PT1	58	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.989	Positive
PANC 765	PANC 765 PLS 1	PANC 765 PT1	48	Female	Caucasian	Pancreas	II	Adenocarcinoma	1.000	Positive
PANC 766	PANC 766 PLS 1	PANC 766 PT1	72	Male	Caucasian	Pancreas	I	Adenocarcinoma	0.995	Positive

Table2.txt

PANC 767	PANC 767 PLS 1	PANC 767 PT1	70	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.457	Negative			
PANC 768	PANC 768 PLS 1	PANC 768 PT1	59	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.125	Negative			
PANC 769	PANC 769 PLS 1	PANC 769 PT1	59	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.804	Negative			
PANCA 1001	PANCA 1001 PLS 1	Not available	74	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.980	Positive			
PANCA 1004	PANCA 1004 PLS 1	Not available	60	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.994	Positive			
PANCA 1005	PANCA 1005 PLS 1	Not available	62	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.993	Positive			
PANCA 1006	PANCA 1006 PLS 1	Not available	78	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.999	Positive			
PANCA 1008	PANCA 1008 PLS 1	Not available	50	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.911	Positive			
PANCA 1009	PANCA 1009 PLS 1	Not available	66	Female	Caucasian	Pancreas
II	Adenocarcinoma	1.000	Positive			
PANCA 1010	PANCA 1010 PLS 1	Not available	86	Male	Caucasian	Pancreas
I	Adenocarcinoma	0.125	Negative			
PANCA 1011	PANCA 1011 PLS 1	Not available	72	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.999	Positive			
PANCA 1012	PANCA 1012 PLS 1	Not available	69	Female	Black	Pancreas
II	Adenocarcinoma	0.794	Negative			
PANCA 1013	PANCA 1013 PLS 1	Not available	61	Male	Caucasian	Pancreas
III	Adenocarcinoma	0.989	Positive			
PANCA 1014	PANCA 1014 PLS 1	Not available	65	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.997	Positive			
PANCA 1015	PANCA 1015 PLS 1	Not available	72	Male	Unknown	Pancreas
III	Adenocarcinoma	0.968	Positive			
PANCA 1016	PANCA 1016 PLS 1	Not available	54	Male	Unknown	Pancreas
I	Adenocarcinoma	0.884	Positive			

Table2.txt

PANCA 1018	PANCA 1018 PLS 1	Not available	53	Female	Caucasian	Pancreas
II	Adenocarcinoma	1.000	Positive			
PANCA 1020	PANCA 1020 PLS 1	Not available	56	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.999	Positive			
PANCA 1022	PANCA 1022 PLS 1	Not available	70	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.994	Positive			
PANCA 1024	PANCA 1024 PLS 1	Not available	58	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.117	Negative			
PANCA 1025	PANCA 1025 PLS 1	Not available	79	Male	Caucasian	Pancreas
III	Adenocarcinoma	0.988	Positive			
PANCA 1028	PANCA 1028 PLS 1	Not available	64	Male	Caucasian	Pancreas
III	Adenocarcinoma	0.910	Positive			
PANCA 1030	PANCA 1030 PLS 1	Not available	69	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.999	Positive			
PANCA 1031	PANCA 1031 PLS 1	Not available	82	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.978	Positive			
PANCA 1034	PANCA 1034 PLS 1	Not available	63	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.969	Positive			
PANCA 1036	PANCA 1036 PLS 1	Not available	69	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.402	Negative			
PANCA 1037	PANCA 1037 PLS 1	Not available	63	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.857	Negative			
PANCA 1039	PANCA 1039 PLS 1	Not available	68	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.693	Negative			
PANCA 1040	PANCA 1040 PLS 1	Not available	63	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.987	Positive			
PANCA 1042	PANCA 1042 PLS 1	Not available	75	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.502	Negative			
PANCA 1043	PANCA 1043 PLS 1	Not available	63	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.998	Positive			
PANCA 1044	PANCA 1044 PLS 1	Not available	56	Female	Caucasian	Pancreas
II	Adenocarcinoma	1.000	Positive			

Table2.txt

PANCA 1047	PANCA 1047 PLS 1	Not available	48	Male	Other	Pancreas	II	Adenocarcinoma	0.824	Negative
PANCA 1048	PANCA 1048 PLS 1	Not available	82	Female	Caucasian	Pancreas	III	Adenocarcinoma	0.929	Positive
PANCA 1050	PANCA 1050 PLS 1	Not available	68	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.947	Positive
PANCA 1051	PANCA 1051 PLS 1	Not available	62	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.993	Positive
PANCA 1052	PANCA 1052 PLS 1	Not available	78	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.406	Negative
PANCA 1053	PANCA 1053 PLS 1	Not available	78	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.987	Positive
PANCA 1054	PANCA 1054 PLS 1	Not available	75	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.986	Positive
PANCA 1055	PANCA 1055 PLS 1	Not available	60	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.122	Negative
PANCA 1056	PANCA 1056 PLS 1	Not available	64	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.997	Positive
PANCA 1057	PANCA 1057 PLS 1	Not available	71	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.284	Negative
PANCA 1058	PANCA 1058 PLS 1	Not available	68	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.957	Positive
PANCA 1059	PANCA 1059 PLS 1	Not available	55	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.877	Positive
PANCA 1061	PANCA 1061 PLS 1	Not available	67	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.999	Positive
PANCA 1063	PANCA 1063 PLS 1	Not available	62	Male	Caucasian	Pancreas	II	Adenocarcinoma	0.701	Negative
PANCA 1149	PANCA 1149 PLS 1	PANCA 1149 PT1	67	Female	Caucasian	Pancreas	II	Adenocarcinoma	0.905	Positive
PANCA 1152	PANCA 1152 PLS 1	PANCA 1152 PT1	66	Male	Caucasian	Pancreas	I	Adenocarcinoma	0.690	Negative

Table2.txt

PANCA 1153	PANCA 1153 PLS 1	PANCA 1153 PT1	73	Male	Caucasian	Pancreas
II	Adenocarcinoma	0.877	Positive			
PANCA 1155	PANCA 1155 PLS 1	PANCA 1155 PT1	79	Female	Caucasian	Pancreas
II	Adenocarcinoma	1.000	Positive			
PANCA 1156	PANCA 1156 PLS 1	PANCA 1156 PT1	76	Female	Caucasian	Pancreas
II	Adenocarcinoma	0.224	Negative			
PAP 938	PAP 938 PLS 1	Not available	76	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 939	PAP 939 PLS 1	Not available	75	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 940	PAP 940 PLS 1	Not available	37	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 941	PAP 941 PLS 1	Not available	46	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 944	PAP 944 PLS 1	Not available	59	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.998	Positive			
PAP 945	PAP 945 PLS 1	Not available	47	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 946	PAP 946 PLS 1	Not available	48	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 947	PAP 947 PLS 1	Not available	71	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.999	Positive			
PAP 949	PAP 949 PLS 1	Not available	81	Female	Black	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 950	PAP 950 PLS 1	Not available	75	Female	Other	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 951	PAP 951 PLS 1	Not available	62	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.836	Negative			
PAP 953	PAP 953 PLS 1	Not available	48	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.998	Positive			
PAP 954	PAP 954 PLS 1	Not available	47	Female	Black	Ovary
III	Epithelial carcinoma	1.000	Positive			

Table2.txt

PAP 955	PAP 955 PLS 1	Not available	53	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 956	PAP 956 PLS 1	Not available	77	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 957	PAP 957 PLS 1	Not available	54	Female	Black	Ovary
III	Epithelial carcinoma	0.983	Positive			
PAP 959	PAP 959 PLS 1	Not available	53	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 961	PAP 961 PLS 1	Not available	67	Female	Black	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAP 962	PAP 962 PLS 1	Not available	74	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.992	Positive			
PAP 974	PAP 974 PLS 1	Not available	75	Female	Caucasian	Ovary
I	Epithelial carcinoma	1.000	Positive			
PAPA 1330	PAPA 1330 PLS 1	Not available	66	Female	Other	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1331	PAPA 1331 PLS 1	Not available	68	Female	Hispanic	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1332	PAPA 1332 PLS 1	Not available	52	Female	Caucasian	Ovary
I	Epithelial carcinoma	0.971	Positive			
PAPA 1333	PAPA 1333 PLS 1	Not available	54	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.994	Positive			
PAPA 1334	PAPA 1334 PLS 1	Not available	66	Female	Black	Ovary
III	Epithelial carcinoma	0.999	Positive			
PAPA 1335	PAPA 1335 PLS 1	Not available	64	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.999	Positive			
PAPA 1336	PAPA 1336 PLS 1	Not available	60	Female	Caucasian	Ovary
I	Epithelial carcinoma	1.000	Positive			
PAPA 1339	PAPA 1339 PLS 1	Not available	66	Female	Caucasian	Ovary
I	Epithelial carcinoma	1.000	Positive			
PAPA 1342	PAPA 1342 PLS 1	Not available	57	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			

Table2.txt

PAPA 1343	PAPA 1343 PLS 1	Not available	74	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1344	PAPA 1344 PLS 1	Not available	59	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.871	Positive			
PAPA 1345	PAPA 1345 PLS 1	Not available	61	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1346	PAPA 1346 PLS 1	Not available	59	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1347	PAPA 1347 PLS 1	Not available	47	Female	Caucasian	Ovary
I	Epithelial carcinoma	1.000	Positive			
PAPA 1348	PAPA 1348 PLS 1	Not available	72	Female	Asian	Ovary
III	Epithelial carcinoma	0.999	Positive			
PAPA 1349	PAPA 1349 PLS 1	Not available	64	Female	Caucasian	Ovary
III	Epithelial carcinoma	1.000	Positive			
PAPA 1350	PAPA 1350 PLS 1	Not available	58	Female	Other	Ovary
II	Epithelial carcinoma	0.941	Positive			
PAPA 1353	PAPA 1353 PLS 1	Not available	55	Female	Caucasian	Ovary
I	Epithelial carcinoma	0.920	Positive			
PAPA 1354	PAPA 1354 PLS 1	Not available	57	Female	Caucasian	Ovary
I	Epithelial carcinoma	0.990	Positive			
PAPA 1355	PAPA 1355 PLS 1	Not available	60	Female	Caucasian	Ovary
III	Epithelial carcinoma	0.999	Positive			
PAPA 1356	PAPA 1356 PLS 1	Not available	49	Female	Caucasian	Ovary
II	Epithelial carcinoma	1.000	Positive			
PAPA 1357	PAPA 1357 PLS 1	Not available	60	Female	Black	Ovary
III	Epithelial carcinoma	1.000	Positive			

NA: Not applicable
NOS: Not otherwise specified
Previously analyzed with a different assay in Cohen et al., PNAS (2017).

Table3.txt

Table 3. Mutations identified in plasma samples from cancer patients and healthy controls.

Patient ID #	Sample ID #	Mutant allele frequency in plasma*	Mutation type	Mutant Tumor Stage	AJCC Stage	CancerSEEK Logistic Regression Score	Plasma DNA concentration (ng/mL)	Plasma volume (mL)	Omega score	Mutant frequency (%)
CRC 455	CRC 455 PLS 1	TP53 p.K120E, c.358A>G	Colorectum	I	5	0.681	6.08	5.1	2.81	0.27
CRC 456	CRC 456 PLS 1	TP53 p.S240I, c.719G>T	Colorectum	I	4	0.986	46.01	3.2	2.52	0.02
CRC 457	CRC 457 PLS 1	TP53 p.R202C, c.604C>T	Colorectum	II	4.5	0.978	6.94	1.4	1.18	0.06
CRC 458	CRC 458 PLS 1	TP53 p.R248Q, c.743G>A	Colorectum	II	7.5	0.693	7.15	3.6	1.61	0.16
CRC 459	CRC 459 PLS 1	TP53 p.A276G, c.827C>G	Colorectum	II	5	0.515	9.81	2.5	1.31	0.08
CRC 460	CRC 460 PLS 1	CTNNB1 p.S45F, c.134C>T	Colorectum	II	5	0.707	16.33	4.9	2.93	0.10
CRC 461	CRC 461 PLS 1	TP53 p.Y220H, c.658T>C	Colorectum	I	7.5	0.117	8.93	0.9	0.96	0.03
CRC 462	CRC 462 PLS 1	TP53 p.A161T, c.481G>A	Colorectum	I	7.5	0.381	5.32	0.4	0.78	0.03
CRC 463	CRC 463 PLS 1	TP53 p.R273H, c.818G>A	Colorectum	I	7.5	0.892	5.47	1.5	0.88	0.09
CRC 464	CRC 464 PLS 1	TP53 p.P12S, c.34C>T	Colorectum	III	7.5	0.557	3.98	0.2	0.96	0.02
CRC 465	CRC 465 PLS 1	TP53 p.L264fs, c.791delT	Colorectum	II	7.5	0.698	2.94	0.5	1.77	0.06
CRC 466	CRC 466 PLS 1	CDKN2A p.A76T, c.226G>A	Colorectum	III	5	0.356	5.56	1.1	0.70	0.07

Table3.txt

CRC 467	CRC 467 PLS 1	Colorectum	III	5	13.69	TP53 p.G245S, c.733G>A
1.12	0.04	1.7	0.878			
CRC 468	CRC 468 PLS 1	Colorectum	III	5	12.99	TP53 p.E286G, c.857A>G
11.42	0.39	15.6	0.998			
CRC 469	CRC 469 PLS 1	Colorectum	II	7.5	4.21	TP53 p.A138T, c.412G>A
0.65	0.04	0.6	0.117			
CRC 470	CRC 470 PLS 1	Colorectum	II	7.5	2.79	APC p.E1306*, c.3916G>T
5.93	0.36	3.1	0.967			
CRC 471	CRC 471 PLS 1	Colorectum	III	7.5	6.65	TP53 p.R196*, c.586C>T
2.80	1.84	37.7	0.915			
CRC 472	CRC 472 PLS 1	Colorectum	II	5	16.78	TP53 p.R273H, c.818G>A
0.72	0.02	1.2	0.574			
CRC 473	CRC 473 PLS 1	Colorectum	II	7.5	6.30	KRAS p.G13D, c.38G>A
3.40	3.68	71.4	0.934			
CRC 474	CRC 474 PLS 1	Colorectum	III	5	16.36	TP53 p.R174G, c.520A>G
1.07	0.03	1.3	0.307			
CRC 475	CRC 475 PLS 1	Colorectum	I	7.5	8.64	TP53 p.G262D, c.785G>A
0.93	0.02	0.5	0.750			
CRC 476	CRC 476 PLS 1	Colorectum	II	5	8.45	TP53 p.R249G, c.745A>G
20.05	7.25	188.8	0.999			
CRC 477	CRC 477 PLS 1	Colorectum	II	5	9.41	TP53 p.R282W, c.844C>T
1.14	0.10	2.8	0.981			
CRC 478	CRC 478 PLS 1	Colorectum	III	5	6.79	FBXW7 p.R465C, c.1393C>T
0.63	0.04	0.8	0.439			
CRC 479	CRC 479 PLS 1	Colorectum	II	5	11.88	KRAS p.G12C, c.34G>T
2.41	0.06	2.4	0.969			
CRC 480	CRC 480 PLS 1	Colorectum	III	5	13.30	CTNNB1 p.T41A, c.121A>G
93.61	0.76	31.0	0.996			
CRC 481	CRC 481 PLS 1	Colorectum	II	5	13.85	PIK3CA p.H1047R, c.3140A>G
3.18	0.19	8.0	0.951			
CRC 482	CRC 482 PLS 1	Colorectum	III	5	4.40	TP53 p.P300S, c.898C>T
1.00	0.05	0.7	0.606			

Table3.txt

CRC 483	CRC 483 PLS 1	Colorectum	I	7.5	5.67	FBXW7 p.R505H, c.1514G>A
0.82	0.02	0.4	0.116			
CRC 484	CRC 484 PLS 1	Colorectum	I	7.5	8.04	TP53 p.R335H, c.1004G>A
1.13	0.04	1.1	0.904			
CRC 486	CRC 486 PLS 1	Colorectum	I	7.5	5.08	KRAS p.G12D, c.35G>A
2.07	0.06	1.0	0.973			
CRC 487	CRC 487 PLS 1	Colorectum	I	7.5	6.05	NRAS p.A59T, c.175G>A
0.92	0.02	0.4	0.117			
CRC 488	CRC 488 PLS 1	Colorectum	II	7.5	5.14	TP53 p.V157F, c.469G>T
4.61	0.59	9.4	0.988			
CRC 489	CRC 489 PLS 1	Colorectum	II	7.5	5.77	KRAS p.Q61K, c.181C>A
4.06	0.17	3.0	0.991			
CRC 490	CRC 490 PLS 1	Colorectum	III	7.5	5.80	TP53 p.L383H, c.1148T>A
1.64	0.02	0.3	0.397			
CRC 491	CRC 491 PLS 1	Colorectum	III	7.5	13.78	FBXW7 p.R465H, c.1394G>A
1.56	0.17	7.1	0.840			
CRC 492	CRC 492 PLS 1	Colorectum	III	7.5	7.38	TP53 p.L348S, c.1043T>C
0.95	0.02	0.5	0.906			
CRC 493	CRC 493 PLS 1	Colorectum	II	7.5	7.91	TP53 p.A347T, c.1039G>A
0.96	0.02	0.4	0.739			
CRC 494	CRC 494 PLS 1	Colorectum	II	7.5	5.11	APC p.R1450*, c.4348C>T
2.21	0.49	7.8	0.448			
CRC 495	CRC 495 PLS 1	Colorectum	I	7	10.65	TP53 p.A119T, c.355G>A
0.80	0.03	1.1	0.116			
CRC 496	CRC 496 PLS 1	Colorectum	I	7.5	8.00	TP53 p.V274A, c.821T>C
0.97	0.07	1.6	0.330			
CRC 497	CRC 497 PLS 1	Colorectum	III	7.5	10.72	FBXW7 p.R479Q, c.1436G>A
2.42	0.46	15.0	0.990			
CRC 498	CRC 498 PLS 1	Colorectum	III	7.5	7.27	TP53 p.R335H, c.1004G>A
1.07	0.05	1.1	0.944			
CRC 499	CRC 499 PLS 1	Colorectum	I	5	10.24	TP53 p.C238Y, c.713G>A
1.83	0.12	3.6	0.543			

Table3.txt

CRC 500	CRC 500 PLS 1	Colorectum	I	7.5	5.79	
TP53 p.P82L, c.245C>T						
0.83	0.02	0.4	0.308			
CRC 501	CRC 501 PLS 1	Colorectum	I	7.5	5.04	
TP53 p.P300fs, c.898delC						
1.04	0.04	0.7	0.490			
CRC 502	CRC 502 PLS 1	Colorectum	I	7.5	9.95	
TP53 p.F328S, c.983T>C						
0.87	0.01	0.2	0.121			
CRC 503	CRC 503 PLS 1	Colorectum	I	7.5	7.15	
TP53 p.R174W, c.520A>T						
1.14	0.01	0.3	0.993			
CRC 504	CRC 504 PLS 1	Colorectum	III	7.5	14.14	
APC p.E1309fs, c.3927delAAAGA						
17.49	1.67	72.6	0.999			
CRC 505	CRC 505 PLS 1	Colorectum	III	7.5	7.98	
TP53 p.R306*, c.916C>T						
0.85	0.03	0.6	0.323			
CRC 506	CRC 506 PLS 1	Colorectum	III	7.5	6.87	
APC p.I1311fs, c.3931insA						
4.40	0.19	4.0	0.680			
CRC 507	CRC 507 PLS 1	Colorectum	I	7.5	3.79	
TP53 p.R273H, c.818G>A						
0.86	0.07	0.8	0.818			
CRC 508	CRC 508 PLS 1	Colorectum	I	7.5	2.69	
PTEN p.R130G, c.388C>G						
1.32	0.05	0.4	0.343			
CRC 509	CRC 509 PLS 1	Colorectum	I	7.5	5.88	
BRAF p.V600M, c.1798G>A						
1.05	0.02	0.4	0.480			
CRC 510	CRC 510 PLS 1	Colorectum	I	7.5	8.25	
TP53 p.R202C, c.604C>T						
1.00	0.04	1.1	0.300			
CRC 511	CRC 511 PLS 1	Colorectum	II	5	16.57	
TP53 p.R202C, c.604C>T						
0.94	0.05	2.3	0.125			
CRC 512	CRC 512 PLS 1	Colorectum	II	7.5	22.90	
KRAS p.G12D, c.35G>A						
2.38	0.08	6.0	0.868			
CRC 513	CRC 513 PLS 1	Colorectum	II	7.5	24.44	
TP53 p.L194H, c.581T>A						
1.64	0.02	1.5	0.994			
CRC 514	CRC 514 PLS 1	Colorectum	II	7	7.21	
KRAS p.G12V, c.35G>T						
8.10	1.27	28.3	0.998			
CRC 515	CRC 515 PLS 1	Colorectum	II	7.5	6.14	
TP53 p.A353V, c.1058C>T						
1.01	0.03	0.6	0.640			

Table3.txt

CRC 516	CRC 516 PLS 1	Colorectum	II	7.5	13.15	CTNNB1 p.T41A, c.121A>G	4.69	0.03	1.4	0.664
CRC 517	CRC 517 PLS 1	Colorectum	II	7.5	9.14	TP53 g.7579311C>T (Splice Site)	1.08	0.02	0.6	0.318
CRC 518	CRC 518 PLS 1	Colorectum	III	7.5	10.91	TP53 p.S215fs, c.644insGTG	87.57	8.48	284.9	0.999
CRC 519	CRC 519 PLS 1	Colorectum	III	7.5	7.62	TP53 p.V217M, c.649G>A	0.93	0.02	0.6	0.117
CRC 520	CRC 520 PLS 1	Colorectum	III	7.5	8.21	KRAS p.G12V, c.35G>T	4.98	0.48	12.1	0.974
CRC 521	CRC 521 PLS 1	Colorectum	III	7.5	5.23	KRAS p.A146V, c.437C>T	3.64	0.45	7.3	0.598
CRC 522	CRC 522 PLS 1	Colorectum	II	7.5	11.83	TP53 p.C176fs, c.528delC	0.77	0.02	0.7	0.868
CRC 523	CRC 523 PLS 1	Colorectum	III	7.5	5.63	TP53 p.R174G, c.520A>G	1.09	0.02	0.4	0.451
CRC 524	CRC 524 PLS 1	Colorectum	II	7.5	7.83	KRAS p.G12V, c.35G>T	4.09	0.36	8.7	0.983
CRC 525	CRC 525 PLS 1	Colorectum	III	7.5	7.88	KRAS p.G13D, c.38G>A	1.34	0.07	1.6	0.968
CRC 526	CRC 526 PLS 1	Colorectum	III	7.5	10.20	AKT1 p.E17K, c.49G>A	2.60	0.10	3.0	0.521
CRC 527	CRC 527 PLS 1	Colorectum	III	7.5	4.72	KRAS p.A146T, c.436G>A	3.10	2.30	33.4	0.937
CRC 528	CRC 528 PLS 1	Colorectum	II	7.5	6.77	TP53 p.R273C, c.817C>T	1.25	0.04	0.8	0.338
CRC 529	CRC 529 PLS 1	Colorectum	II	7.5	4.74	TP53 p.R306*, c.916C>T	0.76	0.04	0.6	0.116
CRC 530	CRC 530 PLS 1	Colorectum	II	7.5	4.99	TP53 p.M384V, c.1150A>G	0.81	0.03	0.5	0.956
CRC 531	CRC 531 PLS 1	Colorectum	III	7.5	4.94	KRAS p.G12V, c.35G>T	2.72	0.14	2.2	0.540

Table3.txt

INDI 001	INDI 001 PLS 1	Lung	II	7.5	2.44	
	TP53 p.K373R, c.1118A>G					
0.82	0.07	0.5	0.926			
INDI 002	INDI 002 PLS 1	Lung	II	7.5	0.86	
	TP53 p.R202C, c.604C>T					
0.54	0.09	0.2	0.621			
INDI 003	INDI 003 PLS 1	Lung	III	7.5	2.72	
	TP53 p.H178P, c.533A>C					
1.69	0.07	0.6	0.999			
INDI 004	INDI 004 PLS 1	Lung	I	7.5	2.43	
	GNAS p.R201H, c.602G>A					
0.67	0.07	0.5	0.936			
INDI 005	INDI 005 PLS 1	Lung	I	7.5	3.15	
	TP53 p.R156fs, c.467delG					
0.74	0.05	0.5	0.779			
INDI 007	INDI 007 PLS 1	Lung	II	7.5	3.24	
	TP53 p.G108S, c.322G>A					
0.86	0.05	0.5	0.614			
INDI 009	INDI 009 PLS 1	Lung	II	7.5	2.59	
	TP53 p.C176F, c.527G>T					
5.51	1.06	8.5	0.985			
INDI 010	INDI 010 PLS 1	Lung	II	7.5	3.14	
	PIK3CA p.A1046V, c.3137C>T					
0.71	0.05	0.5	0.926			
INDI 011	INDI 011 PLS 1	Lung	I	7.5	1.88	
	TP53 p.R175H, c.524G>A					
0.57	0.06	0.3	0.362			
INDI 012	INDI 012 PLS 1	Lung	I	7.5	3.06	
	CDKN2A p.D84V, c.251A>T					
2.31	0.08	0.8	0.966			
INDI 013	INDI 013 PLS 1	Lung	III	7.5	3.27	
	TP53 p.I254F, c.760A>T					
0.98	0.03	0.3	0.852			
INDI 014	INDI 014 PLS 1	Lung	II	7.5	1.61	
	TP53 p.E298*, c.892G>T					
5.89	1.36	6.7	0.965			
INDI 015	INDI 015 PLS 1	Lung	I	7.5	5.45	
	TP53 p.A88D, c.263C>A					
0.81	0.05	0.8	0.121			
INDI 016	INDI 016 PLS 1	Lung	III	7.5	9.56	
	PIK3CA p.E545D, c.1635G>T					
2.38	0.14	4.1	0.990			
INDI 017	INDI 017 PLS 1	Lung	I	7.5	5.22	
	TP53 p.A86T, c.256G>A					
0.50	0.07	1.2	0.397			
INDI 018	INDI 018 PLS 1	Lung	III	7.5	4.29	
	TP53 p.K372fs, c.1114delA					
0.84	0.13	1.7	0.824			

Table3.txt

INDI 022	INDI 022 PLS 1	Lung	III	7.5	3.72	TP53 p.T211fs, c.633delT	7.31	5.99	68.7	0.996
INDI 023	INDI 023 PLS 1	Lung	II	7.5	7.78	TP53 p.G266V, c.797G>T	7.61	0.90	21.7	0.998
INDI 024	INDI 024 PLS 1	Lung	II	7.5	3.11	TP53 p.G244D, c.731G>A	0.44	0.06	0.6	0.606
INDI 025	INDI 025 PLS 1	Lung	I	7.5	3.25	TP53 p.P151A, c.451C>G	1.79	0.16	1.6	0.972
INDI 026	INDI 026 PLS 1	Lung	I	7.5	5.75	TP53 p.A353V, c.1058C>T	0.92	0.05	0.9	0.593
INDI 027	INDI 027 PLS 1	Colorectum	II	7.5	6.11	TP53 p.R175H, c.524G>A	2.79	2.49	46.8	0.981
INDI 028	INDI 028 PLS 1	Colorectum	II	7.5	8.23	TP53 p.G245S, c.733G>A	2.49	1.32	33.4	0.507
INDI 029	INDI 029 PLS 1	Colorectum	II	7.5	6.75	CTNNB1 p.A43T, c.127G>A	0.57	0.00	0.1	0.328
INDI 030	INDI 030 PLS 1	Colorectum	II	7.5	4.52	TP53 p.A189V, c.566C>T	0.60	0.03	0.4	0.940
INDI 031	INDI 031 PLS 1	Colorectum	II	7.5	4.39	KRAS p.G12D, c.35G>A	0.90	0.03	0.4	0.371
INDI 032	INDI 032 PLS 1	Colorectum	III	7.5	4.38	PPP2R1A p.R183W, c.547C>T	0.63	0.05	0.7	0.117
INDI 034	INDI 034 PLS 1	Colorectum	III	7.5	14.89	TP53 p.W53*, c.159G>A	2.65	0.07	3.0	0.997
INDI 035	INDI 035 PLS 1	Colorectum	II	7.5	3.07	KRAS p.G12D, c.35G>A	3.13	0.57	5.4	0.581
INDI 036	INDI 036 PLS 1	Colorectum	I	7.5	12.97	TP53 p.K372fs, c.1114delA	1.00	0.04	1.4	0.801
INDI 037	INDI 037 PLS 1	Colorectum	I	7.5	3.99	TP53 p.K372fs, c.1114delA	0.92	0.05	0.6	0.788
INDI 038	INDI 038 PLS 1	Colorectum	II	7.5	3.25	KRAS p.Q61K, c.181C>A	2.12	0.08	0.8	0.449

Table3.txt

INDI 039	INDI 039 PLS 1	Colorectum	III	7.5	13.81		
	BRAF p.D594G, c.1781A>G						
1.86	0.03	1.3	0.993				
INDI 040	INDI 040 PLS 1	Colorectum	I	7.5	6.86		
	TP53 p.C176fs, c.528delC						
0.83	0.03	0.7	0.387				
INDI 042	INDI 042 PLS 1	Colorectum	I	7.5	4.48		
	KRAS p.G12D, c.35G>A						
1.45	0.10	1.4	0.368				
INDI 043	INDI 043 PLS 1	Colorectum	II	7.5	5.53		
	TP53 g.7577018C>T (Splice Site)						
0.57	0.03	0.5	0.997				
INDI 044	INDI 044 PLS 1	Colorectum	II	7.5	17.02		
	TP53 p.Y236fs, c.708delC						
0.93	0.07	3.5	0.979				
INDI 045	INDI 045 PLS 1	Colorectum	III	7.5	44.22		
	TP53 p.R290C, c.868C>T						
0.56	0.03	4.2	1.000				
INDI 046	INDI 046 PLS 1	Colorectum	II	7.5	37.01		
	CTNNB1 p.S45A, c.133T>G						
0.73	0.01	0.9	0.989				
INDI 047	INDI 047 PLS 1	Colorectum	II	7.5	2.68		
	TP53 p.K372fs, c.1114delA						
0.52	0.05	0.4	0.977				
INDI 048	INDI 048 PLS 1	Breast	II	7.5	3.91		
	TP53 p.T253I, c.758C>T						
0.95	0.06	0.7	0.639				
INDI 049	INDI 049 PLS 1	Breast	III	7.5	2.49		
	TP53 p.R202C, c.604C>T						
0.69	0.05	0.4	0.122				
INDI 050	INDI 050 PLS 1	Breast	II	7.5	2.71		
	CDKN2A p.R58*, c.172C>T						
0.42	0.05	0.4	0.123				
INDI 051	INDI 051 PLS 1	Breast	III	7	4.23		
	TP53 p.P222S, c.664C>T						
0.83	0.05	0.7	0.877				
INDI 052	INDI 052 PLS 1	Breast	II	7.5	3.32		
	TP53 p.R337C, c.1009C>T						
0.37	0.07	0.8	0.886				
INDI 053	INDI 053 PLS 1	Breast	II	7.5	4.62		
	TP53 p.R175H, c.524G>A						
0.63	0.05	0.8	0.121				
INDI 054	INDI 054 PLS 1	Breast	II	7.5	8.96		
	TP53 p.A159T, c.475G>A						
0.86	0.04	1.0	0.121				
INDI 055	INDI 055 PLS 1	Breast	II	7.5	4.40		
	TP53 p.T125T, c.375G>A (Exon End)						
0.61	0.04	0.6	0.404				

Table3.txt

INDI 056	INDI 056 PLS 1	Breast	II	7.5	1.78	TP53 p.R202C, c.604C>T
0.66	0.06	0.3	0.332			
INDI 057	INDI 057 PLS 1	Breast	III	7.5	5.88	TP53 p.K372fs, c.1114delA
1.03	0.06	1.0	0.803			
INDI 058	INDI 058 PLS 1	Breast	I	7.5	2.17	TP53 p.D49N, c.145G>A
0.50	0.06	0.4	0.620			
INDI 059	INDI 059 PLS 1	Breast	II	7.5	6.58	TP53 p.R202C, c.604C>T
1.01	0.04	0.7	0.975			
INDI 060	INDI 060 PLS 1	Breast	II	7.5	37.80	BRAF p.K601E, c.1801A>G
1.30	0.01	1.5	0.993			
INDI 061	INDI 061 PLS 1	Breast	II	7.5	27.99	TP53 p.P47L, c.140C>T
1.04	0.03	2.2	0.961			
INDI 062	INDI 062 PLS 1	Breast	II	7.5	2.95	TP53 p.R306*, c.916C>T
0.46	0.08	0.8	0.571			
INDI 063	INDI 063 PLS 1	Breast	III	7.5	4.86	GNAS p.R201C, c.601C>T
0.56	0.02	0.2	0.727			
INDI 064	INDI 064 PLS 1	Breast	II	7.5	12.86	TP53 p.C242Y, c.725G>A
1.69	0.06	2.5	0.938			
INDI 065	INDI 065 PLS 1	Breast	II	7.5	4.54	TP53 p.R290C, c.868C>T
1.00	0.05	0.7	0.564			
INDI 066	INDI 066 PLS 1	Breast	III	7.5	5.54	KRAS p.V14I, c.40G>A
0.67	0.06	1.0	0.681			
INDI 067	INDI 067 PLS 1	Breast	III	7.5	19.07	CDKN2A p.T79I, c.236C>T
1.23	0.02	1.1	0.997			
INDI 068	INDI 068 PLS 1	Breast	II	7.5	9.78	TP53 p.Q104*, c.310C>T
0.87	0.02	0.7	0.514			
INDI 069	INDI 069 PLS 1	Breast	II	7.5	15.08	TP53 p.G245D, c.734G>A
1.01	0.03	1.2	0.997			
INDI 070	INDI 070 PLS 1	Breast	III	7.5	16.58	PTEN p.C136R, c.406T>C
15.54	0.75	38.2	1.000			
INDI 071	INDI 071 PLS 1	Breast	II	7.5	6.69	TP53 p.R202C, c.604C>T
1.04	0.04	0.9	0.972			

Table3.txt

INDI 072	INDI 072 PLS 1	Breast	II	7.5	6.04	TP53 p.Y205C, c.614A>G	
0.84	0.03	0.6	0.986				
INDI 073	INDI 073 PLS 1	Breast	III	7.5	4.19	TP53 p.L369P, c.1106T>C	
1.14	0.09	1.2	0.861				
INDI 074	INDI 074 PLS 1	Pancreas	II	7.5	7.45	KRAS p.G12V, c.35G>T	
3.43	0.25	5.7	1.000				
INDI 075	INDI 075 PLS 1	Ovary	III	7.5	2.60	TP53 p.Y220C, c.659A>G	
7.16	8.47	67.8	0.955				
INDI 076	INDI 076 PLS 1	Esophagus	II	7.5	5.19	None detected	
NA	NA	NA	0.990				
INDI 077	INDI 077 PLS 1	Liver	II	7.5	62.35	TP53 p.K132R, c.395A>G	
98.06	4.49	862.8	1.000				
INDI 078	INDI 078 PLS 1	Liver	II	7.5	47.19	TP53 p.R249S, c.747G>T	
1.86	0.03	4.2	0.992				
INDI 079	INDI 079 PLS 1	Liver	II	7.5	44.38	TP53 p.C176F, c.527G>T	
2.83	0.05	6.6	0.999				
INDI 080	INDI 080 PLS 1	Liver	I	7.5	5.76	TP53 p.H178P, c.533A>C	
3.14	0.04	0.7	0.984				
INDI 081	INDI 081 PLS 1	Colorectum	II	7.5	25.31	TP53 p.W53*, c.158G>A	
30.50	0.23	18.1	0.997				
INDI 082	INDI 082 PLS 1	Stomach	II	7.5	6.57	TP53 p.A353V, c.1058C>T	
0.97	0.08	1.6	0.117				
INDI 083	INDI 083 PLS 1	Stomach	II	7.5	5.25	None detected	
NA	NA	NA	0.993				
INDI 084	INDI 084 PLS 1	Stomach	II	7.5	19.44	TP53 p.R156C, c.466C>T	
0.71	0.03	2.0	0.997				
INDI 085	INDI 085 PLS 1	Stomach	I	7.5	2.27	None detected	
NA	NA	NA	0.940				
INDI 086	INDI 086 PLS 1	Stomach	I	7.5	34.92	KRAS p.A11V, c.32C>T	
0.81	0.01	1.1	0.997				
INDI 087	INDI 087 PLS 1	Stomach	I	7.5	7.78	TP53 p.R379H, c.1136G>A	
1.18	0.07	1.6	0.999				

Table3.txt

INDI 089	INDI 089 PLS 1	Colorectum	II	7.5	20.39	KRAS p.G12A, c.35G>C		
0.35	0.03	1.8	0.999					
INDI 090	INDI 090 PLS 1	Colorectum	II	7.5	28.80	TP53 p.A138T, c.412G>A		
0.33	0.04	3.9	0.967					
INDI 092	INDI 092 PLS 1	Stomach	II	7.5	3.04	FBXW7 p.R479*, c.1435C>T		
0.48	0.06	0.6	0.848					
INDI 093	INDI 093 PLS 1	Colorectum	I	7.5	7.60	TP53 p.R379H, c.1136G>A		
1.04	0.06	1.5	0.997					
INDI 094	INDI 094 PLS 1	Colorectum	I	7.5	20.90	TP53 p.A353V, c.1058C>T		
0.61	0.06	3.8	0.993					
INDI 095	INDI 095 PLS 1	Stomach	II	7.5	49.78	TP53 p.R202C, c.604C>T		
0.99	0.05	7.2	0.792					
INDI 096	INDI 096 PLS 1	Colorectum	I	7.5	5.59	KRAS p.G13D, c.38G>A		
0.60	0.02	0.4	0.652					
INDI 097	INDI 097 PLS 1	Colorectum	III	7.5	16.40	BRAF p.V600E, c.1799T>A		
4.82	0.28	14.2	0.997					
INDI 098	INDI 098 PLS 1	Colorectum	II	7.5	2.78	TP53 p.R202C, c.604C>T		
0.76	0.07	0.6	0.308					
INDI 100	INDI 100 PLS 1	Colorectum	III	7.5	9.25	TP53 p.V216M, c.646G>A		
1.30	0.07	2.0	0.992					
INDI 101	INDI 101 PLS 1	Colorectum	III	7.5	5.72	TP53 p.H178Q, c.534C>A		
1.17	0.02	0.4	0.793					
INDI 102	INDI 102 PLS 1	Colorectum	III	7.5	11.76	TP53 p.I50fs, c.148insC		
1.13	0.04	1.4	0.977					
INDI 103	INDI 103 PLS 1	Stomach	II	7.5	17.85	KRAS p.A11V, c.32C>T		
0.84	0.01	0.5	0.583					
INDI 104	INDI 104 PLS 1	Stomach	III	7.5	4.21	TP53 p.V272M, c.814G>A		
2.38	0.90	11.7	0.983					
INDI 107	INDI 107 PLS 1	Colorectum	II	7.5	2.43	GNAS p.R201H, c.602G>A		
0.54	0.03	0.2	0.975					
INDI 108	INDI 108 PLS 1	Colorectum	II	7.5	2.95	TP53 p.R267W, c.799C>T		
4.91	16.76	152.3	0.984					

Table3.txt

INDI 109	INDI 109 PLS 1	Colorectum	III	7.5	21.96		
		TP53 p.R248Q, c.743G>A					
3.44	4.87	329.4	0.997				
INDI 110	INDI 110 PLS 1	Stomach	I	7.5	12.51		
		TP53 p.A159T, c.475G>A					
0.98	0.03	1.3	0.972				
INDI 111	INDI 111 PLS 1	Stomach	II	7.5	9.17		
		TP53 p.K372fs, c.1114delA					
0.91	0.02	0.7	0.938				
INDI 112	INDI 112 PLS 1	Esophagus	II	7.5	30.29		
		TP53 p.R249S, c.747G>T					
1.09	0.01	1.3	1.000				
INDI 113	INDI 113 PLS 1	Colorectum	II	7.5	7.73		
		TP53 p.K372fs, c.1114delA					
1.09	0.05	1.1	0.998				
INDI 116	INDI 116 PLS 1	Stomach	I	7.5	39.39		
		TP53 p.S260Y, c.779C>A					
144.55	40.92	4,964.8	1.000				
INDI 119	INDI 119 PLS 1	Esophagus	I	7.5	53.59		
		TP53 p.H179R, c.536A>G					
39.32	2.17	359.0	1.000				
INDI 120	INDI 120 PLS 1	Stomach	III	7.5	58.27		
		TP53 p.R248P, c.743G>C					
0.97	0.00	0.9	0.983				
INDI 121	INDI 121 PLS 1	Stomach	I	7.5	92.85		
		EGFR p.G857E, c.2570G>A					
0.93	0.00	0.9	0.919				
INDI 122	INDI 122 PLS 1	Colorectum	II	7.5	7.61		
		TP53 p.K372fs, c.1114delA					
0.81	0.03	0.6	0.998				
INDI 123	INDI 123 PLS 1	Colorectum	II	7.5	20.99		
		EGFR p.A864T, c.2590G>A					
0.89	0.01	0.6	0.996				
INDI 124	INDI 124 PLS 1	Colorectum	II	7.5	20.63		
		KRAS p.G12D, c.35G>A					
4.80	0.54	34.5	1.000				
INDI 125	INDI 125 PLS 1	Esophagus	II	7.5	23.56		
		TP53 p.L194H, c.581T>A					
5.32	0.72	52.6	0.999				
INDI 126	INDI 126 PLS 1	Stomach	III	7.5	25.59		
		TP53 p.K132R, c.395A>G					
7.89	0.63	49.9	0.999				
INDI 127	INDI 127 PLS 1	Colorectum	II	7.5	23.96		
		TP53 p.P219H, c.656C>A					
1.17	0.01	1.0	1.000				
INDI 128	INDI 128 PLS 1	Colorectum	III	7.5	6.68		
		CTNNB1 p.S45F, c.134C>T					
4.62	0.43	8.9	1.000				

Table3.txt

INDI 129	INDI 129 PLS 1	Liver	II	7.5	80.95		
		TP53 p.H178N, c.532C>A					
0.98	0.00	0.7	0.999				
INDI 130	INDI 130 PLS 1	Stomach	II	7.5	9.63		
		TP53 p.R283C, c.847C>T					
0.82	0.02	0.7	0.982				
INDI 131	INDI 131 PLS 1	Stomach	II	7.5	23.69		
		TP53 p.R158C, c.472C>T					
1.02	0.04	2.6	0.993				
INDI 132	INDI 132 PLS 1	Esophagus	III	7.5	29.99		
		TP53 p.D184G, c.551A>G					
1.00	0.01	1.0	0.918				
INDI 133	INDI 133 PLS 1	Stomach	I	7.5	16.57		
		TP53 p.R248Q, c.743G>A					
1.04	0.04	2.0	0.990				
INDI 134	INDI 134 PLS 1	Stomach	III	7.5	9.09		
		TP53 p.G374fs, c.1120delG					
0.89	0.02	0.7	0.993				
INDI 135	INDI 135 PLS 1	Stomach	III	7.5	52.87		
		TP53 p.R249S, c.747G>T					
1.75	0.04	6.2	0.999				
INDI 136	INDI 136 PLS 1	Colorectum	II	7.5	31.41		
		TP53 p.H115D, c.343C>G					
1.05	0.00	0.4	0.984				
INDI 137	INDI 137 PLS 1	Stomach	II	7.5	23.72		
		TP53 p.E51G, c.152A>G					
1.07	0.01	0.8	0.998				
INDI 139	INDI 139 PLS 1	Stomach	III	7.5	53.26		
		TP53 p.R158L, c.473G>T					
26.38	1.79	293.2	1.000				
INDI 140	INDI 140 PLS 1	Stomach	III	7.5	26.63		
		TP53 p.L194P, c.581T>C					
0.94	0.01	0.9	0.992				
INDI 141	INDI 141 PLS 1	Stomach	III	7.5	5.97		
		TP53 p.R248Q, c.743G>A					
1.11	0.04	0.7	0.965				
INDI 143	INDI 143 PLS 1	Colorectum	II	7.5	16.33		
		CTNNB1 p.S45F, c.134C>T					
1.52	0.03	1.3	0.998				
INDI 144	INDI 144 PLS 1	Colorectum	II	7.5	54.08		
		KRAS p.G12D, c.35G>A					
4.12	0.24	40.6	1.000				
INDI 145	INDI 145 PLS 1	Colorectum	II	7.5	12.18		
		TP53 p.A161T, c.481G>A					
1.22	0.04	1.3	0.999				
INDI 146	INDI 146 PLS 1	Colorectum	II	7.5	19.37		
		PTEN p.A126V, c.377C>T					
1.08	0.01	0.5	0.934				

Table3.txt

INDI 147	INDI 147 PLS 1	Stomach	II	7.5	126.95	
	FBXW7 p.R505H, c.1514G>A					
1.01	0.03	10.9	0.953			
INDI 148	INDI 148 PLS 1	Colorectum	II	7.5	40.76	
	TP53 p.R248W, c.742C>T					
1.02	0.03	3.9	0.998			
INDI 150	INDI 150 PLS 1	Colorectum	II	7.5	78.23	
	TP53 g.7578176C>T (Splice Site)					
189.18	2.43	585.4	1.000			
INDI 151	INDI 151 PLS 1	Stomach	II	7.5	37.78	
	TP53 p.Y220C, c.659A>G					
3.51	0.46	53.6	1.000			
INDI 152	INDI 152 PLS 1	Colorectum	I	7.5	30.66	
	TP53 p.L194P, c.581T>C					
1.21	0.01	0.8	0.988			
INDI 153	INDI 153 PLS 1	Stomach	II	7.5	35.87	
	TP53 p.E346G, c.1037A>G					
0.86	0.02	2.0	0.369			
INDI 155	INDI 155 PLS 1	Colorectum	II	7.5	21.12	
	TP53 p.F19fs, c.55delT					
1.43	0.02	1.0	0.836			
INDI 156	INDI 156 PLS 1	Colorectum	III	7.5	35.66	
	TP53 p.P190fs, c.570delCCT					
323.25	6.15	675.5	1.000			
INDI 158	INDI 158 PLS 1	Colorectum	I	7.5	14.91	
	TP53 p.C176fs, c.528insC					
1.37	0.03	1.6	0.980			
INDI 159	INDI 159 PLS 1	Colorectum	II	7.5	6.04	
	TP53 p.H214Y, c.640C>T					
0.61	0.02	0.3	0.852			
INDI 160	INDI 160 PLS 1	Colorectum	II	7.5	7.01	
	TP53 p.A138T, c.412G>A					
0.83	0.03	0.7	0.890			
INDI 161	INDI 161 PLS 1	Stomach	II	7.5	13.98	
	TP53 p.A138T, c.412G>A					
0.98	0.03	1.5	0.920			
INDI 162	INDI 162 PLS 1	Stomach	III	7.5	74.08	
	TP53 p.A189T, c.565G>A					
0.95	0.01	3.0	0.998			
INDI 163	INDI 163 PLS 1	Colorectum	III	7.5	6.47	
	TP53 p.R282W, c.844C>T					
1.63	0.21	4.1	0.934			
INDI 164	INDI 164 PLS 1	Colorectum	I	7.5	10.85	
	TP53 p.K372fs, c.1114delA					
1.00	0.03	1.1	0.467			
INDI 165	INDI 165 PLS 1	Colorectum	I	7.5	7.25	
	TP53 p.M169T, c.506T>C					
1.21	0.02	0.4	0.995			

Table3.txt

INDI 167	INDI 167 PLS 1	Stomach	II	7.5	56.11	
	TP53 p.R202C, c.604C>T					
0.91	0.04	7.6	0.962			
INDI 168	INDI 168 PLS 1	Stomach	II	7.5	33.93	
	TP53 g.7578555C>G (Splice Site)					
1.86	0.00	0.5	1.000			
INDI 169	INDI 169 PLS 1	Colorectum	III	7.5	35.18	
	TP53 p.G374fs, c.1120delG					
1.01	0.03	3.6	0.965			
INDI 170	INDI 170 PLS 1	Colorectum	I	7.5	28.77	
	TP53 p.M384I, c.1152G>A					
1.24	0.01	0.6	0.992			
INDI 171	INDI 171 PLS 1	Stomach	III	7.5	91.76	
	TP53 p.G199fs, c.597insA					
3.89	0.12	33.6	1.000			
INDI 172	INDI 172 PLS 1	Stomach	II	7.5	70.98	
	TP53 p.R248Q, c.743G>A					
4.20	3.23	706.9	1.000			
INDI 173	INDI 173 PLS 1	Stomach	I	7.5	15.73	
	TP53 p.S215R, c.643A>C					
1.54	0.03	1.5	0.999			
INDI 175	INDI 175 PLS 1	Colorectum	III	7.5	12.58	
	CDKN2A p.D84Y, c.250G>T					
1.67	0.02	0.7	1.000			
INDI 176	INDI 176 PLS 1	Stomach	II	7.5	36.78	
	TP53 g.7578555C>T (Splice Site)					
1.34	0.02	2.0	0.997			
INDI 177	INDI 177 PLS 1	Liver	III	7.5	108.83	
	TP53 p.R249S, c.747G>T					
1.63	0.02	7.7	1.000			
INDI 178	INDI 178 PLS 1	Colorectum	III	7.5	12.90	
	TP53 p.L348M, c.1042T>A					
1.12	0.02	0.8	0.967			
INDI 179	INDI 179 PLS 1	Colorectum	III	7.5	14.15	
	TP53 p.E336G, c.1007A>G					
1.40	0.02	0.7	0.998			
INDI 180	INDI 180 PLS 1	Colorectum	III	7.5	11.31	
	PTEN p.R130G, c.388C>G					
1.11	0.01	0.3	0.921			
INDI 182	INDI 182 PLS 1	Liver	III	7.5	50.25	
	TP53 p.A159P, c.475G>C					
4.64	0.11	17.0	1.000			
INDI 183	INDI 183 PLS 1	Stomach	I	7.5	43.29	
	TP53 p.T256I, c.767C>T					
1.54	0.02	2.6	0.999			
INDI 184	INDI 184 PLS 1	Esophagus	II	7.5	110.40	
	TP53 p.H193R, c.578A>G					
3.10	0.04	14.7	0.983			

Table3.txt

INDI 185	INDI 185 PLS 1	Stomach	II	7.5	44.97	TP53 p.S183fs, c.549insA	41.06	1.40	194.4	1.000
INDI 186	INDI 186 PLS 1	Stomach	II	7.5	86.25	GNAS p.R201C, c.601C>T	3.32	1.20	319.7	1.000
INDI 187	INDI 187 PLS 1	Stomach	I	7.5	7.29	TP53 p.R175C, c.523C>T	0.00	0.12	2.7	0.994
INDI 188	INDI 188 PLS 1	Stomach	I	7.5	44.55	TP53 p.P98T, c.292C>A	0.73	0.02	2.2	0.983
INDI 189	INDI 189 PLS 1	Esophagus	II	7.5	98.02	TP53 p.V274F, c.820G>T	2.09	0.02	5.5	1.000
INDI 190	INDI 190 PLS 1	Liver	III	7.5	62.58	TP53 p.R249S, c.747G>T	1.26	0.01	2.3	0.988
INDI 191	INDI 191 PLS 1	Colorectum	I	7.5	0.37	None detected	NA	NA	NA	0.947
INDI 192	INDI 192 PLS 1	Colorectum	II	7.5	30.45	TP53 p.L43M, c.127T>A	2.11	0.01	0.5	0.992
INDI 194	INDI 194 PLS 1	Colorectum	II	7.5	49.12	TP53 p.E349*, c.1045G>T	1.29	0.00	0.8	0.968
INDI 195	INDI 195 PLS 1	Colorectum	III	7.5	14.49	TP53 p.L369P, c.1106T>C	0.97	0.03	1.3	0.966
INDI 196	INDI 196 PLS 1	Colorectum	III	7.5	12.07	TP53 p.R174W, c.520A>T	0.95	0.01	0.4	0.955
INDI 197	INDI 197 PLS 1	Colorectum	II	7.5	4.59	KRAS p.G12S, c.34G>A	1.62	0.10	1.4	0.998
INDI 198	INDI 198 PLS 1	Stomach	III	7.5	10.36	TP53 p.V274F, c.820G>T	12.36	1.67	53.3	1.000
INDI 199	INDI 199 PLS 1	Stomach	II	7.5	10.21	TP53 p.P60Q, c.179C>A	2.37	0.02	0.8	0.992
INDI 200	INDI 200 PLS 1	Breast	III	7.5	56.36	TP53 p.V216M, c.646G>A	1.76	0.02	3.1	0.936
INDI 202	INDI 202 PLS 1	Colorectum	II	7.5	8.48	TP53 p.R249S, c.747G>T	1.50	0.03	0.7	0.984

Table3.txt

INDI 203	INDI 203 PLS 1		Stomach	II	7.5	7.82			
		TP53 p.R249S, c.747G>T							
2.00	0.07		1.7	0.995					
INDI 205	INDI 205 PLS 1		Liver	III	7.5	71.92			
		CTNNB1 p.S45F, c.134C>T							
2.09	0.03		7.2	0.997					
INDI 206	INDI 206 PLS 1		Stomach	III	7.5	14.92			
		TP53 p.R174M, c.521G>T							
0.89	0.01		0.5	0.957					
INDI 207	INDI 207 PLS 1		Colorectum	II	7.5	15.15			
		TP53 p.R337C, c.1009C>T							
1.03	0.03		1.3	1.000					
INDI 208	INDI 208 PLS 1		Liver	II	7.5	69.07			
		TP53 p.R249S, c.747G>T							
1.90	0.03		7.0	0.997					
INDI 209	INDI 209 PLS 1		Colorectum	II	7.5	13.05			
		TP53 p.N288S, c.863A>G							
1.58	0.03		1.3	0.992					
INDI 210	INDI 210 PLS 1		Stomach	III	7.5	6.85			
		TP53 p.C135*, c.405C>A							
4.85	1.05		22.2	0.991					
INDI 211	INDI 211 PLS 1		Colorectum	II	7.5	13.47			
		TP53 p.R175H, c.524G>A							
1.76	0.25		10.5	0.993					
INDI 212	INDI 212 PLS 1		Colorectum	III	7.5	8.94			
		BRAF p.V600E, c.1799T>A							
33.45	2.63		72.4	1.000					
INDI 213	INDI 213 PLS 1		Colorectum	III	7.5	4.15			
		TP53 p.R248Q, c.743G>A							
1.06	0.07		0.9	0.982					
INDI 214	INDI 214 PLS 1		Stomach	II	7.5	15.37			
		TP53 p.R283H, c.848G>A							
0.94	0.03		1.5	0.935					
INDI 215	INDI 215 PLS 1		Liver	II	7.5	30.64			
		TP53 p.R196*, c.586C>T							
1.96	0.41		38.6	0.903					
INDI 216	INDI 216 PLS 1		Colorectum	III	7.5	4.36			
		TP53 p.M237I, c.711G>A							
1.26	0.08		1.1	0.981					
INDI 218	INDI 218 PLS 1		Colorectum	III	7.5	6.18			
		AKT1 p.E17K, c.49G>A							
1.71	0.06		1.1	0.900					
INDI 219	INDI 219 PLS 1		Liver	III	7.5	51.72			
		KRAS p.G12C, c.34G>T							
7.72	0.57		90.9	0.994					
INDI 220	INDI 220 PLS 1		Lung	I	7.5	19.37			
		TP53 p.R273C, c.817C>T							
1.82	0.17		10.0	0.982					

Table3.txt

INDI 221	INDI 221 PLS 1	Colorectum	III	7.5	4.60		
NRAS p.G12D, c.35G>A							
26.32	5.19	73.6	1.000				
INDI 222	INDI 222 PLS 1	Colorectum	II	7.5	29.31		
TP53 p.G266E, c.797G>A							
62.15	7.25	654.1	1.000				
INDI 223	INDI 223 PLS 1	Colorectum	I	7.5	12.55		
TP53 p.L308Q, c.923T>A							
1.07	0.01	0.3	0.501				
INDI 224	INDI 224 PLS 1	Lung	III	7.5	48.72		
TP53 p.H179R, c.536A>G							
4.74	0.20	30.3	1.000				
INDI 225	INDI 225 PLS 1	Colorectum	I	7.5	70.16		
PIK3CA p.E542K, c.1624G>A							
1.78	0.01	3.2	0.997				
INDI 226	INDI 226 PLS 1	Breast	III	7.5	1.91		
TP53 p.A138T, c.412G>A							
0.52	0.08	0.4	0.117				
INDI 227	INDI 227 PLS 1	Lung	II	7.5	3.40		
FBXW7 p.E471fs, c.1412insA							
1.05	0.08	0.9	0.919				
INDI 228	INDI 228 PLS 1	Breast	II	7.5	6.28		
TP53 p.R306Q, c.917G>A							
0.81	0.07	1.3	0.293				
INDI 229	INDI 229 PLS 1	Colorectum	II	7.5	5.15		
PPP2R1A p.R182W, c.544C>T							
0.88	0.03	0.5	0.968				
INDI 230	INDI 230 PLS 1	Colorectum	I	7.5	5.16		
TP53 p.R273H, c.818G>A							
1.16	0.09	1.4	0.984				
INDI 231	INDI 231 PLS 1	Lung	III	7.5	2.04		
KRAS p.G12D, c.35G>A							
24.34	9.38	59.0	0.999				
INDI 233	INDI 233 PLS 1	Colorectum	I	7.5	6.54		
TP53 p.G154V, c.461G>T							
43.39	7.70	155.0	1.000				
INDI 234	INDI 234 PLS 1	Colorectum	I	7.5	7.55		
TP53 p.R175H, c.524G>A							
0.76	0.02	0.5	0.125				
INDI 236	INDI 236 PLS 1	Stomach	II	7.5	8.20		
KRAS p.D57N, c.169G>A							
1.00	0.07	1.7	0.117				
INDI 237	INDI 237 PLS 1	Breast	I	7.5	2.40		
TP53 p.R202C, c.604C>T							
0.70	0.11	0.8	0.434				
INDI 238	INDI 238 PLS 1	Liver	II	7.5	13.20		
TP53 p.R249S, c.747G>T							
3.85	0.93	37.6	0.999				

Table3.txt

INDI 239	INDI 239 PLS 1	Lung	III	7.5	3.20		
TP53 p.R202C, c.604C>T							
0.92	0.05	0.5	0.987				
INDI 241	INDI 241 PLS 1	Stomach	III	7.5	16.09		
CDKN2A p.A76T, c.226G>A							
0.97	0.03	1.3	0.370				
INDI 243	INDI 243 PLS 1	Colorectum	I	7.5	6.33		
APC p.E1309fs, c.3927delAAAGA							
39.68	2.96	57.7	0.982				
INDI 244	INDI 244 PLS 1	Colorectum	III	7.5	4.06		
KRAS p.G12C, c.34G>T							
5.17	0.65	8.2	0.908				
INDI 245	INDI 245 PLS 1	Colorectum	III	7.5	4.36		
KRAS p.Q61K, c.181C>A							
7.71	1.19	16.0	0.998				
INDI 246	INDI 246 PLS 1	Lung	II	7.5	0.50		
KRAS p.G13D, c.38G>A							
0.00	0.07	0.1	0.314				
INDI 247	INDI 247 PLS 1	Lung	I	7.5	4.09		
TP53 p.V216M, c.646G>A							
2.03	0.26	3.2	0.972				
INDI 248	INDI 248 PLS 1	Colorectum	II	7.5	2.36		
KRAS p.G12D, c.35G>A							
1.09	0.08	0.6	0.453				
INDI 250	INDI 250 PLS 1	Colorectum	II	7.5	6.29		
TP53 p.E286K, c.856G>A							
7.41	0.32	6.2	0.985				
INDI 251	INDI 251 PLS 1	Colorectum	II	7.5	9.61		
TP53 p.S241C, c.722C>G							
2.86	0.03	0.8	0.983				
INDI 252	INDI 252 PLS 1	Lung	II	7.5	13.59		
TP53 g.7576927C>T (Splice Site)							
2.96	0.14	5.9	0.994				
INDI 253	INDI 253 PLS 1	Colorectum	I	7.5	5.84		
GNAS p.L203P, c.608T>C							
0.96	0.02	0.3	0.218				
INDI 255	INDI 255 PLS 1	Colorectum	II	7.5	3.60		
KRAS p.G13V, c.38G>T							
7.72	0.57	6.4	0.950				
INDI 256	INDI 256 PLS 1	Colorectum	III	7.5	5.06		
KRAS p.G12S, c.34G>A							
9.64	3.97	61.8	0.991				
INDI 257	INDI 257 PLS 1	Lung	III	7.5	8.12		
KRAS p.G12R, c.34G>C							
1.45	0.08	2.0	0.991				
INDI 258	INDI 258 PLS 1	Colorectum	I	7.5	13.10		
CDKN2A p.A76V, c.227C>T							
1.05	0.01	0.5	0.503				

Table3.txt

INDI 259	INDI 259 PLS 1	Colorectum	II	7.5	11.59	TP53 p.P151H, c.452C>A	9.52	0.92	33.0	0.942
INDI 260	INDI 260 PLS 1	Stomach	I	7.5	2.24	TP53 p.R181H, c.542G>A	0.70	0.05	0.3	0.256
INDI 261	INDI 261 PLS 1	Breast	II	7.5	2.23	CTNNB1 p.G38D, c.113G>A	0.57	0.01	0.1	0.123
INDI 262	INDI 262 PLS 1	Breast	III	7.5	2.80	AKT1 p.E17K, c.49G>A	2.69	0.31	2.7	0.705
INDI 264	INDI 264 PLS 1	Lung	III	7.5	1.46	TP53 p.H179R, c.536A>G	0.47	0.02	0.1	0.672
INDI 265	INDI 265 PLS 1	Breast	II	7.5	2.55	TP53 p.G374fs, c.1120delG	0.46	0.08	0.6	0.117
INDI 266	INDI 266 PLS 1	Lung	I	7.5	14.77	TP53 p.T230P, c.688A>C	1.29	0.03	1.2	0.930
INDI 267	INDI 267 PLS 1	Esophagus	II	7.5	13.58	TP53 p.Y220C, c.659A>G	1.97	0.11	4.8	0.767
INDI 268	INDI 268 PLS 1	Colorectum	III	7.5	6.66	NRAS p.Q61R, c.182A>G	7.27	3.34	68.5	0.995
INDI 269	INDI 269 PLS 1	Lung	III	7.5	11.25	CDKN2A p.V51L, c.151G>C (Exon Start)	0.99	0.01	0.3	0.618
INDI 270	INDI 270 PLS 1	Breast	II	7.5	1.77	TP53 p.R280G, c.838A>G	0.00	0.10	0.6	0.125
INDI 271	INDI 271 PLS 1	Colorectum	III	7.5	8.04	PPP2R1A p.R182W, c.544C>T	0.99	0.06	1.5	0.609
INDI 273	INDI 273 PLS 1	Lung	I	7.5	3.62	TP53 p.G266*, c.796G>T	1.74	0.28	3.1	0.998
INDI 274	INDI 274 PLS 1	Breast	II	7.5	2.59	TP53 p.R283C, c.847C>T	0.00	0.10	0.8	0.125
INDI 275	INDI 275 PLS 1	Breast	II	7.5	2.61	TP53 p.R282W, c.844C>T	1.27	0.14	1.1	0.335
INDI 276	INDI 276 PLS 1	Liver	II	7	22.94	TP53 p.V157F, c.469G>T	74.98	5.95	420.0	1.000

Table3.txt

INDI 277	INDI 277 PLS 1	Breast	II	7.5	6.39	
	TP53 p.E198*, c.592G>T					
0.72	0.04	0.9	0.116			
INDI 278	INDI 278 PLS 1	Ovary	III	7.5	10.27	
	TP53 p.R273H, c.818G>A					
3.76	11.68	369.5	0.984			
INDI 279	INDI 279 PLS 1	Colorectum	II	7.5	4.79	
	TP53 p.K372fs, c.1114delA					
1.07	0.07	1.1	0.967			
INDI 280	INDI 280 PLS 1	Breast	I	7.5	3.42	
	TP53 p.P36S, c.106C>T					
0.54	0.11	1.2	0.347			
INDI 281	INDI 281 PLS 1	Colorectum	I	7.5	4.49	
	TP53 p.E298*, c.892G>T					
0.80	0.01	0.2	0.724			
INDI 283	INDI 283 PLS 1	Lung	I	7.5	4.72	
	TP53 p.R306*, c.916C>T					
1.06	0.03	0.5	0.593			
INDI 284	INDI 284 PLS 1	Colorectum	II	7.5	17.11	
	APC p.E1309fs, c.3927delAAAGA					
4.74	0.12	6.4	0.918			
INDI 285	INDI 285 PLS 1	Lung	II	7.5	4.88	
	TP53 p.E339*, c.1015G>T					
5.83	1.29	19.4	0.998			
INDI 286	INDI 286 PLS 1	Colorectum	I	7.5	1.46	
	TP53 p.K372fs, c.1114delA					
0.91	0.06	0.3	0.620			
INDI 287	INDI 287 PLS 1	Breast	III	7.5	2.11	
	TP53 p.S94*, c.281C>G					
9.17	1.43	9.3	0.996			
INDI 288	INDI 288 PLS 1	Lung	III	7.5	5.12	
	TP53 p.T125T, c.375G>T (Exon End)					
16.13	8.37	132.1	1.000			
INDI 289	INDI 289 PLS 1	Breast	II	7.5	2.03	
	PTEN p.A126S, c.376G>T					
2.77	0.23	1.4	0.521			
INDI 290	INDI 290 PLS 1	Colorectum	I	7.5	2.19	
	TP53 p.K372fs, c.1114delA					
0.59	0.04	0.3	0.896			
INDI 291	INDI 291 PLS 1	Lung	I	7.5	7.57	
	TP53 p.R342*, c.1024C>T					
0.69	0.04	0.9	0.804			
INDI 292	INDI 292 PLS 1	Lung	III	7.5	8.42	
	TP53 p.N131S, c.392A>G					
1.47	0.03	0.7	0.772			
INDI 293	INDI 293 PLS 1	Colorectum	II	7.5	4.02	
	KRAS p.G12V, c.35G>T					
2.27	0.10	1.3	0.996			

Table3.txt

INDI 295	INDI 295 PLS 1	Colorectum	II	7.5	2.17		
	GNAS p.R201H, c.602G>A						
1.45	0.20	1.3	0.939				
INDI 296	INDI 296 PLS 1	Colorectum	II	7.5	4.40		
	TP53 p.E298K, c.892G>A						
0.89	0.02	0.3	0.940				
INDI 297	INDI 297 PLS 1	Breast	III	7.5	3.07		
	TP53 p.R248Q, c.743G>A						
0.83	0.14	1.3	0.896				
INDI 298	INDI 298 PLS 1	Colorectum	I	7.5	4.58		
	BRAF p.T599I, c.1796C>T						
0.81	0.05	0.7	0.886				
INDI 299	INDI 299 PLS 1	Colorectum	I	7.5	13.08		
	TP53 p.G199E, c.596G>A						
1.21	0.04	1.4	0.924				
INDI 300	INDI 300 PLS 1	Breast	III	7.5	19.40		
	TP53 p.R174G, c.520A>G						
0.86	0.03	1.5	0.917				
INDI 301	INDI 301 PLS 1	Breast	II	7.5	9.18		
	TP53 p.S241fs, c.723delTCC						
3.25	0.06	1.8	0.989				
INDI 302	INDI 302 PLS 1	Colorectum	I	7.5	2.74		
	PPP2R1A p.R182W, c.544C>T						
1.05	0.09	0.8	0.960				
INDI 303	INDI 303 PLS 1	Colorectum	I	7.5	5.30		
	TP53 p.R337H, c.1010G>A						
0.82	0.02	0.3	0.955				
INDI 304	INDI 304 PLS 1	Colorectum	I	7.5	19.49		
	TP53 p.E258K, c.772G>A						
1.12	0.01	0.4	0.997				
INDI 305	INDI 305 PLS 1	Colorectum	II	7.5	20.30		
	TP53 p.S241fs, c.723delTCC						
240.28	8.37	523.1	1.000				
INDI 306	INDI 306 PLS 1	Colorectum	III	7.5	3.55		
	APC p.E1309fs, c.3927delAAAGA						
123.62	36.29	396.8	1.000				
INDI 307	INDI 307 PLS 1	Colorectum	III	7.5	12.09		
	TP53 p.R202C, c.604C>T						
0.94	0.06	2.4	0.944				
INDI 308	INDI 308 PLS 1	Liver	II	7.5	119.55		
	GNAS p.R201S, c.601C>A						
1.61	0.01	3.8	0.974				
INDI 309	INDI 309 PLS 1	Colorectum	II	7.5	20.06		
	TP53 p.P128L, c.383C>T						
0.83	0.01	0.5	0.913				
INDI 310	INDI 310 PLS 1	Colorectum	II	7.5	13.05		
	PIK3CA p.E545A, c.1634A>C						
4.41	0.70	28.2	0.999				

Table3.txt

INDI 311	INDI 311 PLS 1	Colorectum	III	7.5	7.53	
	TP53 p.K372fs, c.1114delA					
0.84	0.05	1.1	0.977			
INDI 312	INDI 312 PLS 1	Breast	II	7.5	3.78	
	TP53 p.K372fs, c.1114delA					
0.80	0.05	0.6	0.751			
INDI 313	INDI 313 PLS 1	Esophagus	II	7.5	19.47	
	GNAS p.R201H, c.602G>A					
0.75	0.03	1.8	0.939			
INDI 314	INDI 314 PLS 1	Colorectum	I	7.5	3.08	
	TP53 p.C176fs, c.528delC					
0.67	0.02	0.2	0.982			
INDI 315	INDI 315 PLS 1	Breast	II	7.5	1.80	
	TP53 p.K372fs, c.1114delA					
0.67	0.08	0.4	0.123			
INDI 316	INDI 316 PLS 1	Breast	II	7.5	1.25	
	TP53 p.P300fs, c.898delC					
0.79	0.06	0.2	0.123			
INDI 317	INDI 317 PLS 1	Breast	II	7.5	1.29	
	FBXW7 p.R465H, c.1394G>A					
0.40	0.07	0.3	0.116			
INDI 318	INDI 318 PLS 1	Stomach	III	7.5	5.16	
	TP53 p.K305*, c.913A>T					
21.62	1.21	19.3	0.997			
INDI 319	INDI 319 PLS 1	Stomach	I	7.5	14.30	
	TP53 p.T125T, c.375G>A (Exon End)					
1.49	0.12	5.3	0.374			
INDI 320	INDI 320 PLS 1	Colorectum	II	7.5	8.18	
	BRAF p.V600E, c.1799T>A					
2.05	0.06	1.5	1.000			
INDI 321	INDI 321 PLS 1	Colorectum	III	7.5	3.54	
	TP53 p.R158H, c.473G>A					
0.47	0.05	0.6	0.836			
INDI 322	INDI 322 PLS 1	Colorectum	III	7.5	10.18	
	KRAS p.A11T, c.31G>A					
1.03	0.01	0.4	0.930			
INDI 323	INDI 323 PLS 1	Breast	I	7.5	1.01	
	TP53 p.R175H, c.524G>A					
0.62	0.11	0.3	0.125			
INDI 324	INDI 324 PLS 1	Lung	I	7.5	2.11	
	TP53 p.K372fs, c.1114delA					
0.48	0.12	0.8	0.877			
INDI 325	INDI 325 PLS 1	Colorectum	III	7.5	1.63	
	TP53 p.A353V, c.1058C>T					
0.92	0.11	0.5	0.933			
INDI 326	INDI 326 PLS 1	Lung	I	7.5	1.94	
	CDKN2A p.H83Y, c.247C>T					
0.00	0.06	0.4	0.992			

Table3.txt

INDI 327	INDI 327 PLS 1	Colorectum	II	7.5	2.83	TP53 p.I195N, c.584T>A	
7.58	0.52	4.6	0.954				
INDI 328	INDI 328 PLS 1	Colorectum	I	7.5	4.56	TP53 p.R202C, c.604C>T	
1.26	0.09	1.2	0.993				
INDI 329	INDI 329 PLS 1	Colorectum	III	7.5	14.29	BRAF p.V600E, c.1799T>A	
89.47	10.04	442.0	1.000				
INDI 331	INDI 331 PLS 1A	Lung	III	7.5	2.53	KRAS p.G12C, c.34G>T	
56.58	10.88	84.8	1.000				
INDI 332	INDI 332 PLS 1	Breast	I	7.5	2.13	CTNNB1 p.T41A, c.121A>G	
1.40	0.00	0.0	0.369				
INDI 333	INDI 333 PLS 1A	Lung	II	7.5	2.17	TP53 p.R248W, c.742C>T	
2.33	1.96	13.1	0.473				
INDI 334	INDI 334 PLS 1	Breast	I	7.5	1.36	HRAS p.G12D, c.35G>A	
0.68	0.03	0.1	0.622				
INDI 335	INDI 335 PLS 1A	Lung	I	7.5	1.61	TP53 p.R267Q, c.800G>A	
0.43	0.08	0.4	0.929				
INDI 336	INDI 336 PLS 1A	Lung	III	7.5	5.42	TP53 g.7578176C>T (Splice Site)	
12.59	0.31	5.1	0.995				
INDI 337	INDI 337 PLS 1	Esophagus	III	7.5	4.63	TP53 p.K372fs, c.1114delA	
0.90	0.04	0.6	0.235				
INDI 338	INDI 338 PLS 1	Colorectum	II	7.5	9.18	KRAS p.A146T, c.436G>A	
1.43	0.05	1.3	0.971				
INDI 339	INDI 339 PLS 1	Breast	II	7.5	1.05	TP53 p.C242Y, c.725G>A	
0.65	0.13	0.4	0.121				
INDI 340	INDI 340 PLS 1	Colorectum	III	7.5	3.43	CTNNB1 p.S37F, c.110C>T	
5.67	0.39	4.2	1.000				
INDI 341	INDI 341 PLS 1	Liver	II	7.5	7.88	CDKN2A p.H83Y, c.247C>T	
2.20	0.15	3.6	0.998				
INDI 342	INDI 342 PLS 1A	Lung	III	5	0.42	FBXW7 p.R479Q, c.1436G>A	
0.81	0.23	0.3	0.125				
INDI 343	INDI 343 PLS 1	Colorectum	III	7.5	0.91	TP53 p.G244V, c.731G>T	
3.44	0.34	1.0	0.573				

Table3.txt

INDI 344	INDI 344 PLS 1	Colorectum	II	7.5	1.91	
	KRAS p.G12S, c.34G>A					
2.73	0.39	2.3	1.000			
INDI 346	INDI 346 PLS 1A	Lung	I	6.5	1.30	
	TP53 p.C176F, c.527G>T					
2.61	0.35	1.4	0.916			
INDI 347	INDI 347 PLS 1	Esophagus	I	7.5	5.20	
	TP53 p.L137P, c.410T>C					
1.16	0.05	0.9	0.650			
INDI 348	INDI 348 PLS 1	Breast	II	7.5	1.92	
	TP53 p.E339D, c.1017G>T					
0.92	0.02	0.1	0.242			
INDI 350	INDI 350 PLS 1	Breast	II	7.5	1.04	
	TP53 p.R202C, c.604C>T					
0.69	0.05	0.2	0.610			
INDI 352	INDI 352 PLS 1	Breast	III	7.5	1.45	
	TP53 p.R196*, c.586C>T					
0.74	0.06	0.3	0.122			
INDI 353	INDI 353 PLS 1A	Lung	II	7.5	2.27	
	TP53 p.K132N, c.396G>T					
17.68	0.24	1.6	0.998			
INDI 354	INDI 354 PLS 1	Colorectum	III	7.5	0.47	
	TP53 p.S367S, c.1101C>T (Exon Start)					
0.00	0.11	0.2	0.989			
INDI 355	INDI 355 PLS 1A	Lung	I	7.5	1.23	
	GNAS p.R201H, c.602G>A					
1.70	0.26	1.0	0.863			
INDI 356	INDI 356 PLS 1	Colorectum	I	7.5	3.14	
	FBXW7 p.R479Q, c.1436G>A					
0.75	0.05	0.5	0.883			
INDI 357	INDI 357 PLS 1A	Lung	I	7.5	0.12	
	TP53 p.R158C, c.472C>T					
0.00	0.08	0.0	0.580			
INDI 358	INDI 358 PLS 1A	Lung	II	7.5	1.31	
	KRAS p.G12C, c.34G>T					
1.22	0.12	0.5	0.686			
INDI 359	INDI 359 PLS 1	Breast	I	7.5	0.67	
	TP53 p.R202C, c.604C>T					
1.14	0.09	0.2	0.850			
INDI 360	INDI 360 PLS 1A	Lung	II	7.5	2.58	
	TP53 p.E336*, c.1006G>T					
3.22	0.59	4.7	0.985			
INDI 361	INDI 361 PLS 1	Breast	III	7.5	4.49	
	TP53 p.A161S, c.481G>T					
1.14	0.05	0.6	0.324			
INDI 362	INDI 362 PLS 1	Breast	II	7.5	2.62	
	KRAS p.G13D, c.38G>A					
0.78	0.06	0.5	0.304			

Table3.txt

INDI 363	INDI 363 PLS 1	Breast	I	7.5	3.14	
	CDKN2A p.R87Q, c.260G>A					
0.60	0.02	0.2	0.121			
INDI 364	INDI 364 PLS 1A	Lung	I	7.5	0.21	
	GNAS p.R201H, c.602G>A					
0.00	0.06	0.0	0.856			
INDI 365	INDI 365 PLS 1	Colorectum	II	7.5	3.06	
	APC p.E1309fs, c.3927delAAAGA					
5.91	0.60	5.6	0.995			
INDI 366	INDI 366 PLS 1	Pancreas	II	7.5	42.88	
	TP53 p.R249S, c.747G>T					
1.19	0.01	1.3	0.998			
INDI 367	INDI 367 PLS 1	Liver	I	7.5	13.22	
	CTNNB1 p.I35S, c.104T>G					
8.39	0.28	11.6	0.965			
INDI 368	INDI 368 PLS 1	Breast	II	7.5	3.09	
	TP53 p.E224*, c.670G>T					
8.24	1.42	13.5	1.000			
INDI 369	INDI 369 PLS 1A	Lung	I	7.5	1.41	
	TP53 g.7576928T>C (Splice Site)					
0.00	0.06	0.3	0.553			
INDI 371	INDI 371 PLS 1A	Lung	III	7.5	1.47	
	KRAS p.G12V, c.35G>T					
20.54	7.71	34.8	0.998			
INDI 372	INDI 372 PLS 1A	Lung	II	7.5	4.77	
	TP53 p.A138S, c.412G>T					
1.58	0.03	0.5	0.995			
INDI 373	INDI 373 PLS 1A	Lung	I	7.5	1.42	
	TP53 p.G245S, c.733G>A					
0.92	0.09	0.4	0.842			
INDI 374	INDI 374 PLS 1	Colorectum	III	7	3.53	
	TP53 p.A159T, c.475G>A					
1.00	0.04	0.4	0.956			
INDI 375	INDI 375 PLS 1	Liver	I	7.5	3.58	
	CTNNB1 p.S33Y, c.98C>A					
0.49	0.05	0.6	0.970			
INDI 376	INDI 376 PLS 1	Colorectum	I	7.5	3.98	
	TP53 p.H178N, c.532C>A					
1.03	0.02	0.3	0.298			
INDI 377	INDI 377 PLS 1	Colorectum	II	7.5	14.70	
	BRAF p.V600E, c.1799T>A					
3.35	0.05	2.2	1.000			
INDI 378	INDI 378 PLS 1	Colorectum	I	7.5	2.49	
	TP53 p.V274I, c.820G>A					
0.72	0.06	0.5	0.155			
INDI 379	INDI 379 PLS 1	Colorectum	III	7.5	3.71	
	TP53 p.R342L, c.1025G>T					
1.07	0.02	0.2	0.312			

Table3.txt

INDI 380 INDI 380 PLS 1 Colorectum II 7.5 3.57
TP53 p.N288fs, c.862delA
4.95 0.32 3.5 0.997
INDI 381 INDI 381 PLS 1A Lung III 6.5 0.32
TP53 p.R175H, c.524G>A
0.00 0.14 0.1 0.640
INDI 382 INDI 382 PLS 1 Breast II 7.5 4.29
TP53 p.N131I, c.392A>T
2.56 0.07 0.9 0.498
INDI 383 INDI 383 PLS 1A Lung III 7.5 2.65
TP53 p.Y205C, c.614A>G
2.61 0.14 1.1 0.976
INDI 384 INDI 384 PLS 1 Pancreas II 7.5 2.35
TP53 p.E346G, c.1037A>G
0.65 0.06 0.4 0.596
INDI 385 INDI 385 PLS 1 Colorectum I 7.5 4.06
TP53 p.A161T, c.481G>A
0.71 0.04 0.5 0.629
INDI 386 INDI 386 PLS 1 Colorectum III 7.5 2.80
TP53 p.P152L, c.455C>T
0.36 0.06 0.5 0.121
INDI 387 INDI 387 PLS 1 Liver I 7.5 3.79
TP53 p.P223L, c.668C>T
1.87 0.07 0.8 0.955
INDI 388 INDI 388 PLS 1 Pancreas II 7.5 7.54
TP53 p.Y220C, c.659A>G
1.41 0.07 1.6 0.992
INDI 389 INDI 389 PLS 1A Lung III 7.5 3.20
KRAS p.G12V, c.35G>T
2.35 0.25 2.5 0.992
INDI 390 INDI 390 PLS 1 Breast II 7.5 2.37
EGFR p.G863D, c.2588G>A
0.48 0.02 0.2 0.578
INDI 391 INDI 391 PLS 1 Liver II 7.5 11.50
PIK3CA p.E545K, c.1633G>A
4.02 0.24 8.7 1.000
INDI 392 INDI 392 PLS 1A Lung I 5 3.56
TP53 p.K372fs, c.1114delA
1.16 0.07 0.8 0.326
INDI 393 INDI 393 PLS 1 Liver II 7.5 5.89
TP53 p.L265V, c.793C>G
1.70 0.03 0.5 0.911
INDI 394 INDI 394 PLS 1A Lung II 7.5 6.92
PIK3CA p.E542K, c.1624G>A
3.31 0.10 2.1 0.960
INDI 395 INDI 395 PLS 1A Lung I 7.5 4.23
TP53 p.T125T, c.375G>T (Exon End)
3.12 0.27 3.5 0.855

Table3.txt

INDI 396	INDI 396 PLS 1	Colorectum	I	7.5	2.41	
		TP53 p.A86T, c.256G>A				
1.08	0.09	0.7	0.965			
INDI 397	INDI 397 PLS 1	Colorectum	III	7.5	7.43	
		PIK3CA p.H1047Q, c.3141T>G				
5.54	0.33	7.6	0.987			
INDI 398	INDI 398 PLS 1	Colorectum	II	7.5	7.40	
		TP53 p.Y220H, c.658T>C				
1.02	0.04	1.0	0.495			
INDI 400	INDI 400 PLS 1	Colorectum	II	7.5	14.64	
		TP53 p.R175H, c.524G>A				
2.94	2.96	133.6	0.980			
INDI 402	INDI 402 PLS 1	Breast	I	7.5	1.35	
		TP53 p.R174K, c.521G>A				
0.73	0.05	0.2	0.322			
INDI 403	INDI 403 PLS 1A	Lung	III	7.5	3.14	
		TP53 p.L369P, c.1106T>C				
0.79	0.03	0.3	0.569			
INDI 404	INDI 404 PLS 1	Breast	III	7.5	1.62	
		KRAS p.G13D, c.38G>A				
0.44	0.07	0.4	0.121			
INDI 405	INDI 405 PLS 1A	Lung	I	7.5	2.66	
		TP53 p.R306Q, c.917G>A				
1.00	0.04	0.3	0.829			
INDI 407	INDI 407 PLS 1	Breast	I	7.5	3.68	
		KRAS p.V14I, c.40G>A				
1.03	0.06	0.7	0.300			
INDI 408	INDI 408 PLS 1	Breast	II	7.5	2.18	
		TP53 p.R202C, c.604C>T				
0.60	0.04	0.3	0.117			
INDI 409	INDI 409 PLS 1	Breast	II	7.5	5.60	
		TP53 p.R174G, c.520A>G				
0.85	0.03	0.5	0.238			
INDI 411	INDI 411 PLS 1	Breast	II	7.5	1.76	
		TP53 p.K372fs, c.1114delA				
1.07	0.10	0.5	0.312			
INDI 412	INDI 412 PLS 1	Breast	II	7.5	6.66	
		TP53 p.K305N, c.915G>T				
1.04	0.01	0.3	0.945			
INDI 413	INDI 413 PLS 1	Lung	I	7.5	9.03	
		TP53 p.A119V, c.356C>T				
0.80	0.01	0.4	0.877			
INDI 414	INDI 414 PLS 1	Lung	II	7.5	1.93	
		TP53 p.A189V, c.566C>T				
0.76	0.08	0.4	0.620			
INDI 415	INDI 415 PLS 1	Lung	II	7.5	3.02	
		TP53 p.H193N, c.577C>A				
7.07	0.51	4.7	0.979			

Table3.txt

INDI 417	INDI 417 PLS 1	Lung	I	7.5	7.71	TP53 p.R337P, c.1010G>C	6.40	0.34
8.2	0.883							
INDI 418	INDI 418 PLS 1	Colorectum	I	7.5	3.00	HRAS p.G12D, c.35G>A	0.33	0.02
0.2	0.953							
INDI 419	INDI 419 PLS 1	Colorectum	I	7.5	10.40	TP53 p.T329I, c.986C>T	0.97	0.02
0.7	0.813							
INDI 421	INDI 421 PLS 1	Colorectum	II	7.5	7.89	TP53 p.E343G, c.1028A>G	1.03	0.01
0.2	0.683							
INDI 422	INDI 422 PLS 1	Colorectum	II	7.5	5.78	TP53 p.L257P, c.770T>C	1.20	0.02
0.4	0.994							
INDI 423	INDI 423 PLS 1	Colorectum	II	7.5	2.97	TP53 p.K372fs, c.1114delA	0.86	0.05
0.5	0.991							
INDI 424	INDI 424 PLS 1	Breast	II	7.5	4.22	TP53 p.R379C, c.1135C>T	0.97	0.04
0.5	0.413							
INDI 425	INDI 425 PLS 1	Breast	II	7.5	11.89	TP53 p.G374fs, c.1120delG	1.21	0.05
1.9	0.690							
INDI 426	INDI 426 PLS 1	Breast	II	7.5	4.78	TP53 p.C176fs, c.528insC	1.50	0.05
0.8	0.666							
INDI 427	INDI 427 PLS 1	Colorectum	II	7.5	6.59	PIK3CA p.N1044K, c.3132T>A	1.45	0.01
0.2	1.000							
INDI 428	INDI 428 PLS 1	Colorectum	III	7.5	16.72	TP53 p.R202C, c.604C>T	0.96	0.03
1.5	0.774							
INDI 429	INDI 429 PLS 1	Colorectum	II	7.5	21.33	TP53 p.L344P, c.1031T>C	0.94	0.01
0.9	1.000							
INDI 431	INDI 431 PLS 1	Colorectum	II	7.5	5.54	KRAS p.A11V, c.32C>T	0.85	0.01
0.2	0.711							
INDI 433	INDI 433 PLS 1	Colorectum	II	7.5	43.71	TP53 p.V173G, c.518T>G	2.27	0.01
0.7	0.985							
INDI 434	INDI 434 PLS 1	Colorectum	II	7.5	2.72	TP53 p.R379C, c.1135C>T	0.82	0.04
0.4	0.817							
INDI 436	INDI 436 PLS 1	Colorectum	III	7.5	20.92	TP53 p.T170A, c.508A>G	0.95	0.01
0.8	0.697							

Table3.txt

INDI 437	INDI 437 PLS 1	Colorectum	I	7.5	36.13	
TP53 p.F134fs, c.400delT						
1.22	0.01	0.8	0.950			
INDI 438	INDI 438 PLS 1	Colorectum	II	7.5	17.94	
TP53 p.G266E, c.797G>A						
1.00	0.01	0.8	0.777			
INDI 439	INDI 439 PLS 1	Colorectum	III	7.5	12.99	
BRAF p.F595L, c.1785T>G						
14.83	0.91	36.2	1.000			
INDI 440	INDI 440 PLS 1	Esophagus	II	7.5	6.90	
TP53 p.R273H, c.818G>A						
1.15	0.15	3.1	0.996			
INDI 441	INDI 441 PLS 1	Esophagus	II	7.5	32.24	
TP53 p.P27H, c.80C>A						
0.78	0.01	0.7	0.980			
INDI 442	INDI 442 PLS 1	Breast	II	7.5	6.17	
KRAS p.G12R, c.34G>C						
1.28	0.03	0.6	0.956			
INDI 443	INDI 443 PLS 1	Breast	II	7.5	4.31	
TP53 p.G374fs, c.1120delG						
0.89	0.03	0.4	0.878			
INDI 444	INDI 444 PLS 1	Colorectum	II	7.5	157.48	
TP53 p.H178P, c.533A>C						
1.14	0.00	2.2	0.993			
INDI 445	INDI 445 PLS 1	Breast	II	7.5	5.43	
TP53 p.E171fs, c.513delGACGGAG						
11.87	0.69	11.6	1.000			
INDI 446	INDI 446 PLS 1	Esophagus	II	7.5	22.51	
TP53 p.R249S, c.747G>T						
2.68	0.21	14.4	0.999			
INDI 447	INDI 447 PLS 1	Breast	III	7.5	26.17	
PIK3CA p.G1049R, c.3145G>C						
209.33	21.72	1,751.3	1.000			
INDI 449	INDI 449 PLS 1	Breast	III	7.5	3.51	
TP53 p.T125T, c.375G>A (Exon End)						
1.17	0.04	0.4	0.985			
INDI 450	INDI 450 PLS 1	Esophagus	II	7.5	7.28	
TP53 p.A347P, c.1039G>C						
0.87	0.01	0.3	0.993			
INDI 452	INDI 452 PLS 1	Colorectum	II	7.5	13.59	
TP53 p.Y234N, c.700T>A						
4.61	0.19	7.8	0.999			
INDI 453	INDI 453 PLS 1	Breast	I	7.5	2.26	
KRAS p.G13D, c.38G>A						
0.94	0.05	0.3	0.900			
INDI 454	INDI 454 PLS 1	Breast	III	7.5	2.94	
TP53 p.L194R, c.581T>G						
2.70	0.15	1.4	0.901			

Table3.txt

INDI 455	INDI 455 PLS 1	Breast	II	7.5	3.99		
	CTNNB1 p.S37F, c.110C>T						
1.41	0.02	0.2	0.855				
INDI 456	INDI 456 PLS 1	Colorectum	II	7.5	35.05		
	TP53 p.L252P, c.755T>C						
1.09	0.01	1.1	0.994				
INDI 457	INDI 457 PLS 1	Esophagus	II	7.5	35.05		
	TP53 p.E221*, c.661G>T						
58.98	1.39	150.0	1.000				
INDI 458	INDI 458 PLS 1	Breast	III	7.5	28.49		
	TP53 p.N263I, c.788A>T						
1.20	0.00	0.1	0.999				
INDI 459	INDI 459 PLS 1	Breast	II	7.5	41.57		
	PIK3CA p.H1047R, c.3140A>G						
399.50	60.44	7,738.7	1.000				
INDI 460	INDI 460 PLS 1	Breast	III	7.5	2.95		
	TP53 p.A307T, c.919G>A (Exon End)						
0.82	0.02	0.2	0.380				
INDI 461	INDI 461 PLS 1	Colorectum	III	7.5	8.60		
	TP53 p.V172F, c.514G>T						
4.56	0.40	10.6	0.989				
INDI 462	INDI 462 PLS 1	Breast	III	7.5	82.66		
	TP53 g.7578176C>A (Splice Site)						
165.23	62.32	15,866.1	1.000				
INDI 463	INDI 463 PLS 1	Colorectum	II	7.5	11.05		
	TP53 p.R273C, c.817C>T						
3.59	2.43	82.6	1.000				
INDI 464	INDI 464 PLS 1	Liver	III	7.5	57.74		
	TP53 p.K132*, c.394A>T						
12.33	0.32	56.3	1.000				
INDI 465	INDI 465 PLS 1	Esophagus	II	7.5	8.91		
	TP53 p.Q38*, c.112C>T						
2.36	0.09	2.4	1.000				
INDI 466	INDI 466 PLS 1	Colorectum	II	7.5	18.81		
	TP53 p.T155fs, c.463insA						
5.88	0.19	11.1	0.998				
INDI 467	INDI 467 PLS 1	Colorectum	II	7.5	36.19		
	TP53 p.H380Y, c.1138C>T						
0.80	0.00	0.3	0.972				
INDI 468	INDI 468 PLS 1	Colorectum	II	7.5	55.36		
	TP53 p.S261N, c.782G>A (Exon End)						
1.16	0.01	1.2	0.971				
INDI 469	INDI 469 PLS 1	Breast	III	7.5	50.88		
	TP53 p.P13H, c.38C>A						
1.07	0.00	0.4	0.695				
INDI 470	INDI 470 PLS 1	Colorectum	III	7.5	8.40		
	TP53 p.Q100*, c.298C>T						
3.75	0.28	7.3	0.988				

Table3.txt

INDI 471	INDI 471 PLS 1	Breast	III	7.5	2.75	
	TP53 p.R202C, c.604C>T					
0.82	0.05	0.4	0.123			
INDI 472	INDI 472 PLS 1	Colorectum	II	7.5	6.22	
	TP53 p.H179R, c.536A>G					
1.07	0.02	0.3	0.991			
INDI 473	INDI 473 PLS 1	Breast	III	7.5	4.59	
	TP53 p.G374fs, c.1120delG					
1.05	0.04	0.6	0.880			
INDI 474	INDI 474 PLS 1	Breast	II	7.5	4.29	
	TP53 p.G374fs, c.1120delG					
0.82	0.02	0.3	0.989			
INDI 475	INDI 475 PLS 1	Liver	III	7.5	17.95	
	PIK3CA p.E81K, c.241G>A					
1.64	0.01	0.5	0.993			
INDI 476	INDI 476 PLS 1	Esophagus	II	7.5	10.06	
	TP53 p.R249S, c.747G>T					
1.39	0.04	1.3	0.996			
INDI 477	INDI 477 PLS 1	Colorectum	III	7.5	4.61	
	TP53 p.K372fs, c.1114delA					
0.86	0.04	0.5	0.928			
INDI 478	INDI 478 PLS 1	Breast	II	7.5	4.43	
	TP53 p.G374fs, c.1120delG					
1.17	0.04	0.6	0.982			
INDI 479	INDI 479 PLS 1	Breast	III	7.5	1.67	
	TP53 p.R175H, c.524G>A					
1.28	0.22	1.1	0.824			
INDI 480	INDI 480 PLS 1	Breast	III	7.5	2.63	
	TP53 p.K372fs, c.1114delA					
0.90	0.03	0.2	0.932			
INDI 482	INDI 482 PLS 1	Liver	II	7.5	63.26	
	TP53 p.R249S, c.747G>T					
2.07	0.04	8.6	0.999			
INDI 483	INDI 483 PLS 1	Colorectum	II	7.5	3.67	
	TP53 p.K372fs, c.1114delA					
0.98	0.06	0.7	0.552			
INDI 484	INDI 484 PLS 1	Colorectum	II	7.5	5.56	
	TP53 p.R273H, c.818G>A					
1.18	0.16	2.7	0.528			
INDI 485	INDI 485 PLS 1	Esophagus	III	7.5	9.58	
	TP53 p.Q331*, c.991C>T					
2.21	0.06	1.7	0.448			
INDI 487	INDI 487 PLS 1	Breast	II	7.5	1.30	
	TP53 p.K351R, c.1052A>G					
0.54	0.06	0.2	0.117			
INDI 488	INDI 488 PLS 1	Breast	III	7.5	9.97	
	TP53 p.P300S, c.898C>T					
0.72	0.02	0.5	0.848			

Table3.txt

INDI 489	INDI 489 PLS 1	Breast	II	7.5	4.09		
CTNNB1 p.G34V, c.101G>T							
1.19	0.02	0.2	0.943				
INDI 490	INDI 490 PLS 1	Breast	III	7.5	8.63		
PIK3CA p.H1047R, c.3140A>G							
2.90	0.30	8.1	1.000				
INDI 491	INDI 491 PLS 1	Lung	I	7.5	5.99		
TP53 p.A138T, c.412G>A							
0.65	0.03	0.5	0.615				
INDI 492	INDI 492 PLS 1	Lung	I	7.5	2.70		
TP53 p.R306*, c.916C>T							
0.69	0.06	0.5	0.572				
INDI 493	INDI 493 PLS 1	Breast	II	7.5	1.96		
TP53 p.R202C, c.604C>T							
0.70	0.29	1.7	0.116				
INDI 494	INDI 494 PLS 1	Lung	III	7.5	4.62		
TP53 p.G244A, c.731G>C							
3.64	0.14	2.0	0.997				
INDI 495	INDI 495 PLS 1	Lung	I	7.5	4.81		
TP53 p.R174G, c.520A>G							
0.65	0.03	0.5	0.122				
INDI 497	INDI 497 PLS 1	Lung	II	7.5	3.07		
TP53 p.R175H, c.524G>A							
0.97	0.12	1.2	0.509				
INDI 498	INDI 498 PLS 1	Colorectum	II	7	4.41		
TP53 p.Y234C, c.701A>G							
2.63	0.50	6.8	0.524				
INDI 499	INDI 499 PLS 1	Lung	I	7.5	6.84		
TP53 p.R267Q, c.800G>A							
0.86	0.02	0.5	0.642				
INDI 501	INDI 501 PLS 1	Colorectum	III	7.5	4.87		
TP53 p.R282Q, c.845G>A							
0.97	0.05	0.8	0.125				
INDI 502	INDI 502 PLS 1	Colorectum	III	7.5	7.58		
TP53 p.I195T, c.584T>C							
2.13	0.11	2.5	0.858				
INDI 503	INDI 503 PLS 1	Lung	I	7.5	3.60		
TP53 p.R306Q, c.917G>A							
0.77	0.07	0.8	0.923				
INDI 504	INDI 504 PLS 1	Breast	III	7.5	3.70		
TP53 p.K372fs, c.1114delA							
0.98	0.07	0.9	0.122				
INDI 505	INDI 505 PLS 1	Lung	II	7.5	34.64		
TP53 p.R267P, c.800G>C							
4.44	0.08	8.3	1.000				
INDI 506	INDI 506 PLS 1	Colorectum	I	7.5	25.63		
TP53 p.K372fs, c.1114insA							
0.95	0.01	0.4	0.947				

Table3.txt

INDI 507	INDI 507 PLS 1	Lung	II	7.5	2.75	TP53 p.R273H, c.818G>A	
1.55	0.61	5.2	0.991				
INDI 508	INDI 508 PLS 1	Colorectum	III	6	8.18	TP53 p.P47L, c.140C>T	
0.79	0.04	1.0	0.122				
INDI 511	INDI 511 PLS 1	Colorectum	III	7.5	4.19	TP53 p.S183fs, c.549insA	
3.80	0.18	2.3	0.637				
INDI 512	INDI 512 PLS 1	Breast	II	7.5	2.24	TP53 p.L369P, c.1106T>C	
0.44	0.06	0.4	0.761				
INDI 513	INDI 513 PLS 1	Lung	I	7.5	7.83	TP53 p.R273H, c.818G>A	
0.91	0.19	4.6	0.502				
INDI 514	INDI 514 PLS 1	Stomach	I	7.5	6.42	CTNNB1 p.T41A, c.121A>G	
5.54	0.04	0.8	0.991				
INDI 515	INDI 515 PLS 1	Colorectum	III	7.5	15.27	TP53 p.K132N, c.396G>T	
4.98	0.04	2.0	0.983				
INDI 516	INDI 516 PLS 1	Pancreas	II	7.5	11.81	KRAS p.G12R, c.34G>C	
2.13	0.10	3.5	0.999				
INDI 517	INDI 517 PLS 1	Breast	III	7.5	2.81	TP53 p.R110H, c.329G>A	
0.55	0.09	0.8	0.588				
INDI 518	INDI 518 PLS 1	Colorectum	III	7.5	9.71	TP53 p.N131fs, c.392delCAA	
6.18	0.18	5.2	0.898				
INDI 519	INDI 519 PLS 1	Lung	I	7.5	8.63	TP53 p.R273H, c.818G>A	
1.15	0.21	5.6	0.852				
INDI 521	INDI 521 PLS 1	Colorectum	II	7.5	16.52	TP53 g.7579311C>A (Splice Site)	
1.52	0.03	1.6	0.933				
INDI 522	INDI 522 PLS 1	Lung	I	7.5	9.02	TP53 p.R337H, c.1010G>A	
0.98	0.03	0.8	0.208				
INDI 523	INDI 523 PLS 1	Colorectum	I	7.5	11.24	TP53 p.V272M, c.814G>A	
1.50	0.05	1.6	0.997				
INDI 524	INDI 524 PLS 1	Lung	III	7.5	0.15	None detected	
NA	NA	NA	0.982				
INDI 525	INDI 525 PLS 1	Colorectum	I	7.5	31.87	TP53 p.C277F, c.830G>T	
3.01	0.03	3.1	0.978				

Table3.txt

INDI 526	INDI 526 PLS 1	Esophagus	III	7.5	2.93		
KRAS p.D57N, c.169G>A							
0.94	0.04	0.4	0.975				
INDI 527	INDI 527 PLS 1	Colorectum	III	7.5	5.83		
TP53 p.E349*, c.1045G>T							
1.00	0.02	0.4	0.932				
INDI 528	INDI 528 PLS 1	Colorectum	II	7.5	4.58		
FBXW7 p.E369*, c.1105G>T							
17.54	5.50	77.6	0.950				
INDI 529	INDI 529 PLS 1	Colorectum	I	7.5	4.86		
KRAS p.A59E, c.176C>A							
2.72	0.12	1.8	0.505				
INDI 530	INDI 530 PLS 1	Breast	I	7.5	3.31		
TP53 p.A353S, c.1057G>T							
0.38	0.05	0.5	0.421				
INDI 532	INDI 532 PLS 1	Lung	I	7.5	2.94		
TP53 p.R273H, c.818G>A							
1.00	0.09	0.8	0.813				
INDI 533	INDI 533 PLS 1	Pancreas	II	7.5	4.15		
TP53 p.D259N, c.775G>A							
0.83	0.04	0.5	0.909				
INDI 534	INDI 534 PLS 1	Stomach	III	7.5	3.20		
TP53 p.R333H, c.998G>A							
0.88	0.05	0.5	0.421				
INDI 535	INDI 535 PLS 1	Lung	I	7.5	6.67		
TP53 p.R202C, c.604C>T							
1.00	0.04	0.8	0.966				
INDI 537	INDI 537 PLS 1	Ovary	I	7.5	15.56		
TP53 p.M44I, c.132G>A							
0.81	0.03	1.3	0.644				
INDI 538	INDI 538 PLS 1	Lung	III	7.5	2.10		
TP53 p.R273H, c.818G>A							
1.34	0.21	1.4	0.959				
INDI 539	INDI 539 PLS 1	Colorectum	II	7.5	8.83		
PTEN p.D92A, c.275A>C							
8.98	0.49	13.4	0.991				
INDI 540	INDI 540 PLS 1	Breast	II	7.5	8.78		
TP53 p.R174G, c.520A>G							
1.18	0.04	1.2	0.630				
INDI 541	INDI 541 PLS 1	Breast	II	7.5	2.10		
TP53 p.K373E, c.1117A>G							
0.58	0.05	0.3	0.571				
INDI 544	INDI 544 PLS 1	Colorectum	III	7.5	2.48		
TP53 p.G334R, c.1000G>C							
185.06	52.81	403.4	1.000				
INDI 545	INDI 545 PLS 1	Lung	I	7.5	7.66		
TP53 p.A159T, c.475G>A							
1.15	0.04	1.0	0.950				

Table3.txt

INDI 546	INDI 546 PLS 1	Lung	II	7.5	9.32		
TP53 p.E62G, c.185A>G							
1.24	0.03	1.0	0.837				
INDI 547	INDI 547 PLS 1	Stomach	III	7.5	5.11		
CTNNB1 p.G34E, c.101G>A							
0.96	0.01	0.1	0.125				
INDI 548	INDI 548 PLS 1	Breast	II	7.5	9.74		
TP53 p.R267Q, c.800G>A							
1.08	0.03	0.8	0.951				
INDI 549	INDI 549 PLS 1	Lung	III	7.5	6.09		
TP53 p.R337H, c.1010G>A							
0.62	0.04	0.7	0.898				
INDI 550	INDI 550 PLS 1	Lung	III	7.5	3.43		
BRAF p.V600M, c.1798G>A							
0.42	0.04	0.4	0.568				
INDI 551	INDI 551 PLS 1	Colorectum	II	7.5	6.37		
TP53 g.7578555C>T (Splice Site)							
1.48	0.04	0.9	0.866				
INDI 555	INDI 555 PLS 1	Colorectum	II	7.5	1.44		
APC p.E1309fs, c.3927delAAAGA							
8.85	0.78	3.5	0.950				
INDI 558	INDI 558 PLS 1	Colorectum	I	7.5	8.45		
TP53 p.H368Y, c.1102C>T							
3.95	0.11	2.8	0.966				
INDI 559	INDI 559 PLS 1	Breast	III	7.5	32.11		
CTNNB1 p.S45A, c.133T>G							
2.36	0.02	1.5	0.847				
INDI 560	INDI 560 PLS 1	Colorectum	I	7.5	6.36		
TP53 p.K373R, c.1118A>G							
0.74	0.02	0.3	0.379				
INDI 561	INDI 561 PLS 1	Breast	III	7.5	4.60		
TP53 p.E286K, c.856G>A							
2.31	0.11	1.6	0.828				
INDI 562	INDI 562 PLS 1	Colorectum	I	7.5	32.71		
TP53 p.V216M, c.646G>A							
1.05	0.01	0.8	0.999				
INDI 564	INDI 564 PLS 1	Colorectum	I	7.5	4.17		
TP53 p.R158C, c.472C>T							
1.17	0.04	0.5	0.955				
INDI 565	INDI 565 PLS 1	Breast	III	7.5	4.43		
TP53 p.K372fs, c.1114delA							
1.12	0.05	0.7	0.640				
INDI 566	INDI 566 PLS 1	Breast	II	7.5	3.30		
TP53 p.L369P, c.1106T>C							
0.95	0.07	0.7	0.412				
INDI 567	INDI 567 PLS 1	Colorectum	II	7.5	3.64		
PIK3CA p.E545K, c.1633G>A							
5.37	0.89	10.0	1.000				

Table3.txt

INDI 568	INDI 568 PLS 1	Breast	II	7.5	3.67	
	TP53 p.G154S, c.460G>A					
0.68	0.05	0.6	0.342			
INDI 569	INDI 569 PLS 1	Breast	III	7.5	6.83	
	TP53 p.V173L, c.517G>T					
1.20	0.05	1.1	0.339			
INDI 570	INDI 570 PLS 1	Colorectum	II	7.5	7.65	
	FBXW7 p.R505H, c.1514G>A					
0.96	0.03	0.8	0.986			
INDI 571	INDI 571 PLS 1	Breast	III	7.5	4.55	
	TP53 p.R306*, c.916C>T					
0.71	0.03	0.4	0.121			
INDI 572	INDI 572 PLS 1	Colorectum	II	7.5	12.78	
	TP53 p.A276V, c.827C>T					
0.89	0.03	1.2	0.834			
INDI 573	INDI 573 PLS 1	Colorectum	I	7.5	2.80	
	TP53 p.R248Q, c.743G>A					
0.65	0.06	0.6	0.372			
INDI 574	INDI 574 PLS 1	Colorectum	III	7.5	3.20	
	TP53 p.G245S, c.733G>A					
1.66	0.17	1.6	0.966			
INDI 575	INDI 575 PLS 1	Breast	II	7.5	11.69	
	TP53 p.M384V, c.1150A>G					
1.11	0.02	0.6	0.974			
INDI 577	INDI 577 PLS 1	Breast	I	7.5	4.14	
	TP53 p.T125M, c.374C>T					
0.75	0.06	0.8	0.351			
INDI 578	INDI 578 PLS 1	Breast	I	7.5	4.61	
	PIK3CA p.E542K, c.1624G>A					
1.08	0.06	0.8	0.811			
INDI 579	INDI 579 PLS 1	Breast	I	7.5	3.43	
	TP53 g.7579310A>G (Splice Site)					
0.49	0.05	0.5	0.698			
INDI 581	INDI 581 PLS 1	Colorectum	II	7.5	6.91	
	TP53 g.7579311C>A (Splice Site)					
4.23	1.40	29.8	0.998			
INDI 582	INDI 582 PLS 1	Colorectum	II	7.5	23.49	
	TP53 p.T125M, c.374C>T					
1.02	0.04	2.6	0.999			
INDI 583	INDI 583 PLS 1	Colorectum	II	7.5	7.26	
	FBXW7 p.R505H, c.1514G>A					
0.88	0.03	0.6	0.979			
INDI 584	INDI 584 PLS 1	Colorectum	II	7.5	6.62	
	TP53 p.K372fs, c.1114delA					
1.02	0.05	1.0	0.974			
INDI 585	INDI 585 PLS 1	Esophagus	III	7.5	14.36	
	PIK3CA p.E545K, c.1633G>A					
5.64	0.25	10.9	0.999			

Table3.txt

INDI 586	INDI 586 PLS 1	Liver	III	7.5	78.17	
	PTEN p.A126V, c.377C>T					
1.07	0.01	1.5	1.000			
INDI 587	INDI 587 PLS 1	Colorectum	II	7.5	8.07	
	TP53 p.G245S, c.733G>A					
0.93	0.03	0.7	0.980			
INDI 588	INDI 588 PLS 1	Breast	III	7.5	8.00	
	TP53 p.R273H, c.818G>A					
0.93	0.10	2.5	0.125			
INDI 589	INDI 589 PLS 1	Breast	II	7.5	10.46	
	TP53 g.7577156C>T (Splice Site)					
0.95	0.01	0.2	0.117			
INDI 591	INDI 591 PLS 1	Colorectum	II	7.5	10.73	
	TP53 p.C242Y, c.725G>A					
2.10	0.14	4.6	0.999			
INDI 592	INDI 592 PLS 1	Breast	II	7.5	10.67	
	TP53 p.A161T, c.481G>A					
1.07	0.03	0.8	0.291			
INDI 593	INDI 593 PLS 1	Breast	II	7.5	12.94	
	TP53 p.G262D, c.785G>A					
0.93	0.01	0.3	0.988			
INDI 594	INDI 594 PLS 1	Colorectum	III	7.5	41.18	
	PIK3CA p.H1047R, c.3140A>G					
1.95	0.03	4.1	0.992			
INDI 595	INDI 595 PLS 1	Esophagus	II	7.5	22.74	
	TP53 g.7578555C>T (Splice Site)					
2.04	0.08	5.5	0.999			
INDI 596	INDI 596 PLS 1	Breast	III	7.5	4.47	
	TP53 p.R379H, c.1136G>A					
0.87	0.05	0.6	0.539			
INDI 597	INDI 597 PLS 1	Breast	II	7.5	19.59	
	TP53 p.K372fs, c.1114delA					
0.94	0.04	2.4	0.591			
INDI 598	INDI 598 PLS 1	Colorectum	II	7.5	7.18	
	TP53 p.R175H, c.524G>A					
1.25	0.07	1.6	0.974			
INDI 599	INDI 599 PLS 1	Colorectum	II	7.5	2.62	
	TP53 p.A159T, c.475G>A					
0.60	0.03	0.3	0.897			
INDI 600	INDI 600 PLS 1	Colorectum	II	7.5	11.91	
	TP53 p.C135Y, c.404G>A					
1.18	0.02	0.9	0.813			
INDI 601	INDI 601 PLS 1	Breast	III	7.5	15.18	
	TP53 p.R213*, c.637C>T					
5.23	9.25	432.4	1.000			
INDI 602	INDI 602 PLS 1	Colorectum	II	7.5	3.35	
	TP53 p.E204*, c.610G>T					
3.05	0.33	3.4	0.998			

Table3.txt

INDI 603	INDI 603 PLS 1	Breast	III	7.5	7.75	
	TP53 p.K372fs, c.1114delA					
0.96	0.04	1.0	0.548			
INDI 604	INDI 604 PLS 1	Breast	II	7.5	3.97	
	TP53 p.E336G, c.1007A>G					
1.06	0.03	0.4	0.948			
INDI 605	INDI 605 PLS 1	Colorectum	II	7.5	14.92	
	TP53 p.R290C, c.868C>T					
0.95	0.04	1.8	0.986			
INDI 606	INDI 606 PLS 1	Breast	II	7.5	12.92	
	TP53 p.E346V, c.1037A>T					
0.77	0.01	0.4	0.681			
INDI 607	INDI 607 PLS 1	Breast	II	7.5	6.54	
	TP53 p.R174G, c.520A>G					
0.88	0.04	0.7	0.667			
INDI 608	INDI 608 PLS 1	Colorectum	II	7.5	11.00	
	TP53 p.R202C, c.604C>T					
1.00	0.05	1.6	0.964			
INDI 609	INDI 609 PLS 1	Colorectum	II	7.5	2.81	
	TP53 p.T253P, c.757A>C					
1.88	0.05	0.4	0.998			
INDI 610	INDI 610 PLS 1	Colorectum	II	7.5	0.99	
	TP53 g.7576928T>C (Splice Site)					
0.75	0.14	0.4	0.965			
INDI 611	INDI 611 PLS 1	Colorectum	II	7.5	6.21	
	TP53 p.A138T, c.412G>A					
0.64	0.03	0.5	0.932			
INDI 612	INDI 612 PLS 1	Colorectum	II	7.5	7.44	
	TP53 p.K372fs, c.1114delA					
0.97	0.03	0.7	0.774			
INDI 613	INDI 613 PLS 1	Breast	II	7.5	7.56	
	TP53 p.K372fs, c.1114delA					
1.09	0.05	1.1	0.931			
INDI 614	INDI 614 PLS 1	Colorectum	II	7.5	21.63	
	NRAS p.G12D, c.35G>A					
3.65	0.12	7.8	0.999			
INDI 615	INDI 615 PLS 1	Colorectum	II	7.5	7.18	
	KRAS p.D57N, c.169G>A					
1.13	0.04	0.8	0.998			
INDI 617	INDI 617 PLS 1	Colorectum	III	7.5	1.57	
	TP53 p.S367S, c.1101C>T (Exon Start)					
0.97	0.07	0.3	0.923			
INDI 618	INDI 618 PLS 1	Colorectum	III	7.5	20.27	
	CTNNB1 p.I35N, c.104T>A					
2.36	0.00	0.3	0.977			
INDI 619	INDI 619 PLS 1	Breast	II	7.5	2.96	
	GNAS p.L203P, c.608T>C					
0.44	0.02	0.2	0.125			

Table3.txt

INDI 620	INDI 620 PLS 1	Colorectum	II	7.5	2.84	TP53 p.Q38R, c.113A>G	0.96	0.05	0.4	0.998
INDI 621	INDI 621 PLS 1	Colorectum	II	7.5	0.75	TP53 p.R249K, c.746G>A	0.00	0.11	0.3	0.910
INDI 622	INDI 622 PLS 1	Liver	III	7.5	85.94	TP53 p.R249S, c.747G>T	2.45	0.06	15.7	1.000
INDI 623	INDI 623 PLS 1	Breast	III	7.5	6.71	TP53 p.R273P, c.818G>C	17.70	2.09	43.1	0.998
INDI 624	INDI 624 PLS 1	Colorectum	II	7.5	4.17	TP53 p.C176Y, c.527G>A	2.00	0.31	4.0	0.986
INDI 625	INDI 625 PLS 1	Colorectum	II	7.5	2.73	KRAS p.G12S, c.34G>A	3.06	0.38	3.2	0.961
INDI 626	INDI 626 PLS 1	Colorectum	II	7.5	11.58	KRAS p.G12D, c.35G>A	4.47	0.43	15.4	1.000
INDI 627	INDI 627 PLS 1	Breast	II	5.66	9.07	TP53 p.K372fs, c.1114delA	0.69	0.04	1.1	0.927
INDI 628	INDI 628 PLS 1	Colorectum	II	5.5	6.27	TP53 p.R379H, c.1136G>A	0.74	0.05	0.9	0.923
INDI 629	INDI 629 PLS 1	Breast	I	7.26	6.14	TP53 p.A353V, c.1058C>T	0.58	0.06	1.1	0.762
INDI 630	INDI 630 PLS 1	Breast	I	7.5	3.63	CDKN2A p.R58*, c.172C>T	0.48	0.14	1.5	0.714
INDI 631	INDI 631 PLS 1	Colorectum	II	5.5	13.47	TP53 p.R156C, c.466C>T	1.04	0.07	3.0	0.998
INDI 632	INDI 632 PLS 1	Colorectum	II	6.52	27.01	TP53 p.F341I, c.1021T>A	1.36	0.01	0.7	0.998
INDI 633	INDI 633 PLS 1	Colorectum	II	7.5	3.87	TP53 p.I251fs, c.753delC	1.69	0.12	1.4	0.993
INDI 635	INDI 635 PLS 1	Colorectum	II	6	5.70	PTEN p.R130Q, c.389G>A	2.29	0.39	6.9	0.991
INDI 636	INDI 636 PLS 1	Liver	III	7.5	27.51	CTNNB1 p.T41A, c.121A>G	310.96	4.60	390.0	1.000

Table3.txt

INDI 637	INDI 637 PLS 1	Breast	III	7.5	5.95	TP53 p.R273H, c.818G>A	
0.43	0.12	2.2	0.877				
INDI 638	INDI 638 PLS 1	Breast	I	7.5	2.81	TP53 p.R248W, c.742C>T	
1.45	0.39	3.3	0.888				
INDI 639	INDI 639 PLS 1	Liver	II	7.5	18.63	TP53 p.R158L, c.473G>T	
4.31	0.18	10.2	1.000				
INDI 640	INDI 640 PLS 1	Colorectum	II	7.5	5.17	TP53 p.C141Y, c.422G>A	
2.72	0.66	10.5	0.998				
INDI 641	INDI 641 PLS 1	Breast	III	7.18	7.46	AKT1 p.E17K, c.49G>A	
1.06	0.04	0.9	0.838				
INDI 643	INDI 643 PLS 1	Colorectum	II	5	4.63	TP53 p.G245S, c.733G>A	
1.75	0.31	4.5	0.999				
INDI 644	INDI 644 PLS 1	Colorectum	I	6	16.82	TP53 p.K372fs, c.1114delA	
0.87	0.03	1.3	0.925				
INDI 645	INDI 645 PLS 1	Liver	III	7.5	27.37	TP53 p.R249S, c.747G>T	
16.21	8.37	706.0	1.000				
INDI 646	INDI 646 PLS 1	Breast	II	7.5	3.10	PPP2R1A p.R182W, c.544C>T	
0.83	0.08	0.7	0.432				
INDI 647	INDI 647 PLS 1	Colorectum	III	7.5	0.11	None detected	
NA	NA	NA	0.999				
INDI 648	INDI 648 PLS 1	Colorectum	III	7.5	1.21	KRAS p.G12V, c.35G>T	
28.57	24.26	90.6	1.000				
INDI 649	INDI 649 PLS 1	Colorectum	III	7.5	0.39	KRAS p.G12S, c.34G>A	
0.00	0.07	0.1	0.999				
INDI 650	INDI 650 PLS 1	Colorectum	III	7.5	1.75	TP53 p.E258G, c.773A>G	
1.12	0.05	0.3	0.857				
INDI 651	INDI 651 PLS 1	Colorectum	III	3	0.30	None detected	
NA	NA	NA	0.881				
INDI 654	INDI 654 PLS 1	Colorectum	II	7.5	1.08	GNAS p.R201H, c.602G>A	
0.36	0.04	0.1	0.932				
INDI 655	INDI 655 PLS 1	Colorectum	II	7.5	2.01	TP53 p.R306*, c.916C>T	
0.88	0.09	0.6	0.854				

Table3.txt

INDI 656	INDI 656 PLS 1	Breast	III	7.5	5.28	
TP53 p.K372fs, c.1114delA						
0.91	0.11	1.7	0.207			
INDI 657	INDI 657 PLS 1	Colorectum	II	7.5	0.28	
KRAS p.G12A, c.35G>C						
2.41	1.66	1.4	1.000			
INDI 658	INDI 658 PLS 1	Colorectum	I	7.5	1.11	
KRAS p.G13D, c.38G>A						
0.51	0.11	0.4	0.997			
INDI 659	INDI 659 PLS 1	Breast	II	7.5	8.16	
TP53 p.K139E, c.415A>G						
1.10	0.05	1.2	0.310			
INDI 660	INDI 660 PLS 1	Colorectum	II	7.5	6.91	
TP53 p.G59S, c.175G>A						
1.13	0.02	0.3	0.955			
INDI 661	INDI 661 PLS 1	Liver	III	7.5	88.95	
TP53 p.R249S, c.747G>T						
1.58	0.02	5.8	0.989			
INDI 662	INDI 662 PLS 1	Breast	I	7.5	6.21	
TP53 p.K351N, c.1053G>T						
0.92	0.06	1.2	0.614			
INDI 663	INDI 663 PLS 1	Esophagus	II	7.5	29.39	
TP53 p.Q331*, c.991C>T						
100.09	1.39	125.9	1.000			
INDI 664	INDI 664 PLS 1	Breast	I	7.5	3.55	
TP53 g.7579310A>G (Splice Site)						
0.50	0.06	0.6	0.641			
INDI 665	INDI 665 PLS 1	Esophagus	III	7.5	14.81	
FGFR2 p.P253R, c.758C>G						
51.21	0.35	16.1	1.000			
INDI 666	INDI 666 PLS 1	Breast	II	7.5	3.52	
TP53 p.R267W, c.799C>T						
0.38	0.07	0.7	0.831			
INDI 667	INDI 667 PLS 1	Breast	II	7.5	2.60	
TP53 p.R306*, c.916C>T						
0.00	0.07	0.6	0.326			
INDI 668	INDI 668 PLS 1	Breast	III	7.5	5.33	
TP53 p.K372fs, c.1114delA						
0.69	0.03	0.5	0.382			
INDI 669	INDI 669 PLS 1	Liver	III	7.5	91.32	
TP53 p.R110L, c.329G>T						
2.32	0.03	8.5	0.996			
INDI 670	INDI 670 PLS 1	Colorectum	III	7.5	2.88	
TP53 p.G117fs, c.350insGGAC						
83.06	14.28	126.9	0.999			
INDI 671	INDI 671 PLS 1	Lung	I	7.5	2.63	
TP53 p.A353V, c.1058C>T						
0.81	0.07	0.5	0.877			

Table3.txt

INDI 672	INDI 672 PLS 1	Breast	II	7.5	1.41	PPP2R1A p.A184V, c.551C>T	
0.41	0.08	0.3	0.117				
INDI 673	INDI 673 PLS 1	Breast	II	7.5	3.75	TP53 p.R273H, c.818G>A	
1.27	0.25	2.8	0.943				
INDI 674	INDI 674 PLS 1	Lung	I	7.5	3.31	TP53 p.R333H, c.998G>A	
1.19	0.07	0.7	0.626				
INDI 675	INDI 675 PLS 1	Colorectum	III	7.5	4.11	TP53 p.R181P, c.542G>C	
2.74	0.10	1.2	0.991				
INDI 677	INDI 677 PLS 1	Colorectum	II	7.5	1.88	KRAS p.G12D, c.35G>A	
1.39	0.07	0.4	0.559				
INDI 678	INDI 678 PLS 1	Colorectum	III	7.5	2.03	TP53 p.E224fs, c.670insG	
13.00	1.10	6.9	0.977				
INDI 679	INDI 679 PLS 1	Colorectum	II	7.5	0.87	TP53 p.A159T, c.475G>A	
0.68	0.03	0.1	0.116				
INDI 681	INDI 681 PLS 1	Lung	II	7.5	3.34	CDKN2A p.R58*, c.172C>T	
0.64	0.03	0.3	0.758				
INDI 682	INDI 682 PLS 1	Colorectum	III	7.5	1.95	TP53 p.C238Y, c.713G>A	
2.26	0.30	1.8	0.778				
INDI 683	INDI 683 PLS 1	Colorectum	II	7.5	2.33	TP53 p.R158C, c.472C>T	
0.89	0.03	0.2	0.589				
INDI 684	INDI 684 PLS 1	Liver	III	7.5	4.11	TP53 p.R181S, c.541C>A	
2.33	0.11	1.3	0.806				
INDI 685	INDI 685 PLS 1	Colorectum	III	7.5	1.59	TP53 p.K372fs, c.1114delA	
0.81	0.05	0.2	0.239				
INDI 686	INDI 686 PLS 1	Pancreas	II	7.5	12.55	TP53 p.R273C, c.817C>T	
1.02	0.03	1.2	0.984				
INDI 687	INDI 687 PLS 1	Lung	III	7.5	11.57	KRAS p.G12V, c.35G>T	
56.40	5.16	183.9	1.000				
INDI 688	INDI 688 PLS 1	Colorectum	II	7.5	3.54	KRAS p.A146T, c.436G>A	
1.84	0.19	2.0	0.908				
INDI 690	INDI 690 PLS 1	Lung	III	7.5	4.42	TP53 p.K373R, c.1118A>G	
0.54	0.02	0.3	0.583				

Table3.txt

INDI 691	INDI 691 PLS 1		Lung	I	7.5	6.03		
		KRAS p.Q61H, c.183A>C						
1.12	0.04		0.8	0.914				
INDI 692	INDI 692 PLS 1		Colorectum	III	7.5	3.61		
		TP53 p.C176fs, c.528delC						
0.84	0.02		0.3	0.955				
INDI 693	INDI 693 PLS 1		Lung	III	7.5	8.08		
		TP53 p.H193Y, c.577C>T						
92.56	22.33		555.6	0.998				
INDI 694	INDI 694 PLS 1		Lung	I	7.5	3.26		
		TP53 p.R273H, c.818G>A						
1.03	0.19		1.9	0.958				
INDI 695	INDI 695 PLS 1		Pancreas	II	7.5	7.79		
		TP53 p.A84T, c.250G>A						
0.67	0.03		0.6	0.378				
INDI 696	INDI 696 PLS 1		Lung	II	7.5	1.71		
		HRAS p.G13V, c.38G>T						
3.20	0.33		1.7	0.948				
INDI 697	INDI 697 PLS 1		Breast	II	7.5	3.86		
		TP53 p.R273H, c.818G>A						
1.28	0.17		2.0	0.974				
INDI 698	INDI 698 PLS 1		Ovary	III	7.5	0.94		
		TP53 p.R158C, c.472C>T						
0.41	0.10		0.3	0.947				
INDI 699	INDI 699 PLS 1		Pancreas	II	7.5	3.47		
		KRAS p.G12D, c.35G>A						
3.27	0.38		4.0	0.997				
INDI 700	INDI 700 PLS 1		Lung	III	7.5	4.48		
		TP53 p.E286*, c.856G>T						
2.64	0.20		2.8	0.986				
INDI 701	INDI 701 PLS 1		Colorectum	II	7.5	1.54		
		BRAF p.V600E, c.1799T>A						
3.67	0.17		0.8	0.874				
INDI 702	INDI 702 PLS 1		Lung	II	7.5	22.55		
		TP53 p.E298*, c.892G>T						
4.22	0.14		9.6	0.997				
INDI 703	INDI 703 PLS 1		Lung	I	7.5	2.98		
		TP53 g.7579310A>G (Splice Site)						
0.69	0.02		0.2	0.656				
INDI 704	INDI 704 PLS 1		Breast	II	7.5	1.94		
		TP53 p.R273H, c.818G>A						
1.71	0.40		2.4	0.395				
INDI 706	INDI 706 PLS 1		Lung	I	7.5	2.69		
		TP53 p.G374fs, c.1120delG						
1.26	0.05		0.4	0.993				
INDI 708	INDI 708 PLS 1		Colorectum	III	7.5	7.20		
		BRAF p.L597R, c.1790T>G						
6.15	0.34		7.4	0.995				

Table3.txt

INDI 709 INDI 709 PLS 1 Colorectum II 7.5 1.71
BRAF p.V600E, c.1799T>A
2.75 0.09 0.5 0.842
INDI 710 INDI 710 PLS 1 Colorectum III 7.5 4.72
PIK3CA p.Q546R, c.1637A>G
3.28 0.16 2.4 0.977
INDI 711 INDI 711 PLS 1 Breast III 7.5 2.28
PIK3CA p.E545K, c.1633G>A
4.38 0.42 2.9 0.979
INDI 712 INDI 712 PLS 1 Breast I 7.5 4.45
TP53 p.C141Y, c.422G>A
1.34 0.11 1.5 0.354
INDI 713 INDI 713 PLS 1 Breast II 7.5 6.30
TP53 p.R273H, c.818G>A
1.28 0.23 4.4 0.342
INDI 714 INDI 714 PLS 1 Breast III 7.5 3.29
TP53 p.R175H, c.524G>A
2.30 2.15 21.8 0.956
INDI 715 INDI 715 PLS 1 Breast III 7.5 11.42
TP53 p.R158C, c.472C>T
1.64 0.20 7.0 0.987
INDI 716 INDI 716 PLS 1 Colorectum III 7.5 5.36
PTEN p.A151T, c.451G>A
1.33 0.01 0.1 0.975
INDI 717 INDI 717 PLS 1 Breast I 7.5 2.38
TP53 p.R273H, c.818G>A
1.04 0.29 2.1 0.812
INDI 718 INDI 718 PLS 1 Colorectum II 7.5 3.33
TP53 p.K372fs, c.1114delA
1.04 0.04 0.5 0.829
INDI 720 INDI 720 PLS 1 Colorectum III 7.5 4.49
KRAS p.G12D, c.35G>A
2.18 0.12 1.6 0.654
INDI 721 INDI 721 PLS 1 Breast II 7.5 3.84
PTEN p.E91fs, c.271delGAAGACCATAACCCACCACAGC (SEQ ID NO:891)
0.99 0.13 1.5 0.598
INDI 722 INDI 722 PLS 1 Breast I 7.5 3.73
TP53 p.P152L, c.455C>T
0.96 0.05 0.5 0.201
INDI 723 INDI 723 PLS 1 Ovary III 7.5 2.80
TP53 p.S215I, c.644G>T
3.13 0.69 6.0 0.993
INDI 724 INDI 724 PLS 1 Colorectum II 7.5 5.51
KRAS p.A11V, c.32C>T
0.90 0.02 0.3 0.230
INDI 725 INDI 725 PLS 1 Colorectum II 7.5 1.64
TP53 p.G245D, c.734G>A
0.59 0.05 0.2 0.636

Table3.txt

INDI 726	INDI 726 PLS 1	Colorectum	I	7.5	5.49	
	TP53 p.R248Q, c.743G>A					
1.15	0.08	1.4	0.315			
INDI 729	INDI 729 PLS 1	Colorectum	II	7.5	3.51	
	TP53 p.L252fs, c.754delTCC					
2.04	0.12	1.3	0.465			
INDI 731	INDI 731 PLS 1	Pancreas	II	7.5	1.84	
	TP53 p.E339K, c.1015G>A					
0.49	0.03	0.1	0.469			
INDI 732	INDI 732 PLS 1	Colorectum	III	7.5	2.84	
	TP53 p.R283C, c.847C>T					
1.10	0.07	0.6	0.756			
INDI 734	INDI 734 PLS 1	Pancreas	II	7.5	6.23	
	KRAS p.G12D, c.35G>A					
2.95	0.38	7.3	0.938			
INDI 735	INDI 735 PLS 1	Pancreas	II	7.5	2.61	
	TP53 p.G266V, c.797G>T					
7.19	2.14	17.2	0.997			
INDI 736	INDI 736 PLS 1	Lung	III	7.5	4.85	
	TP53 p.P278T, c.832C>A					
3.89	0.34	5.1	0.958			
INDI 737	INDI 737 PLS 1	Stomach	I	7.5	5.34	
	TP53 p.K372fs, c.1114delA					
0.86	0.05	0.9	0.944			
INDI 740	INDI 740 PLS 1	Pancreas	II	7.5	13.15	
	TP53 p.R249S, c.747G>T					
1.26	0.04	1.5	0.991			
INDI 741	INDI 741 PLS 1	Pancreas	III	7.5	21.92	
	TP53 p.K132E, c.394A>G					
1.30	0.01	0.8	0.995			
INDI 742	INDI 742 PLS 1	Breast	II	7.5	2.70	
	TP53 p.F109fs, c.327delC					
9.01	0.40	3.4	0.826			
INDI 743	INDI 743 PLS 1	Stomach	II	7.5	3.45	
	TP53 p.T125M, c.374C>T					
0.34	0.03	0.3	0.117			
INDI 745	INDI 745 PLS 1	Pancreas	II	7.5	11.79	
	TP53 p.S241F, c.722C>T					
1.06	0.02	0.9	0.953			
INDI 746	INDI 746 PLS 1	Colorectum	III	7.5	27.04	
	KRAS p.A59T, c.175G>A					
1.18	0.01	0.7	0.993			
INDI 747	INDI 747 PLS 1	Colorectum	III	7.5	4.74	
	TP53 p.K372fs, c.1114delA					
1.06	0.04	0.6	0.988			
INDI 749	INDI 749 PLS 1	Colorectum	III	7.5	3.11	
	TP53 p.K372fs, c.1114delA					
1.02	0.06	0.6	0.900			

Table3.txt

INDI 750	INDI 750 PLS 1	Colorectum	III	7.5	0.79		
KRAS p.D57N, c.169G>A							
0.78	0.16	0.4	0.973				
INDI 751	INDI 751 PLS 1	Colorectum	III	2	1.70		
TP53 p.E336*, c.1006G>T							
3.10	0.88	4.6	0.982				
INDI 752	INDI 752 PLS 1	Colorectum	III	7.5	7.33		
TP53 p.R175H, c.524G>A							
1.93	0.66	14.9	0.975				
INDI 753	INDI 753 PLS 1	Esophagus	III	7.5	8.37		
TP53 p.Y220C, c.659A>G							
4.61	3.46	89.1	0.999				
INDI 754	INDI 754 PLS 1	Breast	III	7.5	2.75		
PIK3CA p.V344M, c.1030G>A							
0.56	0.08	0.7	0.125				
INDI 755	INDI 755 PLS 1	Esophagus	III	7.5	12.96		
TP53 p.M384V, c.1150A>G							
1.26	0.03	1.2	0.996				
INDI 756	INDI 756 PLS 1	Breast	II	7.5	10.17		
TP53 p.R267W, c.799C>T							
0.94	0.03	1.0	0.543				
INDI 757	INDI 757 PLS 1	Breast	II	7.5	3.31		
TP53 p.R248Q, c.743G>A							
0.38	0.04	0.4	0.117				
INDI 758	INDI 758 PLS 1	Colorectum	II	7.5	7.15		
TP53 p.C176fs, c.528delC							
1.21	0.03	0.7	0.987				
INDI 759	INDI 759 PLS 1	Breast	III	7.5	7.72		
TP53 p.R175C, c.523C>T							
0.77	0.05	1.1	0.117				
INDI 760	INDI 760 PLS 1	Liver	III	7.5	101.29		
CDKN2A p.R58*, c.172C>T							
0.85	0.02	6.9	0.997				
INDI 761	INDI 761 PLS 1	Colorectum	II	7.5	11.84		
TP53 p.L383F, c.1147C>T							
1.19	0.01	0.4	0.995				
INDI 762	INDI 762 PLS 1	Esophagus	II	7.5	5.18		
TP53 p.R282Q, c.845G>A							
0.36	0.08	1.3	0.690				
INDI 763	INDI 763 PLS 1	Colorectum	I	7.5	4.48		
TP53 p.E62G, c.185A>G							
0.86	0.02	0.3	0.824				
INDI 764	INDI 764 PLS 1	Colorectum	II	7.5	1.44		
TP53 p.E51fs, c.151delG							
8.55	1.78	7.9	0.993				
INDI 765	INDI 765 PLS 1	Colorectum	I	7.5	33.07		
BRAF p.K601E, c.1801A>G							
2.88	0.02	2.0	1.000				

Table3.txt

INDI 766	INDI 766 PLS 1	Breast	II	7.5	3.86	TP53 p.P190T, c.568C>A	0.78	0.07	0.9	0.125
INDI 767	INDI 767 PLS 1	Colorectum	II	7.5	1.12	KRAS p.G12D, c.35G>A	1.41	0.17	0.6	0.996
INDI 768	INDI 768 PLS 1	Colorectum	II	7.5	4.62	TP53 p.R158C, c.472C>T	0.95	0.04	0.5	0.735
INDI 769	INDI 769 PLS 1	Colorectum	II	7.5	1.51	TP53 p.I251V, c.751A>G	50.33	50.29	234.0	1.000
INDI 770	INDI 770 PLS 1	Colorectum	II	7.5	5.95	APC p.E1306*, c.3916G>T	4.97	0.16	3.0	0.970
INDI 771	INDI 771 PLS 1	Liver	II	7.5	23.39	CTNNB1 p.S45A, c.133T>G	3.36	0.02	1.7	0.994
INDI 772	INDI 772 PLS 1	Colorectum	II	7.5	1.89	TP53 p.A159T, c.475G>A	0.85	0.04	0.3	0.819
INDI 773	INDI 773 PLS 1	Colorectum	II	7.5	2.86	TP53 p.P152L, c.455C>T	1.04	0.07	0.6	0.841
INDI 774	INDI 774 PLS 1	Colorectum	I	7.5	1.14	KRAS p.G13D, c.38G>A	1.05	0.16	0.6	0.984
INDI 775	INDI 775 PLS 1	Liver	II	7.5	105.74	TP53 p.R202C, c.604C>T	1.28	0.10	34.2	0.999
INDI 776	INDI 776 PLS 1	Esophagus	II	7.5	10.35	TP53 p.R379H, c.1136G>A	0.76	0.02	0.7	0.998
INDI 777	INDI 777 PLS 1	Colorectum	II	7.5	23.48	TP53 p.D42fs, c.124insGA	3.27	0.02	1.3	0.994
INDI 778	INDI 778 PLS 1	Liver	II	7.5	16.38	CTNNB1 p.I35S, c.104T>G	4.39	0.08	4.2	0.999
INDI 779	INDI 779 PLS 1	Colorectum	II	7.5	1.88	TP53 p.E11Q, c.31G>C	99.20	50.22	291.5	1.000
INDI 780	INDI 780 PLS 1	Colorectum	II	7.5	1.78	TP53 p.R273C, c.817C>T	1.64	0.27	1.5	0.946
INDI 781	INDI 781 PLS 1	Colorectum	II	7.5	0.85	BRAF p.D594G, c.1781A>G	2.44	0.52	1.4	0.965

Table3.txt

INDI 782	INDI 782 PLS 1	Colorectum	III	7.5	15.27	BRAF p.V600E, c.1799T>A	36.75	2.88	135.7	1.000
INDI 783	INDI 783 PLS 1	Colorectum	III	7.5	12.35	KRAS p.G13D, c.38G>A	1.57	0.18	6.8	0.680
INDI 784	INDI 784 PLS 1	Stomach	I	7.5	10.44	TP53 p.R249S, c.747G>T	1.82	0.04	1.3	0.985
INDI 785	INDI 785 PLS 1	Colorectum	I	7.5	5.62	TP53 p.E346D, c.1038G>T	1.06	0.11	1.9	0.302
INDI 786	INDI 786 PLS 1	Liver	I	7.5	3.23	TP53 p.C135F, c.404G>T	7.05	1.16	11.6	0.978
INDI 787	INDI 787 PLS 1	Breast	II	7.5	3.28	TP53 p.V157I, c.469G>A	0.61	0.07	0.8	0.121
INDI 788	INDI 788 PLS 1	Colorectum	II	7.5	9.94	KRAS p.A146V, c.437C>T	1.16	0.04	1.2	0.688
INDI 789	INDI 789 PLS 1	Breast	II	7.5	3.96	TP53 p.K372fs, c.1114delA	0.87	0.05	0.6	0.117
INDI 790	INDI 790 PLS 1	Breast	II	7.5	1.57	CDKN2A p.R58*, c.172C>T	0.00	0.04	0.2	0.771
INDI 791	INDI 791 PLS 1	Breast	III	7.5	1.88	TP53 p.G374fs, c.1120delG	0.46	0.07	0.4	0.320
INDI 792	INDI 792 PLS 1	Stomach	I	7.5	8.98	TP53 p.A159T, c.475G>A	0.75	0.02	0.6	0.377
INDI 793	INDI 793 PLS 1	Breast	II	7.5	4.67	TP53 p.K372fs, c.1114delA	1.14	0.06	0.8	0.836
INDI 794	INDI 794 PLS 1	Breast	II	7.5	5.64	TP53 p.R337H, c.1010G>A	0.95	0.04	0.7	0.571
INDI 795	INDI 795 PLS 1	Breast	II	7.5	3.30	TP53 p.A138T, c.412G>A	0.84	0.04	0.4	0.595
INDI 797	INDI 797 PLS 1	Stomach	II	7.5	5.15	TP53 p.K372fs, c.1114delA	1.11	0.06	1.0	0.955
INDI 798	INDI 798 PLS 1	Ovary	II	7.5	22.29	TP53 p.Y163C, c.488A>G	52.92	7.31	502.2	1.000

Table3.txt

INDI 799	INDI 799 PLS 1	Stomach	II	7.5	5.36	CTNNB1 p.S33Y, c.98C>A	0.85	0.03	0.4	0.239
INDI 800	INDI 800 PLS 1	Liver	II	7.5	3.60	CTNNB1 p.T41A, c.121A>G	5.78	0.13	1.4	0.997
INDI 801	INDI 801 PLS 1	Stomach	I	7.5	10.75	TP53 p.R158C, c.472C>T	1.00	0.05	1.8	0.293
INDI 802	INDI 802 PLS 1	Pancreas	II	7.5	15.09	CDKN2A p.E88*, c.262G>T	3.80	0.09	4.0	0.987
INDI 803	INDI 803 PLS 1	Esophagus	II	7.5	2.87	PPP2R1A p.R182W, c.544C>T	0.98	0.11	1.0	0.385
INDI 805	INDI 805 PLS 1	Colorectum	II	7.5	6.65	TP53 p.A159T, c.475G>A	0.81	0.05	1.0	0.632
INDI 806	INDI 806 PLS 1	Colorectum	II	7.5	4.68	TP53 p.L369M, c.1105C>A	0.91	0.04	0.5	0.661
INDI 808	INDI 808 PLS 1	Colorectum	III	7.5	16.77	TP53 p.K372fs, c.1114delA	0.98	0.03	1.7	0.601
INDI 809	INDI 809 PLS 1	Colorectum	III	7.5	4.16	TP53 p.G374fs, c.1120delG	0.43	0.05	0.7	0.213
INDI 812	INDI 812 PLS 1	Ovary	II	7.5	3.11	CTNNB1 p.T41A, c.121A>G	77.58	3.18	30.5	1.000
INDI 814	INDI 814 PLS 1	Stomach	I	7.5	4.26	TP53 p.L369P, c.1106T>C	0.73	0.03	0.4	0.386
INDI 815	INDI 815 PLS 1	Colorectum	II	7.5	8.53	BRAF p.V600E, c.1799T>A	4.77	0.22	5.9	0.997
INDI 816	INDI 816 PLS 1	Colorectum	II	7.5	4.72	TP53 p.A276V, c.827C>T	0.43	0.07	1.1	0.336
INDI 817	INDI 817 PLS 1	Liver	III	7.5	11.67	CTNNB1 p.I35S, c.104T>G	5.12	0.11	4.0	0.990
INDI 818	INDI 818 PLS 1	Ovary	III	7.5	6.53	TP53 p.G154fs, c.460delG	41.01	2.83	56.9	1.000
INDI 819	INDI 819 PLS 1	Breast	III	7.5	1.52	AKT1 p.E17K, c.49G>A	8.34	6.06	28.4	0.979

Table3.txt

INDI 821	INDI 821 PLS 1	Colorectum	III	7.5	1.69	
	TP53 p.S241F, c.722C>T					
0.69	0.05	0.3	0.776			
INDI 822	INDI 822 PLS 1	Colorectum	II	7.5	6.72	
	TP53 p.P82L, c.245C>T					
0.99	0.06	1.3	0.123			
INDI 823	INDI 823 PLS 1	Breast	II	7.5	5.00	
	TP53 p.R213Q, c.638G>A					
0.97	0.12	1.8	0.121			
INDI 824	INDI 824 PLS 1	Esophagus	II	7.5	9.40	
	TP53 p.R158P, c.473G>C					
24.02	1.23	35.7	0.998			
INDI 825	INDI 825 PLS 1	Colorectum	III	7.5	4.98	
	TP53 p.E62D, c.186A>T					
1.06	0.03	0.5	0.511			
INDI 826	INDI 826 PLS 1	Colorectum	II	7.5	3.25	
	TP53 p.N239S, c.716A>G					
2.81	0.10	1.0	0.925			
INDI 827	INDI 827 PLS 1	Colorectum	III	7.5	3.01	
	KRAS p.A146T, c.436G>A					
2.05	0.34	3.1	0.956			
INDI 828	INDI 828 PLS 1	Breast	II	7.5	4.03	
	TP53 p.K372fs, c.1114delA					
0.83	0.04	0.5	0.117			
INDI 829	INDI 829 PLS 1	Colorectum	III	7.5	4.98	
	CDKN2A p.R87Q, c.260G>A					
0.90	0.02	0.4	0.122			
INDI 830	INDI 830 PLS 0	Breast	II	7.5	7.99	
	TP53 p.A159T, c.475G>A					
1.16	0.07	1.7	0.954			
INDI 831	INDI 831 PLS 1	Breast	I	7.5	11.33	
	TP53 p.K373R, c.1118A>G					
0.99	0.03	0.9	0.175			
INDI 832	INDI 832 PLS 1	Breast	II	7.5	9.29	
	TP53 p.G154S, c.460G>A					
1.36	0.10	2.7	0.831			
INDI 833	INDI 833 PLS 1	Breast	I	7.5	5.36	
	FBXW7 p.R465C, c.1393C>T					
1.00	0.05	0.8	0.876			
INDI 835	INDI 835 PLS 1	Colorectum	III	7.5	2.80	
	TP53 p.G374fs, c.1120delG					
1.06	0.06	0.5	0.856			
INDI 837	INDI 837 PLS 1	Colorectum	II	7.5	6.63	
	TP53 p.C176fs, c.528delC					
0.91	0.03	0.7	0.609			
INDI 838	INDI 838 PLS 1	Colorectum	III	7.5	4.20	
	APC p.E1306*, c.3916G>T					
3.44	0.11	1.5	0.603			

Table3.txt

INDI 839	INDI 839 PLS 1	Breast	II	7.5	3.74	
TP53 p.K372fs, c.1114delA						
0.81	0.03	0.4	0.125			
INDI 840	INDI 840 PLS 0	Breast	II	7.5	6.27	
TP53 p.A138T, c.412G>A						
0.89	0.03	0.5	0.125			
INDI 841	INDI 841 PLS 1	Colorectum	III	7.5	7.97	
TP53 p.R248W, c.742C>T						
2.22	1.01	24.8	0.994			
INDI 842	INDI 842 PLS 1	Breast	I	7.5	3.46	
TP53 p.R202C, c.604C>T						
1.26	0.14	1.5	0.826			
INDI 843	INDI 843 PLS 1	Esophagus	I	7.5	5.09	
TP53 p.T155I, c.464C>T						
0.83	0.03	0.4	0.122			
INDI 844	INDI 844 PLS 1	Stomach	I	7.5	3.52	
TP53 p.R280T, c.839G>C						
1.75	0.12	1.3	0.876			
INDI 846	INDI 846 PLS 1	Colorectum	II	7.5	1.84	
APC p.E1309fs, c.3927delAAAGA						
0.67	0.08	0.4	0.991			
INDI 847	INDI 847 PLS 1	Liver	III	7.5	113.59	
TP53 p.H179R, c.536A>G						
0.96	0.01	2.1	0.976			
INDI 848	INDI 848 PLS 1	Colorectum	II	7.5	1.68	
TP53 p.R248Q, c.743G>A						
0.61	0.06	0.3	0.876			
INDI 849	INDI 849 PLS 1	Colorectum	II	7.5	1.30	
PPP2R1A p.R183W, c.547C>T						
0.56	0.07	0.3	0.841			
INDI 850	INDI 850 PLS 1	Esophagus	II	7.5	8.01	
TP53 p.H193P, c.578A>C						
124.89	21.37	527.0	1.000			
INDI 853	INDI 853 PLS 1	Esophagus	II	7.5	49.44	
TP53 p.H178Q, c.534C>G						
1.87	0.01	1.3	0.998			
INDI 854	INDI 854 PLS 1	Colorectum	II	7.5	1.03	
FBXW7 p.R465C, c.1393C>T						
0.66	0.14	0.5	0.991			
INDI 855	INDI 855 PLS 1	Colorectum	II	7.5	9.62	
TP53 g.7576927C>T (Splice Site)						
1.18	0.01	0.4	0.999			
INDI 856	INDI 856 PLS 1	Breast	III	7.5	5.72	
KRAS p.D57N, c.169G>A						
0.77	0.03	0.5	0.116			
INDI 857	INDI 857 PLS 1	Breast	III	7.5	6.54	
TP53 p.C176G, c.526T>G						
1.30	0.04	0.8	0.356			

Table3.txt

INDI 858	INDI 858 PLS 1	Breast	I	7.5	6.21	TP53 p.A159T, c.475G>A		
0.82	0.03	0.6	0.480					
INDI 859	INDI 859 PLS 1	Esophagus	II	7.5	15.56	TP53 p.Y234N, c.700T>A		
7.28	0.59	28.3	0.992					
INDI 860	INDI 860 PLS 1	Breast	I	7.5	2.77	TP53 p.D49N, c.145G>A		
0.40	0.08	0.7	0.121					
INDI 861	INDI 861 PLS 1	Liver	II	7.5	49.26	TP53 p.R249S, c.747G>T		
1.32	0.02	3.3	0.997					
INDI 862	INDI 862 PLS 1	Pancreas	II	7.5	12.94	TP53 p.M133I, c.399G>T		
1.15	0.01	0.4	0.910					
INDI 864	INDI 864 PLS 1	Liver	III	7.5	40.15	PTEN p.R130*, c.388C>T		
1.36	0.02	2.5	0.999					
INDI 865	INDI 865 PLS 1	Breast	III	7.5	3.59	TP53 p.V157I, c.469G>A		
0.80	0.08	0.9	0.392					
INDI 867	INDI 867 PLS 1	Esophagus	II	7.5	20.52	TP53 p.R181P, c.542G>C		
1.33	0.01	0.6	0.995					
INDI 868	INDI 868 PLS 1	Liver	III	7.5	79.15	KRAS p.A146V, c.437C>T		
2.83	0.05	11.8	0.993					
INDI 870	INDI 870 PLS 1	Breast	II	7.5	20.48	TP53 p.R202C, c.604C>T		
1.07	0.04	2.5	0.947					
INDI 872	INDI 872 PLS 1	Breast	III	7.5	5.17	PIK3CA p.H1047L, c.3140A>T		
13.66	0.89	14.2	0.986					
INDI 873	INDI 873 PLS 1	Breast	III	7.5	8.85	KRAS p.A59E, c.176C>A		
1.00	0.02	0.7	0.527					
INDI 875	INDI 875 PLS 1	Breast	II	7.5	5.66	TP53 p.R337C, c.1009C>T		
0.54	0.03	0.5	0.252					
INDI 876	INDI 876 PLS 1	Breast	II	7.5	8.23	TP53 p.R306L, c.917G>T		
0.41	0.02	0.5	0.331					
INDI 877	INDI 877 PLS 1	Breast	I	7.5	37.49	TP53 p.P85H, c.254C>A		
1.05	0.01	0.9	0.999					
INDI 878	INDI 878 PLS 1	Breast	III	7.5	8.88	TP53 p.L369M, c.1105C>A		
1.22	0.03	0.9	0.992					

Table3.txt

INDI 879	INDI 879 PLS 1	Breast	II	7.5	5.37	
	TP53 p.R282W, c.844C>T					
0.76	0.04	0.7	0.340			
INDI 880	INDI 880 PLS 1	Breast	II	7.5	72.89	
	FBXW7 p.R465H, c.1394G>A					
0.84	0.02	3.4	0.675			
INDI 881	INDI 881 PLS 1	Breast	II	7.5	18.05	
	HRAS p.G12S, c.34G>A					
1.08	0.08	4.7	0.835			
INDI 882	INDI 882 PLS 1	Breast	II	7.5	21.10	
	TP53 p.K373E, c.1117A>G					
1.00	0.01	0.8	0.779			
INDI 883	INDI 883 PLS 1	Breast	II	7.5	11.03	
	TP53 p.K372fs, c.1114delA					
1.05	0.05	1.8	0.602			
INDI 884	INDI 884 PLS 1	Breast	II	7.5	17.62	
	TP53 p.Y220C, c.659A>G					
12.84	11.77	638.8	0.999			
INDI 885	INDI 885 PLS 1	Breast	II	7.5	5.89	
	FBXW7 p.R505H, c.1514G>A					
0.93	0.03	0.6	0.547			
INDI 886	INDI 886 PLS 1	Breast	II	7.5	2.52	
	TP53 p.K372fs, c.1114delA					
0.66	0.09	0.7	0.123			
INDI 887	INDI 887 PLS 1	Breast	III	7.5	20.27	
	CDKN2A p.R87Q, c.260G>A					
0.84	0.02	1.5	0.987			
INDI 888	INDI 888 PLS 1	Pancreas	II	7.5	8.94	
	TP53 p.G108S, c.322G>A					
1.03	0.04	1.0	0.976			
INDI 889	INDI 889 PLS 1	Colorectum	II	7.5	2.44	
	TP53 p.P190L, c.569C>T					
3.86	0.35	2.6	0.999			
INDI 892	INDI 892 PLS 1	Stomach	I	7.5	4.34	
	TP53 p.K372fs, c.1114delA					
0.90	0.03	0.4	0.561			
INDI 893	INDI 893 PLS 1	Pancreas	II	7.5	14.46	
	BRAF p.A598T, c.1792G>A					
1.01	0.01	0.5	0.972			
INDI 896	INDI 896 PLS 1	Lung	I	7.5	3.34	
	TP53 p.R337L, c.1010G>T					
5.64	2.20	22.6	0.864			
INDI 897	INDI 897 PLS 1	Breast	III	7.5	1.91	
	TP53 p.T155I, c.464C>T					
7.02	7.02	41.2	0.993			
INDI 898	INDI 898 PLS 1	Breast	I	7.5	1.21	
	TP53 p.K372fs, c.1114delA					
1.14	0.09	0.4	0.967			

Table3.txt

INDI 899	INDI 899 PLS 1	Breast	I	7.5	4.02	
TP53 p.A161S, c.481G>T						
0.96	0.02	0.2	0.154			
INDI 902	INDI 902 PLS 1	Breast	III	7.5	7.00	
PIK3CA p.H1047R, c.3140A>G						
26.55	9.21	198.7	0.997			
INDI 903	INDI 903 PLS 1	Breast	I	7.5	0.56	
TP53 p.E62K, c.184G>A						
0.00	0.14	0.2	0.651			
INDI 905	INDI 905 PLS 1	Esophagus	II	7.5	19.99	
TP53 p.K132R, c.395A>G						
8.45	0.61	37.4	1.000			
INDI 907	INDI 907 PLS 1	Esophagus	II	7.5	18.15	
TP53 p.T256fs, c.767insCACT						
1.06	0.02	1.3	0.971			
INDI 908	INDI 908 PLS 1	Esophagus	II	7.5	41.43	
TP53 p.G266V, c.797G>T						
2.61	0.02	1.9	0.999			
INDI 909	INDI 909 PLS 1	Esophagus	II	7.5	22.67	
TP53 p.P152L, c.455C>T						
1.16	0.06	4.1	0.987			
INDI 911	INDI 911 PLS 1	Esophagus	II	7.5	12.33	
TP53 p.A159T, c.475G>A						
0.95	0.05	1.8	0.887			
INDI 913	INDI 913 PLS 1	Esophagus	III	7.5	24.11	
PIK3CA p.N345K, c.1035T>A						
0.89	0.01	0.6	0.835			
INDI 915	INDI 915 PLS 1	Breast	II	7.5	4.83	
TP53 p.R273H, c.818G>A						
1.32	0.22	3.2	0.328			
INDI 917	INDI 917 PLS 1	Liver	III	7.5	27.49	
PTEN p.C136R, c.406T>C						
7.49	0.18	15.4	0.997			
INDI 919	INDI 919 PLS 1	Breast	II	7.5	5.89	
TP53 p.P152L, c.455C>T						
1.99	0.61	11.0	0.458			
INDI 920	INDI 920 PLS 1	Ovary	III	7.5	4.16	
TP53 p.R273H, c.818G>A						
1.36	0.23	2.9	0.944			
INDI 921	INDI 921 PLS 1	Breast	II	7.5	5.20	
TP53 p.N288fs, c.864insCCCAAGTGAC (SEQ ID NO:892)						
1.25	0.08	1.2	0.458			
INDI 922	INDI 922 PLS 1	Breast	II	7.5	4.92	
TP53 p.R273H, c.818G>A						
0.90	0.14	2.1	0.125			
INDI 923	INDI 923 PLS 1	Esophagus	I	7.5	12.24	
TP53 p.A138T, c.412G>A						
1.02	0.03	1.1	0.306			

Table3.txt

INDI 924	INDI 924 PLS 1	Breast	III	7.5	4.69		
	GNAS p.R201H, c.602G>A						
1.61	0.32	4.6	0.395				
INDI 926	INDI 926 PLS 1	Breast	II	7.5	4.98		
	TP53 p.R273H, c.818G>A						
1.29	0.24	3.7	0.343				
INDI 927	INDI 927 PLS 1	Breast	II	7.5	2.73		
	TP53 p.R273H, c.818G>A						
1.15	0.40	3.4	0.304				
INDI 928	INDI 928 PLS 1	Stomach	II	7.5	6.23		
	TP53 p.F338fs, c.1014delC						
4.08	0.16	3.0	0.998				
INDI 929	INDI 929 PLS 1	Stomach	II	7.5	15.27		
	TP53 p.V216L, c.646G>C						
1.45	0.03	1.6	0.719				
INDI 930	INDI 930 PLS 1	Stomach	II	7.5	5.92		
	TP53 p.R273H, c.818G>A						
1.18	0.21	3.8	0.672				
INDI 931	INDI 931 PLS 1	Ovary	III	7.5	6.52		
	TP53 p.R273H, c.818G>A						
1.29	0.27	5.4	0.955				
INDI 932	INDI 932 PLS 1	Ovary	III	7.5	5.40		
	TP53 p.L252fs, c.754delTCC						
69.94	10.81	179.8	0.999				
INDI 933	INDI 933 PLS 1	Esophagus	III	7.5	7.05		
	TP53 p.R273H, c.818G>A						
1.26	0.19	4.1	0.527				
INDI 935	INDI 935 PLS 1	Esophagus	I	7	9.06		
	TP53 p.R273H, c.818G>A						
1.10	0.14	4.0	0.810				
INDI 936	INDI 936 PLS 1	Ovary	I	7.5	8.81		
	TP53 p.C176fs, c.528insC						
1.41	0.12	3.3	0.363				
INDI 937	INDI 937 PLS 1	Esophagus	III	7.5	8.18		
	TP53 p.R273H, c.818G>A						
1.08	0.16	4.1	0.541				
LCR 588	LCR 588 PLS1	Normal	NA	7.5	7.34		
	TP53 p.K372R, c.1115A>G						
0.47	0.01	0.2	0.260				
LCR 589	LCR 589 PLS1	Normal	NA	7.5	7.48		
	TP53 p.K372fs, c.1114insA						
0.94	0.01	0.2	0.186				
LCR 590	LCR 590 PLS1	Normal	NA	7.5	8.50		
	TP53 p.G302fs, c.904delG						
0.91	0.01	0.3	0.235				
LCR 591	LCR 591 PLS1	Normal	NA	7.5	10.50		
	TP53 p.R175C, c.523C>T						
0.66	0.03	1.0	0.125				

Table3.txt

LCR 592	LCR 592 PLS1	Normal	NA	7.5	5.04	
		TP53 p.K372fs, c.1114delA				
0.95	0.04	0.6	0.117			
LCR 593	LCR 593 PLS1	Normal	NA	7.5	11.14	
		TP53 p.K372fs, c.1114delA				
0.84	0.06	2.1	0.175			
LCR 594	LCR 594 PLS1	Normal	NA	7.5	4.84	
		PIK3CA p.A1046V, c.3137C>T				
0.89	0.06	1.0	0.121			
LCR 595	LCR 595 PLS1	Normal	NA	7.5	3.73	
		TP53 p.K372fs, c.1114delA				
1.00	0.04	0.5	0.296			
LCR 596	LCR 596 PLS1	Colorectum	I	7.5	2.88	
		TP53 p.A83T, c.247G>A				
0.39	0.08	0.7	0.181			
LCR 597	LCR 597 PLS1	Normal	NA	7.5	4.77	
		TP53 p.L369P, c.1106T>C				
1.07	0.05	0.7	0.435			
LCR 599	LCR 599 PLS1	Normal	NA	7.5	3.41	
		TP53 p.K372fs, c.1114delA				
1.22	0.10	1.1	0.339			
LCR 600	LCR 600 PLS1	Normal	NA	7.5	4.65	
		TP53 p.R158H, c.473G>A				
0.51	0.14	2.0	0.121			
LCR 601	LCR 601 PLS1	Normal	NA	7.5	3.19	
		TP53 p.L369P, c.1106T>C				
1.05	0.04	0.4	0.307			
LCR 602	LCR 602 PLS1	Normal	NA	7.5	9.94	
		TP53 p.R335H, c.1004G>A				
0.62	0.03	1.0	0.315			
LCR 603	LCR 603 PLS1	Normal	NA	7.5	2.92	
		KRAS p.G13D, c.38G>A				
0.57	0.19	1.7	0.125			
LCR 604	LCR 604 PLS1	Normal	NA	7.5	7.73	
		HRAS p.G12D, c.35G>A				
0.87	0.02	0.4	0.121			
LCR 605	LCR 605 PLS1	Normal	NA	7.5	5.75	
		KRAS p.G13D, c.38G>A				
1.15	0.07	1.2	0.326			
LCR 606	LCR 606 PLS1	Normal	NA	7.5	6.06	
		KRAS p.G13D, c.38G>A				
1.07	0.06	1.1	0.779			
LCR 607	LCR 607 PLS1	Normal	NA	7.5	8.85	
		KRAS p.G13D, c.38G>A				
0.90	0.10	2.8	0.585			
LCR 608	LCR 608 PLS1	Normal	NA	7.5	3.74	
		TP53 p.P142L, c.425C>T				
0.68	0.06	0.7	0.593			

Table3.txt

LCR 610	LCR 610 PLS1	Normal	NA	7.5	2.05
		TP53 p.P47L, c.140C>T			
0.00	0.06	0.4	0.125		
LCR 611	LCR 611 PLS1	Normal	NA	7.5	2.71
		KRAS p.G13D, c.38G>A			
0.49	0.09	0.7	0.196		
LCR 612	LCR 612 PLS1	Normal	NA	7.5	4.86
		TP53 p.R335H, c.1004G>A			
0.36	0.07	1.1	0.116		
LCR 613	LCR 613 PLS1	Normal	NA	7.5	2.46
		HRAS p.G12D, c.35G>A			
0.41	0.07	0.5	0.117		
LCR 614	LCR 614 PLS1	Normal	NA	7.5	5.18
		TP53 p.N200fs, c.598delCCGAGTGGAAGGAA (SEQ ID NO:747)			
0.74	0.04	0.6	0.239		
LCR 616	LCR 616 PLS1	Normal	NA	7.5	9.30
		HRAS p.G13D, c.38G>A			
0.59	0.02	0.4	0.125		
LCR 617	LCR 617 PLS1	Normal	NA	7.5	8.47
		TP53 p.G374fs, c.1120delG			
0.93	0.08	2.1	0.122		
LCR 618	LCR 618 PLS1	Normal	NA	7.5	3.18
		KRAS p.D57N, c.169G>A			
0.45	0.08	0.8	0.293		
LCR 619	LCR 619 PLS1	Normal	NA	7.5	5.61
		KRAS p.A11V, c.32C>T			
0.00	0.02	0.4	0.122		
LCR 620	LCR 620 PLS1	Normal	NA	7.5	5.33
		FBXW7 p.G477S, c.1429G>A			
0.47	0.03	0.5	0.494		
LCR 621	LCR 621 PLS1	Normal	NA	7.5	2.80
		TP53 p.Y234H, c.700T>C			
0.31	0.11	0.9	0.117		
LCR 622	LCR 622 PLS1	Normal	NA	7.5	16.35
		TP53 p.K372fs, c.1114delA			
0.98	0.04	2.2	0.125		
LCR 623	LCR 623 PLS1	Normal	NA	7.5	5.34
		TP53 p.R282Q, c.845G>A			
0.67	0.12	1.9	0.835		
LCR 624	LCR 624 PLS1	Normal	NA	7.5	3.81
		TP53 p.P177S, c.529C>T			
0.61	0.09	1.0	0.116		
LCR 625	LCR 625 PLS1	Normal	NA	7.5	17.16
		TP53 p.P36Q, c.107C>A			
1.40	0.03	1.7	0.486		
LCR 626	LCR 626 PLS1	Normal	NA	7.5	3.95
		TP53 p.S121Y, c.362C>A			
0.59	0.06	0.8	0.603		

Table3.txt

LCR 627	LCR 627 PLS1	Normal	NA	7.5	2.76	
	TP53 p.R290H, c.869G>A					
0.00	0.10	0.9	0.861			
LCR 628	LCR 628 PLS1	Normal	NA	7.5	2.29	
	CDKN2A p.V51I, c.151G>A (Exon Start)					
0.00	0.08	0.6	0.117			
LCR 629	LCR 629 PLS1	Normal	NA	7.5	7.50	
	TP53 p.T118I, c.353C>T					
1.06	0.06	1.3	0.639			
LCR 630	LCR 630 PLS1	Normal	NA	7.5	14.32	
	TP53 p.C182Y, c.545G>A					
1.04	0.08	3.5	0.298			
LCR 631	LCR 631 PLS1	Normal	NA	7.5	3.87	
	TP53 p.R181C, c.541C>T					
0.54	0.15	1.8	0.220			
LCR 632	LCR 632 PLS1	Normal	NA	7.5	7.22	
	TP53 p.R202C, c.604C>T					
0.67	0.05	1.2	0.123			
LCR 633	LCR 633 PLS1	Normal	NA	7.5	10.48	
	TP53 p.L348M, c.1042T>A					
0.92	0.03	0.9	0.547			
LCR 634	LCR 634 PLS1	Normal	NA	7.5	5.81	
	CDKN2A p.R87Q, c.260G>A					
0.55	0.04	0.8	0.121			
LCR 635	LCR 635 PLS1	Normal	NA	7.5	4.11	
	FBXW7 p.R479*, c.1435C>T					
0.68	0.04	0.5	0.125			
LCR 636	LCR 636 PLS1	Normal	NA	7.5	4.08	
	PIK3CA p.N1044S, c.3131A>G					
1.26	0.18	2.3	0.345			
LCR 637	LCR 637 PLS1	Normal	NA	7.5	2.56	
	TP53 p.P142H, c.425C>A					
0.00	0.06	0.5	0.125			
LCR 638	LCR 638 PLS1	Normal	NA	7.5	3.27	
	TP53 p.L308M, c.922C>A					
0.00	0.07	0.8	0.123			
LCR 639	LCR 639 PLS1	Normal	NA	7.5	5.42	
	FBXW7 p.R505H, c.1514G>A					
0.63	0.04	0.7	0.122			
LCR 640	LCR 640 PLS1	Normal	NA	7.5	9.99	
	GNAS p.R201C, c.601C>T					
0.81	0.04	1.1	0.125			
LCR 641	LCR 641 PLS1	Normal	NA	7.5	5.50	
	TP53 p.P47L, c.140C>T					
0.62	0.07	1.2	0.705			
LCR 642	LCR 642 PLS1	Normal	NA	7.5	6.58	
	GNAS p.R201H, c.602G>A					
0.55	0.03	0.5	0.229			

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LCR 643	LCR 643 PLS1	Normal	NA	7.5	2.70
		TP53 p.A159T, c.475G>A			
0.54	0.14	1.1	0.116		
LCR 644	LCR 644 PLS1	Normal	NA	7.5	4.70
		TP53 p.Q104R, c.311A>G			
0.49	0.05	0.7	0.117		
LCR 645	LCR 645 PLS1	Normal	NA	7.5	8.55
		GNAS p.R201H, c.602G>A			
0.76	0.05	1.3	0.510		
LCR 646	LCR 646 PLS1	Normal	NA	7.5	7.59
		GNAS p.R201H, c.602G>A			
0.64	0.07	1.6	0.117		
LCR 647	LCR 647 PLS1	Normal	NA	7.5	7.61
		TP53 p.G374fs, c.1120delG			
0.89	0.07	1.5	0.168		
LCR 648	LCR 648 PLS1	Normal	NA	7.5	5.30
		KRAS p.V14I, c.40G>A			
0.41	0.05	0.8	0.122		
LCR 649	LCR 649 PLS1	Normal	NA	7.5	7.69
		TP53 p.P177L, c.530C>T			
0.62	0.05	1.2	0.125		
LCR 650	LCR 650 PLS1	Normal	NA	7.5	4.06
		TP53 p.T170K, c.509C>A			
0.00	0.08	1.0	0.747		
LCR 652	LCR 652 PLS1	Normal	NA	7.5	4.71
		TP53 p.L299P, c.896T>C			
0.00	0.05	0.7	0.122		
LCR 653	LCR 653 PLS1	Normal	NA	7	23.33
		TP53 p.E339K, c.1015G>A			
0.67	0.03	2.5	0.329		
LCR 654	LCR 654 PLS1	Normal	NA	7.5	3.38
		TP53 p.T125T, c.375G>A (Exon End)			
0.34	0.09	0.9	0.117		
LCR 655	LCR 655 PLS1	Normal	NA	7.5	3.34
		TP53 p.P152L, c.455C>T			
0.40	0.12	1.2	0.122		
LCR 658	LCR 658 PLS1	Normal	NA	7.5	1.80
		TP53 p.N30K, c.90C>G			
0.00	0.10	0.6	0.117		
LCR 659	LCR 659 PLS1	Normal	NA	7.5	4.23
		FBXW7 p.R505C, c.1513C>T			
0.42	0.02	0.3	0.125		
LCR 660	LCR 660 PLS1	Normal	NA	7.5	1.72
		TP53 p.R379H, c.1136G>A			
0.49	0.19	1.0	0.125		
LCR 661	LCR 661 PLS1	Normal	NA	7.5	1.04
		PIK3CA p.R88Q, c.263G>A			
0.00	0.08	0.3	0.117		

Table3.txt

LCR 662	LCR 662 PLS1	Normal	NA	7.5	3.35	TP53 p.L369P, c.1106T>C
0.63	0.15	1.6	0.193			
LCR 663	LCR 663 PLS1	Normal	NA	7.5	4.40	TP53 p.R290C, c.868C>T
1.10	0.12	1.6	0.317			
LCR 665	LCR 665 PLS1	Normal	NA	7.5	8.49	TP53 p.A119T, c.355G>A
0.86	0.04	1.0	0.117			
LCR 666	LCR 666 PLS1	Normal	NA	7.5	1.95	TP53 p.T125T, c.375G>A (Exon End)
0.00	0.03	0.2	0.123			
LCR 667	LCR 667 PLS1	Normal	NA	7.5	2.13	TP53 p.S116Y, c.347C>A
0.00	0.02	0.2	0.122			
LCR 668	LCR 668 PLS1	Normal	NA	7.5	5.91	TP53 p.R202C, c.604C>T
0.66	0.08	1.4	0.121			
LCR 670	LCR 670 PLS1	Normal	NA	7.5	2.93	CDKN2A p.A76T, c.226G>A
0.94	0.15	1.3	0.125			
LCR 671	LCR 671 PLS1	Normal	NA	7.5	0.90	FBXW7 p.R479Q, c.1436G>A
0.00	0.15	0.4	0.123			
LCR 672	LCR 672 PLS1	Normal	NA	7.5	2.56	TP53 p.T125T, c.375G>A (Exon End)
0.00	0.06	0.5	0.601			
LCR 673	LCR 673 PLS1	Normal	NA	7.5	2.67	TP53 p.P153L, c.458C>T
0.60	0.07	0.6	0.116			
LCR 674	LCR 674 PLS1	Normal	NA	7.5	5.50	TP53 p.K372fs, c.1114delA
0.91	0.05	0.8	0.179			
LCR 675	LCR 675 PLS1	Normal	NA	7.5	8.63	CDKN2A p.R58*, c.172C>T
0.75	0.04	1.1	0.187			
LCR 676	LCR 676 PLS1	Normal	NA	7.5	3.34	TP53 p.R158H, c.473G>A
0.51	0.06	0.6	0.245			
LCR 677	LCR 677 PLS1	Normal	NA	7.5	12.26	TP53 p.R196Q, c.587G>A
0.82	0.04	1.7	0.156			
LCR 678	LCR 678 PLS1	Normal	NA	7.5	3.13	FBXW7 p.G477S, c.1429G>A
0.00	0.07	0.7	0.186			
LCR 679	LCR 679 PLS1	Normal	NA	7.5	5.80	TP53 p.V157I, c.469G>A
0.36	0.04	0.7	0.125			

Table3.txt

LCR 680	LCR 680 PLS1	Normal	NA	7.5	4.18	TP53 p.F113L, c.337T>C
4.77	0.24	3.1	0.699			
LCR 681	LCR 681 PLS1	Normal	NA	7.5	5.83	GNAS p.R201H, c.602G>A
0.41	0.02	0.4	0.597			
LCR 682	LCR 682 PLS1	Normal	NA	7.5	6.17	TP53 p.V10I, c.28G>A
0.64	0.05	0.9	0.631			
LCR 683	LCR 683 PLS1	Normal	NA	7.5	6.17	TP53 p.R267W, c.799C>T
1.27	0.28	5.2	0.322			
LCR 684	LCR 684 PLS1	Normal	NA	7.5	4.83	TP53 p.A161V, c.482C>T
0.69	0.05	0.7	0.121			
LCR 685	LCR 685 PLS1	Normal	NA	7.5	8.62	PTEN p.G129E, c.386G>A
0.63	0.02	0.4	0.845			
LCR 686	LCR 686 PLS1	Normal	NA	7.5	4.78	TP53 p.A83V, c.248C>T
0.50	0.06	0.9	0.122			
LCR 687	LCR 687 PLS1	Normal	NA	7.5	1.96	TP53 p.A119S, c.355G>T
0.60	0.09	0.5	0.121			
LCR 688	LCR 688 PLS1	Normal	NA	7.5	7.42	TP53 p.L369P, c.1106T>C
1.06	0.05	1.2	0.419			
LCR 689	LCR 689 PLS1	Normal	NA	7.5	1.99	FBXW7 p.E471*, c.1411G>T
0.00	0.10	0.6	0.125			
LCR 690	LCR 690 PLS1	Normal	NA	7.5	6.21	TP53 p.A119V, c.356C>T
0.00	0.01	0.3	0.123			
LCR 691	LCR 691 PLS1	Normal	NA	7.5	3.99	TP53 p.T125T, c.375G>A (Exon End)
0.53	0.09	1.1	0.123			
LCR 692	LCR 692 PLS1	Normal	NA	7.5	3.42	TP53 p.K372fs, c.1114delA
0.76	0.06	0.7	0.770			
LCR 693	LCR 693 PLS1	Normal	NA	7.5	2.57	TP53 p.R175H, c.524G>A
0.48	0.16	1.2	0.116			
LCR 694	LCR 694 PLS1	Normal	NA	7.5	1.54	CDKN2A p.R58*, c.172C>T
0.57	0.18	0.9	0.122			
LCR 697	LCR 697 PLS1	Normal	NA	7.5	12.02	GNAS p.R201H, c.602G>A
1.08	0.03	1.2	0.308			

Table3.txt

LCR 698	LCR 698 PLS1	Normal	NA	7.5	6.49
		FBXW7 p.E471fs, c.1412delA			
0.74	0.04	0.8	0.328		
LCR 699	LCR 699 PLS1	Normal	NA	7.5	0.90
		CTNNB1 p.S33C, c.98C>G			
0.00	0.06	0.2	0.123		
LCR 700	LCR 700 PLS1	Normal	NA	7.5	3.76
		TP53 p.P300fs, c.898delC			
0.71	0.02	0.3	0.755		
LCR 701	LCR 701 PLS1	Normal	NA	7.5	1.86
		TP53 p.R110C, c.328C>T			
0.49	0.06	0.4	0.630		
LCR 702	LCR 702 PLS1	Normal	NA	7.5	3.95
		TP53 p.R202C, c.604C>T			
0.76	0.04	0.5	0.968		
LCR 703	LCR 703 PLS1	Normal	NA	7.5	0.65
		KRAS p.V14I, c.40G>A			
0.00	0.14	0.3	0.117		
LCR 704	LCR 704 PLS1	Normal	NA	7.5	7.32
		TP53 p.T125M, c.374C>T			
1.05	0.05	1.1	1.000		
LCR 705	LCR 705 PLS1	Normal	NA	7.5	5.14
		GNAS p.R201C, c.601C>T			
1.24	0.11	1.8	0.485		
LCR 706	LCR 706 PLS1	Normal	NA	7.5	10.62
		CDKN2A p.V82M, c.244G>A			
0.80	0.04	1.3	0.192		
LCR 707	LCR 707 PLS1	Normal	NA	7.5	3.90
		TP53 p.P222L, c.665C>T			
0.51	0.10	1.2	0.216		
LCR 709	LCR 709 PLS1	Normal	NA	7.5	2.36
		TP53 p.N131T, c.392A>C			
0.00	0.14	1.0	0.400		
LCR 710	LCR 710 PLS1	Normal	NA	7.5	7.20
		TP53 p.T150K, c.449C>A			
1.02	0.02	0.5	0.758		
LCR 711	LCR 711 PLS1	Normal	NA	7.5	2.26
		TP53 p.M237K, c.710T>A			
0.69	0.09	0.6	0.123		
LCR 712	LCR 712 PLS1	Normal	NA	7.5	11.51
		TP53 p.A161V, c.482C>T			
0.69	0.03	1.2	0.121		
LCR 713	LCR 713 PLS1	Normal	NA	7.5	9.78
		PTEN p.A137T, c.409G>A			
1.14	0.02	0.7	0.861		
LCR 714	LCR 714 PLS1	Normal	NA	7.5	1.93
		TP53 p.D49N, c.145G>A			
0.55	0.26	1.5	0.123		

Table3.txt

LCR 715	LCR 715 PLS1	Normal	NA	7.5	0.50
		TP53 p.R156C, c.466C>T			
0.00	0.15	0.2	0.122		
LCR 716	LCR 716 PLS1	Normal	NA	7.5	5.21
		TP53 p.A119V, c.356C>T			
0.74	0.01	0.2	0.538		
LCR 717	LCR 717 PLS1	Normal	NA	7.5	1.27
		TP53 p.A119T, c.355G>A			
0.00	0.01	0.1	0.507		
LCR 718	LCR 718 PLS1	Normal	NA	7.5	3.12
		TP53 p.P47L, c.140C>T			
0.52	0.10	0.9	0.523		
LCR 719	LCR 719 PLS1	Normal	NA	7.5	3.19
		TP53 p.R306*, c.916C>T			
0.56	0.03	0.3	0.125		
LCR 720	LCR 720 PLS1	Normal	NA	7.5	3.36
		TP53 p.R283C, c.847C>T			
0.51	0.07	0.7	0.116		
LCR 721	LCR 721 PLS1	Normal	NA	7.5	5.91
		CDKN2A p.R58*, c.172C>T			
0.66	0.02	0.4	0.517		
LCR 722	LCR 722 PLS1	Normal	NA	7.5	5.16
		TP53 p.R335H, c.1004G>A			
0.80	0.03	0.5	0.377		
LCR 723	LCR 723 PLS1	Normal	NA	7.5	5.22
		TP53 p.R202C, c.604C>T			
0.98	0.02	0.3	0.117		
LCR 724	LCR 724 PLS1	Normal	NA	7.5	0.83
		TP53 p.T118I, c.353C>T			
0.00	0.04	0.1	0.122		
LCR 725	LCR 725 PLS1	Normal	NA	7.5	2.85
		TP53 p.S303G, c.907A>G			
0.77	0.02	0.2	0.184		
LCR 726	LCR 726 PLS1	Normal	NA	7.5	1.45
		TP53 p.R267Q, c.800G>A			
0.58	0.11	0.5	0.564		
LCR 727	LCR 727 PLS1	Normal	NA	7.5	1.80
		PPP2R1A p.R182W, c.544C>T			
0.52	0.08	0.4	0.125		
LCR 728	LCR 728 PLS1	Normal	NA	7.5	1.82
		TP53 p.R174G, c.520A>G			
0.53	0.08	0.4	0.303		
LCR 729	LCR 729 PLS1	Normal	NA	7.5	1.61
		TP53 p.P153L, c.458C>T			
0.64	0.05	0.3	0.122		
LCR 730	LCR 730 PLS1	Normal	NA	7.5	2.75
		TP53 p.R273C, c.817C>T			
0.44	0.07	0.6	0.117		

Table3.txt

LCR 731	LCR 731 PLS1	Normal	NA	7.5	1.45
		TP53 p.S94P, c.280T>C			
0.60	0.06	0.3	0.294		
LCR 732	LCR 732 PLS1	Normal	NA	7.5	0.76
		TP53 p.T125T, c.375G>A (Exon End)			
0.31	0.04	0.1	0.125		
LCR 733	LCR 733 PLS1	Normal	NA	7.5	3.81
		TP53 p.R337H, c.1010G>A			
0.61	0.03	0.4	0.305		
LCR 734	LCR 734 PLS1	Normal	NA	7.5	3.43
		TP53 g.7577017A>G (Splice Site)			
0.74	0.03	0.4	0.377		
LCR 736	LCR 736 PLS1	Normal	NA	7.5	2.97
		TP53 p.L369P, c.1106T>C			
0.67	0.06	0.5	0.404		
LCR 737	LCR 737 PLS1	Normal	NA	7.5	2.65
		PPP2R1A p.P179L, c.536C>T			
0.68	0.07	0.5	0.863		
LCR 738	LCR 738 PLS1	Normal	NA	7.5	7.94
		TP53 p.D228E, c.684C>A			
0.69	0.04	1.0	0.591		
LCR 739	LCR 739 PLS1	Normal	NA	7.5	1.95
		TP53 p.P219S, c.655C>T			
0.00	0.09	0.6	0.390		
LCR 740	LCR 740 PLS1	Normal	NA	7.5	37.74
		TP53 p.P309S, c.925C>T			
0.46	0.06	7.4	0.411		
LCR 741	LCR 741 PLS1	Normal	NA	7.5	100.42
		TP53 p.V274A, c.821T>C			
0.60	0.05	14.3	0.374		
LCR 742	LCR 742 PLS1	Normal	NA	7.5	5.67
		GNAS p.R201H, c.602G>A			
0.30	0.02	0.4	0.860		
LCR 743	LCR 743 PLS1	Normal	NA	7.5	4.22
		TP53 p.E298K, c.892G>A			
0.48	0.03	0.4	0.603		
LCR 745	LCR 745 PLS1	Normal	NA	7.5	1.30
		PPP2R1A p.R183Q, c.548G>A			
0.00	0.05	0.2	0.680		
LCR 746	LCR 746 PLS1	Normal	NA	7.5	25.18
		TP53 p.R175H, c.524G>A			
0.77	0.06	5.0	0.553		
LCR 747	LCR 747 PLS1	Normal	NA	7.5	1.78
		TP53 p.A161T, c.481G>A			
0.76	0.04	0.2	0.327		
LCR 749	LCR 749 PLS1	Normal	NA	7.5	1.96
		TP53 p.R337H, c.1010G>A			
0.00	0.05	0.3	0.221		

Table3.txt

LCR 750	LCR 750 PLS1	Normal	NA	7.5	1.36
		APC p.R1450*, c.4348C>T			
0.00	0.06	0.2	0.851		
LCR 751	LCR 751 PLS1	Normal	NA	7.5	2.10
		TP53 p.R158H, c.473G>A			
0.74	0.06	0.4	0.125		
LCR 752	LCR 752 PLS1	Normal	NA	7.5	9.31
		TP53 p.G302W, c.904G>T			
0.91	0.01	0.3	0.855		
LCR 753	LCR 753 PLS1	Normal	NA	7.5	1.52
		TP53 p.D48N, c.142G>A			
0.66	0.06	0.3	0.193		
LCR 754	LCR 754 PLS1	Normal	NA	7.5	2.21
		TP53 p.T125M, c.374C>T			
0.80	0.03	0.2	0.121		
LCR 755	LCR 755 PLS1	Normal	NA	7.5	1.39
		TP53 p.R158H, c.473G>A			
0.00	0.08	0.3	0.125		
LCR 757	LCR 757 PLS1	Normal	NA	7.5	1.62
		TP53 p.T125M, c.374C>T			
0.40	0.21	1.0	0.387		
LCR 758	LCR 758 PLS1	Normal	NA	7.5	67.40
		TP53 p.R283H, c.848G>A			
0.49	0.06	12.9	0.473		
LCR 759	LCR 759 PLS1	Normal	NA	7.5	1.97
		TP53 p.R283H, c.848G>A			
0.48	0.06	0.4	0.736		
LCR 760	LCR 760 PLS1	Normal	NA	7.5	0.65
		TP53 p.L114M, c.340T>A			
0.00	0.08	0.1	0.401		
LCR 761	LCR 761 PLS1	Normal	NA	7.5	0.94
		TP53 p.E298K, c.892G>A			
0.45	0.08	0.2	0.117		
LCR 762	LCR 762 PLS1	Normal	NA	7.5	135.67
		TP53 p.V203M, c.607G>A			
0.82	0.02	7.1	0.117		
LCR 763	LCR 763 PLS1	Normal	NA	7	39.88
		TP53 p.S303N, c.908G>A			
0.95	0.05	5.9	0.121		
LCR 764	LCR 764 PLS1	Normal	NA	7.5	71.68
		TP53 p.P300fs, c.898delC			
0.85	0.03	7.4	0.184		
LCR 765	LCR 765 PLS1	Normal	NA	7.5	64.69
		TP53 p.R202C, c.604C>T			
1.26	0.09	17.3	0.339		
LCR 766	LCR 766 PLS1	Normal	NA	7.5	6.85
		TP53 p.R342*, c.1024C>T			
0.77	0.08	1.7	0.116		

Table3.txt

LCR 768	LCR 768 PLS1	Normal	NA	7.5	4.67	
		GNAS p.R201H, c.602G>A				
0.46	0.05	0.7	0.886			
LCR 769	LCR 769 PLS1	Normal	NA	7.5	4.49	
		TP53 p.R202C, c.604C>T				
0.95	0.06	0.9	0.338			
LCR 770	LCR 770 PLS1	Normal	NA	7.5	3.25	
		TP53 p.P152L, c.455C>T				
0.43	0.07	0.7	0.121			
LCR 771	LCR 771 PLS1	Normal	NA	7.5	100.85	
		KRAS p.D57N, c.169G>A				
0.40	0.03	8.7	0.388			
LCR 772	LCR 772 PLS1	Normal	NA	7.5	7.79	
		TP53 p.C176fs, c.528insC				
0.94	0.06	1.5	0.121			
LCR 773	LCR 773 PLS1	Normal	NA	7.5	5.23	
		FBXW7 p.R367*, c.1099C>T				
0.65	0.05	0.8	0.156			
LCR 774	LCR 774 PLS1	Normal	NA	7.5	7.43	
		TP53 p.R202C, c.604C>T				
0.75	0.03	0.7	0.600			
LCR 775	LCR 775 PLS1	Normal	NA	7.5	5.50	
		TP53 p.A307T, c.919G>A (Exon End)				
0.99	0.02	0.3	0.935			
LCR 776	LCR 776 PLS1	Normal	NA	7.5	2.82	
		TP53 p.K372fs, c.1114delA				
0.71	0.06	0.6	0.117			
LCR 777	LCR 777 PLS1	Normal	NA	7.5	4.78	
		TP53 p.A161T, c.481G>A				
0.65	0.05	0.7	0.511			
LCR 778	LCR 778 PLS1	Normal	NA	7.5	3.11	
		TP53 p.E336K, c.1006G>A				
0.56	0.04	0.3	0.209			
LCR 779	LCR 779 PLS1	Normal	NA	7.5	11.52	
		CTNNB1 p.S33P, c.97T>C				
0.97	0.01	0.3	0.721			
LCR 780	LCR 780 PLS1	Normal	NA	7.5	5.49	
		TP53 p.R202C, c.604C>T				
0.87	0.06	1.0	0.122			
LCR 781	LCR 781 PLS1	Normal	NA	7.5	3.34	
		TP53 p.E11K, c.31G>A				
0.44	0.11	1.1	0.125			
LCR 782	LCR 782 PLS1	Normal	NA	7.5	3.10	
		TP53 p.R248Q, c.743G>A				
0.44	0.13	1.2	0.220			
LCR 783	LCR 783 PLS1	Normal	NA	7.5	4.26	
		TP53 p.K373R, c.1118A>G				
1.06	0.05	0.7	0.703			

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LCR 784	LCR 784 PLS1	Normal	NA	7.5	4.30
		TP53 p.T118I, c.353C>T			
1.13	0.05	0.7	0.638		
LCR 785	LCR 785 PLS1	Normal	NA	7.5	6.71
		TP53 p.L369P, c.1106T>C			
0.89	0.05	1.0	0.827		
LCR 786	LCR 786 PLS1	Normal	NA	7.5	5.05
		TP53 p.E298K, c.892G>A			
0.65	0.02	0.3	0.333		
LCR 812	LCR 812 PLS1	Pancreas	II	7.5	31.37
		TP53 p.R249S, c.747G>T			
2.19	0.10	9.8	0.999		
LCR 814	LCR 814 PLS1	Pancreas	II	7.5	5.46
		TP53 p.K372fs, c.1114delA			
1.09	0.05	0.9	0.711		
NL 918	NL PLS 918	Normal	NA	7.5	3.67
		TP53 g.7577018C>T (Splice Site)			
0.00	0.03	0.3	0.117		
NL 919	NL PLS 919	Normal	NA	7.5	1.98
		TP53 p.R248Q, c.743G>A			
0.85	0.07	0.5	0.875		
NL 920	NL PLS 920	Normal	NA	7.5	2.89
		TP53 p.R333H, c.998G>A			
0.89	0.07	0.6	0.122		
NL 921	NL PLS 921	Normal	NA	7.5	0.88
		TP53 p.V157I, c.469G>A			
0.00	0.09	0.2	0.125		
NL 922	NL PLS 922	Normal	NA	7.5	3.69
		TP53 p.C242Y, c.725G>A			
0.55	0.03	0.3	0.116		
NL 923	NL PLS 923	Normal	NA	7.5	1.25
		TP53 p.R248Q, c.743G>A			
0.00	0.03	0.1	0.610		
NL 924	NL PLS 924	Normal	NA	7.5	0.87
		TP53 p.S313G, c.937A>G			
1.18	0.15	0.4	0.335		
NL 925	NL PLS 925	Normal	NA	7.5	3.08
		TP53 p.R181C, c.541C>T			
0.38	0.02	0.2	0.121		
NL 930	NL PLS 930	Normal	NA	7.5	2.79
		TP53 p.R175H, c.524G>A			
0.59	0.07	0.6	0.192		
NL 931	NL PLS 931	Normal	NA	7.5	6.06
		TP53 g.7576927C>T (Splice Site)			
1.00	0.01	0.2	0.300		
NL 932	NL PLS 932	Normal	NA	7.5	0.57
		CTNNB1 p.A43T, c.127G>A			
0.47	0.05	0.1	0.116		

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NL 938	NL PLS 938	Normal	NA	7.5	2.43
		KRAS p.G12A, c.35G>C			
0.42	0.03	0.2	0.117		
NL 939	NL PLS 939	Normal	NA	7.5	4.19
		TP53 p.K351R, c.1052A>G			
0.70	0.05	0.6	0.599		
NL 940	NL PLS 940	Normal	NA	7.5	2.27
		TP53 p.R379H, c.1136G>A			
0.54	0.05	0.4	0.117		
NL 941	NL PLS 941	Normal	NA	7.5	3.08
		TP53 p.P309S, c.925C>T			
0.85	0.09	0.9	0.116		
NL 942	NL PLS 942	Normal	NA	7.5	13.09
		TP53 p.R379P, c.1136G>C			
0.91	0.01	0.3	0.660		
NL 943	NL PLS 943	Normal	NA	7.5	2.60
		KRAS p.G60D, c.179G>A			
0.48	0.04	0.3	0.122		
NL 944	NL PLS 944	Normal	NA	7.5	1.99
		TP53 p.R282Q, c.845G>A			
0.83	0.09	0.5	0.341		
NL 945	NL PLS 945	Normal	NA	7.5	2.20
		CDKN2A p.E88D, c.264G>T			
0.70	0.02	0.1	0.843		
NL 946	NL PLS 946	Normal	NA	7.5	1.61
		TP53 p.R181C, c.541C>T			
0.53	0.13	0.7	0.382		
NL 947	NL PLS 947	Normal	NA	7.5	11.63
		TP53 p.A86T, c.256G>A			
0.90	0.02	0.7	0.558		
NL 948	NL PLS 948	Normal	NA	7.5	2.42
		TP53 p.W91G, c.271T>G			
0.00	0.05	0.3	0.125		
NL 949	NL PLS 949	Normal	NA	7.5	3.08
		TP53 p.V274G, c.821T>G			
0.83	0.04	0.4	0.117		
NL 950	NL PLS 950	Normal	NA	7.5	10.82
		TP53 p.P60L, c.179C>T			
1.15	0.02	0.8	0.320		
NL 951	NL PLS 951	Normal	NA	7.5	3.64
		TP53 p.R333H, c.998G>A			
0.67	0.06	0.7	0.116		
NL 952	NL PLS 952	Normal	NA	7.5	3.19
		TP53 p.G226D, c.677G>A			
0.67	0.05	0.5	0.230		
NL 964	NL PLS 964	Normal	NA	7.5	3.43
		TP53 p.P278R, c.833C>G			
0.92	0.06	0.7	0.125		

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NL 965	NL PLS 965	Normal	NA	7.5	3.49
		TP53 p.A161V, c.482C>T			
1.10	0.03	0.3	0.612		
NL 1160	NL PLSA 1160	Normal	NA	7.5	5.60
		TP53 p.L348S, c.1043T>C			
1.00	0.06	1.1	0.677		
NL 1163	NL PLSA 1163	Normal	NA	7.5	5.59
		TP53 p.A138T, c.412G>A			
0.73	0.03	0.6	0.125		
NL 1164	NL PLSA 1164	Normal	NA	7.5	6.27
		TP53 p.Q354H, c.1062G>T			
1.10	0.02	0.5	0.319		
NL 1165	NL PLSA 1165	Normal	NA	7.5	5.04
		TP53 p.L369M, c.1105C>A			
1.04	0.03	0.5	0.303		
NL 1166	NL PLSA 1166	Normal	NA	7.5	4.96
		TP53 p.K373N, c.1119G>T			
0.91	0.01	0.2	0.117		
NL 1167	NL PLSA 1167	Normal	NA	7.5	3.00
		TP53 p.G374fs, c.1120delG			
1.24	0.06	0.5	0.329		
NL 1168	NL PLSA 1168	Normal	NA	7.5	2.17
		PTEN p.D153N, c.457G>A			
0.60	0.03	0.2	0.121		
NL 1169	NL PLSA 1169	Normal	NA	7.5	3.98
		TP53 p.A276V, c.827C>T			
0.71	0.08	0.9	0.125		
NL 1170	NL PLSA 1170	Normal	NA	7.5	2.15
		TP53 p.C176fs, c.528insC			
0.68	0.07	0.4	0.125		
NL 1171	NL PLSA 1171	Normal	NA	7.5	2.66
		TP53 p.G374S, c.1120G>A			
0.87	0.04	0.3	0.122		
NL 1172	NL PLSA 1172	Normal	NA	7.5	6.58
		TP53 p.G374fs, c.1120delG			
1.26	0.05	1.0	0.334		
NL 1173	NL PLSA 1173	Normal	NA	7.5	5.93
		TP53 p.R174M, c.521G>T			
0.89	0.03	0.6	0.125		
NL 1174	NL PLSA 1174	Normal	NA	7.5	2.60
		TP53 p.A138T, c.412G>A			
0.48	0.04	0.3	0.122		
NL 1175	NL PLSA 1175	Normal	NA	7.5	4.11
		TP53 p.A161V, c.482C>T			
0.91	0.04	0.5	0.121		
NL 1176	NL PLSA 1176	Normal	NA	7.5	7.64
		PIK3CA p.E81K, c.241G>A			
0.95	0.02	0.5	0.125		

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NL 1177	NL PLSA 1177	Normal	NA	7.5	7.08
	TP53 p.G374fs, c.1120insG				
1.29	0.02	0.4	0.338		
NL 1178	NL PLSA 1178	Normal	NA	7.5	2.18
	TP53 p.K372fs, c.1114delA				
0.66	0.03	0.2	0.123		
NL 1179	NL PLSA 1179	Normal	NA	7.5	1.86
	TP53 p.R283H, c.848G>A				
1.07	0.10	0.6	0.316		
NL 1180	NL PLSA 1180	Normal	NA	7.5	3.46
	TP53 p.K372fs, c.1114delA				
0.80	0.03	0.4	0.121		
NL 1181	NL PLSA 1181	Normal	NA	7.5	1.80
	TP53 p.R202C, c.604C>T				
1.06	0.17	1.0	0.633		
NL 1182	NL PLSA 1182	Normal	NA	7.5	4.79
	PPP2R1A p.A184V, c.551C>T				
1.16	0.06	0.9	0.322		
NL 1183	NL PLSA 1183	Normal	NA	7.5	3.63
	TP53 p.P36S, c.106C>T				
1.02	0.07	0.8	0.297		
NL 1184	NL PLSA 1184	Normal	NA	7.5	4.58
	CTNNB1 p.G34R, c.100G>C				
0.80	0.01	0.1	0.357		
NL 1185	NL PLSA 1185	Normal	NA	7.5	2.85
	TP53 p.K373E, c.1117A>G				
0.58	0.01	0.1	0.125		
NL 1186	NL PLSA 1186	Normal	NA	7.5	3.38
	TP53 p.R306*, c.916C>T				
0.70	0.02	0.2	0.117		
NL 1187	NL PLSA 1187	Normal	NA	7.5	1.63
	TP53 p.K372fs, c.1114delA				
0.62	0.04	0.2	0.117		
NL 1188	NL PLSA 1188	Normal	NA	7.5	1.61
	FBXW7 p.R505H, c.1514G>A				
0.67	0.06	0.3	0.316		
NL 1189	NL PLSA 1189	Normal	NA	7.5	3.02
	TP53 p.R273H, c.818G>A				
0.94	0.09	0.9	0.317		
NL 1190	NL PLSA 1190	Normal	NA	7.5	6.88
	TP53 p.R379H, c.1136G>A				
0.68	0.04	0.8	0.121		
NL 1191	NL PLSA 1191	Normal	NA	7.5	5.24
	GNAS p.R201H, c.602G>A				
1.16	0.06	1.0	0.320		
NL 1192	NL PLSA 1192	Normal	NA	7.5	5.67
	TP53 p.E336G, c.1007A>G				
0.75	0.01	0.2	0.125		

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NL 1193	NL PLSA 1193	Normal	NA	7.5	6.97
		TP53 p.R267W, c.799C>T			
0.96	0.05	1.0	0.125		
NL 1194	NL PLSA 1194	Normal	NA	7.5	3.12
		TP53 p.E298K, c.892G>A			
0.65	0.10	0.9	0.334		
NL 1195	NL PLSA 1195	Normal	NA	7.5	7.64
		TP53 p.A84T, c.250G>A			
0.93	0.02	0.4	0.311		
NL 1196	NL PLSA 1196	Normal	NA	7.5	6.18
		CDKN2A p.S56N, c.167G>A			
1.06	0.02	0.5	0.309		
NL 1197	NL PLSA 1197	Normal	NA	7.5	4.67
		TP53 p.K372fs, c.1114delA			
1.07	0.05	0.7	0.489		
NL 1198	NL PLSA 1198	Normal	NA	7.5	2.74
		TP53 p.P89L, c.266C>T			
0.52	0.03	0.3	0.125		
NL 1199	NL PLSA 1199	Normal	NA	7.5	5.06
		TP53 p.A86T, c.256G>A			
0.66	0.03	0.4	0.125		
NL 1200	NL PLSA 1200	Normal	NA	7.5	2.12
		GNAS p.R201H, c.602G>A			
1.09	0.15	1.0	0.316		
NL 1201	NL PLSA 1201	Normal	NA	7.5	2.12
		TP53 p.A129T, c.385G>A			
0.61	0.05	0.3	0.125		
NL 1202	NL PLSA 1202	Normal	NA	7.5	3.17
		TP53 g.7576928T>C (Splice Site)			
0.53	0.03	0.3	0.117		
NL 1203	NL PLSA 1203	Normal	NA	7.5	6.06
		TP53 p.F341S, c.1022T>C			
1.18	0.02	0.4	0.322		
NL 1204	NL PLSA 1204	Normal	NA	7.5	8.29
		KRAS p.G13D, c.38G>A			
0.88	0.02	0.6	0.125		
NL 1205	NL PLSA 1205	Normal	NA	7.5	1.48
		TP53 p.K373R, c.1118A>G			
0.85	0.08	0.4	0.125		
NL 1206	NL PLSA 1206	Normal	NA	7.5	9.14
		TP53 p.R273H, c.818G>A			
1.17	0.15	4.1	0.323		
NL 1207	NL PLSA 1207	Normal	NA	7.5	0.13
		None detected			
NA	NA	NA	0.125		
NL 1208	NL PLSA 1208	Normal	NA	7.5	3.99
		TP53 p.A189T, c.565G>A			
0.82	0.02	0.3	0.125		

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NL 1209	NL PLSA 1209	Normal	NA	7.5	7.98
		TP53 p.R202C, c.604C>T			
1.05	0.05	1.1	0.302		
NL 1210	NL PLSA 1210	Normal	NA	7.5	3.60
		TP53 p.R337H, c.1010G>A			
0.40	0.03	0.3	0.123		
NL 1211	NL PLSA 1211	Normal	NA	7.5	3.60
		TP53 p.I254F, c.760A>T			
1.06	0.08	0.9	0.310		
NL 1212	NL PLSA 1212	Normal	NA	7.5	3.21
		TP53 p.R342*, c.1024C>T			
0.95	0.08	0.8	0.121		
NL 1213	NL PLSA 1213	Normal	NA	7.5	5.61
		PPP2R1A p.R183W, c.547C>T			
0.76	0.03	0.4	0.122		
NL 1214	NL PLSA 1214	Normal	NA	7.5	2.82
		TP53 p.R283C, c.847C>T			
0.65	0.04	0.4	0.121		
NL 1215	NL PLSA 1215	Normal	NA	7.5	1.75
		TP53 p.R273H, c.818G>A			
0.78	0.08	0.4	0.122		
NL 1216	NL PLSA 1216	Normal	NA	7.5	3.06
		TP53 p.P36S, c.106C>T			
0.31	0.05	0.5	0.565		
NL 1217	NL PLSA 1217	Normal	NA	7.5	1.42
		TP53 p.R175L, c.524G>T			
0.00	0.09	0.4	0.121		
NL 1218	NL PLSA 1218	Normal	NA	7.5	6.73
		GNAS p.R201C, c.601C>T			
1.18	0.05	1.0	0.320		
NL 1219	NL PLSA 1219	Normal	NA	7.5	9.54
		TP53 p.S260T, c.778T>A			
0.89	0.01	0.3	0.117		
NL 1220	NL PLSA 1220	Normal	NA	7.5	4.83
		TP53 p.P309S, c.925C>T			
0.73	0.04	0.6	0.117		
NL 1221	NL PLSA 1221	Normal	NA	7.5	3.08
		CDKN2A p.H83Y, c.247C>T			
0.00	0.04	0.3	0.125		
NL 1222	NL PLSA 1222	Normal	NA	7.5	3.49
		TP53 p.L369P, c.1106T>C			
0.71	0.06	0.6	0.121		
NL 1223	NL PLSA 1223	Normal	NA	7.5	3.21
		TP53 p.R335H, c.1004G>A			
0.68	0.07	0.7	0.121		
NL 1224	NL PLSA 1224	Normal	NA	7.5	6.25
		PTEN p.F154fs, c.461delT			
0.80	0.03	0.5	0.116		

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NL 1225	NL PLSA 1225	Normal	NA	7.5	5.68
		TP53 p.R174G, c.520A>G			
0.68	0.04	0.7	0.123		
NL 1226	NL PLSA 1226	Normal	NA	7.5	2.18
		TP53 p.K372fs, c.1114delA			
0.89	0.05	0.4	0.117		
NL 1227	NL PLSA 1227	Normal	NA	7.5	4.17
		TP53 p.Q192H, c.576G>C			
0.75	0.01	0.2	0.125		
NL 1228	NL PLSA 1228	Normal	NA	7.5	1.53
		TP53 p.A159T, c.475G>A			
0.43	0.09	0.4	0.117		
NL 1229	NL PLSA 1229	Normal	NA	7.5	4.69
		PPP2R1A p.R183Q, c.548G>A			
0.89	0.06	0.8	0.125		
NL 1230	NL PLSA 1230	Normal	NA	7.5	1.63
		TP53 p.R202C, c.604C>T			
0.81	0.10	0.5	0.125		
NL 1231	NL PLSA 1231	Normal	NA	7.5	5.06
		TP53 p.K372fs, c.1114delA			
0.86	0.05	0.7	0.121		
NL 1232	NL PLSA 1232	Normal	NA	7.5	5.50
		TP53 p.L93P, c.278T>C			
0.83	0.03	0.5	0.117		
NL 1233	NL PLSA 1233	Normal	NA	7.5	3.84
		TP53 p.R202C, c.604C>T			
1.37	0.11	1.3	0.355		
NL 1234	NL PLSA 1234	Normal	NA	7.5	5.01
		TP53 p.K372fs, c.1114delA			
0.91	0.05	0.7	0.121		
NL 1235	NL PLSA 1235	Normal	NA	7.5	3.19
		TP53 p.P222L, c.665C>T			
0.87	0.15	1.4	0.575		
NL 1236	NL PLSA 1236	Normal	NA	7.5	5.35
		TP53 p.L369P, c.1106T>C			
0.68	0.03	0.5	0.122		
NL 1237	NL PLSA 1237	Normal	NA	7.5	11.50
		TP53 p.G374fs, c.1120delG			
0.78	0.02	0.8	0.121		
NL 1238	NL PLSA 1238	Normal	NA	7.5	7.90
		HRAS p.G12C, c.34G>T			
1.16	0.01	0.2	0.320		
NL 1239	NL PLSA 1239	Normal	NA	7.5	3.06
		TP53 p.A353V, c.1058C>T			
0.54	0.06	0.6	0.121		
NL 1240	NL PLSA 1240	Normal	NA	7.5	5.08
		TP53 p.A189V, c.566C>T			
0.93	0.04	0.6	0.258		

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NL 1241	NL PLSA 1241	Normal	NA	7.5	7.23
		TP53 p.Y236C, c.707A>G			
1.16	0.03	0.7	0.532		
NL 1242	NL PLSA 1242	Normal	NA	7.5	5.15
		KRAS p.V14I, c.40G>A			
0.57	0.03	0.4	0.123		
NL 1243	NL PLSA 1243	Normal	NA	7.5	5.93
		PPP2R1A p.A184V, c.551C>T			
0.62	0.04	0.6	0.121		
NL 1244	NL PLSA 1244	Normal	NA	7.5	9.27
		TP53 p.P85T, c.253C>A			
1.16	0.02	0.5	0.321		
NL 1245	NL PLSA 1245	Normal	NA	7.5	11.82
		TP53 p.A276V, c.827C>T			
1.05	0.03	1.0	0.309		
NL 1246	NL PLSA 1246	Normal	NA	7.5	6.82
		TP53 p.A138T, c.412G>A			
0.85	0.03	0.5	0.123		
NL 1247	NL PLSA 1247	Normal	NA	7.5	5.34
		TP53 p.R306Q, c.917G>A			
1.39	0.08	1.3	0.727		
NL 1248	NL PLSA 1248	Normal	NA	7.5	6.67
		TP53 p.A353V, c.1058C>T			
0.91	0.04	0.9	0.121		
NL 1249	NL PLSA 1249	Normal	NA	7.5	3.68
		TP53 p.R290C, c.868C>T			
0.29	0.03	0.3	0.123		
NL 1250	NL PLSA 1250	Normal	NA	7.5	4.29
		TP53 p.T125M, c.374C>T			
0.76	0.07	1.0	0.248		
NL 1251	NL PLSA 1251	Normal	NA	7.5	1.46
		TP53 p.R335H, c.1004G>A			
0.79	0.07	0.3	0.121		
NL 1252	NL PLSA 1252	Normal	NA	7.5	0.85
		TP53 p.S260fs, c.778insT			
0.00	0.09	0.2	0.374		
NL 1253	NL PLSA 1253	Normal	NA	7.5	1.16
		KRAS p.G13D, c.38G>A			
0.45	0.06	0.2	0.121		
NL 1254	NL PLSA 1254	Normal	NA	7.5	1.68
		TP53 p.R273H, c.818G>A			
0.96	0.27	1.4	0.584		
NL 1255	NL PLSA 1255	Normal	NA	7.5	1.06
		TP53 p.R273H, c.818G>A			
0.90	0.61	2.0	0.297		
NL 1256	NL PLSA 1256	Normal	NA	7.5	3.88
		TP53 p.R273H, c.818G>A			
0.89	0.09	1.0	0.117		

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NL 1257	NL PLSA 1257	Normal	NA	7.5	1.85	
		TP53 p.G262D, c.785G>A				
0.62	0.08	0.4	0.341			
NL 1258	NL PLSA 1258	Normal	NA	7.5	1.21	
		TP53 p.R273H, c.818G>A				
1.11	0.53	2.0	0.324			
NL 1259	NL PLSA 1259	Normal	NA	7.5	1.62	
		TP53 p.R290C, c.868C>T				
0.00	0.04	0.2	0.604			
NL 1260	NL PLSA 1260	Normal	NA	7.5	0.03	
		None detected				
NA	NA	NA	0.116			
NL 1291	NL PLSA 1291	Normal	NA	7.5	5.28	
		TP53 p.E298K, c.892G>A				
0.61	0.03	0.4	0.117			
NL 1292	NL PLSA 1292	Normal	NA	7.5	2.31	
		TP53 p.R273H, c.818G>A				
1.45	0.27	1.9	0.376			
NL 1293	NL PLSA 1293	Normal	NA	7.5	2.12	
		TP53 p.S260fs, c.779insC				
1.16	0.06	0.4	0.514			
NL 1294	NL PLSA 1294	Normal	NA	7.5	1.27	
		TP53 p.R273H, c.818G>A				
1.73	0.47	1.8	0.416			
NL 1295	NL PLSA 1295	Normal	NA	7.5	2.70	
		TP53 p.R337C, c.1009C>T				
0.37	0.03	0.2	0.117			
NL 1296	NL PLSA 1296	Normal	NA	7.5	4.08	
		FBXW7 p.R465H, c.1394G>A				
0.31	0.04	0.5	0.116			
NL 1297	NL PLSA 1297	Normal	NA	7.5	3.27	
		TP53 p.K372fs, c.1114delA				
0.86	0.04	0.4	0.117			
NL 1298	NL PLSA 1298	Normal	NA	7.5	2.88	
		TP53 p.L93P, c.278T>C				
0.92	0.05	0.5	0.122			
NL 1299	NL PLSA 1299	Normal	NA	7.5	4.87	
		TP53 p.F134V, c.400T>G				
0.93	0.02	0.3	0.125			
NL 1300	NL PLSA 1300	Normal	NA	7.5	4.81	
		TP53 p.C176fs, c.528insC				
0.36	0.03	0.5	0.242			
NL 1301	NL PLSA 1301	Normal	NA	7.5	1.98	
		TP53 p.R175C, c.523C>T				
0.47	0.12	0.7	0.573			
NL 1302	NL PLSA 1302	Normal	NA	7.5	8.45	
		FBXW7 p.R505L, c.1514G>T				
1.18	0.04	1.0	0.833			

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NL 1303	NL PLSA 1303	Normal	NA	7.5	23.63	TP53 p.L348S, c.1043T>C
0.98	0.02	1.6	0.122			
NL 1304	NL PLSA 1304	Normal	NA	7.5	13.29	TP53 p.K372fs, c.1114delA
0.96	0.06	2.4	0.117			
NL 1305	NL PLSA 1305	Normal	NA	7.5	6.96	TP53 p.A189V, c.566C>T
0.72	0.02	0.4	0.192			
NL 1306	NL PLSA 1306	Normal	NA	7.5	3.66	TP53 p.G279R, c.835G>C
1.78	0.10	1.2	0.409			
NL 1307	NL PLSA 1307	Normal	NA	7.5	2.63	TP53 p.E287D, c.861G>T
0.47	0.03	0.3	0.125			
NL 1308	NL PLSA 1308	Normal	NA	7.5	8.50	TP53 p.F134L, c.400T>C
0.77	0.01	0.3	0.121			
NL 1309	NL PLSA 1309	Normal	NA	7.5	5.78	TP53 p.R342*, c.1024C>T
0.57	0.02	0.3	0.125			
NL 1310	NL PLSA 1310	Normal	NA	7.5	0.12	None detected
NA	NA	NA	0.414			
NL 1311	NL PLSA 1311	Normal	NA	7.5	0.39	TP53 p.M133I, c.399G>T
0.00	0.12	0.1	0.553			
NL 1312	NL PLSA 1312	Normal	NA	7.5	0.33	TP53 p.E11K, c.31G>A
0.00	0.10	0.1	0.121			
NL 1313	NL PLSA 1313	Normal	NA	7.5	0.80	TP53 p.P301T, c.901C>A
0.00	0.08	0.2	0.117			
NL 1314	NL PLSA 1314	Normal	NA	7.5	3.34	TP53 p.A353V, c.1058C>T
0.62	0.06	0.6	0.125			
NL 1315	NL PLSA 1315	Normal	NA	7.5	3.83	TP53 p.R273H, c.818G>A
0.66	0.09	1.0	0.576			
NL 1316	NL PLSA 1316	Normal	NA	7.5	26.99	TP53 p.A353V, c.1058C>T
0.97	0.03	2.1	0.117			
NL 1317	NL PLSA 1317	Normal	NA	7.5	6.83	TP53 p.K372fs, c.1114insA
0.63	0.02	0.4	0.362			
NL 1318	NL PLSA 1318	Normal	NA	7.5	2.49	TP53 p.R273H, c.818G>A
0.70	0.12	0.9	0.121			

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NL 1319	NL PLSA 1319	Normal	NA	7.5	5.24
		GNAS p.R201H, c.602G>A			
0.83	0.05	0.8	0.116		
NL 1320	NL PLSA 1320	Normal	NA	7.5	4.61
		TP53 p.R306*, c.916C>T			
0.81	0.05	0.7	0.125		
NL 1321	NL PLSA 1321	Normal	NA	7.5	1.52
		TP53 p.P177H, c.530C>A			
0.58	0.08	0.4	0.121		
NL 1322	NL PLSA 1322	Normal	NA	7.5	2.85
		TP53 p.Y234C, c.701A>G			
0.57	0.07	0.6	0.125		
NL 1323	NL PLSA 1323	Normal	NA	7.5	0.09
		None detected			
NA	NA	NA	0.121		
NL 1324	NL PLSA 1324	Normal	NA	7.5	0.02
		None detected			
NA	NA	NA	0.123		
NL 1325	NL PLSA 1325	Normal	NA	7.5	0.08
		None detected			
NA	NA	NA	0.331		
NL 1326	NL PLSA 1326	Normal	NA	7.5	6.36
		EGFR p.E868G, c.2603A>G			
1.37	0.09	1.8	0.356		
NL 1327	NL PLSA 1327	Normal	NA	7.5	0.08
		None detected			
NA	NA	NA	0.122		
NL 1328	NL PLSA 1328	Normal	NA	7.5	2.14
		TP53 p.K372fs, c.1114delA			
0.78	0.05	0.3	0.125		
NL 1329	NL PLSA 1329	Normal	NA	7.5	1.05
		TP53 p.E339G, c.1016A>G			
0.78	0.03	0.1	0.125		
NL 1330	NL PLSA 1330	Normal	NA	7.5	1.62
		TP53 p.R273H, c.818G>A			
0.97	0.18	0.9	0.121		
NL 1331	NL PLSA 1331	Normal	NA	7.5	1.04
		TP53 p.A138T, c.412G>A			
0.68	0.06	0.2	0.122		
NL 1332	NL PLSA 1332	Normal	NA	7.5	2.01
		TP53 p.L264P, c.791T>C			
0.91	0.03	0.2	0.117		
NL 1333	NL PLSA 1333	Normal	NA	7.5	3.52
		TP53 p.A161V, c.482C>T			
0.85	0.03	0.3	0.123		
NL 1334	NL PLSA 1334	Normal	NA	7.5	3.12
		TP53 p.G154S, c.460G>A			
1.16	0.04	0.4	0.489		

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NL 1335	NL PLSA 1335	Normal	NA	7.5	2.00
		TP53 p.R306*, c.916C>T			
1.15	0.08	0.5	0.849		
NL 1336	NL PLSA 1336	Normal	NA	7.5	1.44
		TP53 p.A138T, c.412G>A			
1.22	0.07	0.3	0.325		
NL 1337	NL PLSA 1337	Normal	NA	7.5	2.29
		TP53 p.Q375*, c.1123C>T			
0.90	0.02	0.1	0.122		
NL 1338	NL PLSA 1338	Normal	NA	7.5	2.59
		TP53 p.M384V, c.1150A>G			
0.91	0.03	0.3	0.188		
NL 1339	NL PLSA 1339	Normal	NA	7.5	2.72
		CDKN2A p.V82M, c.244G>A			
0.77	0.03	0.2	0.117		
NL 1340	NL PLSA 1340	Normal	NA	7.5	3.30
		TP53 p.P250S, c.748C>T			
0.77	0.02	0.2	0.125		
NL 1341	NL PLSA 1341	Normal	NA	7.5	2.13
		TP53 p.R202C, c.604C>T			
0.88	0.06	0.4	0.125		
NL 1342	NL PLSA 1342	Normal	NA	7.5	1.86
		TP53 p.R273H, c.818G>A			
0.99	0.09	0.5	0.205		
NL 1343	NL PLSA 1343	Normal	NA	7.5	1.22
		TP53 p.R273H, c.818G>A			
0.65	0.10	0.4	0.122		
NL 1344	NL PLSA 1344	Normal	NA	7.5	1.63
		TP53 g.7577156C>G (Splice Site)			
0.77	0.01	0.1	0.125		
NL 1345	NL PLSA 1345	Normal	NA	7.5	0.75
		TP53 p.G108S, c.322G>A			
0.57	0.15	0.4	0.125		
NL 1346	NL PLSA 1346	Normal	NA	7.5	1.31
		TP53 p.K373R, c.1118A>G			
0.74	0.03	0.1	0.346		
NL 1347	NL PLSA 1347	Normal	NA	7.5	2.67
		TP53 p.A189V, c.566C>T			
0.85	0.02	0.2	0.343		
NL 1348	NL PLSA 1348	Normal	NA	7.5	1.94
		TP53 p.E336G, c.1007A>G			
0.82	0.02	0.1	0.125		
NL 1349	NL PLSA 1349	Normal	NA	7.5	4.77
		TP53 p.R202C, c.604C>T			
0.82	0.04	0.5	0.117		
NL 1350	NL PLSA 1350	Normal	NA	7.5	2.11
		TP53 p.L369P, c.1106T>C			
0.77	0.03	0.2	0.397		

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NL 1351	NL PLSA 1351	Normal	NA	7.5	1.86
		TP53 p.E258D, c.774A>T			
1.10	0.05	0.3	0.317		
NL 1352	NL PLSA 1352	Normal	NA	7.5	1.12
		TP53 p.K373R, c.1118A>G			
0.83	0.03	0.1	0.125		
NL 1353	NL PLSA 1353	Normal	NA	7.5	3.05
		TP53 p.L130P, c.389T>C			
1.09	0.02	0.2	0.593		
NL 1354	NL PLSA 1354	Normal	NA	7.5	7.82
		TP53 p.P300T, c.898C>A			
1.04	0.00	0.1	0.299		
NL 1355	NL PLSA 1355	Normal	NA	7.5	1.15
		TP53 g.7576928T>C (Splice Site)			
0.87	0.04	0.1	0.116		
NL 1356	NL PLSA 1356	Normal	NA	7.5	2.61
		EGFR p.A864T, c.2590G>A			
1.15	0.02	0.1	0.327		
NL 1357	NL PLSA 1357	Normal	NA	7.5	1.41
		TP53 p.L369P, c.1106T>C			
0.88	0.08	0.3	0.121		
NL 1358	NL PLSA 1358	Normal	NA	7.5	1.83
		TP53 p.A138T, c.412G>A			
1.14	0.05	0.3	0.553		
NL 1359	NL PLSA 1359	Normal	NA	7.5	0.72
		TP53 p.R283C, c.847C>T			
0.38	0.05	0.1	0.570		
NL 1360	NL PLSA 1360	Normal	NA	7.5	0.89
		TP53 p.R283H, c.848G>A			
0.74	0.07	0.2	0.125		
NL 1361	NL PLSA 1361	Normal	NA	7.5	1.59
		TP53 p.D281G, c.842A>G			
0.70	0.05	0.3	0.123		
NL 1362	NL PLSA 1362	Normal	NA	7.5	0.47
		TP53 p.R333H, c.998G>A			
0.29	0.06	0.1	0.122		
NL 1363	NL PLSA 1363	Normal	NA	7.5	0.83
		TP53 p.E346G, c.1037A>G			
0.39	0.05	0.1	0.125		
NL 1364	NL PLSA 1364	Normal	NA	7.5	1.82
		TP53 p.S261S, c.783T>C (Exon Start)			
1.10	0.03	0.2	0.441		
NL 1365	NL PLSA 1365	Normal	NA	7.5	1.58
		TP53 p.K370E, c.1108A>G			
1.17	0.03	0.1	0.325		
NL 1366	NL PLSA 1366	Normal	NA	7.5	1.98
		TP53 p.R335C, c.1003C>T			
0.65	0.03	0.2	0.125		

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NL 1367	NL PLSA 1367	Normal	NA	7.5	1.81	1.47
	TP53 p.A138V, c.413C>T					
0.04	0.2	0.383				
NL 1368	NL PLSA 1368	Normal	NA	7.5	3.16	0.95
	TP53 p.P36S, c.106C>T					
0.06	0.6	0.121				
NL 1369	NL PLSA 1369	Normal	NA	7.5	3.21	1.00
	FBXW7 p.R505H, c.1514G>A					
0.03	0.3	0.618				
NL 1370	NL PLSA 1370	Normal	NA	7.5	1.65	1.03
	TP53 p.R273H, c.818G>A					
0.11	0.6	0.304				
NL 1371	NL PLSA 1371	Normal	NA	7.5	1.20	0.58
	TP53 p.R283H, c.848G>A					
0.03	0.1	0.116				
NL 1372	NL PLSA 1372	Normal	NA	7.5	1.19	0.66
	KRAS p.A11V, c.32C>T					
0.05	0.2	0.125				
NL 1373	NL PLSA 1373	Normal	NA	7.5	7.04	1.10
	TP53 p.L194P, c.581T>C					
0.01	0.1	0.311				
NL 1374	NL PLSA 1374	Normal	NA	7.5	1.77	0.79
	TP53 p.R337C, c.1009C>T					
0.05	0.3	0.117				
NL 1375	NL PLSA 1375	Normal	NA	7.5	1.51	0.50
	TP53 p.C135Y, c.404G>A					
0.02	0.1	0.117				
NL 1376	NL PLSA 1376	Normal	NA	7.5	1.53	0.79
	TP53 p.A161T, c.481G>A					
0.04	0.2	0.121				
NL 1377	NL PLSA 1377	Normal	NA	7.5	2.06	1.14
	TP53 p.R202C, c.604C>T					
0.06	0.3	0.319				
NL 1378	NL PLSA 1378	Normal	NA	7.5	5.39	0.99
	FBXW7 p.R465C, c.1393C>T					
0.07	1.2	0.122				
NL 1379	NL PLSA 1379	Normal	NA	7.5	1.79	0.84
	KRAS p.A146T, c.436G>A					
0.02	0.1	0.125				
NL 1380	NL PLSA 1380	Normal	NA	7.5	1.80	0.69
	TP53 p.A159T, c.475G>A					
0.06	0.3	0.125				
NL 1381	NL PLSA 1381	Normal	NA	7.5	1.94	0.59
	TP53 p.A159T, c.475G>A					
0.04	0.2	0.123				
NL 1382	NL PLSA 1382	Normal	NA	7.5	2.05	1.05
	TP53 p.P36S, c.106C>T					
0.04	0.3	0.305				

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NL 1383	NL PLSA 1383	Normal	NA	7.5	1.85
		TP53 p.A86T, c.256G>A			
0.65	0.02	0.1	0.337		
NL 1384	NL PLSA 1384	Normal	NA	7.5	1.93
		FBXW7 p.E369*, c.1105G>T			
1.01	0.02	0.1	0.301		
NL 1385	NL PLSA 1385	Normal	NA	7.5	1.36
		TP53 p.A189V, c.566C>T			
0.57	0.03	0.1	0.366		
NL 1386	NL PLSA 1386	Normal	NA	7.5	1.73
		TP53 p.R202C, c.604C>T			
0.97	0.09	0.5	0.122		
NL 1387	NL PLSA 1387	Normal	NA	7.5	3.35
		TP53 p.A189fs, c.566delC			
1.17	0.01	0.1	0.489		
NL 1388	NL PLSA 1388	Normal	NA	7.5	1.66
		TP53 p.R202C, c.604C>T			
1.06	0.06	0.3	0.303		
NL 1389	NL PLSA 1389	Normal	NA	7.5	1.41
		TP53 p.R209fs, c.627delA			
1.56	0.08	0.3	0.388		
NL 1390	NL PLSA 1390	Normal	NA	7.5	4.87
		EGFR p.L858R, c.2573T>G			
1.66	0.06	0.9	0.403		
NL 1391	NL PLSA 1391	Normal	NA	7.5	1.25
		TP53 p.G244D, c.731G>A			
0.83	0.04	0.1	0.590		
NL 1392	NL PLSA 1392	Normal	NA	7.5	1.50
		TP53 p.A138T, c.412G>A			
0.60	0.03	0.2	0.123		
NL 1393	NL PLSA 1393	Normal	NA	7.5	5.66
		TP53 p.A276V, c.827C>T			
0.95	0.04	0.7	0.481		
NL 1394	NL PLSA 1394	Normal	NA	7.5	1.38
		TP53 p.P60L, c.179C>T			
0.65	0.03	0.1	0.191		
NL 1395	NL PLSA 1395	Normal	NA	7.5	0.58
		TP53 p.T125M, c.374C>T			
0.55	0.13	0.2	0.117		
NL 1396	NL PLSA 1396	Normal	NA	7.5	1.06
		HRAS p.G13D, c.38G>A			
0.68	0.03	0.1	0.117		
NL 1397	NL PLSA 1397	Normal	NA	7.5	2.60
		TP53 p.L369P, c.1106T>C			
1.09	0.05	0.4	0.320		
NL 1398	NL PLSA 1398	Normal	NA	7.5	2.79
		TP53 p.R202C, c.604C>T			
0.81	0.03	0.3	0.123		

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NL 1399	NL PLSA 1399	Normal	NA	7.5	3.11
		TP53 p.A189V, c.566C>T			
0.75	0.03	0.3	0.121		
NL 1400	NL PLSA 1400	Normal	NA	7.5	3.46
		TP53 p.A138T, c.412G>A			
0.86	0.05	0.5	0.307		
NL 1401	NL PLSA 1401	Normal	NA	7.5	6.61
		TP53 p.R248Q, c.743G>A			
0.61	0.03	0.5	0.116		
NL 1402	NL PLSA 1402	Normal	NA	7.5	1.98
		TP53 p.G245S, c.733G>A			
0.61	0.05	0.3	0.125		
NL 1403	NL PLSA 1403	Normal	NA	7.5	6.82
		TP53 p.K372fs, c.1114delA			
1.07	0.05	1.0	0.311		
NL 1404	NL PLSA 1404	Normal	NA	7.5	3.03
		TP53 p.L369P, c.1106T>C			
0.55	0.05	0.4	0.125		
NL 1405	NL PLSA 1405	Normal	NA	7.5	4.49
		TP53 p.R342Q, c.1025G>A			
0.57	0.02	0.3	0.123		
NL 1406	NL PLSA 1406	Normal	NA	7.5	6.08
		TP53 p.V10I, c.28G>A			
1.12	0.04	0.7	0.841		
NL 1407	NL PLSA 1407	Normal	NA	7.5	2.94
		BRAF p.T599I, c.1796C>T			
0.89	0.05	0.5	0.125		
NL 1408	NL PLSA 1408	Normal	NA	7.5	3.29
		TP53 p.R181H, c.542G>A			
0.34	0.06	0.6	0.125		
NL 1409	NL PLSA 1409	Normal	NA	7.5	4.96
		TP53 p.R306Q, c.917G>A			
0.73	0.06	1.0	0.390		
NL 1410	NL PLSA 1410	Normal	NA	7.5	1.49
		TP53 p.R290H, c.869G>A			
0.00	0.04	0.2	0.219		
NL 1411	NL PLSA 1411	Normal	NA	7.5	3.13
		TP53 p.R282W, c.844C>T			
0.36	0.05	0.5	0.116		
NL 1412	NL PLSA 1412	Normal	NA	7.5	6.22
		TP53 p.V217M, c.649G>A			
0.60	0.02	0.4	0.299		
NL 1413	NL PLSA 1413	Normal	NA	7.5	11.01
		TP53 p.A86T, c.256G>A			
0.81	0.02	0.7	0.123		
NL 1414	NL PLSA 1414	Normal	NA	7.5	3.18
		TP53 p.R335C, c.1003C>T			
1.31	0.07	0.7	0.345		

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NL 1425	NL PLSA 1425	Normal	NA	7.5	1.28
		TP53 p.L348M, c.1042T>A			
0.65	0.04	0.2	0.121		
NL 1426	NL PLSA 1426	Normal	NA	7.5	1.48
		TP53 p.R335H, c.1004G>A			
0.58	0.02	0.1	0.123		
NL 1427	NL PLSA 1427	Normal	NA	7.5	1.81
		FBXW7 p.R505C, c.1513C>T			
0.85	0.03	0.1	0.125		
NL 1428	NL PLSA 1428	Normal	NA	7.5	2.08
		TP53 p.P300fs, c.898delC			
0.63	0.04	0.2	0.553		
NL 1429	NL PLSA 1429	Normal	NA	7.5	1.05
		KRAS p.V14I, c.40G>A			
0.61	0.05	0.2	0.121		
NL 1430	NL PLSA 1430	Normal	NA	7.5	2.09
		TP53 p.R110C, c.328C>T			
1.07	0.05	0.3	0.307		
NL 1431	NL PLSA 1431	Normal	NA	7.5	3.13
		TP53 g.7577018C>T (Splice Site)			
0.91	0.02	0.2	0.219		
NL 1432	NL PLSA 1432	Normal	NA	7.5	2.16
		GNAS p.R201H, c.602G>A			
0.83	0.04	0.3	0.122		
NL 1433	NL PLSA 1433	Normal	NA	7.5	2.31
		TP53 p.R158H, c.473G>A			
0.61	0.05	0.4	0.125		
NL 1434	NL PLSA 1434	Normal	NA	7.5	3.00
		TP53 p.G244A, c.731G>C			
0.99	0.01	0.1	0.125		
NL 1435	NL PLSA 1435	Normal	NA	7.5	2.82
		TP53 p.R283H, c.848G>A			
0.68	0.02	0.1	0.125		
NL 1436	NL PLSA 1436	Normal	NA	7.5	0.93
		TP53 p.R202C, c.604C>T			
0.52	0.08	0.2	0.237		
NL 1437	NL PLSA 1437	Normal	NA	7.5	0.77
		TP53 p.G279E, c.836G>A			
0.97	0.09	0.2	0.117		
NL 1438	NL PLSA 1438	Normal	NA	7.5	2.90
		TP53 p.R202C, c.604C>T			
0.87	0.04	0.4	0.122		
NL 1439	NL PLSA 1439	Normal	NA	7.5	1.65
		TP53 p.R273H, c.818G>A			
0.81	0.13	0.7	0.117		
NL 1440	NL PLSA 1440	Normal	NA	7.5	5.15
		TP53 p.L369P, c.1106T>C			
0.80	0.03	0.5	0.117		

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NL 1441	NL PLSA 1441	Normal	NA	7.5	1.05	
		TP53 p.R290C, c.868C>T				
0.74	0.15	0.5	0.125			
NL 1442	NL PLSA 1442	Normal	NA	7.5	1.11	
		HRAS p.G13D, c.38G>A				
0.43	0.03	0.1	0.117			
NL 1443	NL PLSA 1443	Normal	NA	7.5	1.71	
		TP53 p.M384V, c.1150A>G				
1.10	0.05	0.2	0.317			
NL 1444	NL PLSA 1444	Normal	NA	7.5	1.87	
		TP53 p.P300S, c.898C>T				
1.06	0.03	0.2	0.816			
NL 1445	NL PLSA 1445	Normal	NA	7.5	2.20	
		TP53 p.A129V, c.386C>T				
0.97	0.02	0.2	0.117			
NL 1482	NL PLSA 1482	Normal	NA	7.5	1.74	
		TP53 p.A189V, c.566C>T				
0.63	0.05	0.2	0.125			
NL 1483	NL PLSA 1483	Normal	NA	7.5	1.78	
		TP53 p.P36S, c.106C>T				
0.65	0.05	0.3	0.575			
NL 1484	NL PLSA 1484	Normal	NA	7.5	4.03	
		TP53 p.T329A, c.985A>G				
1.42	0.07	0.8	0.357			
NL 1485	NL PLSA 1485	Normal	NA	7	2.80	
		TP53 p.R337H, c.1010G>A				
0.90	0.09	0.8	0.117			
NL 1486	NL PLSA 1486	Normal	NA	7.5	2.60	
		TP53 p.A189V, c.566C>T				
0.85	0.04	0.3	0.125			
NL 1487	NL PLSA 1487	Normal	NA	7.5	2.87	
		TP53 p.M133T, c.398T>C				
1.21	0.09	0.8	0.338			
NL 1488	NL PLSA 1488	Normal	NA	7.5	3.72	
		TP53 p.R196Q, c.587G>A				
0.56	0.04	0.5	0.116			
NL 1489	NL PLSA 1489	Normal	NA	7.5	2.70	
		TP53 p.S261G, c.781A>G				
1.06	0.07	0.6	0.818			
NL 1490	NL PLSA 1490	Normal	NA	7.5	2.21	
		TP53 p.R202C, c.604C>T				
0.52	0.10	0.7	0.125			
NL 1491	NL PLSA 1491	Normal	NA	7.5	3.50	
		TP53 p.R181H, c.542G>A				
1.18	0.06	0.6	0.325			
NL 1492	NL PLSA 1492	Normal	NA	7.5	2.83	
		FBXW7 p.R465C, c.1393C>T				
0.75	0.06	0.5	0.123			

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NL 1493	NL PLSA 1493	Normal	NA	7	6.78	
		TP53 p.S371F, c.1112C>T				
1.00	0.02	0.3	0.297			
NL 1494	NL PLSA 1494	Normal	NA	7.5	1.99	
		TP53 p.P36S, c.106C>T				
0.77	0.04	0.3	0.116			
NL 1495	NL PLSA 1495	Normal	NA	7.5	2.78	
		PPP2R1A p.R183W, c.547C>T				
1.32	0.11	0.9	0.355			
NL 1496	NL PLSA 1496	Normal	NA	7.5	7.53	
		TP53 p.A353V, c.1058C>T				
1.04	0.04	0.9	0.413			
NL 1497	NL PLSA 1497	Normal	NA	7.5	3.37	
		TP53 p.R273H, c.818G>A				
0.67	0.07	0.7	0.117			
NL 1498	NL PLSA 1498	Normal	NA	7.5	5.73	
		TP53 p.A86T, c.256G>A				
0.88	0.02	0.4	0.125			
NL 1499	NL PLSA 1499	Normal	NA	7.5	5.03	
		TP53 p.L369P, c.1106T>C				
1.04	0.06	0.9	0.308			
NL 1500	NL PLSA 1500	Normal	NA	7.5	21.02	
		TP53 p.R333H, c.998G>A				
0.88	0.07	4.3	0.193			
NL 1501	NL PLSA 1501	Normal	NA	7.5	7.00	
		TP53 p.R202C, c.604C>T				
0.70	0.05	1.1	0.125			
NL 1502	NL PLSA 1502	Normal	NA	7.5	11.11	
		TP53 p.A189T, c.565G>A				
0.70	0.01	0.4	0.123			
NL 1503	NL PLSA 1503	Normal	NA	7.5	5.63	
		TP53 p.M169I, c.507G>T				
0.90	0.03	0.5	0.117			
NL 1504	NL PLSA 1504	Normal	NA	7.5	2.51	
		TP53 p.A138T, c.412G>A				
1.00	0.11	0.9	0.117			
NL 1505	NL PLSA 1505	Normal	NA	7.5	3.53	
		TP53 p.A353V, c.1058C>T				
1.14	0.07	0.8	0.457			
NL 1506	NL PLSA 1506	Normal	NA	7.5	4.43	
		TP53 p.R110C, c.328C>T				
1.38	0.10	1.3	0.509			
NL 1507	NL PLSA 1507	Normal	NA	7.5	4.87	
		TP53 p.A276V, c.827C>T				
1.12	0.05	0.7	0.731			
NL 1508	NL PLSA 1508	Normal	NA	7.5	5.26	
		TP53 p.R174G, c.520A>G				
0.87	0.04	0.6	0.125			

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NL 1509	NL PLSA 1509	Normal	NA	7.5	3.99
		TP53 p.H168Y, c.502C>T			
1.22	0.02	0.3	0.328		
NL 1510	NL PLSA 1510	Normal	NA	7.5	4.36
		FBXW7 p.R505H, c.1514G>A			
1.05	0.03	0.4	0.300		
NL 1511	NL PLSA 1511	Normal	NA	7.5	4.09
		TP53 p.Q167R, c.500A>G			
1.05	0.02	0.3	0.514		
NL 1512	NL PLSA 1512	Normal	NA	7.5	3.48
		TP53 p.A86E, c.257C>A			
0.80	0.03	0.3	0.121		
NL 1513	NL PLSA 1513	Normal	NA	7.5	6.15
		TP53 p.A138T, c.412G>A			
0.82	0.03	0.5	0.185		
NL 1514	NL PLSA 1514	Normal	NA	7.5	2.99
		PPP2R1A p.R183Q, c.548G>A			
1.14	0.07	0.6	0.329		
NL 1515	NL PLSA 1515	Normal	NA	7.5	3.68
		GNAS p.R201H, c.602G>A			
0.46	0.01	0.1	0.238		
NL 1516	NL PLSA 1516	Normal	NA	7.5	4.02
		TP53 p.A138T, c.412G>A			
0.63	0.03	0.4	0.117		
NL 1517	NL PLSA 1517	Normal	NA	7.5	3.34
		TP53 p.L369P, c.1106T>C			
1.00	0.04	0.4	0.305		
NL 1518	NL PLSA 1518	Normal	NA	7.5	5.74
		TP53 p.A353V, c.1058C>T			
1.11	0.05	0.8	0.443		
NL 1519	NL PLSA 1519	Normal	NA	7.5	4.30
		KRAS p.D57N, c.169G>A			
0.85	0.02	0.3	0.122		
NL 1520	NL PLSA 1520	Normal	NA	7.5	6.00
		TP53 p.R202C, c.604C>T			
0.99	0.06	1.1	0.125		
NL 1521	NL PLSA 1521	Normal	NA	7.5	4.06
		TP53 p.A353V, c.1058C>T			
1.07	0.04	0.5	0.314		
NL 1522	NL PLSA 1522	Normal	NA	7.5	2.73
		TP53 p.E51G, c.152A>G			
0.70	0.04	0.4	0.116		
NL 1523	NL PLSA 1523	Normal	NA	7.5	9.04
		PIK3CA p.Q546H, c.1638G>T			
1.06	0.01	0.3	0.314		
NL 1524	NL PLSA 1524	Normal	NA	7.5	11.25
		TP53 p.S376P, c.1126T>C			
1.11	0.01	0.4	0.600		

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NL 1525	NL PLSA 1525	Normal	NA	7.5	9.45
		TP53 p.A353V, c.1058C>T			
1.00	0.03	0.8	0.550		
NL 1526	NL PLSA 1526	Normal	NA	7.5	9.48
		TP53 p.C176Y, c.527G>A			
0.94	0.02	0.5	0.117		
NL 1527	NL PLSA 1527	Normal	NA	7.5	7.99
		TP53 p.A138T, c.412G>A			
1.10	0.07	1.8	0.296		
NL 1528	NL PLSA 1528	Normal	NA	7.5	6.24
		TP53 p.C141Y, c.422G>A			
1.03	0.03	0.6	0.301		
NL 1529	NL PLSA 1529	Normal	NA	7.5	8.39
		TP53 p.A189fs, c.566delC			
1.40	0.01	0.2	0.814		
NL 1530	NL PLSA 1530	Normal	NA	7.5	3.93
		TP53 p.C176fs, c.528delC			
0.68	0.04	0.5	0.421		
NL 1531	NL PLSA 1531	Normal	NA	7.5	2.30
		TP53 p.G262D, c.785G>A			
0.80	0.04	0.3	0.116		
NL 1532	NL PLSA 1532	Normal	NA	7.5	7.77
		TP53 p.H179Q, c.537T>A			
1.68	0.07	1.7	0.409		
NL 1533	NL PLSA 1533	Normal	NA	7.5	3.21
		TP53 p.M384V, c.1150A>G			
1.09	0.03	0.3	0.295		
NL 1534	NL PLSA 1534	Normal	NA	7.5	3.15
		TP53 p.Q38R, c.113A>G			
1.21	0.05	0.5	0.490		
NL 1535	NL PLSA 1535	Normal	NA	7.5	6.29
		PPP2R1A p.R183W, c.547C>T			
0.84	0.02	0.4	0.229		
NL 1536	NL PLSA 1536	Normal	NA	7.5	2.80
		TP53 p.A189V, c.566C>T			
0.82	0.02	0.2	0.125		
NL 1537	NL PLSA 1537	Normal	NA	7.5	3.02
		TP53 p.P36L, c.107C>T			
0.98	0.04	0.3	0.125		
NL 1538	NL PLSA 1538	Normal	NA	7.5	9.57
		TP53 p.R175H, c.524G>A			
1.03	0.07	2.2	0.297		
NL 1539	NL PLSA 1539	Normal	NA	7.5	10.01
		TP53 p.H179Q, c.537T>A			
0.97	0.03	0.8	0.425		
NL 1540	NL PLSA 1540	Normal	NA	7.5	2.95
		TP53 p.R213*, c.637C>T			
0.70	0.08	0.8	0.123		

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NL 1541	NL PLSA 1541	Normal	NA	7.5	7.27
		TP53 p.A353V, c.1058C>T			
1.03	0.04	0.8	0.617		
NL 1542	NL PLSA 1542	Normal	NA	7.5	4.84
		TP53 p.A353V, c.1058C>T			
0.90	0.04	0.5	0.213		
NL 1543	NL PLSA 1543	Normal	NA	7.5	2.89
		TP53 p.S37P, c.109T>C			
0.67	0.03	0.3	0.338		
NL 1544	NL PLSA 1544	Normal	NA	7.5	4.45
		TP53 p.A189V, c.566C>T			
0.76	0.02	0.2	0.117		
NL 1545	NL PLSA 1545	Normal	NA	7.5	8.20
		TP53 p.R213*, c.637C>T			
0.73	0.05	1.2	0.451		
NL 1546	NL PLSA 1546	Normal	NA	7.5	8.19
		TP53 p.R174G, c.520A>G			
1.20	0.04	0.9	0.338		
NL 1547	NL PLSA 1547	Normal	NA	7.5	3.18
		TP53 p.A189V, c.566C>T			
0.71	0.02	0.2	0.246		
NL 1548	NL PLSA 1548	Normal	NA	7.5	2.59
		CTNNB1 p.T42I, c.125C>T			
0.64	0.02	0.1	0.125		
NL 1549	NL PLSA 1549	Normal	NA	7.5	3.90
		FBXW7 p.R505H, c.1514G>A			
0.90	0.05	0.5	0.731		
NL 1550	NL PLSA 1550	Normal	NA	7.5	6.28
		TP53 p.R273H, c.818G>A			
0.84	0.08	1.5	0.542		
NL 1551	NL PLSA 1551	Normal	NA	7.5	5.38
		TP53 p.A353V, c.1058C>T			
0.65	0.03	0.6	0.123		
NL 1552	NL PLSA 1552	Normal	NA	7.5	6.18
		PIK3CA p.E545Q, c.1633G>C			
0.80	0.02	0.3	0.415		
NL 1553	NL PLSA 1553	Normal	NA	7.5	4.75
		TP53 p.S99P, c.295T>C			
1.03	0.02	0.3	0.307		
NL 1554	NL PLSA 1554	Normal	NA	7.5	6.13
		TP53 p.L369P, c.1106T>C			
0.97	0.03	0.5	0.117		
NL 1555	NL PLSA 1555	Normal	NA	7.5	5.38
		TP53 p.P222S, c.664C>T			
1.15	0.04	0.6	0.435		
NL 1556	NL PLSA 1556	Normal	NA	7.5	2.93
		TP53 p.K372fs, c.1114delA			
1.06	0.06	0.5	0.305		

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NL 1557	NL PLSA 1557	Normal	NA	7.5	2.63
		TP53 p.A161V, c.482C>T			
1.05	0.10	0.8	0.673		
NL 1558	NL PLSA 1558	Normal	NA	7.5	3.85
		TP53 p.P301T, c.901C>A			
1.01	0.04	0.5	0.465		
NL 1559	NL PLSA 1559	Normal	NA	7.5	6.18
		TP53 p.S185G, c.553A>G			
1.12	0.03	0.6	0.518		
NL 1560	NL PLSA 1560	Normal	NA	7.5	7.00
		TP53 p.R202C, c.604C>T			
1.18	0.12	2.6	0.847		
NL 1561	NL PLSA 1561	Normal	NA	7.5	4.78
		TP53 p.A138T, c.412G>A			
1.10	0.07	1.0	0.472		
NL 1562	NL PLSA 1562	Normal	NA	7.5	8.41
		CDKN2A p.A86fs, c.257delC			
1.34	0.02	0.4	0.976		
NL 1563	NL PLSA 1563	Normal	NA	7.5	6.71
		PPP2R1A p.A184V, c.551C>T			
0.84	0.03	0.6	0.399		
NL 1564	NL PLSA 1564	Normal	NA	7.5	1.55
		TP53 p.C135Y, c.404G>A			
2.19	0.27	1.3	0.485		
NL 1565	NL PLSA 1565	Normal	NA	7.5	2.15
		TP53 p.R267Q, c.800G>A			
0.51	0.09	0.6	0.121		
NL 1566	NL PLSA 1566	Normal	NA	7.5	3.57
		FBXW7 p.R367*, c.1099C>T			
0.95	0.06	0.7	0.305		
NL 1567	NL PLSA 1567	Normal	NA	7.5	2.40
		CTNNB1 p.T42I, c.125C>T			
0.77	0.02	0.1	0.116		
NL 1568	NL PLSA 1568	Normal	NA	7.5	3.59
		TP53 p.L348S, c.1043T>C			
0.55	0.02	0.2	0.207		
NL 1569	NL PLSA 1569	Normal	NA	7.5	4.89
		TP53 p.R273H, c.818G>A			
1.10	0.12	1.7	0.616		
NL 1570	NL PLSA 1570	Normal	NA	7.5	7.36
		TP53 p.L369Q, c.1106T>A			
1.02	0.01	0.3	0.295		
NL 1571	NL PLSA 1571	Normal	NA	7.5	2.64
		GNAS p.L203P, c.608T>C			
1.05	0.02	0.2	0.303		
NL 1572	NL PLSA 1572	Normal	NA	7.5	4.46
		TP53 p.T170A, c.508A>G			
0.96	0.02	0.3	0.125		

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NL 1573	NL PLSA 1573	Normal	NA	7.5	5.18
		TP53 p.K101fs, c.301delA			
0.85	0.01	0.2	0.195		
NL 1574	NL PLSA 1574	Normal	NA	7.5	13.15
		TP53 p.A189V, c.566C>T			
0.97	0.02	1.0	0.554		
NL 1575	NL PLSA 1575	Normal	NA	7.5	7.39
		TP53 p.R174G, c.520A>G			
0.99	0.03	0.6	0.333		
NL 1576	NL PLSA 1576	Normal	NA	7.5	3.74
		TP53 p.R283H, c.848G>A			
0.94	0.04	0.4	0.121		
NL 1577	NL PLSA 1577	Normal	NA	7.5	1.36
		TP53 p.S20*, c.59C>A			
0.87	0.03	0.1	0.543		
NL 1578	NL PLSA 1578	Normal	NA	7.5	2.14
		TP53 p.R202C, c.604C>T			
0.99	0.11	0.7	0.117		
NL 1579	NL PLSA 1579	Normal	NA	7.5	1.51
		TP53 p.R333H, c.998G>A			
0.49	0.22	1.0	0.256		
NL 1580	NL PLSA 1580	Normal	NA	7.5	1.53
		TP53 p.R202C, c.604C>T			
0.69	0.13	0.6	0.242		
NL 1581	NL PLSA 1581	Normal	NA	7.5	6.46
		TP53 p.R267Q, c.800G>A			
0.78	0.02	0.4	0.125		
NL 1582	NL PLSA 1582	Normal	NA	7.5	1.78
		TP53 p.R181H, c.542G>A			
0.84	0.17	0.9	0.197		
NL 1583	NL PLSA 1583	Normal	NA	7.5	4.88
		KRAS p.A11T, c.31G>A			
0.90	0.02	0.3	0.334		
NL 1584	NL PLSA 1584	Normal	NA	7.5	1.83
		TP53 p.A138T, c.412G>A			
0.96	0.10	0.6	0.117		
NL 1585	NL PLSA 1585	Normal	NA	7.5	3.32
		TP53 p.A83T, c.247G>A			
0.51	0.03	0.3	0.117		
NL 1586	NL PLSA 1586	Normal	NA	7.5	1.67
		TP53 p.R282Q, c.845G>A			
0.45	0.06	0.3	0.382		
NL 1587	NL PLSA 1587	Normal	NA	7.5	2.55
		TP53 p.P92L, c.275C>T			
1.13	0.02	0.2	0.719		
NL 1588	NL PLSA 1588	Normal	NA	7.5	2.44
		TP53 p.R342*, c.1024C>T			
0.82	0.09	0.7	0.508		

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NL 1589	NL PLSA 1589	Normal	NA	7.5	4.50	
		TP53 p.M169T, c.506T>C				
1.35	0.02	0.3	0.666			
NL 1590	NL PLSA 1590	Normal	NA	7.5	3.19	
		TP53 p.Q100R, c.299A>G				
0.52	0.03	0.2	0.123			
NL 1591	NL PLSA 1591	Normal	NA	7.5	2.13	
		TP53 p.K351N, c.1053G>T				
0.64	0.05	0.3	0.188			
NL 1592	NL PLSA 1592	Normal	NA	7.5	2.94	
		TP53 p.R202C, c.604C>T				
1.09	0.06	0.5	0.320			
NL 1593	NL PLSA 1593	Normal	NA	7.5	2.35	
		TP53 p.R273H, c.818G>A				
0.82	0.14	1.0	0.122			
NL 1594	NL PLSA 1594	Normal	NA	7.5	2.09	
		TP53 p.P300S, c.898C>T				
0.51	0.04	0.3	0.117			
NL 1595	NL PLSA 1595	Normal	NA	7.5	3.70	
		APC p.R1450*, c.4348C>T				
0.94	0.04	0.4	0.396			
NL 1596	NL PLSA 1596	Normal	NA	7.5	6.14	
		TP53 p.Q104R, c.311A>G				
1.10	0.02	0.4	0.321			
NL 1597	NL PLSA 1597	Normal	NA	7.5	2.78	
		HRAS p.S17G, c.49A>G				
0.91	0.00	0.0	0.125			
NL 1598	NL PLSA 1598	Normal	NA	7.5	9.90	
		TP53 p.A84V, c.251C>T				
0.92	0.01	0.4	0.238			
NL 1599	NL PLSA 1599	Normal	NA	7.5	4.42	
		TP53 g.7579311C>T (Splice Site)				
0.95	0.03	0.3	0.116			
NL 1600	NL PLSA 1600	Normal	NA	7.5	5.45	
		FBXW7 p.R505H, c.1514G>A				
0.90	0.03	0.6	0.338			
NL 1601	NL PLSA 1601	Normal	NA	7.5	3.56	
		TP53 p.R196*, c.586C>T				
0.49	0.03	0.3	0.318			
NL 1602	NL PLSA 1602	Normal	NA	7.5	3.75	
		TP53 p.R273H, c.818G>A				
0.93	0.07	0.8	0.242			
NL 1603	NL PLSA 1603	Normal	NA	7.5	3.53	
		TP53 p.A189V, c.566C>T				
0.88	0.03	0.3	0.125			
NL 1604	NL PLSA 1604	Normal	NA	7.5	2.06	
		TP53 p.R273H, c.818G>A				
0.45	0.08	0.5	0.331			

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NL 1605	NL PLSA 1605	Normal	NA	7.5	2.51	
		FBXW7 p.R465C, c.1393C>T				
0.53	0.03	0.2	0.125			
NL 1606	NL PLSA 1606	Normal	NA	7.5	1.80	
		TP53 p.R267Q, c.800G>A				
0.87	0.05	0.3	0.121			
NL 1607	NL PLSA 1607	Normal	NA	7.5	2.47	
		TP53 p.R273H, c.818G>A				
0.74	0.16	1.2	0.381			
NL 1608	NL PLSA 1608	Normal	NA	7.5	4.78	
		TP53 p.P309S, c.925C>T				
0.90	0.03	0.4	0.121			
NL 1609	NL PLSA 1609	Normal	NA	7.5	3.27	
		TP53 p.G108S, c.322G>A				
1.13	0.10	1.0	0.301			
NL 1610	NL PLSA 1610	Normal	NA	7.5	3.49	
		TP53 p.R290C, c.868C>T				
0.77	0.03	0.4	0.121			
NL 1611	NL PLSA 1611	Normal	NA	7.5	34.53	
		TP53 p.H179Q, c.537T>A				
0.82	0.01	1.1	0.538			
NL 1612	NL PLSA 1612	Normal	NA	7.5	2.52	
		TP53 p.K373R, c.1118A>G				
0.89	0.03	0.3	0.125			
NL 1613	NL PLSA 1613	Normal	NA	7.5	3.33	
		FBXW7 p.R505C, c.1513C>T				
0.83	0.04	0.4	0.117			
NL 1614	NL PLSA 1614	Normal	NA	7.5	3.86	
		TP53 p.A138T, c.412G>A				
0.76	0.03	0.3	0.125			
NL 1615	NL PLSA 1615	Normal	NA	7.5	4.06	
		TP53 p.H115Y, c.343C>T				
0.89	0.03	0.4	0.125			
NL 1616	NL PLSA 1616	Normal	NA	7.5	17.87	
		TP53 p.R342*, c.1024C>T				
0.88	0.04	2.5	0.815			
NL 1617	NL PLSA 1617	Normal	NA	7.5	2.80	
		TP53 p.R273H, c.818G>A				
0.85	0.14	1.2	0.121			
NL 1618	NL PLSA 1618	Normal	NA	7.5	3.05	
		TP53 p.A88V, c.263C>T				
0.84	0.02	0.2	0.116			
NL 1619	NL PLSA 1619	Normal	NA	7.5	5.09	
		TP53 p.R306Q, c.917G>A				
0.83	0.05	0.8	0.200			
NL 1620	NL PLSA 1620	Normal	NA	7.5	7.50	
		TP53 p.E298K, c.892G>A				
1.03	0.04	1.0	0.301			

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NL 1621	NL PLSA 1621	Normal	NA	7.5	2.27	
		TP53 p.R273H, c.818G>A				
0.93	0.06	0.4	0.117			
NL 1622	NL PLSA 1622	Normal	NA	7.5	4.74	
		CTNNB1 p.S45A, c.133T>G				
2.21	0.04	0.5	0.480			
NL 1623	NL PLSA 1623	Normal	NA	7.5	3.29	
		TP53 p.R249M, c.746G>T				
0.81	0.12	1.2	0.122			
NL 1624	NL PLSA 1624	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.121			
NL 1625	NL PLSA 1625	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.117			
NL 1626	NL PLSA 1626	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.125			
NL 1627	NL PLSA 1627	Normal	NA	7.5	0.06	
		None detected				
NA	NA	NA	0.192			
NL 1628	NL PLSA 1628	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.116			
NL 1629	NL PLSA 1629	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.187			
NL 1630	NL PLSA 1630	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.121			
NL 1631	NL PLSA 1631	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.123			
NL 1632	NL PLSA 1632	Normal	NA	7.5	0.04	
		None detected				
NA	NA	NA	0.117			
NL 1633	NL PLSA 1633	Normal	NA	7.5	0.00	
		None detected				
NA	NA	NA	0.122			
NL 1634	NL PLSA 1634	Normal	NA	7.5	0.04	
		None detected				
NA	NA	NA	0.180			
NL 1635	NL PLSA 1635	Normal	NA	6	0.81	
		None detected				
NA	NA	NA	0.335			
NL 1636	NL PLSA 1636	Normal	NA	7.5	0.21	
		None detected				
NA	NA	NA	0.125			

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NL 1637	NL PLSA 1637	Normal	NA	7.5	0.00	None detected
NA	NA	NA	0.125			
NL 1638	NL PLSA 1638	Normal	NA	7.5	0.00	None detected
NA	NA	NA	0.310			
NL 1639	NL PLSA 1639	Normal	NA	7.5	0.39	None detected
NA	NA	NA	0.187			
NL 1640	NL PLSA 1640	Normal	NA	7.5	0.04	None detected
NA	NA	NA	0.121			
NL 1641	NL PLSA 1641	Normal	NA	7.5	0.01	None detected
NA	NA	NA	0.123			
NL 1642	NL PLSA 1642	Normal	NA	7.5	0.38	None detected
NA	NA	NA	0.175			
NL 1643	NL PLSA 1643	Normal	NA	7.5	0.40	None detected
NA	NA	NA	0.122			
NL 1644	NL PLSA 1644	Normal	NA	7.5	0.15	None detected
NA	NA	NA	0.222			
NL 1645	NL PLSA 1645	Normal	NA	7.5	0.03	None detected
NA	NA	NA	0.117			
NL 1646	NL PLSA 1646	Normal	NA	7.5	0.07	None detected
NA	NA	NA	0.125			
NL 1647	NL PLSA 1647	Normal	NA	7.5	0.05	None detected
NA	NA	NA	0.125			
NL 1648	NL PLSA 1648	Normal	NA	7.5	13.03	TP53 p.R202C, c.604C>T
1.04	0.06	2.5	0.306			
NL 1649	NL PLSA 1649	Normal	NA	7.5	5.00	TP53 p.R202C, c.604C>T
1.10	0.06	1.0	0.747			
NL 1650	NL PLSA 1650	Normal	NA	7.5	4.22	TP53 p.G112D, c.335G>A
0.90	0.06	0.8	0.125			
NL 1651	NL PLSA 1651	Normal	NA	7.5	4.49	TP53 p.A189V, c.566C>T
1.07	0.04	0.5	0.311			
NL 1652	NL PLSA 1652	Normal	NA	7.5	4.36	TP53 p.A138T, c.412G>A
1.07	0.04	0.5	0.317			

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NL 1653	NL PLSA 1653	Normal	NA	7.5	4.65
		TP53 p.C176fs, c.528delC			
0.86	0.03	0.4	0.568		
NL 1654	NL PLSA 1654	Normal	NA	7.5	4.77
		TP53 p.L369P, c.1106T>C			
0.99	0.02	0.3	0.121		
NL 1655	NL PLSA 1655	Normal	NA	7.5	3.19
		TP53 p.A276V, c.827C>T			
0.68	0.05	0.5	0.720		
NL 1656	NL PLSA 1656	Normal	NA	7.5	7.47
		TP53 p.S215N, c.644G>A			
1.05	0.02	0.4	0.522		
NL 1657	NL PLSA 1657	Normal	NA	7.5	3.06
		GNAS p.R201H, c.602G>A			
0.66	0.05	0.5	0.320		
NL 1658	NL PLSA 1658	Normal	NA	7.5	4.21
		PPP2R1A p.R182W, c.544C>T			
0.74	0.02	0.3	0.324		
NL 1659	NL PLSA 1659	Normal	NA	7.5	6.67
		PPP2R1A p.R183Q, c.548G>A			
1.00	0.05	1.1	0.300		
NL 1660	NL PLSA 1660	Normal	NA	7.5	0.05
		None detected			
NA	NA	NA	0.333		
NL 1661	NL PLSA 1661	Normal	NA	7.5	0.12
		None detected			
NA	NA	NA	0.334		
NL 1662	NL PLSA 1662	Normal	NA	7.5	0.52
		HRAS p.G13D, c.38G>A			
0.21	0.00	0.0	0.121		
NL 1663	NL PLSA 1663	Normal	NA	7.5	1.86
		TP53 g.7578175A>G (Splice Site)			
0.79	0.04	0.2	0.116		
NL 1664	NL PLSA 1664	Normal	NA	7.5	7.61
		TP53 p.A88G, c.263C>G			
1.05	0.01	0.1	0.308		
NL 1665	NL PLSA 1665	Normal	NA	7.5	3.86
		PPP2R1A p.R183W, c.547C>T			
0.80	0.05	0.6	0.471		
NL 1666	NL PLSA 1666	Normal	NA	7.5	4.86
		TP53 p.A353V, c.1058C>T			
1.06	0.04	0.6	0.304		
NL 1667	NL PLSA 1667	Normal	NA	7.5	4.81
		TP53 p.A138T, c.412G>A			
1.10	0.04	0.6	0.313		
NL 1668	NL PLSA 1668	Normal	NA	7.5	5.56
		TP53 p.L369P, c.1106T>C			
1.08	0.04	0.6	0.309		

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NL 1669	NL PLSA 1669	Normal	NA	7.5	5.42
		TP53 p.K372fs, c.1114delA			
0.96	0.04	0.7	0.577		
NL 1701	NL PLSA 1701	Normal	NA	7.5	1.94
		TP53 p.Q331R, c.992A>G			
0.95	0.02	0.1	0.528		
NL 1702	NL PLSA 1702	Normal	NA	7.5	2.96
		TP53 p.P47L, c.140C>T			
0.80	0.03	0.3	0.214		
NL 1703	NL PLSA 1703	Normal	NA	7.5	2.23
		TP53 p.A83T, c.247G>A			
1.05	0.02	0.1	0.713		
NL 1704	NL PLSA 1704	Normal	NA	7.5	2.81
		TP53 p.M384V, c.1150A>G			
1.29	0.03	0.2	0.338		
NL 1705	NL PLSA 1705	Normal	NA	7.5	2.54
		TP53 p.R306Q, c.917G>A			
0.96	0.05	0.4	0.117		
NL 1706	NL PLSA 1706	Normal	NA	7.5	1.28
		TP53 p.G187D, c.560G>A (Exon Start)			
1.02	0.02	0.1	0.308		
NL 1707	NL PLSA 1707	Normal	NA	7.5	1.97
		TP53 p.P222S, c.664C>T			
1.13	0.03	0.2	0.314		
NL 1708	NL PLSA 1708	Normal	NA	7.5	4.38
		TP53 p.H179R, c.536A>G			
2.19	0.04	0.5	0.576		
NL 1709	NL PLSA 1709	Normal	NA	7.5	3.30
		PIK3CA p.H1047R, c.3140A>G			
1.73	0.05	0.5	0.566		
NL 1710	NL PLSA 1710	Normal	NA	7.5	2.96
		TP53 p.R337H, c.1010G>A			
0.78	0.02	0.2	0.323		
NL 1711	NL PLSA 1711	Normal	NA	7.5	1.19
		TP53 p.A161T, c.481G>A			
0.94	0.02	0.1	0.123		
NL 1712	NL PLSA 1712	Normal	NA	7.5	2.86
		TP53 p.V203M, c.607G>A			
1.16	0.03	0.3	0.305		
NL 1713	NL PLSA 1713	Normal	NA	7.5	3.33
		TP53 g.7579311C>T (Splice Site)			
0.97	0.02	0.2	0.178		
NL 1714	NL PLSA 1714	Normal	NA	7.5	3.13
		TP53 p.Q38R, c.113A>G			
0.89	0.02	0.2	0.121		
NL 1715	NL PLSA 1715	Normal	NA	7.5	1.15
		TP53 g.7579311C>T (Splice Site)			
0.76	0.03	0.1	0.187		

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NL 1716	NL PLSA 1716	Normal	NA	7.5	2.45
		TP53 p.R267W, c.799C>T			
0.82	0.06	0.5	0.125		
NL 1717	NL PLSA 1717	Normal	NA	7.5	1.11
		TP53 p.A84V, c.251C>T			
1.31	0.03	0.1	0.353		
NL 1718	NL PLSA 1718	Normal	NA	7.5	0.95
		HRAS p.G13D, c.38G>A			
1.33	0.03	0.1	0.349		
NL 1719	NL PLSA 1719	Normal	NA	7.5	1.31
		TP53 p.A161T, c.481G>A			
0.63	0.04	0.2	0.121		
NL 1720	NL PLSA 1720	Normal	NA	7.5	3.02
		TP53 p.A189V, c.566C>T			
0.92	0.04	0.3	0.444		
NL 1721	NL PLSA 1721	Normal	NA	7.5	1.76
		TP53 p.H168R, c.503A>G			
0.97	0.04	0.2	0.123		
NL 1722	NL PLSA 1722	Normal	NA	7.5	2.62
		TP53 p.A353V, c.1058C>T			
0.85	0.03	0.2	0.125		
NL 1723	NL PLSA 1723	Normal	NA	7.5	2.90
		TP53 p.G245D, c.734G>A			
0.87	0.02	0.1	0.116		
NL 1724	NL PLSA 1724	Normal	NA	7.5	2.31
		TP53 p.A138T, c.412G>A			
1.02	0.05	0.4	0.599		
NL 1725	NL PLSA 1725	Normal	NA	7.5	0.04
		None detected			
NA	NA	NA	0.624		
NL 1726	NL PLSA 1726	Normal	NA	7.5	0.04
		None detected			
NA	NA	NA	0.123		
NL 1727	NL PLSA 1727	Normal	NA	7.5	0.19
		TP53 p.R196*, c.586C>T			
0.95	0.07	0.0	0.123		
NL 1728	NL PLSA 1728	Normal	NA	7.5	0.11
		None detected			
NA	NA	NA	0.735		
NL 1729	NL PLSA 1729	Normal	NA	7.5	0.03
		None detected			
NA	NA	NA	0.322		
NL 1730	NL PLSA 1730	Normal	NA	7.5	0.01
		None detected			
NA	NA	NA	0.599		
NL 1731	NL PLSA 1731	Normal	NA	7.5	0.03
		None detected			
NA	NA	NA	0.236		

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NL 1732	NL PLSA 1732	Normal	NA	7.5	0.06	None detected
NA	NA	NA	0.125			
NL 1733	NL PLSA 1733	Normal	NA	7.5	0.05	None detected
NA	NA	NA	0.125			
NL 1734	NL PLSA 1734	Normal	NA	7.5	0.04	None detected
NA	NA	NA	0.155			
NL 1735	NL PLSA 1735	Normal	NA	7.5	0.06	None detected
NA	NA	NA	0.187			
NL 1736	NL PLSA 1736	Normal	NA	7.5	0.05	None detected
NA	NA	NA	0.564			
NL 1737	NL PLSA 1737	Normal	NA	7.5	0.07	None detected
NA	NA	NA	0.183			
NL 1738	NL PLSA 1738	Normal	NA	7.5	0.08	None detected
NA	NA	NA	0.175			
NL 1739	NL PLSA 1739	Normal	NA	7.5	0.03	None detected
NA	NA	NA	0.122			
NL 1740	NL PLSA 1740	Normal	NA	7.5	0.18	None detected
NA	NA	NA	0.121			
NL 1741	NL PLSA 1741	Normal	NA	7.5	0.09	None detected
NA	NA	NA	0.117			
NL 1742	NL PLSA 1742	Normal	NA	7.5	0.02	None detected
NA	NA	NA	0.125			
NL 1743	NL PLSA 1743	Normal	NA	7.5	0.05	None detected
NA	NA	NA	0.125			
NL 1744	NL PLSA 1744	Normal	NA	7.5	0.11	None detected
NA	NA	NA	0.116			
NL 1745	NL PLSA 1745	Normal	NA	7.5	0.19	EGFR p.L858Q, c.2573T>A
0.00	0.04	0.0	0.154			
NL 1746	NL PLSA 1746	Normal	NA	7.5	0.08	None detected
NA	NA	NA	0.344			
NL 1747	NL PLSA 1747	Normal	NA	7.5	0.07	None detected
NA	NA	NA	0.121			

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NL 1748	NL PLSA 1748	Normal	NA	7.5	0.13	None detected	NA	NA	0.182
NL 1749	NL PLSA 1749	Normal	NA	7.5	2.78	TP53 p.G226D, c.677G>A	1.11	0.04	0.3	0.323
NL 1750	NL PLSA 1750	Normal	NA	7.5	0.10	None detected	NA	NA	NA	0.117
NL 1751	NL PLSA 1751	Normal	NA	7.5	2.09	TP53 p.A159T, c.475G>A	0.84	0.03	0.2	0.116
NL 1752	NL PLSA 1752	Normal	NA	7.5	0.29	TP53 p.R196Q, c.587G>A	1.07	0.10	0.1	0.303
NL 1753	NL PLSA 1753	Normal	NA	7.5	3.67	TP53 p.Q38R, c.113A>G	1.37	0.02	0.3	0.810
NL 1754	NL PLSA 1754	Normal	NA	7.5	0.75	TP53 p.A86E, c.257C>A	0.71	0.04	0.1	0.116
NL 1755	NL PLSA 1755	Normal	NA	7.5	0.14	None detected	NA	NA	NA	0.122
NL 1756	NL PLSA 1756	Normal	NA	7.5	3.75	PTEN p.A148T, c.442G>A	1.20	0.03	0.3	0.332
NL 1757	NL PLSA 1757	Normal	NA	7.5	0.26	KRAS p.A146T, c.436G>A	0.00	0.04	0.0	0.116
NL 1758	NL PLSA 1758	Normal	NA	7.5	1.35	FBXW7 p.R465H, c.1394G>A	1.19	0.07	0.3	0.554
NL 1759	NL PLSA 1759	Normal	NA	7.5	0.77	FBXW7 p.R465C, c.1393C>T	0.90	0.04	0.1	0.122
NL 1760	NL PLSA 1760	Normal	NA	7.5	0.15	TP53 p.R156C, c.466C>T	1.25	0.11	0.1	0.337
NL 1761	NL PLSA 1761	Normal	NA	7.5	0.15	CTNNB1 p.S37Y, c.110C>A	0.00	0.07	0.0	0.117
NL 1762	NL PLSA 1762	Normal	NA	7.5	0.47	TP53 p.E298K, c.892G>A	0.75	0.04	0.1	0.297
NL 1763	NL PLSA 1763	Normal	NA	7.5	0.26	None detected	NA	NA	NA	0.237

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NL 1764	NL PLSA 1764	Normal	NA	7.5	0.42
		APC p.N1455fs, c.4364delA			
0.00	0.05	0.1	0.116		
NL 1765	NL PLSA 1765	Normal	NA	7.5	0.46
		TP53 p.T230I, c.689C>T			
0.00	0.07	0.1	0.125		
NL 1766	NL PLSA 1766	Normal	NA	7.5	0.29
		TP53 p.R158H, c.473G>A			
1.19	0.13	0.1	0.327		
NL 1767	NL PLSA 1767	Normal	NA	7.5	0.19
		TP53 p.P222S, c.664C>T			
0.00	0.08	0.0	0.226		
NL 1768	NL PLSA 1768	Normal	NA	7.5	0.46
		TP53 p.R335C, c.1003C>T			
1.16	0.06	0.1	0.332		
NL 1769	NL PLSA 1769	Normal	NA	7.5	1.01
		TP53 p.C238Y, c.713G>A			
0.87	0.03	0.1	0.125		
NL 1770	NL PLSA 1770	Normal	NA	7.5	1.90
		TP53 p.P142L, c.425C>T			
1.10	0.02	0.1	0.428		
NL 1771	NL PLSA 1771	Normal	NA	7.5	1.67
		TP53 p.R335C, c.1003C>T			
0.81	0.04	0.2	0.245		
NL 1772	NL PLSA 1772	Normal	NA	7.5	1.43
		TP53 p.R283H, c.848G>A			
0.86	0.03	0.1	0.178		
NL 1773	NL PLSA 1773	Normal	NA	7.5	0.47
		TP53 p.R158H, c.473G>A			
0.00	0.05	0.1	0.117		
NL 1774	NL PLSA 1774	Normal	NA	7.5	0.29
		FBXW7 p.R465C, c.1393C>T			
0.00	0.05	0.0	0.319		
NL 1775	NL PLSA 1775	Normal	NA	7.5	0.20
		TP53 p.R158G, c.472C>G			
0.00	0.06	0.0	0.125		
NL 1776	NL PLSA 1776	Normal	NA	7.5	0.18
		TP53 p.V157A, c.470T>C			
0.00	0.05	0.0	0.123		
NL 1777	NL PLSA 1777	Normal	NA	7.5	0.23
		TP53 p.R196Q, c.587G>A			
0.00	0.11	0.1	0.240		
NL 1778	NL PLSA 1778	Normal	NA	7.5	0.10
		None detected			
NA	NA	NA	0.117		
NL 1779	NL PLSA 1779	Normal	NA	7.5	0.19
		TP53 p.R156H, c.467G>A			
0.00	0.05	0.0	0.198		

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NL 1780	NL PLSA 1780	Normal	NA	7.5	0.27
		EGFR p.A864T, c.2590G>A			
0.00	0.03	0.0	0.125		
NL 1781	NL PLSA 1781	Normal	NA	7.5	0.79
		KRAS p.V14I, c.40G>A			
0.25	0.01	0.0	0.121		
NL 1782	NL PLSA 1782	Normal	NA	7.5	0.24
		TP53 p.V157F, c.469G>T			
1.65	0.06	0.0	0.405		
NL 1783	NL PLSA 1783	Normal	NA	7.5	0.35
		TP53 p.R248fs, c.743delG			
0.00	0.03	0.0	0.122		
NL 1784	NL PLSA 1784	Normal	NA	7.5	0.18
		TP53 p.M160I, c.480G>T			
0.00	0.05	0.0	0.122		
NL 1785	NL PLSA 1785	Normal	NA	7.5	0.34
		CTNNB1 p.A43T, c.127G>A			
0.82	0.05	0.0	0.117		
NL 1786	NL PLSA 1786	Normal	NA	7.5	1.96
		BRAF p.T599I, c.1796C>T			
0.92	0.02	0.1	0.125		
NL 1787	NL PLSA 1787	Normal	NA	7.5	0.23
		EGFR p.L858Q, c.2573T>A			
0.00	0.05	0.0	0.236		
NL 1788	NL PLSA 1788	Normal	NA	7.5	1.58
		TP53 p.S261I, c.782G>T (Exon End)			
1.14	0.02	0.1	0.436		
NL 1789	NL PLSA 1789	Normal	NA	7.5	3.36
		TP53 p.C242S, c.725G>C			
1.44	0.02	0.2	0.670		
NL 1790	NL PLSA 1790	Normal	NA	7.5	0.29
		TP53 g.7573009C>T (Splice Site)			
0.00	0.04	0.0	0.121		
NL 1791	NL PLSA 1791	Normal	NA	7.5	0.55
		TP53 p.L369M, c.1105C>A			
1.08	0.04	0.1	0.313		
NL 1792	NL PLSA 1792	Normal	NA	7.5	0.69
		CTNNB1 p.T41I, c.122C>T			
1.26	0.02	0.0	0.338		
NL 1793	NL PLSA 1793	Normal	NA	7.5	1.36
		TP53 p.R202C, c.604C>T			
0.93	0.03	0.1	0.345		
NL 1794	NL PLSA 1794	Normal	NA	7.5	2.12
		TP53 p.M40V, c.118A>G			
1.36	0.01	0.1	0.354		
NL 1795	NL PLSA 1795	Normal	NA	7.5	1.12
		CTNNB1 p.S33Y, c.98C>A			
0.67	0.02	0.1	0.240		

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NL 1796	NL PLSA 1796	Normal	NA	7.5	0.41
		TP53 p.P47L, c.140C>T			
0.55	0.11	0.1	0.248		
NL 1797	NL PLSA 1797	Normal	NA	7.5	1.09
		KRAS p.G60D, c.179G>A			
0.63	0.02	0.1	0.221		
NL 1798	NL PLSA 1798	Normal	NA	7.5	1.79
		TP53 p.V272M, c.814G>A			
0.76	0.04	0.2	0.116		
NL 1799	NL PLSA 1799	Normal	NA	7.5	2.29
		TP53 p.A189V, c.566C>T			
0.83	0.03	0.2	0.234		
NL 1800	NL PLSA 1800	Normal	NA	7.5	3.81
		TP53 p.P219L, c.656C>T			
0.80	0.02	0.2	0.123		
NL 1801	NL PLSA 1801	Normal	NA	7.5	1.06
		TP53 p.P82L, c.245C>T			
0.35	0.04	0.1	0.331		
NL 1802	NL PLSA 1802	Normal	NA	7.5	2.36
		TP53 p.A276V, c.827C>T			
0.67	0.03	0.2	0.125		
NL 1803	NL PLSA 1803	Normal	NA	7.5	0.95
		TP53 p.C176fs, c.528delC			
0.59	0.04	0.1	0.125		
NL 1804	NL PLSA 1804	Normal	NA	7.5	1.17
		PTEN p.R142Q, c.425G>A			
0.82	0.08	0.3	0.322		
NL 1805	NL PLSA 1805	Normal	NA	7.5	0.52
		CDKN2A p.R87Q, c.260G>A			
0.53	0.10	0.2	0.176		
NL 1806	NL PLSA 1806	Normal	NA	7.5	1.71
		TP53 p.S15G, c.43A>G			
0.58	0.01	0.1	0.125		
NL 1807	NL PLSA 1807	Normal	NA	7.5	2.26
		PTEN p.G129R, c.385G>A			
0.65	0.01	0.1	0.125		
NL 1808	NL PLSA 1808	Normal	NA	7.5	2.03
		TP53 p.P300S, c.898C>T			
0.82	0.02	0.1	0.306		
NL 1809	NL PLSA 1809	Normal	NA	7.5	0.81
		TP53 p.R174W, c.520A>T			
0.50	0.02	0.1	0.117		
NL 1810	NL PLSA 1810	Normal	NA	7.5	2.91
		FBXW7 p.R465H, c.1394G>A			
0.72	0.06	0.5	0.125		
NL 1811	NL PLSA 1811	Normal	NA	7.5	1.26
		TP53 p.A138V, c.413C>T			
0.68	0.07	0.3	0.121		

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NL 1812	NL PLSA 1812	Normal	NA	7.5	0.63
		TP53 p.G245S, c.733G>A			
0.35	0.04	0.1	0.596		
NL 1813	NL PLSA 1813	Normal	NA	7.5	0.95
		TP53 p.M384I, c.1152G>A			
0.48	0.04	0.1	0.121		
NL 1814	NL PLSA 1814	Normal	NA	7.5	1.83
		TP53 p.A138T, c.412G>A			
1.13	0.04	0.2	0.322		
NL 1815	NL PLSA 1815	Normal	NA	7.5	3.45
		TP53 p.E180G, c.539A>G			
0.77	0.02	0.2	0.116		
NL 1816	NL PLSA 1816	Normal	NA	7.5	0.83
		TP53 p.A83T, c.247G>A			
0.66	0.06	0.1	0.121		
NL 1817	NL PLSA 1817	Normal	NA	7.5	2.16
		TP53 p.T329A, c.985A>G			
0.81	0.03	0.2	0.125		
NL 1818	NL PLSA 1818	Normal	NA	7.5	6.00
		TP53 p.Q38R, c.113A>G			
0.82	0.01	0.3	0.125		
NL 1819	NL PLSA 1819	Normal	NA	7.5	1.74
		NRAS p.G12D, c.35G>A			
0.71	0.02	0.1	0.117		
NL 1820	NL PLSA 1820	Normal	NA	7.5	0.84
		TP53 p.Q136*, c.406C>T			
0.40	0.04	0.1	0.125		
NL 1821	NL PLSA 1821	Normal	NA	7.5	1.46
		TP53 p.R342Q, c.1025G>A			
0.50	0.04	0.2	0.117		
NL 1822	NL PLSA 1822	Normal	NA	7.5	1.00
		TP53 p.R273C, c.817C>T			
0.58	0.07	0.2	0.121		
NL 1823	NL PLSA 1823	Normal	NA	7.5	2.03
		GNAS p.L203P, c.608T>C			
0.92	0.02	0.1	0.125		
NL 1824	NL PLSA 1824	Normal	NA	7.5	1.55
		PPP2R1A p.R183W, c.547C>T			
0.62	0.04	0.2	0.125		
NL 1825	NL PLSA 1825	Normal	NA	7.5	1.44
		TP53 p.C277Y, c.830G>A			
0.64	0.05	0.2	0.122		
NL 1826	NL PLSA 1826	Normal	NA	7.5	1.75
		TP53 p.Q38H, c.114A>T			
0.45	0.02	0.1	0.805		
NL 1827	NL PLSA 1827	Normal	NA	7.5	0.79
		TP53 p.R174W, c.520A>T			
0.57	0.05	0.1	0.125		

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NL 1828	NL PLSA 1828	Normal	NA	7.5	2.33	
		TP53 p.R202C, c.604C>T				
0.78	0.07	0.5	0.116			
NL 1829	NL PLSA 1829	Normal	NA	7.5	1.41	
		TP53 p.A353V, c.1058C>T				
0.70	0.05	0.2	0.121			
NL 1830	NL PLSA 1830	Normal	NA	7.5	1.96	
		TP53 p.A159T, c.475G>A				
0.74	0.03	0.2	0.125			
NL 1831	NL PLSA 1831	Normal	NA	7.5	1.90	
		TP53 p.G245S, c.733G>A				
0.67	0.02	0.1	0.710			
NL 1832	NL PLSA 1832	Normal	NA	7.5	0.88	
		TP53 p.C176Y, c.527G>A				
0.31	0.03	0.1	0.123			
NL 1833	NL PLSA 1833	Normal	NA	7.5	1.23	
		PIK3CA p.N1044S, c.3131A>G				
0.66	0.07	0.3	0.587			
NL 1834	NL PLSA 1834	Normal	NA	7.5	0.57	
		HRAS p.G12S, c.34G>A				
0.39	0.02	0.0	0.125			
NL 1835	NL PLSA 1835	Normal	NA	7.5	1.31	
		TP53 p.L369P, c.1106T>C				
0.64	0.06	0.2	0.117			
NL 1836	NL PLSA 1836	Normal	NA	7.5	2.26	
		TP53 p.R333H, c.998G>A				
0.62	0.03	0.2	0.125			
NL 1837	NL PLSA 1837	Normal	NA	7.5	2.75	
		TP53 p.C176fs, c.528delC				
0.86	0.02	0.1	0.253			
NL 1838	NL PLSA 1838	Normal	NA	7.5	1.19	
		TP53 p.S99P, c.295T>C				
0.68	0.04	0.1	0.117			
NL 1839	NL PLSA 1839	Normal	NA	7.5	3.38	
		TP53 p.R202C, c.604C>T				
1.03	0.05	0.5	0.309			
NL 1840	NL PLSA 1840	Normal	NA	7.5	0.92	
		TP53 p.R174G, c.520A>G				
0.64	0.04	0.1	0.123			
NL 1841	NL PLSA 1841	Normal	NA	7.5	1.14	
		TP53 g.7579310A>G (Splice Site)				
0.31	0.03	0.1	0.121			
NL 1842	NL PLSA 1842	Normal	NA	7.5	1.70	
		TP53 p.S33fs, c.98delC				
1.01	0.03	0.1	0.305			
NL 1843	NL PLSA 1843	Normal	NA	7.5	3.50	
		TP53 p.R306*, c.916C>T				
0.81	0.04	0.4	0.122			

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NL 1844	NL PLSA 1844	Normal	NA	7.5	6.53
		TP53 g.7579311C>T (Splice Site)			
0.78	0.01	0.3	0.184		
NL 1845	NL PLSA 1845	Normal	NA	7.5	3.97
		BRAF p.V600E, c.1799T>A			
2.42	0.06	0.7	0.515		
NL 1846	NL PLSA 1846	Normal	NA	7.5	1.57
		TP53 p.R202C, c.604C>T			
0.86	0.03	0.1	0.125		
NL 1847	NL PLSA 1847	Normal	NA	7.5	1.18
		TP53 p.A86T, c.256G>A			
0.82	0.06	0.2	0.122		
NL 1848	NL PLSA 1848	Normal	NA	7.5	0.67
		PPP2R1A p.R182W, c.544C>T			
0.00	0.07	0.2	0.123		
NL 1849	NL PLSA 1849	Normal	NA	7.5	1.65
		TP53 p.G262S, c.784G>A			
0.67	0.07	0.3	0.125		
NL 1850	NL PLSA 1850	Normal	NA	7.5	1.36
		TP53 p.L130F, c.388C>T			
0.72	0.03	0.1	0.121		
NL 1851	NL PLSA 1851	Normal	NA	7.5	2.20
		KRAS p.V14I, c.40G>A			
0.71	0.02	0.1	0.125		
NL 1852	NL PLSA 1852	Normal	NA	7.5	4.27
		TP53 p.L348V, c.1042T>G			
0.97	0.01	0.1	0.116		
NL 1853	NL PLSA 1853	Normal	NA	7.5	0.66
		GNAS p.L203P, c.608T>C			
0.40	0.04	0.1	0.117		
NL 1854	NL PLSA 1854	Normal	NA	7.5	0.59
		GNAS p.L203P, c.608T>C			
0.50	0.03	0.1	0.125		
NL 1855	NL PLSA 1855	Normal	NA	7.5	2.50
		TP53 p.A353V, c.1058C>T			
0.79	0.04	0.3	0.125		
NL 1856	NL PLSA 1856	Normal	NA	7.5	3.11
		TP53 p.I255F, c.763A>T			
0.99	0.05	0.5	0.191		
NL 1857	NL PLSA 1857	Normal	NA	7.5	4.26
		TP53 p.E339G, c.1016A>G			
0.81	0.01	0.2	0.117		
NL 1858	NL PLSA 1858	Normal	NA	7.5	1.14
		TP53 p.L369P, c.1106T>C			
0.69	0.05	0.2	0.234		
NL 1859	NL PLSA 1859	Normal	NA	7.5	2.20
		TP53 p.A276V, c.827C>T			
1.15	0.04	0.3	0.325		

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NL 1860	NL PLSA 1860	Normal	NA	7.5	3.32	
		TP53 p.A189V, c.566C>T				
1.06	0.03	0.3	0.803			
NL 1861	NL PLSA 1861	Normal	NA	7.5	3.09	
		BRAF p.V600A, c.1799T>C				
0.78	0.02	0.2	0.116			
NL 1862	NL PLSA 1862	Normal	NA	7.5	2.06	
		TP53 p.E258*, c.772G>T				
0.84	0.01	0.1	0.125			
NL 1863	NL PLSA 1863	Normal	NA	7.5	7.63	
		KRAS p.A146T, c.436G>A				
0.87	0.01	0.3	0.116			
NL 1864	NL PLSA 1864	Normal	NA	7.5	3.46	
		KRAS p.A146T, c.436G>A				
1.09	0.02	0.2	0.317			
NL 1865	NL PLSA 1865	Normal	NA	7.5	2.79	
		FBXW7 p.R465C, c.1393C>T				
0.53	0.02	0.1	0.116			
NL 1866	NL PLSA 1866	Normal	NA	7.5	2.17	
		TP53 p.S376P, c.1126T>C				
1.12	0.02	0.1	0.324			
NL 1867	NL PLSA 1867	Normal	NA	7.5	0.89	
		TP53 p.D186N, c.556G>A				
0.91	0.09	0.2	0.122			
NL 1868	NL PLSA 1868	Normal	NA	7.5	1.29	
		CDKN2A p.A76T, c.226G>A				
0.49	0.05	0.2	0.125			
NL 1869	NL PLSA 1869	Normal	NA	7.5	0.49	
		KRAS p.G12A, c.35G>C				
0.33	0.03	0.1	0.121			
NL 1870	NL PLSA 1870	Normal	NA	7.5	0.77	
		TP53 p.G302R, c.904G>A				
0.67	0.03	0.1	0.123			
PANC 669	PANC 669 PLS 1	Pancreas	II	7.5	16.28	
		TP53 p.C176fs, c.528delC				
1.12	0.03	1.4	0.982			
PANC 670	PANC 670 PLS 1	Pancreas	II	7.5	3.29	
		KRAS p.G12V, c.35G>T				
0.81	0.07	0.7	0.560			
PANC 671	PANC 671 PLS 1	Pancreas	II	7.5	27.73	
		KRAS p.G12V, c.35G>T				
1.69	0.04	3.0	0.994			
PANC 672	PANC 672 PLS 1	Pancreas	II	7.5	8.17	
		TP53 p.A159T, c.475G>A				
1.08	0.03	0.8	0.982			
PANC 673	PANC 673 PLS 1	Pancreas	II	7.5	4.94	
		KRAS p.G12V, c.35G>T				
1.09	0.10	1.5	0.423			

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PANC 674	PANC 674 PLS 1	Pancreas	II	7.5	7.53	
	KRAS p.G12D, c.35G>A					
1.19	0.04	1.0	0.993			
PANC 675	PANC 675 PLS 1	Pancreas	II	7.5	3.97	
	TP53 p.F109V, c.325T>G					
19.28	2.16	26.4	1.000			
PANC 676	PANC 676 PLS 1	Pancreas	II	7.5	5.18	
	GNAS p.R201H, c.602G>A					
1.19	0.05	0.7	0.977			
PANC 677	PANC 677 PLS 1	Pancreas	II	7.5	14.44	
	TP53 p.C238Y, c.713G>A					
2.91	0.60	26.5	1.000			
PANC 678	PANC 678 PLS 1	Pancreas	II	7.5	14.28	
	FBXW7 p.R367*, c.1099C>T					
0.66	0.02	1.0	0.463			
PANC 679	PANC 679 PLS 1	Pancreas	II	7.5	7.76	
	TP53 p.K372fs, c.1114delA					
0.75	0.07	1.7	0.605			
PANC 680	PANC 680 PLS 1	Pancreas	II	7.5	5.40	
	TP53 p.K372fs, c.1114delA					
1.22	0.08	1.3	0.822			
PANC 757	PANC 757 PLS 1	Pancreas	II	7.5	13.14	
	TP53 p.K372fs, c.1114delA					
0.85	0.05	2.2	0.231			
PANC 758	PANC 758 PLS 1	Pancreas	II	7.5	3.49	
	TP53 p.L369M, c.1105C>A					
0.71	0.03	0.3	0.679			
PANC 759	PANC 759 PLS 1	Pancreas	II	7.5	11.66	
	KRAS p.G12V, c.35G>T					
0.98	0.02	0.8	0.832			
PANC 760	PANC 760 PLS 1	Pancreas	II	7.5	1.97	
	BRAF p.T599I, c.1796C>T					
0.43	0.04	0.2	0.872			
PANC 761	PANC 761 PLS 1	Pancreas	II	7.5	2.01	
	TP53 p.P309S, c.925C>T					
0.63	0.01	0.1	0.904			
PANC 762	PANC 762 PLS 1	Pancreas	II	7.5	10.33	
	KRAS p.G12R, c.34G>C					
1.90	0.05	1.6	1.000			
PANC 764	PANC 764 PLS 1	Pancreas	II	7.5	9.08	
	TP53 p.C176Y, c.527G>A					
1.15	0.03	0.7	0.989			
PANC 765	PANC 765 PLS 1	Pancreas	II	7.5	12.46	
	KRAS p.G12D, c.35G>A					
2.14	0.07	2.6	1.000			
PANC 766	PANC 766 PLS 1	Pancreas	I	7	8.57	
	TP53 p.C176fs, c.528delC					
1.13	0.03	0.7	0.995			

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PANC 767	PANC 767 PLS 1	Pancreas	II	7.5	1.71	TP53 p.V173L, c.517G>T
1.19	0.03	0.2	0.457			
PANC 768	PANC 768 PLS 1	Pancreas	II	7.5	1.77	TP53 p.L348S, c.1043T>C
0.89	0.03	0.2	0.125			
PANC 769	PANC 769 PLS 1	Pancreas	II	7.5	2.84	TP53 p.A161T, c.481G>A
0.90	0.02	0.2	0.804			
PANCA 1001	PANCA 1001 PLS 1	Pancreas	II	6	4.44	TP53 p.G245D, c.734G>A
0.81	0.04	0.6	0.980			
PANCA 1004	PANCA 1004 PLS 1	Pancreas	II	7	3.08	TP53 p.K139N, c.417G>T
2.97	0.20	1.9	0.994			
PANCA 1005	PANCA 1005 PLS 1	Pancreas	II	7.5	3.90	TP53 p.R333H, c.998G>A
0.89	0.04	0.5	0.993			
PANCA 1006	PANCA 1006 PLS 1	Pancreas	II	7.5	109.97	TP53 p.G374fs, c.1120delG
1.03	0.03	11.0	0.999			
PANCA 1008	PANCA 1008 PLS 1	Pancreas	II	7.5	6.96	GNAS p.R201H, c.602G>A
1.44	0.16	3.5	0.911			
PANCA 1009	PANCA 1009 PLS 1	Pancreas	II	7.5	2.59	TP53 p.I195F, c.583A>T
11.87	1.73	13.8	1.000			
PANCA 1010	PANCA 1010 PLS 1	Pancreas	I	7.5	4.18	TP53 g.7577156C>T (Splice Site)
0.88	0.06	0.7	0.125			
PANCA 1011	PANCA 1011 PLS 1	Pancreas	II	7.5	14.89	KRAS p.G12D, c.35G>A
1.84	0.06	2.8	0.999			
PANCA 1012	PANCA 1012 PLS 1	Pancreas	II	7.5	3.04	TP53 p.P47L, c.140C>T
0.42	0.05	0.5	0.794			
PANCA 1013	PANCA 1013 PLS 1	Pancreas	III	7.5	12.68	TP53 p.P47L, c.140C>T
1.09	0.04	1.6	0.989			
PANCA 1014	PANCA 1014 PLS 1	Pancreas	II	7.5	25.75	TP53 p.R283P, c.848G>C
2.66	0.06	4.7	0.997			
PANCA 1015	PANCA 1015 PLS 1	Pancreas	III	7.5	3.57	TP53 p.R283H, c.848G>A
0.44	0.12	1.3	0.968			
PANCA 1016	PANCA 1016 PLS 1	Pancreas	I	7.5	3.82	GNAS p.R201S, c.601C>A
0.55	0.05	0.6	0.884			

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PANCA 1018	PANCA 1018 PLS 1	Pancreas	II	7.5	10.34	TP53 p.R202C, c.604C>T	1.04	0.04	1.3	1.000
PANCA 1020	PANCA 1020 PLS 1	Pancreas	II	7.5	8.66	TP53 p.R202C, c.604C>T	1.02	0.07	1.7	0.999
PANCA 1022	PANCA 1022 PLS 1	Pancreas	II	7.5	13.86	TP53 p.C176fs, c.528delC	1.15	0.03	1.2	0.994
PANCA 1024	PANCA 1024 PLS 1	Pancreas	II	7.5	1.49	TP53 p.A159T, c.475G>A	0.61	0.08	0.4	0.117
PANCA 1025	PANCA 1025 PLS 1	Pancreas	III	7.5	3.82	KRAS p.G12D, c.35G>A	3.81	1.17	13.8	0.988
PANCA 1028	PANCA 1028 PLS 1	Pancreas	III	7.5	3.06	TP53 p.A159T, c.475G>A	1.19	0.05	0.5	0.910
PANCA 1030	PANCA 1030 PLS 1	Pancreas	II	7.5	12.93	TP53 p.I255N, c.764T>A	2.95	0.10	4.1	0.999
PANCA 1031	PANCA 1031 PLS 1	Pancreas	II	7.5	1.97	TP53 p.R202C, c.604C>T	0.90	0.08	0.5	0.978
PANCA 1034	PANCA 1034 PLS 1	Pancreas	II	7.5	3.16	TP53 p.A88fs, c.263delC	0.00	0.06	0.6	0.969
PANCA 1036	PANCA 1036 PLS 1	Pancreas	II	7.5	2.21	TP53 p.R379S, c.1135C>A	0.00	0.16	1.1	0.402
PANCA 1037	PANCA 1037 PLS 1	Pancreas	II	7.5	29.96	TP53 p.P177R, c.530C>G	1.49	0.02	2.0	0.857
PANCA 1039	PANCA 1039 PLS 1	Pancreas	II	7.5	6.89	TP53 p.K372fs, c.1114delA	0.68	0.05	1.1	0.693
PANCA 1040	PANCA 1040 PLS 1	Pancreas	II	7.5	10.00	TP53 p.P300fs, c.898delC	1.30	0.03	0.9	0.987
PANCA 1042	PANCA 1042 PLS 1	Pancreas	II	7.5	6.70	KRAS p.G12V, c.35G>T	2.44	0.18	3.8	0.502
PANCA 1043	PANCA 1043 PLS 1	Pancreas	II	7.5	2.41	TP53 p.A159T, c.475G>A	0.55	0.07	0.5	0.998
PANCA 1044	PANCA 1044 PLS 1	Pancreas	II	7.5	4.25	KRAS p.G12R, c.34G>C	2.91	0.24	3.1	1.000

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PANCA 1047	PANCA 1047 PLS 1	Pancreas	II	7	2.13	TP53 p.P151fs, c.451insC	0.00	0.07	0.4	0.824
PANCA 1048	PANCA 1048 PLS 1	Pancreas	III	7.5	77.12	TP53 p.R174G, c.520A>G	0.98	0.02	4.4	0.929
PANCA 1050	PANCA 1050 PLS 1	Pancreas	II	7.5	37.90	CTNNB1 p.G34R, c.100G>A	1.06	0.01	1.6	0.947
PANCA 1051	PANCA 1051 PLS 1	Pancreas	II	7.5	26.98	TP53 p.K372fs, c.1114delA	1.03	0.04	3.2	0.993
PANCA 1052	PANCA 1052 PLS 1	Pancreas	II	7.5	4.34	TP53 p.R283C, c.847C>T	0.60	0.16	2.1	0.406
PANCA 1053	PANCA 1053 PLS 1	Pancreas	II	7	22.34	TP53 p.E336G, c.1007A>G	1.10	0.02	1.2	0.987
PANCA 1054	PANCA 1054 PLS 1	Pancreas	II	7.5	8.34	TP53 p.R202C, c.604C>T	0.41	0.03	0.7	0.986
PANCA 1055	PANCA 1055 PLS 1	Pancreas	II	7	1.92	TP53 p.R156H, c.467G>A	0.00	0.06	0.3	0.122
PANCA 1056	PANCA 1056 PLS 1	Pancreas	II	7.5	8.77	TP53 p.I232N, c.695T>A	1.37	0.11	3.0	0.997
PANCA 1057	PANCA 1057 PLS 1	Pancreas	II	7.5	2.44	TP53 p.R175C, c.523C>T	0.00	0.07	0.6	0.284
PANCA 1058	PANCA 1058 PLS 1	Pancreas	II	7.5	7.76	TP53 p.R202C, c.604C>T	0.91	0.05	1.1	0.957
PANCA 1059	PANCA 1059 PLS 1	Pancreas	II	7.5	3.11	KRAS p.Q61H, c.183A>T	0.78	0.11	1.1	0.877
PANCA 1061	PANCA 1061 PLS 1	Pancreas	II	7.5	17.39	TP53 p.S241fs, c.722delC	5.83	0.27	14.6	0.999
PANCA 1063	PANCA 1063 PLS 1	Pancreas	II	7.5	2.67	KRAS p.Q61H, c.183A>C	0.00	0.12	1.0	0.701
PANCA 1149	PANCA 1149 PLS 1	Pancreas	II	4	19.28	TP53 p.A138T, c.412G>A	1.03	0.04	2.4	0.905
PANCA 1152	PANCA 1152 PLS 1	Pancreas	I	3	11.79	TP53 p.R273H, c.818G>A	1.39	0.42	15.4	0.690

Table3.txt

PANCA 1153	PANCA 1153 PLS 1	Pancreas	II	7.5		10.42
		TP53 p.E346D, c.1038G>T				
0.98	0.02	0.5		0.877		
PANCA 1155	PANCA 1155 PLS 1	Pancreas	II	7.5		9.02
		KRAS p.G12D, c.35G>A				
2.69	0.11	2.9		1.000		
PANCA 1156	PANCA 1156 PLS 1	Pancreas	II	7.5		1.60
		TP53 p.A161T, c.481G>A				
0.75	0.03	0.2		0.224		
PAP 938	PAP 938 PLS 1	Ovary	III	5		6.59
		TP53 p.S127fs, c.380delC				
60.45	18.18	369.1		1.000		
PAP 939	PAP 939 PLS 1	Ovary	III	5		10.83
		TP53 p.Y163C, c.488A>G				
252.57	43.92	1,464.8		1.000		
PAP 940	PAP 940 PLS 1	Ovary	III	5		11.54
		TP53 p.Y163C, c.488A>G				
20.13	2.42	86.1		1.000		
PAP 941	PAP 941 PLS 1	Ovary	III	5		9.21
		BRAF p.V600E, c.1799T>A				
8.02	0.36	10.3		1.000		
PAP 944	PAP 944 PLS 1	Ovary	III	5		4.35
		KRAS p.G12D, c.35G>A				
1.65	0.24	3.3		0.998		
PAP 945	PAP 945 PLS 1	Ovary	III	5		10.63
		TP53 p.D259V, c.776A>T				
260.70	9.47	310.1		1.000		
PAP 946	PAP 946 PLS 1	Ovary	III	5		5.59
		TP53 p.S241F, c.722C>T				
3.22	0.29	5.1		1.000		
PAP 947	PAP 947 PLS 1	Ovary	III	5		6.81
		TP53 p.H168Q, c.504C>G				
10.49	0.24	5.0		0.999		
PAP 949	PAP 949 PLS 1	Ovary	III	5		13.59
		TP53 g.7576852C>T (Splice Site)				
3.31	0.13	5.6		1.000		
PAP 950	PAP 950 PLS 1	Ovary	III	5		10.15
		TP53 p.L130F, c.388C>T				
15.94	1.96	61.3		1.000		
PAP 951	PAP 951 PLS 1	Ovary	III	5		4.12
		TP53 p.G245D, c.734G>A				
1.51	0.05	0.6		0.836		
PAP 953	PAP 953 PLS 1	Ovary	III	5		6.60
	TP53 p.F341fs, c.1022delGTGGGCGTGAGCGCTTCGAGATGTT (SEQ ID NO:748)					
2.03	0.03	0.5		0.998		
PAP 954	PAP 954 PLS 1	Ovary	III	5		33.14
		TP53 p.R175H, c.524G>A				
6.20	23.40	2,388.5		1.000		

Table3.txt

PAP 955	PAP 955 PLS 1	Ovary	III	5	5.75		
TP53 p.T155N, c.464C>A							
9.22	0.45	8.0	1.000				
PAP 956	PAP 956 PLS 1	Ovary	III	5	22.89		
TP53 p.P278S, c.832C>T							
210.57	52.34	3,690.7	1.000				
PAP 957	PAP 957 PLS 1	Ovary	III	5	5.85		
TP53 p.M340fs, c.1018delTCGAGA							
1.91	0.07	1.2	0.983				
PAP 959	PAP 959 PLS 1	Ovary	III	5	4.72		
TP53 p.E336fs, c.1006insGAGCGCTTC							
10.55	0.60	8.7	1.000				
PAP 961	PAP 961 PLS 1	Ovary	III	5	21.78		
TP53 p.T211A, c.631A>G							
9.98	0.44	29.7	1.000				
PAP 962	PAP 962 PLS 1	Ovary	III	5	13.61		
TP53 p.V218G, c.653T>G							
7.50	0.31	13.0	0.992				
PAP 974	PAP 974 PLS 1	Ovary	I	5	8.88		
TP53 p.V216L, c.646G>C							
56.77	4.58	125.3	1.000				
PAPA 1330	PAPA 1330 PLS 1	Ovary	III	3.5	29.23		
BRAF p.G596R, c.1786G>C							
17.73	1.00	90.3	1.000				
PAPA 1331	PAPA 1331 PLS 1	Ovary	III	3.5	45.45		
TP53 p.R306*, c.916C>T							
3.70	2.96	414.6	1.000				
PAPA 1332	PAPA 1332 PLS 1	Ovary	I	3.5	61.19		
TP53 p.K372fs, c.1114delA							
1.18	0.07	12.8	0.971				
PAPA 1333	PAPA 1333 PLS 1	Ovary	III	3.5	19.89		
TP53 p.A353V, c.1058C>T							
0.92	0.04	2.6	0.994				
PAPA 1334	PAPA 1334 PLS 1	Ovary	III	3.5	17.60		
TP53 p.R267P, c.800G>C							
10.16	1.36	73.8	0.999				
PAPA 1335	PAPA 1335 PLS 1	Ovary	III	3.5	8.71		
TP53 p.F341fs, c.1023delC							
24.76	2.93	78.4	0.999				
PAPA 1336	PAPA 1336 PLS 1	Ovary	I	3.5	29.40		
CTNNB1 p.S33Y, c.98C>A							
26.13	11.72	1,061.3	1.000				
PAPA 1339	PAPA 1339 PLS 1	Ovary	I	3.5	52.87		
CTNNB1 p.S33P, c.97T>C							
169.01	6.15	1,001.5	1.000				
PAPA 1342	PAPA 1342 PLS 1	Ovary	III	3.5	21.31		
TP53 p.L264fs, c.792delA							
35.67	4.77	312.9	1.000				

Table3.txt

PAPA 1343	PAPA 1343 PLS 1		Ovary	III	3.5	89.38		
		TP53 p.S127F, c.380C>T						
6.48	2.09	574.1	1.000					
PAPA 1344	PAPA 1344 PLS 1		Ovary	III	3.5	17.07		
		TP53 p.C176fs, c.528delC						
1.07	0.02	1.2	0.871					
PAPA 1345	PAPA 1345 PLS 1		Ovary	III	3.5	39.86		
		TP53 p.P177R, c.530C>G						
70.80	2.00	245.1	1.000					
PAPA 1346	PAPA 1346 PLS 1		Ovary	III	3.5	42.94		
		TP53 p.R249G, c.745A>G						
40.97	15.62	2,066.3	1.000					
PAPA 1347	PAPA 1347 PLS 1		Ovary	I	3.5	30.11		
		PIK3CA p.H1047R, c.3140A>G						
3.00	0.18	16.3	1.000					
PAPA 1348	PAPA 1348 PLS 1		Ovary	III	3.5	47.69		
		TP53 p.R273L, c.818G>T						
4.71	0.19	28.5	0.999					
PAPA 1349	PAPA 1349 PLS 1		Ovary	III	3.5	24.47		
		TP53 p.S241F, c.722C>T						
35.28	6.38	480.6	1.000					
PAPA 1350	PAPA 1350 PLS 1		Ovary	II	3.5	5.73		
		CDKN2A p.R87Q, c.260G>A						
0.49	0.05	0.8	0.941					
PAPA 1353	PAPA 1353 PLS 1		Ovary	I	3.5	6.55		
		TP53 p.P300fs, c.898delC						
0.97	0.03	0.6	0.920					
PAPA 1354	PAPA 1354 PLS 1		Ovary	I	3.5	22.83		
		TP53 p.R249G, c.745A>G						
3.84	0.74	51.9	0.990					
PAPA 1355	PAPA 1355 PLS 1		Ovary	III	3.5	64.51		
		TP53 g.7579311C>G (Splice Site)						
10.11	1.88	374.1	0.999					
PAPA 1356	PAPA 1356 PLS 1		Ovary	II	3.5	13.71		
		TP53 p.R282W, c.844C>T						
0.73	0.05	2.2	1.000					
PAPA 1357	PAPA 1357 PLS 1		Ovary	III	3.5	19.81		
		TP53 g.7576927C>T (Splice Site)						
1.42	0.03	1.6	1.000					

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

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Table 4. Concentrations of assayed protein biomarker in plasma samples from cancer patients and healthy controls.

Angiopoietin-2 (pg/ml)	AXL (pg/ml)	CA125 (U/ml)	CA15-3 (U/ml)	AJCC CA19-9 (U/ml)	AFP CD44 (ng/ml)	CEA (pg/ml)
CYFRA 21-1 (pg/ml)	DKK1 (ng/ml)	Endoglin (pg/ml)	FGF2 (pg/ml)	Follistatin (pg/ml)	Galectin-3 (ng/ml)	
Patient ID #	Sample ID #	Tumor type	Stage			
CRC 455	CRC 455 PLS 1	Colorectum	I	1583.45		
5598.50	3621.04	5.09	19.08	*2.742	9.81	540.1
*323.109	0.78	2882.65	92.02	2144.33	11.19	
CRC 456	CRC 456 PLS 1	Colorectum	I	*119.218		
20936.35	2772.96	7.27	10.04	40.91	27.57	5,902.4
*323.109	0.77	3921.77	164.06	1646.26	9.9	
CRC 457	CRC 457 PLS 1	Colorectum	II	4365.53		
2350.93	4120.77	*0.809	16.96	*2.742	14.59	973.8
1976.94	0.9	2410.16	154.77	2486.88	11.61	
CRC 458	CRC 458 PLS 1	Colorectum	II	*119.218		
1604.34	2029.96	5.39	8.31	*2.742	7.78	2,027.5
*323.109	0.64	1284.96	227.57	829.43	4.8	
CRC 459	CRC 459 PLS 1	Colorectum	II	801.3		
2087.57	2069.17	*0.809	11.73	*2.742	12.21	614.5
*323.109	0.78	2552.72	134.72	2168.23	8.92	
CRC 460	CRC 460 PLS 1	Colorectum	II	*119.218		
1147.55	2054.9	*0.809	5.49	39.51	6.97	1,242.3
*323.109	0.75	2459.5	123.75	1341.11	6.25	
CRC 461	CRC 461 PLS 1	Colorectum	I	1975.13		
1900.89	3499.99	6.33	16.65	*2.742	12.21	755.77
3329.43	0.86	1566.22	172.95	1765.41	7.67	
CRC 462	CRC 462 PLS 1	Colorectum	I	992.17		
1783.54	2478.39	*0.809	11.44	*2.742	11.23	478.98
*323.109	0.71	1574.6	145.02	1484.83	8.25	
CRC 463	CRC 463 PLS 1	Colorectum	I	1039.85		
1103.02	954.25	5.7	6.23	36.31	*1.367	895.66
1976.94	0.59	1513.17	205.52	790.19	5.63	
CRC 464	CRC 464 PLS 1	Colorectum	III	6002.13		
1942.35	1692.65	*0.809	7.29	*2.742	10.87	818.81
*323.109	0.64	2392.78	177.27	1229.47	14.81	
CRC 465	CRC 465 PLS 1	Colorectum	II	772.64		
2371.75	4878.84	6.02	6.25	45.91	17.2	2,038.8
2129.61	0.69	1931.79	99.02	1291.93	14.62	
CRC 466	CRC 466 PLS 1	Colorectum	III	868.13		
1198.96	2375.93	*0.809	15.11	*2.742	11.64	672.19
*323.109	0.81	2581.94	177.27	1831.13	10.06	
CRC 467	CRC 467 PLS 1	Colorectum	III	*119.218		
2747.35	2370.46	*0.809	7.98	19.32	11.05	22,271.3

Table4.txt

*323.109	0.98	2687.53	111.94	1246.24	11.95		
CRC 468	CRC 468 PLS 1		Colorectum	III	2387.08		
1597.46	1777.87	*0.809	24.41	*2.742	9.29	8,587.4	
*323.109	0.72	1917.63	123.75	2564.16	6.09		
CRC 469	CRC 469 PLS 1		Colorectum	II	3003.1		
764.67	1089.96	*0.809	11.00	*2.742	10.74	911.83	
*323.109	1.3	2280.16	111.94	1341.11	7.26		
CRC 470	CRC 470 PLS 1		Colorectum	II	1545.28		
1343.05	1018.57	14.64	17.44	26.84	7.37	3,352.6	
3181.21	0.81	1796.21	213.06	1476.98	14.21		
CRC 471	CRC 471 PLS 1		Colorectum	III	1182.88		
761.26	752.44	5.09	26.84	26.03	*1.367	2,209.4	
*323.109	0.62	1376.69	189.77	910.64	8.42		
CRC 472	CRC 472 PLS 1		Colorectum	II	4189.1		
2778.72	2637.05	*0.809	26.23	115.84	7.49	17219.93	
*323.109	0.72	1994.19	123.75	819.68	10.3		
CRC 473	CRC 473 PLS 1		Colorectum	II	1573.91		
1260.68	1909.47	*0.809	13.18	*2.742	9.77	2,163.7	
2129.61	0.73	1613.75	111.94	980.12	8.65		
CRC 474	CRC 474 PLS 1		Colorectum	III	*119.218		
1075.63	1500.21	*0.809	11.85	*2.742	8.49	537.1	
*323.109	0.74	1711.85	123.75	559.01	8.1		
CRC 475	CRC 475 PLS 1		Colorectum	I	4149.94		
901.22	428.41	6.64	7.34	*2.742	8.18	*74.59	
*323.109	0.68	1931.79	159.46	1139.99	11.37		
CRC 476	CRC 476 PLS 1		Colorectum	II	*119.218		
2066.81	2341.33	*0.809	9.54	*2.742	7.49	2,696.2	
3550.97	0.96	1616.55	172.95	984.69	8.99		
CRC 477	CRC 477 PLS 1		Colorectum	II	2291.16		
1935.44	2079.89	*0.809	13.79	*2.742	17.39	*74.59	
*323.109	0.94	2125.25	111.94	1867.27	8.13		
CRC 478	CRC 478 PLS 1		Colorectum	III	2396.68		
2170.66	1713.47	*0.809	12.30	*2.742	14.1	3910.80	
*323.109	0.69	*26.35	201.67	625.11	0.7		
CRC 479	CRC 479 PLS 1		Colorectum	II	*119.218		
2198.37	3323.7	*0.809	20.40	23.39	10.99	4,489.4	
*323.109	0.69	2699.29	111.94	1113.95	6.25		
CRC 480	CRC 480 PLS 1		Colorectum	III	*119.218		
2174.12	2625.93	*0.809	4.21	*2.742	8.57	*74.59	
*323.109	0.87	1176.64	123.75	891.78	6.49		
CRC 481	CRC 481 PLS 1		Colorectum	II	7022.24		
2413.41	2256.06	*0.809	19.57	292.07	8.26	2,110.5	
*323.109	0.72	731.81	111.94	1043.36	10.02		
CRC 482	CRC 482 PLS 1		Colorectum	III	*119.218		
624.96	970.28	*0.809	12.51	19.11	*1.367	1,753.1	
*323.109	0.69	1532.71	273.79	952.55	2.75		
CRC 483	CRC 483 PLS 1		Colorectum	I	*119.218		
2073.73	1703.06	*0.809	10.84	*2.742	10.77	1006.64	

Table4.txt

*323.109	0.71	1588.58	111.94	1065.61	3.89		
CRC 484	CRC 484 PLS 1		Colorectum	I	1965.57		
2517.64	2203.7	*0.809	12.01	123.22	10.68	2,125.7	
*323.109	0.75	1672.57	149.95	1052.28	5.17		
CRC 486	CRC 486 PLS 1		Colorectum	I	9728.86		
679.45	1231.3	5.7	19.68	17.68	*1.367	2,046.3	
3918.28	0.58	1265.52	326.05	352.26	5.46		
CRC 487	CRC 487 PLS 1		Colorectum	I	1850.84		
2219.16	2936.38	8.53	21.77	18.91	8.79	1113.21	
*323.109	1.02	1818.75	111.94	1254.59	6.41		
CRC 488	CRC 488 PLS 1		Colorectum	II	*119.218		
1945.80	1671.88	5.7	3.35	*2.742	9.5	3,004.8	
*323.109	0.78	1154.42	145.02	1433.55	4.58		
CRC 489	CRC 489 PLS 1		Colorectum	II	*119.218		
1377.39	2361.35	48.49	5.11	88.34	*1.367	8,477.7	
2883.42	0.78	1254.41	134.72	1324.79	7.02		
CRC 490	CRC 490 PLS 1		Colorectum	III	*119.218		
1044.83	2104.92	*0.809	6.23	*2.742	11.61	1,651.3	
*323.109	0.77	1432.35	99.02	1935.22	3.92		
CRC 491	CRC 491 PLS 1		Colorectum	III	858.58		
1952.71	3585.82	5.39	11.60	39.31	15.92	1,479.4	
*323.109	0.78	2005.56	99.02	998.34	7.54		
CRC 492	CRC 492 PLS 1		Colorectum	III	*119.218		
4254.90	841.52	57.91	21.49	18.91	11.79	8487.66	
*323.109	0.73	466.66	279.93	435.56	15.7		
CRC 493	CRC 493 PLS 1		Colorectum	II	3516.3		
720.35	2592.62	5.09	27.44	65.15	8.45	4806.52	
*323.109	0.57	1337.76	111.94	755.25	8.14		
CRC 494	CRC 494 PLS 1		Colorectum	II	*119.218		
1542.39	1462.8	*0.809	10.13	*2.742	19.18	560.7	
*323.109	0.6	1813.12	*14.089	943.3	6.84		
CRC 495	CRC 495 PLS 1		Colorectum	I	*119.218		
400.65	3010.15	*0.809	15.15	*2.742	*1.367	*74.59	
*323.109	0.78	1566.22	84.54	1152.93	8.59		
CRC 496	CRC 496 PLS 1		Colorectum	I	*119.218		
3040.55	3585.82	*0.809	4.90	66.53	16.16	1099.78	
*323.109	0.63	2145.26	92.02	2506.28	11.24		
CRC 497	CRC 497 PLS 1		Colorectum	III	782.2		
4173.41	7223.76	5.09	13.52	*2.742	23.89	15,904.1	
*323.109	0.77	3064.83	181.51	887.04	8.27		
CRC 498	CRC 498 PLS 1		Colorectum	III	1030.32		
1907.80	2187.49	5.39	24.17	124.19	10.01	578.6	
*323.109	0.71	2056.77	181.51	1341.11	7.47		
CRC 499	CRC 499 PLS 1		Colorectum	I	*119.218		
567.11	1181.73	*0.809	7.29	*2.742	8.41	*74.59	
*323.109	1.09	813.86	164.06	1204.16	4.7		
CRC 500	CRC 500 PLS 1		Colorectum	I	8295.07		
2587.19	4479.12	*0.809	7.07	*2.742	18.56	812.47	

Table4.txt

*323.109	0.76	1387.82	145.02	1034.42	12.59	
CRC 501	CRC 501 PLS 1		Colorectum	I	*119.218	
1212.67	1990.86	*0.809	24.57	*2.742	17.22	895.7
2281.58	1.08	1555.04	164.06	1668.84	12.54	
CRC 502	CRC 502 PLS 1		Colorectum	I	*119.218	
1243.53	2212.72	*0.809	7.70	24.00	*1.367	1479.41
*323.109	0.65	2148.13	154.77	1308.4	10.42	
CRC 503	CRC 503 PLS 1		Colorectum	I	*119.218	
1852.56	2237.99	*0.809	5.48	*2.742	10.99	737.0
*323.109	0.84	590.99	*14.089	760.28	7.74	
CRC 504	CRC 504 PLS 1		Colorectum	III	4140.16	
4684.89	2083.46	7.58	9.38	57.83	*1.367	79,678.8
3918.28	0.77	1215.52	168.55	1357.35	15.29	
CRC 505	CRC 505 PLS 1		Colorectum	III	*119.218	
1473.60	1289.49	*0.809	6.15	16.45	10.24	5435.06
*323.109	0.64	1151.64	84.54	1208.39	4.65	
CRC 506	CRC 506 PLS 1		Colorectum	III	*119.218	
1449.54	877.83	*0.809	14.10	*2.742	12.46	1,150.3
*323.109	0.69	2308.97	99.02	943.3	6.63	
CRC 507	CRC 507 PLS 1		Colorectum	I	*133.814	
992.76	3019.58	5.24	9.09	*2.745	11.04	4524.32
*328.934	0.84	584.2	110.68	978.25	3.92	
CRC 508	CRC 508 PLS 1		Colorectum	I	*133.814	
2548.80	4892.6	*0.83	6.26	*2.745	27.13	2,287.1
*328.934	0.88	1618.37	*14.113	864.9	8.79	
CRC 509	CRC 509 PLS 1		Colorectum	I	*133.814	
1316.41	1718.73	*0.83	12.64	*2.745	16.99	577.4
*328.934	1.03	2110.06	110.68	418.05	4.7	
CRC 510	CRC 510 PLS 1		Colorectum	I	905.21	
1746.69	2083.3	4.98	4.01	*2.745	15.63	1503.59
*328.934	0.74	1841.97	84.68	1012.2	0.86	
CRC 511	CRC 511 PLS 1		Colorectum	II	*133.814	
1586.62	1950.29	8.31	6.68	*2.745	15.76	*74.812
*328.934	0.73	1004	150.94	185.72	4.36	
CRC 512	CRC 512 PLS 1		Colorectum	II	1513.35	
14107.58	2111.12	*0.83	12.44	*2.745	22.1	13,183.2
*328.934	1.05	1895.31	98.45	2113.67	12.2	
CRC 513	CRC 513 PLS 1		Colorectum	II	*133.814	
2733.88	3591.1	*0.83	52.72	*2.745	51.76	608.3
*328.934	1.47	3102.55	84.68	1491.11	3.63	
CRC 514	CRC 514 PLS 1		Colorectum	II	2500.76	
1096.07	2947.15	*0.83	35.69	22.57	16.26	2,960.4
*328.934	1.15	1432.17	*14.113	1286.89	7.07	
CRC 515	CRC 515 PLS 1		Colorectum	II	843.61	
1799.04	2730.25	*0.83	4.31	*2.745	14.35	1751.77
*328.934	0.83	1747.51	84.68	1037.41	4.95	
CRC 516	CRC 516 PLS 1		Colorectum	II	*133.814	
2311.34	3267.52	*0.83	3.18	*2.745	27.4	906.9

Table4.txt

*328.934	0.8	2140.06	84.68	1371.35	2.66		
CRC 517	CRC 517 PLS 1		Colorectum	II	1221.64		
694.14	2963.24	*0.83	3.23	*2.745	11.93	476.2	
*328.934	0.9	1691.64	*14.113	569.68	0.53		
CRC 518	CRC 518 PLS 1		Colorectum	III	*133.814		
1531.17	4413.2	5.77	8.25	19.81	17.73	1,385.1	
1973.6	0.85	2576.62	*14.113	801.71	7.44		
CRC 519	CRC 519 PLS 1		Colorectum	III	2075.04		
867.21	1498.01	*0.83	16.17	*2.745	11.55	582.53	
*328.934	1.06	1208	110.68	943.88	0.26		
CRC 520	CRC 520 PLS 1		Colorectum	III	*133.814		
1857.99	1274.4	*0.83	5.07	*2.745	14.94	603.1	
*328.934	1.09	*28.66	110.68	600.29	13.33		
CRC 521	CRC 521 PLS 1		Colorectum	III	*133.814		
1436.71	2146.92	*0.83	4.08	*2.745	13.98	2,482.4	
*328.934	0.7	1841.97	*14.113	995.27	4.19		
CRC 522	CRC 522 PLS 1		Colorectum	II	*133.814		
870.42	1521.61	4.98	11.69	*2.745	19.81	*74.812	
*328.934	1.89	2152.07	*14.113	1446.61	3.26		
CRC 523	CRC 523 PLS 1		Colorectum	III	*133.814		
2087.64	2077.33	6.84	16.20	*2.745	11.49	885.0	
*328.934	0.7	1516.3	*14.113	*20.74	3.53		
CRC 524	CRC 524 PLS 1		Colorectum	II	*133.814		
970.19	2346.15	9.53	4.37	21.47	15.55	1,420.4	
*328.934	0.73	1927.97	141.81	769.47	0.67		
CRC 525	CRC 525 PLS 1		Colorectum	III	*133.814		
6809.77	2288.32	*0.83	12.92	*2.745	19.21	17,514.4	
*328.934	0.62	2092.08	98.45	383.14	1.43		
CRC 526	CRC 526 PLS 1		Colorectum	III	*133.814		
774.14	719.4	4.98	6.81	*2.745	11.93	466.2	
*328.934	0.71	764.47	84.68	838.02	5.76		
CRC 527	CRC 527 PLS 1		Colorectum	III	*133.814		
851.14	2890.86	*0.83	18.76	51.46	14.98	5,106.8	
*328.934	1.24	2290.69	84.68	630.37	6.03		
CRC 528	CRC 528 PLS 1		Colorectum	II	*133.814		
1044.38	2150.9	*0.83	7.11	*2.745	16.95	755.4	
*328.934	0.65	1630.08	132.15	610.37	7.23		
CRC 529	CRC 529 PLS 1		Colorectum	II	*133.814		
1151.06	2226.54	*0.83	5.42	*2.745	18.7	665.50	
*328.934	0.8	1516.3	110.68	620.4	2.48		
CRC 530	CRC 530 PLS 1		Colorectum	II	*133.814		
1799.04	2822.56	*0.83	11.95	*2.745	26.56	2584.50	
*328.934	0.77	2068.13	*14.113	1454.06	4.89		
CRC 531	CRC 531 PLS 1		Colorectum	III	*133.814		
854.36	2684.13	*0.83	9.78	*2.745	10.57	2,242.0	
*328.934	0.78	1630.08	98.45	474.1	7.86		
INDI 001	INDI 001 PLS 1		Lung	II	*130.232		
4050.94	2561.78	*0.795	5.27	*2.633	25.95	*73.413	

Table4.txt

*1033.785	2.11	1211.27	106.93	993.91	8.31		
INDI 002	INDI 002 PLS 1		Lung	II	*130.232		
1204.80	918.55	5.49	19.86	22.76	11.51	1959.21	
*1033.785	1.01	985.45	143.4	542.59	3.98		
INDI 003	INDI 003 PLS 1		Lung	III	5337		
1034.19	2507.12	169.14	36.28	476.96	18.42	34,562.2	
*1033.785	0.7	2205.23	*13.973	1274.11	5.84		
INDI 004	INDI 004 PLS 1		Lung	I	*130.232		
2203.07	2782.18	*0.795	11.09	149.33	17.29	1885.07	
*1033.785	0.8	1817.61	83.84	1131.28	7.55		
INDI 005	INDI 005 PLS 1		Lung	I	*130.232		
1860.67	4122.82	*0.795	5.36	*2.633	9.71	885.64	
*1033.785	0.75	873.48	*13.973	774.77	2.92		
INDI 007	INDI 007 PLS 1		Lung	II	*130.232		
513.82	1853.65	9.85	32.40	22.76	21.65	91090.52	
*1033.785	0.68	1975.85	106.93	542.59	3.83		
INDI 009	INDI 009 PLS 1		Lung	II	*130.232		
1200.19	442.58	8.39	16.50	*2.633	10.53	*73.413	
*1033.785	0.74	837.8	106.93	626.68	2.31		
INDI 010	INDI 010 PLS 1		Lung	II	*130.232		
2376.25	391.11	39.67	16.84	307.79	10.42	*73.413	
*1033.785	0.99	1066.47	*13.973	1162.95	5.07		
INDI 011	INDI 011 PLS 1		Lung	I	*130.232		
1177.16	1290.04	*0.795	8.15	17.62	19.32	1085.49	
*1033.785	0.6	1729.53	158.9	576.84	5.49		
INDI 012	INDI 012 PLS 1		Lung	I	*130.232		
3217.17	1446.5	*0.795	20.36	*2.633	11.97	512.7	
*1033.785	0.77	1864.07	83.84	626.68	5.39		
INDI 013	INDI 013 PLS 1		Lung	III	908.66		
1567.71	2326.22	*0.795	20.52	*2.633	18.62	617.83	
*1033.785	0.96	1466.85	126.31	471.17	4.67		
INDI 014	INDI 014 PLS 1		Lung	II	*130.232		
3647.90	2251.89	*0.795	9.11	*2.633	14.73	2,303.1	
*1033.785	0.92	1471.44	126.31	1053.71	3.05		
INDI 015	INDI 015 PLS 1		Lung	I	*130.232		
2102.72	4967.26	*0.795	32.57	29.87	26.27	1155.54	
*1033.785	1.09	1480.62	126.31	1007.33	5.08		
INDI 016	INDI 016 PLS 1		Lung	III	1710.54		
1508.10	1511.27	*0.795	16.73	47.86	11.72	34,150.7	
*1033.785	1.11	1604.8	126.31	618.49	4.57		
INDI 017	INDI 017 PLS 1		Lung	I	*130.232		
2011.43	2406.08	6.93	23.44	*2.633	19.03	1226.57	
*1033.785	0.85	2455.01	106.93	939.47	6.73		
INDI 018	INDI 018 PLS 1		Lung	III	*130.232		
1663.92	2912	16.33	13.42	16.06	20.32	44341.86	
*1033.785	1.35	1632.47	83.84	855.2	6.48		
INDI 022	INDI 022 PLS 1		Lung	III	*130.232		
3185.41	970.09	*0.795	16.74	*2.633	17.37	787.3	

Table4.txt

*1033.785	0.95	779.98	126.31	876.58	5.35		
INDI 023	INDI 023	PLS 1	Lung	II	*130.232		
1434.68	2223.79	*0.795	32.73	*2.633	18.13	2,267.1	
*1033.785	0.86	2469.19	*13.973	759.77	7.37		
INDI 024	INDI 024	PLS 1	Lung	II	2331.68		
4544.00	2494.13	*0.795	11.08	*2.633	32.6	1353.09	
*1033.785	1.46	1845.48	*13.973	*72.59	4.21		
INDI 025	INDI 025	PLS 1	Lung	I	1323.96		
2631.16	1703.17	6.57	9.62	*2.633	10.15	4,045.1	
*1033.785	0.94	1655.55	126.31	966.85	6.87		
INDI 026	INDI 026	PLS 1	Lung	I	4433.47		
881.57	1231.5	*0.795	72.06	*2.633	11.56	923.20	
*1033.785	0.9	1457.68	143.4	1286.2	7.7		
INDI 027	INDI 027	PLS 1	Colorectum	II	5170.73		
1874.38	2223.79	*0.795	3.92	*2.633	17.96	2,205.8	
*1033.785	0.78	2106.73	*13.973	1000.63	5.5		
INDI 028	INDI 028	PLS 1	Colorectum	II	2518		
918.61	1591.01	*0.795	7.25	*2.633	18.38	1,085.5	
*1033.785	0.75	1416.44	83.84	*72.59	4.59		
INDI 029	INDI 029	PLS 1	Colorectum	II	1110.73		
1718.86	1076.72	*0.795	25.76	*2.633	20.16	2862.66	
*1033.785	0.79	2711.21	*13.973	364.62	3.25		
INDI 030	INDI 030	PLS 1	Colorectum	II	4699.57		
4887.50	4748.93	4.77	19.16	22.76	26.66	2965.77	
*1033.785	1	1878.02	126.31	1945.45	4.54		
INDI 031	INDI 031	PLS 1	Colorectum	II	3240.13		
2553.81	738.43	4.77	16.92	*2.633	21.26	2008.99	
*1033.785	0.87	1152.33	264.43	1261.96	6.12		
INDI 032	INDI 032	PLS 1	Colorectum	III	1722.98		
1741.75	2023.6	*0.795	12.60	16.58	14.32	1680.98	
*1033.785	0.76	2720.73	83.84	2451.7	4.36		
INDI 034	INDI 034	PLS 1	Colorectum	III	*130.232		
3226.24	2137.28	*0.795	23.09	*2.633	44.71	4,899.1	
*1033.785	0.81	1512.76	106.93	1188.03	9.81		
INDI 035	INDI 035	PLS 1	Colorectum	II	1223.77		
2703.92	1264.23	*0.795	3.22	*2.633	22.87	479.9	
*1033.785	1.22	771.1	106.93	626.68	4.49		
INDI 036	INDI 036	PLS 1	Colorectum	I	1273.9		
2626.61	1851.17	*0.795	20.20	*2.633	18.46	572.3	
*1033.785	0.75	2988.22	83.84	*72.59	4.83		
INDI 037	INDI 037	PLS 1	Colorectum	I	*130.232		
2166.59	2016.06	*0.795	70.12	52.30	18.99	3252.07	
*1033.785	1.2	1947.87	*13.973	1219.06	5.32		
INDI 038	INDI 038	PLS 1	Colorectum	II	1047.76		
1034.19	2711.04	*0.795	15.60	*2.633	16.9	*73.413	
*1033.785	0.96	1873.37	186.6	1695	4.14		
INDI 039	INDI 039	PLS 1	Colorectum	III	6200.29		
1103.41	2147.43	10.22	4.69	24.80	11.41	1,244.5	

Table4.txt

*1033.785	0.94	335.03	186.6	658.99	9.3	INDI 040	INDI 040 PLS 1	Colorectum	I
1959.14	639.98	501.08	*0.795	14.65	*2.633	20.24	1235.51		
*1033.785	1.01	642.98	186.6	2250.23	6.56	INDI 042	INDI 042 PLS 1	Colorectum	I
3841.1	1952.06	1154.87	*0.795	12.85	*2.633	18.71	1,894.9		
*1033.785	0.86	1320.49	83.84	1684.24	6.29	INDI 043	INDI 043 PLS 1	Colorectum	II
*130.232	1498.92	1516.09	9.12	5.95	*2.633	11.67	7170.88		
*1033.785	0.8	3122.62	274.05	568.36	2.98	INDI 044	INDI 044 PLS 1	Colorectum	II
1518.46	1461.82	1169.82	46.46	13.71	*2.689	13.58	*77.55		
*319.819	0.88	1466.89	*13.517	536.43	7.93	INDI 045	INDI 045 PLS 1	Colorectum	III
*159.986	1516.92	1048.57	17.46	20.25	*2.689	12.2	11828.89		
2725.41	1.32	1663.27	206.36	678.86	51.61	INDI 046	INDI 046 PLS 1	Colorectum	II
*159.986	2307.35	1406.29	8.14	17.49	*2.689	11.98	2628.56		
2413.21	0.73	892.07	144.85	1315.85	4.04	INDI 047	INDI 047 PLS 1	Colorectum	II
*159.986	2794.99	495.64	5.18	8.48	*2.689	12.62	2746.89		
4936.36	0.7	724.28	236.7	573.27	7.51	INDI 048	INDI 048 PLS 1	Breast	II
*130.232	2075.34	2512.31	20.63	41.03	*2.633	19.84	11062.71		
*1033.785	0.85	1669.41	83.84	1619.03	5.95	INDI 049	INDI 049 PLS 1	Breast	III
2965.8	1462.22	1439.33	8.39	15.80	*2.633	10.74	579.79		
*1033.785	0.73	1265.82	*13.973	1007.33	2.17	INDI 050	INDI 050 PLS 1	Breast	II
*130.232	471.62	949.87	8.39	10.62	*2.633	11.46	*73.413		
*1033.785	0.81	1859.42	106.93	525.13	2.17	INDI 051	INDI 051 PLS 1	Breast	III
*130.232	3801.92	2406.08	64.31	18.70	24.29	16.64	2390.97		
*1033.785	0.84	1034.92	143.4	1237.52	6.11	INDI 052	INDI 052 PLS 1	Breast	II
*130.232	3003.83	2890.74	*0.795	5.61	*2.633	20.16	1271.43		
*1033.785	1.08	2228.72	83.84	1112.1	2.86	INDI 053	INDI 053 PLS 1	Breast	II
946.68	1974.90	2369.96	5.85	25.91	*2.633	14.92	1533.81		
*1033.785	1.03	2266.33	126.31	1060.26	6.26	INDI 054	INDI 054 PLS 1	Breast	II
*130.232	2025.13	2512.31	*0.795	6.54	*2.633	23.66	*73.413		
*1033.785	0.92	1443.93	*13.973	1462.35	3.24	INDI 055	INDI 055 PLS 1	Breast	II
*130.232	244.85	1910.88	5.85	11.07	*2.633	15.55	982.30		
*1033.785	0.69	208.39	244.28	507.41	4.3	INDI 056	INDI 056 PLS 1	Breast	II
*130.232	2685.73	1035.68	*0.795	13.70	*2.633	13.57	2835.66		

Table4.txt

*1033.785	1.01	1554.14	83.84	576.84	4.44		
INDI 057	INDI 057 PLS 1		Breast	III	*130.232		
1255.43	1351.35	*0.795	8.64	*2.633	16.94	1,137.9	
*1033.785	0.91	1016.91	83.84	1020.67	6.6		
INDI 058	INDI 058 PLS 1		Breast	I	*130.232		
1158.73	777.45	6.21	21.80	*2.633	12.71	1984.06	
*1033.785	0.72	1297.69	106.93	452.61	2.45		
INDI 059	INDI 059 PLS 1		Breast	II	5870.64		
1204.30	1704.54	10.97	20.18	22.69	16.16	1235.59	
*319.819	1.02	2353.93	129.61	678.86	9.13		
INDI 060	INDI 060 PLS 1		Breast	II	1752.17		
1491.48	1012.87	6.68	7.44	*2.689	15.13	*77.55	
2087.71	0.9	1019.3	183.89	831.88	6.76		
INDI 061	INDI 061 PLS 1		Breast	II	*159.986		
3285.53	877.09	*0.816	6.19	17.01	22.86	1,432.2	
2413.21	0.95	1931.89	158.79	2515.41	8.31		
INDI 062	INDI 062 PLS 1		Breast	II	*159.986		
699.44	224.04	*0.816	4.13	*2.689	9.15	*77.55	
3026.76	1.3	2368.34	272.84	1014.25	7.25		
INDI 063	INDI 063 PLS 1		Breast	III	*159.986		
1754.98	2058.55	*0.816	27.02	*2.689	16.08	3726.45	
*319.819	0.95	1188.56	195.4	1833.6	9.2		
INDI 064	INDI 064 PLS 1		Breast	II	4248.51		
1904.33	1646.63	5.75	17.16	20.34	12.67	777.0	
2725.41	0.77	1814.95	289.56	1337.92	8.09		
INDI 065	INDI 065 PLS 1		Breast	II	*159.986		
1162.25	1483.01	*0.816	20.48	26.39	20.25	1497.89	
5189.04	1.3	2716.45	137.42	734.88	8.19		
INDI 066	INDI 066 PLS 1		Breast	III	*159.986		
1720.90	1704.54	*0.816	7.56	*2.689	16.33	1443.17	
3603.35	1.27	1733.72	206.36	1617.74	9.57		
INDI 067	INDI 067 PLS 1		Breast	III	*159.986		
2596.10	1829.71	*0.816	16.31	*2.689	8.34	777.0	
*319.819	1.08	1628.1	112.55	1849.2	12.61		
INDI 068	INDI 068 PLS 1		Breast	II	*159.986		
927.78	1163.32	*0.816	10.00	*2.689	7.29	*77.55	
*319.819	1.14	874.91	206.36	762.29	5.98		
INDI 069	INDI 069 PLS 1		Breast	II	*159.986		
2346.07	3383.08	*0.816	8.42	*2.689	21.72	2,136.9	
*319.819	1.21	271.82	281.29	1964.66	11.19		
INDI 070	INDI 070 PLS 1		Breast	III	4529.89		
2816.64	832.55	*0.816	30.22	31.24	16.66	733.2	
21984.63	1.01	837.2	195.4	1609.54	4.72		
INDI 071	INDI 071 PLS 1		Breast	II	*159.986		
2591.79	1372.85	*0.816	5.58	*2.689	17.11	1,006.5	
*319.819	1.88	1133.19	183.89	1239.73	18.16		
INDI 072	INDI 072 PLS 1		Breast	II	2367.68		
1559.34	1172.42	*0.816	7.72	*2.689	18.68	3030.32	

Table4.txt

2252.31	1.01	1638.65	255.28	1802.25	8.53		
INDI 073	INDI 073 PLS 1		Breast	III	1171.83		
1449.12	2509.64	*0.816	12.97	34.53	17.46	1,366.6	
2087.71	1.53	1974.53	*13.517	1543.36	4		
INDI 074	INDI 074 PLS 1		Pancreas	II	1823.22		
2228.39	2167.67	25.55	33.61	2136.83	20.09	4,158.0	
7562.35	0.81	2078.57	99.23	1217.75	4.71		
INDI 075	INDI 075 PLS 1		Ovary	III	2302.37		
1018.56	2655.01	113.65	13.91	*2.624	23.8	1,102.6	
9240.89	0.97	1890.23	112.06	1618.34	4.68		
INDI 076	INDI 076 PLS 1		Esophagus	II	1989.46		
2829.63	1660.39	*0.816	23.02	31.91	16.16	5507.57	
2877.32	0.62	1091.73	158.79	*77	11.73		
INDI 077	INDI 077 PLS 1		Liver	II	7843.86		
1644.30	2868.99	9.57	12.85	41.97	21.06	3,104.4	
4152.37	0.66	3313.49	171.73	326.66	4.71		
INDI 078	INDI 078 PLS 1		Liver	II	2030.92		
852.82	762.79	*0.816	21.49	26.39	13.78	1,783.3	
5189.04	0.64	1882.22	171.73	561.09	7.67		
INDI 079	INDI 079 PLS 1		Liver	II	*159.986		
4155.29	1302.39	*0.816	22.27	*2.689	11.76	1,552.7	
*319.819	0.63	2174.35	*13.517	511.34	9.7		
INDI 080	INDI 080 PLS 1		Liver	I	7417.29		
937.12	7194.25	*0.795	5.79	*2.633	17.12	978.1	
*1033.785	0.82	2431.37	*13.973	1020.67	4.63		
INDI 081	INDI 081 PLS 1		Colorectum	II	*130.232		
3620.72	2076.54	*0.795	25.54	22.76	15.72	1,899.9	
*1033.785	0.82	2892.49	83.84	1033.94	6.28		
INDI 082	INDI 082 PLS 1		Stomach	II	*130.232		
812.04	3366.34	*0.795	18.90	*2.633	21.46	1850.70	
*1033.785	0.72	1416.44	83.84	452.61	2.87		
INDI 083	INDI 083 PLS 1		Stomach	II	4467.66		
3137.66	811.64	*0.816	11.76	*2.689	16.08	4042.02	
3318.97	0.66	1327.41	137.42	821.32	10.55		
INDI 084	INDI 084 PLS 1		Stomach	II	49326.37		
2432.19	1198.5	14.42	20.98	46.09	13.39	1290.18	
14369.30	0.57	1501.86	226.96	2618.59	9.79		
INDI 085	INDI 085 PLS 1		Stomach	I	*159.986		
1166.46	631.07	*0.816	8.67	*2.689	11.87	3195.82	
4679.62	0.55	1896.4	206.36	391.81	6.53		
INDI 086	INDI 086 PLS 1		Stomach	I	*159.986		
4471.57	2747.31	*0.816	22.93	*2.689	37.16	2533.06	
3318.97	1.13	1938.99	171.73	894.22	7.95		
INDI 087	INDI 087 PLS 1		Stomach	I	*159.986		
1153.85	362.66	19.46	5.40	30.57	11.92	1,772.3	
3027	0.6	1600	206.36	1043.41	7.12		
INDI 089	INDI 089 PLS 1		Colorectum	II	*159.986		
836.19	737.34	*0.816	6.42	29.20	11.53	*77.55	

Table4.txt

4679.62	1.29	2804.14	313.33	805.39	7.87	
INDI 090	INDI 090 PLS 1		Colorectum	II	*159.986	
2114.09	778.61	*0.816	9.94	*2.689	11.18	*77.55
3880.89	1.02	570.82	171.73	1359.86	5.81	
INDI 092	INDI 092 PLS 1		Stomach	II	*159.986	
2596.10	1120.55	*0.816	5.28	*2.689	14.4	1970.77
2087.71	0.99	1825.56	129.61	964.93	6.29	
INDI 093	INDI 093 PLS 1		Colorectum	I	*159.986	
2131.25	3662.82	9.92	41.44	*2.689	19.26	1,093.8
11116.5	1.06	1617.56	183.89	974.86	11.95	
INDI 094	INDI 094 PLS 1		Colorectum	I	*159.986	
3800.44	2320.73	14.59	7.56	*2.689	28.33	2583.58
3603.35	1.67	1758.42	272.84	2354	7	
INDI 095	INDI 095 PLS 1		Stomach	II	*159.986	
1250.61	2574.64	7.05	9.68	*2.689	13.78	490.38
3318.97	1.55	1765.48	289.56	1355.48	9.02	
INDI 096	INDI 096 PLS 1		Colorectum	I	*159.986	
1831.74	586.52	5.18	4.98	*2.689	*1.35	787.95
6866.41	0.87	1931.89	206.36	1072.27	3.46	
INDI 097	INDI 097 PLS 1		Colorectum	III	947.92	
3016.05	3819.22	25.37	14.95	43.17	36.23	2,956.4
2725.41	1.45	3068.78	264.17	1394.68	6.63	
INDI 098	INDI 098 PLS 1		Colorectum	II	*159.986	
4436.39	783.49	*0.816	11.71	*2.689	8.11	820.78
*319.819	1.08	796.1	112.55	1175.68	5.27	
INDI 100	INDI 100 PLS 1		Colorectum	III	*159.986	
2872.95	1154.22	*0.816	2.94	*2.689	10.46	1,028.3
*319.819	1.54	892.07	195.4	1584.85	11.13	
INDI 101	INDI 101 PLS 1		Colorectum	III	*159.986	
1989.86	1277.28	*0.816	5.67	*2.689	10.34	1,148.3
6635.12	0.99	898.93	112.55	419.45	8.17	
INDI 102	INDI 102 PLS 1		Colorectum	III	*159.986	
2165.57	1707.3	*0.816	10.35	*2.689	16.74	523.7
*319.819	2.97	3039.25	343.07	1625.92	7.22	
INDI 103	INDI 103 PLS 1		Stomach	II	4169.69	
1237.98	884.55	*0.816	4.44	*2.689	11.87	601.17
3462.07	2.14	926.41	183.89	3271.93	11.64	
INDI 104	INDI 104 PLS 1		Stomach	III	390698.43	
2509.79	924.51	*0.816	8.39	*2.689	15.26	19,906.4
*319.819	2.02	2567.27	305.56	548.82	11.53	
INDI 107	INDI 107 PLS 1		Colorectum	II	4026.98	
3940.50	2259.77	*0.816	5.22	*2.689	14.49	1959.72
2413.21	1.6	2375.55	144.85	1147.83	9.18	
INDI 108	INDI 108 PLS 1		Colorectum	II	*159.986	
1925.70	173.03	7.41	1.88	17.01	9.28	634.3
38779.71	1.34	1917.69	255.28	2047.72	13.45	
INDI 109	INDI 109 PLS 1		Colorectum	III	*159.986	
3011.71	1112.8	5.93	31.24	*2.689	13.63	2,136.9

Table4.txt

3880.89	0.71	2958.22	144.85	341.54	6.26		
INDI 110	INDI 110 PLS 1		Stomach	I	*159.986		
1246.40	1621.91	*0.816	3.39	*2.689	10.46	3,013.3	
*319.819	1.61	1889.31	*13.517	2047.72	8.46		
INDI 111	INDI 111 PLS 1		Stomach	II	*159.986		
1720.90	967.26	*0.816	10.66	*2.689	12.2	886.38	
*319.819	0.79	2253.23	*13.517	924.77	10.32		
INDI 112	INDI 112 PLS 1		Esophagus	II	4930.94		
1917.15	751.87	*0.816	44.94	*2.689	15.99	941.0	
*319.819	1.44	1355.25	144.85	756.84	13.81		
INDI 113	INDI 113 PLS 1		Colorectum	II	*159.986		
2242.87	740.97	*0.816	10.56	99.93	9.69	120,958.6	
*319.819	0.86	1868.05	171.73	1115.01	5.79		
INDI 116	INDI 116 PLS 1		Stomach	I	*159.986		
5053.37	1656.26	*0.816	16.79	*2.689	21.56	*77.55	
*319.819	0.65	1445.93	*13.517	1257.79	5.79		
INDI 119	INDI 119 PLS 1		Esophagus	I	*159.986		
1406.80	307.22	187.03	**54.442	224.73	12.73	2,303.8	
11016.84	1.16	1924.79	216.86	767.73	13.13		
INDI 120	INDI 120 PLS 1		Stomach	III	*159.986		
3717.36	3379.98	7.41	6.44	*2.689	15.82	804.37	
*319.819	0.91	1237.08	*13.517	632.76	91.98		
INDI 121	INDI 121 PLS 1		Stomach	I	*159.986		
1263.25	2816.3	8.5	6.59	*2.689	12.52	689.25	
*319.819	1.55	940.15	144.85	1337.92	4.58		
INDI 122	INDI 122 PLS 1		Colorectum	II	145090.58		
**9999.94	1967.61	11.32	31.75	*2.689	10.21	656.27	
*319.819	1.16	1882.22	343.07	2529.26	19.07		
INDI 123	INDI 123 PLS 1		Colorectum	II	*159.986		
654.06	1379.53	18.46	17.85	35.81	14.76	4183.26	
3603.35	1.37	830.34	226.96	1004.46	19.3		
INDI 124	INDI 124 PLS 1		Colorectum	II	*159.986		
4014.97	1189.36	50.41	12.58	*2.689	29.04	3,494.7	
3026.76	0.97	570.82	158.79	934.87	16.91		
INDI 125	INDI 125 PLS 1		Esophagus	II	3640.27		
2414.96	888.29	*0.816	10.33	*2.689	8.93	557.0	
2725.41	0.95	1404.04	158.79	377.71	11.61		
INDI 126	INDI 126 PLS 1		Stomach	III	*159.986		
3102.90	982.43	*0.816	19.49	*2.689	12.2	1,629.4	
*319.819	1.16	1303.06	*13.517	964.93	13.92		
INDI 127	INDI 127 PLS 1		Colorectum	II	*159.986		
3037.76	1857.72	*0.816	25.92	*2.689	11.98	2,606.1	
*319.819	1.03	2006.55	158.79	740.4	29.53		
INDI 128	INDI 128 PLS 1		Colorectum	III	5345.11		
2847.97	864.37	12.06	4.11	147.22	18.95	14,732.4	
11119.95	*0.107	1627.35	217.27	2133.98	8.17		
INDI 129	INDI 129 PLS 1		Liver	II	**100101.482		
2242.08	1047.07	6.29	9.58	50.35	8.98	1530.86	

Table4.txt

6047.91	1.54	2512.5	290.33	910.59	12.48		
INDI 130	INDI 130 PLS 1		Stomach	II	*168.118		
1317.90	609.74	11.48	9.22	*2.915	13.18	936.72	
4204.12	*0.107	1841.6	250.9	793.8	6.31		
INDI 131	INDI 131 PLS 1		Stomach	II	1015.37		
2163.90	2232.8	86.55	15.37	21.56	15.96	664.1	
4624.15	1.38	1247.64	116.99	820.42	14.52		
INDI 132	INDI 132 PLS 1		Esophagus	III	*168.118		
1765.49	2866	5.61	4.30	*2.915	7.94	1,331.4	
*347.375	*0.107	1386.8	105.39	996.74	45.32		
INDI 133	INDI 133 PLS 1		Stomach	I	*168.118		
2259.46	1581.43	*0.845	11.45	*2.915	8.9	1,233.4	
2203	*0.107	1677.92	*15.378	947.96	24.05		
INDI 134	INDI 134 PLS 1		Stomach	III	*168.118		
2612.15	1962.2	*0.845	18.72	34.28	15.67	2672.50	
*347.375	*0.107	1588.48	105.39	497.5	36.54		
INDI 135	INDI 135 PLS 1		Stomach	III	*168.118		
2272.50	2893.2	101.49	336.25	19.24	11.75	2,272.7	
8555	*0.107	125.29	177.94	739.25	7.24		
INDI 136	INDI 136 PLS 1		Colorectum	II	1960.36		
2992.32	1168.99	7.25	15.68	*2.915	8.34	2,130.0	
*347.375	*0.107	1062.73	146.25	638.87	32.61		
INDI 137	INDI 137 PLS 1		Stomach	II	29205.8		
2233.39	2869.2	7.25	12.56	*2.915	16.44	79,953.9	
*347.375	*0.107	1970.52	*15.378	638.87	5.95		
INDI 139	INDI 139 PLS 1		Stomach	III	*168.118		
1834.63	2226.63	26.87	16.90	*2.915	9.22	**56071.331	
722034	1.32	2150.68	191.89	1385.14	74.85		
INDI 140	INDI 140 PLS 1		Stomach	III	3829.74		
2931.06	1261.22	14.4	4.84	*2.915	10.29	910.88	
*347.375	*0.107	1947.06	127.5	1436.33	15.04		
INDI 141	INDI 141 PLS 1		Stomach	III	2244.47		
2042.43	553.16	6.15	8.03	*2.915	11.55	957.5	
*347.375	*0.107	2793.05	*15.378	793.8	5.09		
INDI 143	INDI 143 PLS 1		Colorectum	II	*168.118		
1253.63	1525.68	24.07	12.64	*2.915	9.06	576.7	
*347.375	*0.107	1008.95	*15.378	1091.09	7.01		
INDI 144	INDI 144 PLS 1		Colorectum	II	*168.118		
1674.85	290.09	24.69	20.14	115.33	8.47	8,796.4	
*347.375	*0.107	1101.19	127.5	353.44	24.73		
INDI 145	INDI 145 PLS 1		Colorectum	II	*168.118		
848.75	343.48	16.18	8.09	30.82	11.07	3,657.4	
*347.375	*0.107	924.58	127.5	711.26	8.95		
INDI 146	INDI 146 PLS 1		Colorectum	II	*168.118		
3005.46	772.86	10.48	4.47	*2.915	10.72	4,435.2	
*347.375	1.34	1479.79	105.39	623.93	11.28		
INDI 147	INDI 147 PLS 1		Stomach	II	3115.12		
2189.95	743.55	*0.845	11.11	168.89	11.58	2,041.7	

Table4.txt

*347.375	*0.107	1705.17	127.5	419.33	28.06	INDI 148	INDI 148	PLS 1	
Colorectum	II	2673.94	3246.46	2896.4	8.92	23.57	*2.915	18.48	1901.61
4204.12	1.27	985.92	177.94	885.27	48.8	INDI 150	INDI 150	PLS 1	
Colorectum	II	*168.118	2129.17	1329.92	*0.845	5.65	167.18	7.14	**56071.331
13239.38	1.18	916.91	191.89	*76.56	76.28	INDI 151	INDI 151	PLS 1	
Stomach	II	5187.97	1800.05	3362.79	17.07	13.40	*2.915	8.56	193,910.0
*347.375	1.24	1093.5	162.85	480.65	84.07	INDI 152	INDI 152	PLS 1	
Colorectum	I	16759.56	692.28	5505.36	*0.845	4.89	26.20	22.48	1,051.7
*347.375	*0.107	2611.15	105.39	711.26	4.8	INDI 153	INDI 153	PLS 1	
Stomach	II	*168.118	984.68	2174.3	5.34	2.93	*2.915	14.44	*76.457
*347.375	1.57	1572.94	105.39	401.03	140.43	INDI 155	INDI 155	PLS 1	
Colorectum	II	*168.118	6069.42	3747.51	*0.845	*0.236	*2.915	9.62	567.1
*347.375	1.49	771.67	*15.378	1008.75	78.02	INDI 156	INDI 156	PLS 1	
Colorectum	III	1042.06	1236.51	2155.87	*0.845	20.69	117.04	15.1	50,868.3
24724.77	*0.107	2437.61	*15.378	1364.42	47.81	INDI 158	INDI 158	PLS 1	
Colorectum	I	*168.118	1403.71	2051.85	8.36	3.25	*2.915	8.69	586.3
*347.375	*0.107	1865.02	*15.378	1613.98	10.29	INDI 159	INDI 159	PLS 1	
Colorectum	II	*168.118	4082.35	2999.14	*0.845	7.92	*2.915	10.72	*76.457
*347.375	1.1	2607.2	*15.378	1415.96	7.86	INDI 160	INDI 160	PLS 1	
Colorectum	II	*168.118	1895.18	2030.53	*0.845	7.02	*2.915	11.51	1342.38
*347.375	1.36	1771.39	146.25	1395.45	6.47	INDI 161	INDI 161	PLS 1	
Stomach	II	*168.118	4064.71	1819.03	*0.845	6.05	*2.915	15.36	1,158.1
*347.375	1.45	897.77	127.5	1296.01	5.98	INDI 162	INDI 162	PLS 1	
Stomach	III	*168.118	3914.80	6484.12	*0.845	14.68	*2.915	9.06	664.10
*347.375	1.39	901.6	105.39	2146.6	10.46	INDI 163	INDI 163	PLS 1	
Colorectum	III	*168.118	925.15	1750.26	*0.845	12.69	*2.915	7.14	703.5
*347.375	*0.107	1093.5	*15.378	2184.27	7.38	INDI 164	INDI 164	PLS 1	
Colorectum	I	*168.118	1903.83	2738.53	*0.845	2.93	*2.915	7.85	813.76
*347.375	1.59	1232.2	146.25	1979.62	7.23	INDI 165	INDI 165	PLS 1	
Colorectum	I	*168.118	2957.31	1997.08	*0.845	4.13	*2.915	11.21	1,677.6
*347.375	*0.107	1043.51	154.77	4165.56	4.6	INDI 167	INDI 167	PLS 1	
Stomach	II	*168.118	1232.23	1268.35	5.07	5.78	*2.915	14.33	1364.35

Table4.txt

*347.375	*0.107	2343.14	*15.378	2100.14	18.85		
INDI 168	INDI 168 PLS 1		Stomach	II	*168.118		
3119.33	3441.52	*0.845	5.33	98.26	11.35	2,944.9	
*347.375	1.6	1131.98	177.94	793.8	66.23		
INDI 169	INDI 169 PLS 1		Colorectum	III	*168.118		
486.48	1711.55	5.61	7.45	*2.915	9.77	2,428.9	
*347.375	1.34	1904.08	162.85	570.25	47.29		
INDI 170	INDI 170 PLS 1		Colorectum	I	*168.118		
937.90	1391.88	14.69	9.38	*2.915	9.22	813.8	
*347.375	1.47	206.32	*15.378	247.38	51.64		
INDI 171	INDI 171 PLS 1		Stomach	III	9498.91		
1986.09	935.24	6.15	21.48	329.76	9.62	10,006.2	
3776.79	1.16	2009.65	271.24	353.44	39.74		
INDI 172	INDI 172 PLS 1		Stomach	II	*168.118		
2939.81	2001.64	59.78	18.40	9615.69	11.88	24,029.0	
21718.99	*0.107	2410.05	162.85	846.64	67.34		
INDI 173	INDI 173 PLS 1		Stomach	I	*168.118		
1438.07	2372.22	5.61	6.01	*2.915	12.07	15,825.7	
*347.375	1.33	3281.75	*15.378	3877.33	34.66		
INDI 175	INDI 175 PLS 1		Colorectum	III	3813.23		
4563.92	5085.46	27.5	18.81	*2.915	26.97	1,677.6	
11299.06	1.68	400.41	105.39	1020.71	53.94		
INDI 176	INDI 176 PLS 1		Stomach	II	*168.118		
4705.55	1616.77	5.61	21.84	52.64	11.71	2,623.5	
*347.375	1.12	407.92	92.27	739.25	35.45		
INDI 177	INDI 177 PLS 1		Liver	III	**100101.482		
1696.42	2181.98	8.36	10.60	40.03	10	978.3	
3777	1.32	1201.34	228.97	343.56	32.99		
INDI 178	INDI 178 PLS 1		Colorectum	III	2519.15		
2185.61	1084.71	*0.845	13.16	27.35	8.03	1,126.0	
*347.375	1.72	695.47	162.85	247.38	5.19		
INDI 179	INDI 179 PLS 1		Colorectum	III	*168.118		
1666.23	446.05	11.48	6.49	19.24	7.28	1,458.3	
3776.79	1.44	1031.99	280.93	1181.75	46.7		
INDI 180	INDI 180 PLS 1		Colorectum	III	*168.118		
278.81	1913.81	8.22	2.73	*2.915	9.92	1,700.4	
*347.375	*0.107	1915.8	162.85	910.59	12.35		
INDI 182	INDI 182 PLS 1		Liver	III	3879.35		
3866.33	2604.03	5.61	22.78	23.30	14.47	1,694.7	
18146.52	*0.107	2103.63	105.39	1038.51	10.36		
INDI 183	INDI 183 PLS 1		Stomach	I	*168.118		
1856.25	2269.86	11.77	3.60	*2.915	12.48	773.4	
*347.375	1.99	1670.13	146.25	*76.56	95.28		
INDI 184	INDI 184 PLS 1		Esophagus	II	1177.11		
3611.02	1696.69	9.77	4.90	*2.915	9.81	864.7	
*347.375	1.42	1441.02	127.5	1877.98	79.36		
INDI 185	INDI 185 PLS 1		Stomach	II	*168.118		
2808.63	2265.23	18.88	7.20	*2.915	11.48	335,550.1	

Table4.txt

2668.03	2.22	1880.64	105.39	1176.18	68.66	
INDI 186	INDI 186 PLS 1		Stomach	II	*168.118	
2581.62	1900.23	16.18	10.37	*2.915	8.12	**56071.331
*347.375	1.49	1301.71	198.52	480.65	42.98	
INDI 187	INDI 187 PLS 1		Stomach	I	*168.118	
1326.47	1383.21	6.42	2.96	*2.915	11.48	1711.75
*347.375	*0.107	2052.71	*15.378	291.97	9.23	
INDI 188	INDI 188 PLS 1		Stomach	I	1015.37	
8540.58	2372.22	6.69	3.94	*2.915	7.38	491.35
2895.27	1.25	1001.27	*15.378	463.52	70.15	
INDI 189	INDI 189 PLS 1		Esophagus	II	*168.118	
2450.89	288.92	6.29	4.74	*2.915	*1.372	576.7
3776.79	1.64	642.25	217.27	1604.36	92.26	
INDI 190	INDI 190 PLS 1		Liver	III	*134.509	
3110.53	2786.58	5.07	10.15	18.38	9.78	618.6
*336.028	1.91	1105.4	*14.024	670.34	23.85	
INDI 191	INDI 191 PLS 1		Colorectum	I	*134.509	
3595.17	1842.57	*0.821	7.33	*2.73	11.54	1473.58
*336.028	1.52	1911.55	170.71	1082.47	30.79	
INDI 192	INDI 192 PLS 1		Colorectum	II	2506.97	
1653.10	4757.01	*0.821	12.12	*2.73	18.19	1,648.0
3526	2.17	3065.73	177.18	1058.33	30.62	
INDI 194	INDI 194 PLS 1		Colorectum	II	*134.509	
1438.86	1377.23	*0.821	13.43	*2.73	10.27	540.9
*336.028	2.49	*26.403	116.7	637.41	29.43	
INDI 195	INDI 195 PLS 1		Colorectum	III	*134.509	
1424.21	2078.27	15.81	8.81	17.39	9.68	1016.44
*336.028	1.57	1613.18	189.51	569.62	46.97	
INDI 196	INDI 196 PLS 1		Colorectum	III	*134.509	
1160.87	2237.14	6.2	7.83	*2.73	8.83	1658.10
2467.28	1.3	1514.11	201.16	1030.5	50.22	
INDI 197	INDI 197 PLS 1		Colorectum	II	*134.509	
2130.90	1496.19	7.36	3.43	*2.73	11.75	5,719.9
2106.97	2.21	1347.2	287.53	789.07	52.95	
INDI 198	INDI 198 PLS 1		Stomach	III	**98718.787	
2122.02	6817.13	*0.821	22.96	*2.73	*1.364	8,698.2
2106.97	0.82	109.47	116.7	471.29	7.39	
INDI 199	INDI 199 PLS 1		Stomach	II	3007.38	
1977.14	1648.03	*0.821	5.17	18.38	12.28	1,035.2
*336.028	1.38	901.3	134.22	364.89	8.87	
INDI 200	INDI 200 PLS 1		Breast	III	*134.509	
506.98	1358.05	*0.821	8.87	*2.73	7.64	706.4
*336.028	1.26	1687.89	201.16	*96.087	59.19	
INDI 202	INDI 202 PLS 1		Colorectum	II	*134.509	
518.67	3104.56	5.92	6.49	92.78	8.83	3,904.1
3351.56	0.96	1543.77	233.01	301.96	6.35	
INDI 203	INDI 203 PLS 1		Stomach	II	*134.509	
2326.63	2794.41	*0.821	3.58	324.93	10.27	*76.419

Table4.txt

*336.028	1.69	1528.93	149.81	861.02	7.76	
INDI 205	INDI 205 PLS 1		Liver	III	6066.84	
3998.62	3274.1	*0.821	17.51	17.39	27.97	1,548.0
11917.86	1.21	2794.24	96.2	1474.26	13.93	
INDI 206	INDI 206 PLS 1		Stomach	III	*134.509	
3291.72	2392.52	*0.821	2.59	*2.73	10.6	809.46
*336.028	1.22	426.15	164.02	815.84	23.4	
INDI 207	INDI 207 PLS 1		Colorectum	II	*134.509	
2279.12	2194.48	5.35	4.65	29.13	*1.364	34,340.2
3526	1.33	157.64	242.81	1009.45	11.49	
INDI 208	INDI 208 PLS 1		Liver	II	195444.75	
2696.21	5918.39	7.07	14.34	21.35	11.83	859.4
19067	1.1	967.33	270.39	1113.22	8.94	
INDI 209	INDI 209 PLS 1		Colorectum	II	22535.23	
2290.99	2177.04	*0.821	9.98	*2.73	9.78	614.2
*336.028	1.54	1652.98	*14.024	569.62	18.52	
INDI 210	INDI 210 PLS 1		Stomach	III	*134.509	
1650.16	2361.41	*0.821	6.36	26.72	10.74	549.5
*336.028	0.92	2693.95	*14.024	480.52	9.15	
INDI 211	INDI 211 PLS 1		Colorectum	II	*134.509	
2720.14	784.54	*0.821	11.54	*2.73	10.92	1,311.9
*336.028	1.19	1873.65	*14.024	2797.46	12.58	
INDI 212	INDI 212 PLS 1		Colorectum	III	*134.509	
1770.75	1312.05	*0.821	5.81	16.38	*1.364	1,021.1
3176.33	1.01	1206.4	116.7	2689.27	9.97	
INDI 213	INDI 213 PLS 1		Colorectum	III	*134.509	
2582.68	1503.87	*0.821	9.43	*2.73	8.83	1,063.3
4045.81	1.47	3980.45	96.2	1648.9	8.34	
INDI 214	INDI 214 PLS 1		Stomach	II	*134.509	
1856.18	1490.43	*0.821	2.64	*2.73	23	*76.419
4900.90	2.12	1737.89	96.2	1788.52	14.62	
INDI 215	INDI 215 PLS 1		Liver	II	18789.42	
1026.51	1580.72	*0.821	64.61	17.39	12.83	877.7
*336.028	0.93	789.12	149.81	872.18	9.33	
INDI 216	INDI 216 PLS 1		Colorectum	III	*134.509	
1324.64	1848.36	*0.821	6.13	30.57	15.92	2,141.2
8060.05	1.84	2344.09	212.24	789.07	8.79	
INDI 218	INDI 218 PLS 1		Colorectum	III	*134.509	
425.07	1634.56	*0.821	2.47	19.38	6.82	*76.419
3526	1.72	242.62	370.07	838.54	8.25	
INDI 219	INDI 219 PLS 1		Liver	III	*134.509	
2015.55	2739.63	*0.821	2.92	*2.73	8.08	*76.419
2467.28	1.18	3173.11	96.2	534.62	5.64	
INDI 220	INDI 220 PLS 1		Lung	I	2965.8	
2399.03	786.16	12.43	4.18	*2.633	20.48	1,366.8
*1033.785	0.73	542.22	106.93	1020.67	5.25	
INDI 221	INDI 221 PLS 1		Colorectum	III	*130.232	
2248.67	1836.29	41.6	23.16	16.06	17.07	26,173.8

Table4.txt

*1033.785	1.12	1985.18	83.84	1547.11	3.2		
INDI 222	INDI 222 PLS 1		Colorectum	II	*130.232		
2940.24	2152.51	10.58	20.43	17.62	37.33	37,253.1	
*1033.785	0.86	2162.98	244.28	1007.33	5.3		
INDI 223	INDI 223 PLS 1		Colorectum	I	2667.14		
677.25	849.76	10.22	33.85	*2.633	15.46	490.8	
*1033.785	0.77	2559.18	106.93	585.27	4.75		
INDI 224	INDI 224 PLS 1		Lung	III	*130.232		
5077.25	2390.59	50.87	16.46	*2.633	16.51	965.3	
*1033.785	0.98	438.04	*13.973	1530.32	6.33		
INDI 225	INDI 225 PLS 1		Colorectum	I	*130.232		
2189.39	708.3	6.93	8.71	159.25	30.71	2,664.3	
*1033.785	1.01	2658.88	126.31	1780.12	4.89		
INDI 226	INDI 226 PLS 1		Breast	III	*130.232		
1663.92	1417.85	8.57	16.08	*2.633	14.73	516.41	
*1033.785	0.76	1206.73	199.23	593.65	3.28		
INDI 227	INDI 227 PLS 1		Lung	II	*130.232		
2485.54	2285.17	*0.795	21.75	*2.633	20.56	1,362.2	
*1033.785	0.83	1521.95	*13.973	1853.21	4.89		
INDI 228	INDI 228 PLS 1		Breast	II	845.14		
1131.08	1499.24	*0.795	28.65	*2.633	12.76	1353.09	
*1033.785	0.73	2398.3	*13.973	690.65	4.03		
INDI 229	INDI 229 PLS 1		Colorectum	II	*130.232		
941.75	2106.88	16.7	16.18	*2.633	13.43	3969.27	
*1033.785	1.08	1752.68	*13.973	610.26	3.64		
INDI 230	INDI 230 PLS 1		Colorectum	I	5055.85		
1544.79	2246.78	*0.795	24.34	*2.633	24.03	3,692.3	
*1033.785	0.88	2069.29	96	953.2	4.92		
INDI 231	INDI 231 PLS 1		Lung	III	*130.232		
1411.72	970.09	8.2	10.98	17.62	17.2	7,733.9	
*1033.785	0.95	1147.8	244.28	980.42	4.98		
INDI 233	INDI 233 PLS 1		Colorectum	I	*130.232		
2912.99	1417.85	30.67	45.38	*2.633	22.26	2,878.9	
10264.95	1.01	1850.13	126.31	1345.99	3.14		
INDI 234	INDI 234 PLS 1		Colorectum	I	1499.85		
934.44	3290.78	5.4	18.30	*2.624	29.98	2048.43	
2904.45	1.45	1811.03	227.98	1065.72	4.78		
INDI 236	INDI 236 PLS 1		Stomach	II	*130.232		
1066.50	1710.53	*0.795	5.52	*2.633	13.86	549.76	
*1033.785	0.74	520.43	83.84	752.22	3.96		
INDI 237	INDI 237 PLS 1		Breast	I	*154.94		
1574.84	1674.31	*0.816	13.05	*2.737	14.91	3336.38	
*331.366	0.82	2614.85	106.15	572.89	5.41		
INDI 238	INDI 238 PLS 1		Liver	II	3889.22		
4371.08	1125.69	15.18	27.72	73.69	12.66	1,284.1	
5598	0.75	4549.13	216.16	818.73	5.29		
INDI 239	INDI 239 PLS 1		Lung	III	9644.2		
5326.65	3690.17	12.38	9.63	*2.737	30.4	3797.63	

Table4.txt

*331.366	0.91	3159.07	147.26	1439.1	6.72		
INDI 241	INDI 241 PLS 1		Stomach	III	*154.94		
1396.65	1917.82	*0.816	13.51	*2.737	19.44	524.13	
*331.366	0.97	1594.55	106.15	1572.27	3.84		
INDI 243	INDI 243 PLS 1		Colorectum	I	2540.54		
2459.77	3683.33	5.11	23.18	*2.624	33.47	1,247.0	
*315.949	0.9	818.84	123.81	1458.36	11.59		
INDI 244	INDI 244 PLS 1		Colorectum	III	2380.99		
2589.82	5575.16	*0.817	24.53	*2.624	31.36	3,829.3	
2805.47	0.87	2974.45	112.06	1522.32	5.03		
INDI 245	INDI 245 PLS 1		Colorectum	III	2433.83		
1073.37	2965.44	*0.817	18.84	21.80	39.49	2,114.3	
3003.07	0.83	2349.24	112.06	1118.92	7.72		
INDI 246	INDI 246 PLS 1		Lung	II	*154.94		
2974.73	3152.02	6.72	18.76	20.78	23.99	2656.90	
*331.366	0.85	2069.14	*14.107	1048.83	4.86		
INDI 247	INDI 247 PLS 1		Lung	I	1342.4		
1570.51	2392.38	*0.816	16.27	*2.737	23.38	2,299.0	
*331.366	1.41	2548.94	*14.107	1350.87	9.09		
INDI 248	INDI 248 PLS 1		Colorectum	II	3411.52		
1241.20	3249.7	*0.817	32.39	*2.624	21.57	2,239.0	
1895.7	0.88	2393.41	99.23	1605.95	5.5		
INDI 250	INDI 250 PLS 1		Colorectum	II	1987.56		
4218.73	2032.99	5.4	9.26	18.57	29.98	2,892.7	
*315.949	0.88	1529.11	84.9	618.39	7.52		
INDI 251	INDI 251 PLS 1		Colorectum	II	2504.82		
2235.63	3112.92	*0.817	5.41	*2.624	31.93	12,282.7	
*315.949	0.91	778.42	112.06	935.4	9.42		
INDI 252	INDI 252 PLS 1		Lung	II	2826.15		
2633.29	1997.12	*0.816	86.17	*2.737	19.85	*77.037	
7477	1.77	2274.02	128.6	1701.09	7.29		
INDI 253	INDI 253 PLS 1		Colorectum	I	2139		
2492.29	3606.34	*0.817	25.89	*2.624	21	897.10	
1998.75	0.98	2459.82	99.23	735.83	11.16		
INDI 255	INDI 255 PLS 1		Colorectum	II	3093.82		
3109.40	2521.99	*0.817	16.81	16.96	17.07	1,753.2	
3394.29	0.83	1674.92	99.23	612.29	4.19		
INDI 256	INDI 256 PLS 1		Colorectum	III	2980.6		
2036.57	4306.88	*0.817	60.78	18.17	23.8	3,721.2	
2904.45	2.55	1440.75	129.37	695.65	13.64		
INDI 257	INDI 257 PLS 1		Lung	III	*154.94		
6493.46	3958.73	18.18	17.82	16.98	29.02	10,666.9	
4121.95	1.21	2405.61	147.26	1070.7	5.29		
INDI 258	INDI 258 PLS 1		Colorectum	I	*126.474		
556.21	3003.65	8.17	14.26	*2.624	15.6	657.9	
4542	0.76	1167.97	197.94	457.12	4.15		
INDI 259	INDI 259 PLS 1		Colorectum	II	4997.86		
1007.59	2194.65	*0.817	6.21	*2.624	30.25	770.9	

Table4.txt

4541.87	0.88	1592.99	173.01	618.39	3.53		
INDI 260	INDI 260 PLS 1		Stomach	I	2692.17		
3289.73	873.35	14.52	14.49	*2.737	9.13	964.23	
*331.366	0.95	1116.84	178.29	1208.82	4.65		
INDI 261	INDI 261 PLS 1		Breast	II	*154.94		
2953.41	1917.82	5.13	23.77	*2.737	16.64	477.61	
*331.366	0.91	1679.36	128.6	1037.83	5.83		
INDI 262	INDI 262 PLS 1		Breast	III	*154.94		
1055.53	896.12	*0.816	18.12	52.88	18.42	2,064.0	
*331.366	0.65	1205.42	*14.107	515.9	3.24		
INDI 264	INDI 264 PLS 1		Lung	III	2178.73		
1353.08	1202.14	*0.816	**196.241	23.93	14.31	2332.96	
*331.366	0.88	708.37	147.26	775.88	3.95		
INDI 265	INDI 265 PLS 1		Breast	II	3292.66		
2552.04	3131.98	*0.816	10.05	*2.737	21.52	1066.51	
*331.366	0.93	1795.06	106.15	812.67	4.15		
INDI 266	INDI 266 PLS 1		Lung	I	*154.94		
1985.47	900.68	*0.816	16.41	*2.737	17.08	466.1	
*331.366	0.7	445.78	204.36	1370.67	3.89		
INDI 267	INDI 267 PLS 1		Esophagus	II	5319.71		
3328.00	2414.38	*0.816	18.18	*2.737	22.55	*77.037	
*331.366	0.66	3174.66	*14.107	1380.53	4.68		
INDI 268	INDI 268 PLS 1		Colorectum	III	*126.474		
1069.71	4102.31	*0.817	6.22	*2.624	23.13	4,666.1	
2304.69	1.06	1209.64	134.74	562.54	6.04		
INDI 269	INDI 269 PLS 1		Lung	III	*154.94		
2269.25	2441.28	46.05	18.33	*2.737	16.9	2083.04	
*331.366	0.95	1876.09	*14.107	1285.69	4.37		
INDI 270	INDI 270 PLS 1		Breast	II	*154.94		
1570.51	1033.47	*0.816	20.82	*2.737	18.72	1346.09	
*331.366	0.85	2444.33	*14.107	1270.47	4.65		
INDI 271	INDI 271 PLS 1		Colorectum	III	*126.474		
2286.26	3381.22	16.01	5.86	*2.624	15.45	823.1	
*315.949	0.76	4242.37	145.03	575.14	7.34		
INDI 273	INDI 273 PLS 1		Lung	I	*154.94		
1509.73	1655.32	5.13	14.41	29.00	23.76	3,315.7	
2190	0.63	1517.47	227.33	1048.83	7		
INDI 274	INDI 274 PLS 1		Breast	II	2014.65		
1626.88	2304.59	*0.816	13.05	*2.737	27.58	747.90	
*331.366	0.68	1286.31	128.6	1015.68	4.74		
INDI 275	INDI 275 PLS 1		Breast	II	*154.94		
1353.08	1288.23	*0.816	15.81	*2.737	21.96	938.9	
*331.366	0.64	2452.08	*14.107	1140.59	4.18		
INDI 276	INDI 276 PLS 1		Liver	II	**99069.977		
4235.63	4061.6	6.4	17.94	24.44	27.55	1,489.3	
*331.366	1.23	4012.44	147.26	1395.26	4.95		
INDI 277	INDI 277 PLS 1		Breast	II	3412.18		
2936.36	3618.92	*0.816	18.82	*2.737	25.32	686.96	

Table4.txt

*331.366	0.86	2042.1	*14.107	818.73	3.21		
INDI 278	INDI 278 PLS 1		Ovary	III	*126.474		
3278.81	4622.76	1217.96	108.24	25.03	28.79	674.9	
5659	2.24	754.91	235.06	925.08	7.77		
INDI 279	INDI 279 PLS 1		Colorectum	II	1569.23		
1452.37	3003.65	*0.817	14.64	*2.624	32.6	*76.03	
*315.949	0.9	1426.65	99.23	524.03	6.52		
INDI 280	INDI 280 PLS 1		Breast	I	*154.94		
1825.88	2358.21	*0.816	18.52	*2.737	13.11	6659.72	
*331.366	0.57	1795.06	128.6	744.69	5.71		
INDI 281	INDI 281 PLS 1		Colorectum	I	*126.474		
949.08	2916.34	5.97	10.24	*2.624	40.61	*76.03	
2203.21	0.99	1836.19	154.78	429.24	6.95		
INDI 283	INDI 283 PLS 1		Lung	I	*154.94		
2654.66	1570.05	*0.816	13.01	19.71	23.61	2,543.2	
*331.366	0.81	2424.97	*14.107	1182.76	7.11		
INDI 284	INDI 284 PLS 1		Colorectum	II	1868.52		
2651.31	1487.51	*0.824	3.56	*2.781	24.4	8,648.0	
*327.606	1.19	2588.17	*15.64	1644.42	6.09		
INDI 285	INDI 285 PLS 1		Lung	II	1527.73		
1596.53	1445.11	21.71	9.85	*2.737	18.8	30,535.7	
7565.62	0.77	1556	128.6	1129.95	5.73		
INDI 286	INDI 286 PLS 1		Colorectum	I	906.77		
1565.06	2205.44	*0.817	8.69	*2.624	20.41	890.01	
*315.949	0.79	1447.8	99.23	463.99	7.38		
INDI 287	INDI 287 PLS 1		Breast	III	1682.38		
1700.50	1433.36	8.96	26.07	20.78	9.53	37,524.4	
3171.34	1.12	1086.02	243.12	1086.99	7.91		
INDI 288	INDI 288 PLS 1		Lung	III	1328.01		
5115.33	2202.51	113.04	**196.241	47.47	30.05	2,927.3	
33810.21	2.21	1294.01	221.82	1525.24	9.38		
INDI 289	INDI 289 PLS 1		Breast	II	1626.35		
1335.64	665.65	*0.816	5.22	*2.737	16.24	*77.037	
3554.71	0.76	2351.41	106.15	976.46	1.46		
INDI 290	INDI 290 PLS 1		Colorectum	I	790.34		
5320.30	5916.5	*0.817	26.87	*2.624	38.41	2475.64	
*315.949	0.85	2064.03	99.23	648.55	10.99		
INDI 291	INDI 291 PLS 1		Lung	I	2719		
1046.74	1253.28	*0.816	10.43	*2.737	13.49	4107.85	
*331.366	0.96	970.46	128.6	700.13	5.9		
INDI 292	INDI 292 PLS 1		Lung	III	*154.94		
3854.37	1551.14	*0.816	11.54	*2.737	21	4,237.6	
*331.366	0.92	2003.48	106.15	*74.42	7.02		
INDI 293	INDI 293 PLS 1		Colorectum	II	2549.49		
4477.89	3260.65	5.83	13.08	17.77	33.21	26,271.8	
2203	0.88	1696.35	99.23	1263.68	5.72		
INDI 295	INDI 295 PLS 1		Colorectum	II	1707.99		
3059.31	2400.29	*0.821	3.43	30.09	*1.364	25,046.6	

Table4.txt

*336.028	1.24	1232.99	164.02	1672.46	5.45		
INDI 296	INDI 296 PLS 1		Colorectum	II	1258.19		
4183.13	2904.14	6.78	3.33	17.39	*1.364	688.73	
*336.028	1.5	722	233.01	1157.11	4.09		
INDI 297	INDI 297 PLS 1		Breast	III	*134.509		
839.74	1067.1	*0.821	21.15	16.38	9.83	914.40	
*336.028	1.24	2256.27	116.7	1498.78	6.63		
INDI 298	INDI 298 PLS 1		Colorectum	I	*134.509		
4411.69	3337.32	*0.821	7.25	*2.73	13.36	*76.419	
*336.028	1.7	1583.39	177.18	586.83	5.91		
INDI 299	INDI 299 PLS 1		Colorectum	I	3420.77		
6774.65	3366.99	*0.821	8.39	*2.73	8.01	733.1	
2556.7	1.79	2528.72	134.22	1005.93	12.27		
INDI 300	INDI 300 PLS 1		Breast	III	*134.509		
348.87	1734.64	*0.821	9.76	33.43	9.32	1215.40	
*336.028	1.23	1469.74	134.22	894.34	4.88		
INDI 301	INDI 301 PLS 1		Breast	II	*134.509		
2514.09	1126.37	11.06	16.35	*2.73	16.95	1,234.6	
*336.028	0.96	1071.92	*14.024	1136.93	9.15		
INDI 302	INDI 302 PLS 1		Colorectum	I	*134.509		
4380.74	2606.79	*0.821	8.08	*2.73	6.96	997.8	
*336.028	0.91	2662.38	149.81	645.69	7.07		
INDI 303	INDI 303 PLS 1		Colorectum	I	4931.01		
3802.59	5720.18	5.63	7.66	23.32	22.76	1488.41	
*336.028	1.52	1964.75	195.41	2265.75	6.07		
INDI 304	INDI 304 PLS 1		Colorectum	I	*134.509		
7292.68	2618.5	*0.821	14.00	*2.73	13.94	1,390.0	
*336.028	1.36	1876.17	116.7	1406.07	7.59		
INDI 305	INDI 305 PLS 1		Colorectum	II	*134.509		
3586.04	1371.47	*0.821	6.94	33.91	9.73	14,690.7	
6578.56	1.5	2458.31	164.02	938.1	6.38		
INDI 306	INDI 306 PLS 1		Colorectum	III	*134.509		
5476.43	2390.57	26.49	6.80	*2.73	9.27	93,510.4	
6661.5	1.16	1742.9	134.22	2234.07	12		
INDI 307	INDI 307 PLS 1		Colorectum	III	*134.509		
4691.17	4319.42	*0.821	9.01	*2.73	7.95	719.77	
2106.97	1.47	929.55	*14.024	1130.17	6.91		
INDI 308	INDI 308 PLS 1		Liver	II	**98718.787		
1829.65	1421.34	40.28	16.26	*2.73	11.15	644.7	
2106.97	1.18	2636.11	201.16	*96.087	43.87		
INDI 309	INDI 309 PLS 1		Colorectum	II	2757.97		
1210.56	624.42	6.2	6.07	23.81	14.08	3933.21	
2287.68	1.68	2375.17	164.02	*96.087	16.16		
INDI 310	INDI 310 PLS 1		Colorectum	II	*134.509		
6764.87	3467.96	23.42	6.86	*2.73	15.83	1,587.9	
6412.44	1.56	3081.81	*14.024	1252.94	46.07		
INDI 311	INDI 311 PLS 1		Colorectum	III	*134.509		
1155.02	277.76	*0.821	8.24	27.20	*1.364	8076.31	

Table4.txt

2106.97	1.19	1712.87	177.18	*96.087	55.56		
INDI 312	INDI 312 PLS 1		Breast	II	1101.89		
1055.71	2283.71	*0.821	16.30	*2.73	12.4	601.17	
7404.47	1.04	2107.38	222.84	414.47	33.6		
INDI 313	INDI 313 PLS 1		Esophagus	II	1882.49		
848.49	2305.07	7.36	22.76	*2.73	9.16	768.91	
3000.34	0.93	1136.57	149.81	842.3	25.53		
INDI 314	INDI 314 PLS 1		Colorectum	I	*134.509		
1564.98	2035.71	8.82	3.65	18.38	10.65	566.63	
3264.04	0.9	1657.97	189.51	*96.087	41.2		
INDI 315	INDI 315 PLS 1		Breast	II	*134.509		
682.19	2194.48	*0.821	9.08	*2.73	11.96	786.90	
5239.60	1.02	5472.55	177.18	354.69	5.88		
INDI 316	INDI 316 PLS 1		Breast	II	*134.509		
1067.39	1588.41	*0.821	18.13	*2.73	14.89	*76.419	
*336.028	0.92	1660.46	*14.024	516.82	6.14		
INDI 317	INDI 317 PLS 1		Breast	II	*134.509		
1137.49	4001.89	*0.821	5.06	*2.73	15.09	1688.34	
*336.028	0.79	1538.82	*14.024	*96.087	10.79		
INDI 318	INDI 318 PLS 1		Stomach	III	975.05		
4311.83	1377.06	10.26	21.91	275.78	15.79	30,584.3	
2783.08	0.67	2103.91	178.29	890.2	3.73		
INDI 319	INDI 319 PLS 1		Stomach	I	*154.94		
2415.04	4333.12	5.76	16.01	20.25	31	469.9	
*331.366	1.08	1024.39	204.36	326.21	9.58		
INDI 320	INDI 320 PLS 1		Colorectum	II	3219.96		
1544.99	4789.23	9.88	3.79	*2.688	29.57	12,114.0	
2981.75	1.59	562.62	253.52	650.06	5.24		
INDI 321	INDI 321 PLS 1		Colorectum	III	13904.55		
1879.58	2166.45	111.49	12.57	*2.688	19.95	978.30	
1984.23	0.86	1944.44	180.85	1042.89	0.9		
INDI 322	INDI 322 PLS 1		Colorectum	III	3705.16		
1745.08	3693.3	*0.819	7.61	25.82	31.92	957.5	
2981.75	1.26	941.24	282.31	859.63	2.48		
INDI 323	INDI 323 PLS 1		Breast	I	*154.94		
1418.41	1309.23	*0.816	4.90	*2.737	13.35	*77.037	
*331.366	0.61	1035.95	178.29	627.71	4.57		
INDI 324	INDI 324 PLS 1		Lung	I	*154.94		
1261.44	1598.44	*0.816	16.44	*2.737	14.4	4032.52	
*331.366	0.69	1186.17	138.29	493.89	4.46		
INDI 325	INDI 325 PLS 1		Colorectum	III	3439.28		
342.14	4967.71	8.77	15.27	*2.688	20.39	1120.64	
2981.75	1.02	984.63	201.81	1067.05	2.01		
INDI 326	INDI 326 PLS 1		Lung	I	*154.94		
701.80	470.49	5.61	30.58	22.36	18.38	9033.13	
*331.366	0.88	1995.76	237.97	725.73	4.78		
INDI 327	INDI 327 PLS 1		Colorectum	II	*147.882		
1560.39	3846.14	6.3	11.91	*2.688	18.5	1,703.9	

Table4.txt

2502.31	0.8	2015.9	220.56	981.39	1.91		
INDI 328	INDI 328 PLS 1		Colorectum	I	2169.31		
1398.55	2915.87	99.6	7.28	*2.688	14.93	953.4	
*330.705	0.95	1564.49	220.56	255.15	2.21		
INDI 329	INDI 329 PLS 1		Colorectum	III	5114.01		
2021.63	4190.88	8.55	13.69	70.89	27.01	2,083.6	
71827.39	2.39	1941.2	201.81	1269.44	5.85		
INDI 331	INDI 331 PLS 1A		Lung	III	*166.572		
4950.43	1323.05	6.1	4.38	*2.781	24.92	6,718.2	
2252.24	0.98	1300.84	161.07	*78.14	2.22		
INDI 332	INDI 332 PLS 1		Breast	I	4895.14		
1422.77	2818.08	*0.816	16.17	*2.737	20.3	*77.037	
*331.366	0.91	1825.92	*14.107	1290.75	4.86		
INDI 333	INDI 333 PLS 1A		Lung	II	*166.572		
2299.29	2109.42	*0.824	8.86	*2.781	17.42	*76.889	
*327.606	1.02	1386.68	*15.64	981.84	3.54		
INDI 334	INDI 334 PLS 1		Breast	I	1973.44		
1448.87	1452.16	*0.816	6.27	*2.737	14.78	739.74	
*331.366	0.64	1798.92	163.59	842.82	3.5		
INDI 335	INDI 335 PLS 1A		Lung	I	3292.88		
1976.13	1638.22	*0.824	48.42	*2.781	26.46	4261.12	
*327.606	1.09	1541.42	115.58	1581.5	5.32		
INDI 336	INDI 336 PLS 1A		Lung	III	*166.572		
857.79	713.04	6.1	5.72	*2.781	22.32	1,084.5	
*327.606	0.65	939.71	*15.64	417.51	3.32		
INDI 337	INDI 337 PLS 1		Esophagus	III	*154.94		
2226.32	2865.21	8.96	31.91	27.50	21.68	2045.02	
*331.366	0.96	2801.15	106.15	732.07	4.23		
INDI 338	INDI 338 PLS 1		Colorectum	II	3304.7		
1004.42	4713.05	24.71	18.21	*2.688	28.23	1,040.9	
3433.08	0.92	2484.86	220.56	1114.69	3.27		
INDI 339	INDI 339 PLS 1		Breast	II	*154.94		
2705.93	1367.69	*0.816	9.25	*2.737	23.34	2410.81	
*331.366	1.01	3104.53	106.15	706.56	5.23		
INDI 340	INDI 340 PLS 1		Colorectum	III	3967.29		
408.84	1263.58	24.92	8.89	*2.688	22.15	636.4	
4865.43	0.93	762.78	455.84	879.33	2.14		
INDI 341	INDI 341 PLS 1		Liver	II	*154.94		
3021.60	1555.87	9.93	40.03	3446.30	13.74	1,453.3	
8180	0.78	2065.28	369.52	530.38	5.53		
INDI 342	INDI 342 PLS 1A		Lung	III	*166.572		
1553.70	270.52	5.01	156.65	*2.781	23.15	2451.24	
*327.606	0.71	2601.6	105.47	562.96	5.85		
INDI 343	INDI 343 PLS 1		Colorectum	III	5082.7		
2795.03	4198.55	8.1	20.09	*2.688	23.81	1,637.8	
*330.705	1.16	2139.78	180.85	1275.01	1.84		
INDI 344	INDI 344 PLS 1		Colorectum	II	5859.15		
2588.59	2634	24.09	20.51	77.70	31.14	12,819.2	

Table4.txt

3433.08	0.98	1663.75	156.67	826.35	1.41		
INDI 346	INDI 346 PLS 1A		Lung	I	*166.572		
424.08	517.75	*0.824	14.40	*2.781	22.04	608.2	
*327.606	0.97	1154.93	161.07	585.83	4.11		
INDI 347	INDI 347 PLS 1		Esophagus	I	1255.73		
3400.25	2706.76	*0.816	17.62	*2.737	13.01	634.7	
*331.366	0.84	1332.53	147.26	1310.91	5.32		
INDI 348	INDI 348 PLS 1		Breast	II	*154.94		
1200.23	1574.78	9.28	32.43	19.17	19.97	821.92	
*331.366	0.91	1424.99	*14.107	936.6	4.26		
INDI 350	INDI 350 PLS 1		Breast	II	*154.94		
1230.84	918.93	5.61	16.73	*2.737	19.85	650.74	
*331.366	0.73	1378.76	248.15	1081.57	6.26		
INDI 352	INDI 352 PLS 1		Breast	III	*154.94		
1326.92	4551.88	*0.816	15.90	*2.737	23.45	2145.07	
*331.366	0.74	2812.8	106.15	456.29	6.79		
INDI 353	INDI 353 PLS 1A		Lung	II	*166.572		
772.79	229.52	*0.824	3.47	*2.781	28.27	461.3	
*327.606	1.33	601.93	*15.64	667.1	7.23		
INDI 354	INDI 354 PLS 1		Colorectum	III	5519		
2489.12	2368.6	8.77	12.68	17.58	30.71	2750.33	
2981.75	0.88	1602.86	320.3	2023.77	1.22		
INDI 355	INDI 355 PLS 1A		Lung	I	*166.572		
1056.34	1646.31	*0.824	8.49	*2.781	25.65	1,289.3	
*327.606	0.93	2189	*15.64	328.31	5.26		
INDI 356	INDI 356 PLS 1		Colorectum	I	5735.69		
1614.28	819.68	*0.819	22.43	*2.688	27.77	928.57	
1984.23	0.98	1341.93	156.67	1541.74	3.23		
INDI 357	INDI 357 PLS 1A		Lung	I	*166.572		
1767.21	1682.79	*0.824	25.08	24.73	19.24	608.21	
*327.606	0.92	1056.1	231.82	270.37	5.83		
INDI 358	INDI 358 PLS 1A		Lung	II	*166.572		
1027.96	554.38	6.24	9.95	*2.781	21.4	1,269.7	
*327.606	0.67	1887.35	161.07	*78.14	4.61		
INDI 359	INDI 359 PLS 1		Breast	I	4802.4		
1064.32	1111.82	7.35	13.30	*2.737	19.18	826.1	
*331.366	0.63	1988.03	*14.107	667.6	5.67		
INDI 360	INDI 360 PLS 1A		Lung	II	*166.572		
2099.65	2271.23	*0.824	21.08	*2.781	30.1	719.0	
*327.606	1.59	2035.56	*15.64	724	4.38		
INDI 361	INDI 361 PLS 1		Breast	III	2096.83		
3076.97	1017.39	7.35	6.93	*2.737	23.34	*77.037	
*331.366	0.7	2150.29	106.15	993.35	4.08		
INDI 362	INDI 362 PLS 1		Breast	II	1959.68		
2774.26	889.29	*0.816	7.47	*2.737	13.54	586.99	
*331.366	0.83	1344.09	147.26	544.69	4.78		
INDI 363	INDI 363 PLS 1		Breast	I	*154.94		
3429.99	4651.3	6.56	11.81	26.49	32.82	1363.88	

Table4.txt

*331.366	0.83	2781.73	106.15	1320.94	9.5		
INDI 364	INDI 364 PLS 1A		Lung	I	*166.572		
2204.21	1825.62	5.28	6.40	*2.781	28.22	3434.55	
*327.606	0.88	3353.24	115.58	467.79	3.37		
INDI 365	INDI 365 PLS 1		Colorectum	II	1799.72		
919.16	950.21	*0.819	7.00	25.16	20.17	1,385.2	
6149.65	1.14	1526.18	295.56	*77.47	2.48		
INDI 366	INDI 366 PLS 1		Pancreas	II	2173.1		
2383.88	2186.55	18.56	18.86	172.97	53.77	1,673.9	
3588.09	1.08	2997.04	274.74	925.08	5.01		
INDI 367	INDI 367 PLS 1		Liver	I	5266.58		
1257.07	2365.53	15.52	35.00	33.42	26.89	1,471.3	
*331.366	0.86	3182.46	*14.107	1380.53	3.91		
INDI 368	INDI 368 PLS 1		Breast	II	*154.94		
3926.43	5671.81	8.32	5.13	92.00	36.66	**56207.571	
*331.366	0.91	2715.72	128.6	1320.94	8.28		
INDI 369	INDI 369 PLS 1A		Lung	I	*166.572		
2432.45	960.84	12.7	74.46	*2.781	35.32	4554.64	
*327.606	0.73	2013.71	*15.64	*78.14	8		
INDI 371	INDI 371 PLS 1A		Lung	III	*166.572		
2827.43	1445.66	47.51	29.87	53.38	22.88	2,635.4	
10275.15	0.84	1266.51	161.07	709.94	3.75		
INDI 372	INDI 372 PLS 1A		Lung	II	2062.31		
4969.54	2084.35	*0.824	6.06	*2.781	22.21	1,215.0	
*327.606	0.78	1378.09	147.81	508.23	3.22		
INDI 373	INDI 373 PLS 1A		Lung	I	*166.572		
838.90	2750.42	*0.824	18.61	17.41	25.85	6310.62	
*327.606	0.84	2202.2	*15.64	724	5.1		
INDI 374	INDI 374 PLS 1		Colorectum	III	1488.62		
841.57	1916.89	7.43	7.64	44.92	33.16	24236.29	
4274.50	1.05	2025.66	253.52	701.32	2.03		
INDI 375	INDI 375 PLS 1		Liver	I	11030.57		
4675.66	2957.2	169.14	28.84	*2.737	17.3	4615.26	
*331.366	1.94	3847.4	*14.107	1590.92	8.37		
INDI 376	INDI 376 PLS 1		Colorectum	I	*138.956		
800.55	2757.32	*0.815	13.15	*2.744	20.14	500.9	
*323.192	0.56	2079.62	*14.413	729.21	4.15		
INDI 377	INDI 377 PLS 1		Colorectum	II	6373.14		
720.35	2675.29	18.04	5.12	*2.744	24.26	1,087.6	
4734.29	1.15	1267.85	734.55	1115.93	4.88		
INDI 378	INDI 378 PLS 1		Colorectum	I	*138.956		
3124.88	12247.31	*0.815	46.85	*2.744	39.79	2024.99	
*323.192	0.99	1940.72	99.02	710.11	9.46		
INDI 379	INDI 379 PLS 1		Colorectum	III	8497.3		
850.61	2005.28	*0.815	7.84	*2.744	63.88	*77.473	
*323.192	0.69	3125.56	128.85	610.75	4.45		
INDI 380	INDI 380 PLS 1		Colorectum	II	*138.956		
780.51	6167.15	*0.815	7.08	*2.744	59.24	2,030.3	

Table4.txt

2535.48	0.8	1764.91	166.55	*84.63	5.77		
INDI 381	INDI 381 PLS 1A		Lung	III	*166.572		
1146.24	666.15	8.62	11.59	*2.781	19.61	1825.47	
*327.606	1.04	831.3	*15.64	328.31	2.68		
INDI 382	INDI 382 PLS 1		Breast	II	4418.48		
1501.04	1891.44	*0.816	25.59	*2.737	22.2	1,381.7	
*331.366	1	2312.71	106.15	1015.68	3.74		
INDI 383	INDI 383 PLS 1A		Lung	III	*166.572		
1278.81	749.39	10.06	15.37	*2.781	30.56	570.9	
*327.606	1.05	1090.5	231.82	364.94	5.27		
INDI 384	INDI 384 PLS 1		Pancreas	II	5598.93		
1561.43	2611.55	*0.817	19.22	*2.624	12.76	1295.85	
*315.949	1.04	1199.21	84.9	*71.31	3.18		
INDI 385	INDI 385 PLS 1		Colorectum	I	*138.956		
1526.22	4966.31	*0.815	40.28	*2.744	72.63	1004.15	
*323.192	0.6	1703.17	*14.413	3532.45	7.25		
INDI 386	INDI 386 PLS 1		Colorectum	III	*138.956		
740.41	2977.23	*0.815	4.47	*2.744	29.56	958.35	
*323.192	0.62	997.21	166.55	366.62	4.66		
INDI 387	INDI 387 PLS 1		Liver	I	*154.94		
3349.25	2875.14	*0.816	6.63	*2.737	21.88	1,621.0	
*331.366	1.01	2614.85	216.16	1772.98	4.57		
INDI 388	INDI 388 PLS 1		Pancreas	II	1522.87		
941.76	3039.14	6.55	12.50	26.65	21.64	3,749.3	
4730	0.92	1370.38	99.23	660.45	6.62		
INDI 389	INDI 389 PLS 1A		Lung	III	17193.3		
2589.44	912.01	28.03	20.54	48.87	22.32	869.0	
7678	1.05	2145.06	503.3	1633.99	6.49		
INDI 390	INDI 390 PLS 1		Breast	II	*154.94		
865.99	1917.82	*0.816	55.18	*2.737	27.73	1884.75	
*331.366	0.83	1394.17	*14.107	1224.35	3.95		
INDI 391	INDI 391 PLS 1		Liver	II	*154.94		
4980.07	2328.95	24.93	15.98	18.08	20.79	2,548.1	
1988	1.07	2847.77	163.59	2003.38	6.58		
INDI 392	INDI 392 PLS 1A		Lung	I	1354.34		
1226.72	1441.68	*0.824	20.57	*2.781	17.63	*76.889	
*327.606	0.7	931.06	115.58	400.27	4.65		
INDI 393	INDI 393 PLS 1		Liver	II	**99069.977		
4430.32	1740.91	5.45	50.39	19.71	17.04	955.8	
*331.366	0.71	2999.41	359.1	1092.39	2.99		
INDI 394	INDI 394 PLS 1A		Lung	II	*166.572		
1700.76	3719.06	*0.824	39.57	*2.781	22.77	574.3	
*327.606	1.56	2263.88	*15.64	467.79	4.79		
INDI 395	INDI 395 PLS 1A		Lung	I	1429.31		
1236.19	1715.3	*0.824	13.04	*2.781	27.74	1,910.9	
2061.47	0.9	624.33	184.36	1285.89	4.17		
INDI 396	INDI 396 PLS 1		Colorectum	I	4454.42		
1675.93	4294.27	*0.815	17.23	*2.744	28.08	*77.473	

Table4.txt

*323.192	0.64	1068.31	*14.413	1438.63	4.11		
INDI 397	INDI 397 PLS 1		Colorectum	III	*138.956		
1100.48	3628.65	*0.815	6.75	*2.744	29.91	58,578.6	
*323.192	0.58	1359.26	202.76	2290.1	4.45		
INDI 398	INDI 398 PLS 1		Colorectum	II	*138.956		
1579.45	2300.24	*0.815	23.20	*2.744	36.78	788.2	
*323.192	0.79	1132.57	99.02	1640.41	4.76		
INDI 400	INDI 400 PLS 1		Colorectum	II	*138.956		
3131.62	8347.78	6.52	13.84	*2.744	148.44	3,869.6	
*323.192	0.8	1768.34	*14.413	2601.61	6.79		
INDI 402	INDI 402 PLS 1		Breast	I	2341.76		
2002.71	3866.41	*0.816	19.68	20.25	20.59	3336.38	
*331.366	0.91	3843.48	155.66	471.47	4.73		
INDI 403	INDI 403 PLS 1A		Lung	III	*166.572		
1577.42	1358.5	*0.824	4.83	*2.781	20.7	684.00	
*327.606	0.87	1343.75	*15.64	1086.57	3.22		
INDI 404	INDI 404 PLS 1		Breast	III	*154.94		
2560.59	3573.19	5.76	4.00	*2.737	13.64	2002.39	
*331.366	1	1949.42	106.15	674.15	3.52		
INDI 405	INDI 405 PLS 1A		Lung	I	*166.572		
1715.00	2981.23	*0.824	8.18	*2.781	24.55	1211.15	
*327.606	1.27	1287.97	*15.64	681.49	4.15		
INDI 407	INDI 407 PLS 1		Breast	I	*154.94		
3795.01	3368.22	*0.816	5.74	*2.737	18.97	508.6	
*331.366	0.65	1633.1	128.6	1290.75	6.51		
INDI 408	INDI 408 PLS 1		Breast	II	*154.94		
3187.64	1051.87	5.92	6.59	*2.737	21.52	764.27	
*331.366	0.71	1656.23	*14.107	1092.39	6.43		
INDI 409	INDI 409 PLS 1		Breast	II	1654.39		
967.52	3049.46	10.26	22.21	23.41	17.12	715.31	
*331.366	0.75	1301.72	106.15	884.33	3.67		
INDI 411	INDI 411 PLS 1		Breast	II	10065.51		
2019.93	2880.11	*0.816	30.64	*2.737	19.89	1,708.2	
*331.366	0.75	1825.92	118	763.47	4.86		
INDI 412	INDI 412 PLS 1		Breast	II	7616.1		
1243.96	1617.38	12.22	16.53	58.19	13.4	3,269.2	
2587	0.7	2483.06	257.94	1310.91	5.83		
INDI 413	INDI 413 PLS 1		Lung	I	*154.94		
2569.15	1755.21	95.89	10.43	*2.737	9.19	590.95	
*331.366	0.98	1818.21	*14.107	1124.62	4.44		
INDI 414	INDI 414 PLS 1		Lung	II	*154.94		
1313.83	1051.87	*0.816	16.30	*2.737	16.46	2040.27	
*331.366	0.95	854.87	106.15	913.52	0.88		
INDI 415	INDI 415 PLS 1		Lung	II	63012.68		
1230.84	2141.94	*0.816	34.89	*2.737	20.02	1,218.2	
*331.366	0.89	2208.28	*14.107	1156.48	5.58		
INDI 417	INDI 417 PLS 1		Lung	I	1779.95		
2080.19	3433.88	*0.816	10.57	19.71	17.78	723.4	

Table4.txt

*331.366	1.24	623.49	128.6	1054.32	3.68		
INDI 418	INDI 418 PLS 1		Colorectum	I	*134.509		
3473.57	565.36	*0.821	7.63	*2.73	14.49	706.44	
*336.028	1.33	1376.52	157.06	1492.66	12.07		
INDI 419	INDI 419 PLS 1		Colorectum	I	*134.509		
1888.61	7113.41	10.31	6.29	*2.73	19.61	498.42	
8386.27	1.36	1105.4	*14.024	754.17	8.29		
INDI 421	INDI 421 PLS 1		Colorectum	II	*134.509		
3340.15	1258.42	8.82	12.80	*2.73	12.28	1,995.3	
*336.028	1.04	*26.403	201.16	1233.34	5.45		
INDI 422	INDI 422 PLS 1		Colorectum	II	*134.509		
2618.51	3754.14	*0.821	1.81	*2.73	11.83	1,892.1	
3088.43	1.89	1707.87	217.6	1153.75	10.32		
INDI 423	INDI 423 PLS 1		Colorectum	II	*134.509		
3857.64	6834.25	6.78	2.58	*2.73	11.62	1678.25	
2645.88	1.19	761.28	189.51	934.48	8.79		
INDI 424	INDI 424 PLS 1		Breast	II	12620.43		
1647.22	2056.98	5.07	4.38	*2.73	7.89	579.55	
*336.028	1.24	1048.06	311.77	702.69	5.88		
INDI 425	INDI 425 PLS 1		Breast	II	3365.77		
1307.08	3165.61	*0.821	6.10	*2.73	16.86	532.4	
*336.028	1.19	2276.9	164.02	864.74	5.63		
INDI 426	INDI 426 PLS 1		Breast	II	*134.509		
2048.06	1471.23	*0.821	6.94	*2.73	7.76	*76.419	
*336.028	2.12	2993.55	*14.024	595.36	8.85		
INDI 427	INDI 427 PLS 1		Colorectum	II	*134.509		
5966.93	2450.88	10.61	6.88	32.96	20.58	26,090.8	
*336.028	2.89	1110.19	233.01	1226.78	7.68		
INDI 428	INDI 428 PLS 1		Colorectum	III	*117.693		
3595.17	5059.3	6.52	5.13	36.54	9.73	34148.35	
*311.017	1.83	430.56	134.25	734.52	6.45		
INDI 429	INDI 429 PLS 1		Colorectum	II	1940.15		
5072.71	6684.75	44.35	3.20	18.38	14.59	2983.16	
*336.028	2.18	1095.83	116.7	1642.99	6.99		
INDI 431	INDI 431 PLS 1		Colorectum	II	*134.509		
5091.55	3712.31	5.07	8.24	16.38	9.88	662.29	
*336.028	1.25	752.02	116.7	475.92	6.82		
INDI 433	INDI 433 PLS 1		Colorectum	II	*134.509		
2033.28	7364.24	29.93	10.41	44.71	25.78	473.2	
*336.028	1.41	1337.44	116.7	1103	4.33		
INDI 434	INDI 434 PLS 1		Colorectum	II	940.72		
6108.05	5034.72	*0.821	2.09	*2.73	11.36	1210.60	
*336.028	1.07	1533.88	*14.024	*96.087	9.24		
INDI 436	INDI 436 PLS 1		Colorectum	III	*134.509		
4072.34	700.65	*0.821	6.63	*2.73	6.82	1258.70	
*336.028	1.11	1206.4	*14.024	603.85	4.86		
INDI 437	INDI 437 PLS 1		Colorectum	I	*134.509		
1641.34	1906.25	*0.821	13.68	*2.73	8.83	481.6	

Table4.txt

2106.97	2.1	1692.89	170.71	1180.5	6.05	
INDI 438	INDI 438 PLS 1		Colorectum	II	*134.509	
2190.14	1365.72	*0.821	5.77	*2.73	9.88	566.63
*336.028	2.11	768.23	116.7	1327.11	3.44	
INDI 439	INDI 439 PLS 1		Colorectum	III	2168.78	
1468.17	2857.09	5.07	4.16	58.09	9.88	662.3
*336.028	1.95	673.73	116.7	1123.4	10.8	
INDI 440	INDI 440 PLS 1		Esophagus	II	*134.509	
3888.25	673.97	*0.821	22.13	*2.73	11.32	1,253.9
*336.028	1.43	1163.01	*14.024	742.4	8.06	
INDI 441	INDI 441 PLS 1		Esophagus	II	2147.81	
1852.64	1850.37	*0.83	4.94	17.24	12.29	1239.39
2639.08	1.29	1942.16	159.22	2426.62	27.17	
INDI 442	INDI 442 PLS 1		Breast	II	*147.82	
1370.17	1984.28	*0.83	12.57	*2.755	13.3	*75.938
*325.95	1.13	951.61	159.22	279.99	16.72	
INDI 443	INDI 443 PLS 1		Breast	II	1409.49	
1546.58	1363.58	*0.83	24.97	*2.755	15.25	3974.29
2055.05	0.96	1776.29	86.07	764.01	11.66	
INDI 444	INDI 444 PLS 1		Colorectum	II	11637.12	
616.77	2310.12	9.32	30.59	46.90	22.06	46,050.8
2924.55	1.35	1113.16	204.08	773.24	14.16	
INDI 445	INDI 445 PLS 1		Breast	II	964.78	
460.45	1736.21	6.83	10.49	31.79	17.46	4,655.0
4572.73	2.28	*26.781	180.46	469.13	5.23	
INDI 446	INDI 446 PLS 1		Esophagus	II	3276.17	
4986.42	1556.16	6.83	77.24	*2.755	22.93	4,776.1
2349	1.27	2744.94	159.22	1242.17	11.16	
INDI 447	INDI 447 PLS 1		Breast	III	12912.11	
1414.25	2344.22	3269.27	**172.378	4333.59	29.28	195,227.2
685439.58	1.52	1932.36	403.56	854.25	7.87	
INDI 449	INDI 449 PLS 1		Breast	III	*147.82	
701.29	1192.15	7.14	10.78	*2.755	11.75	11,343.6
6315	1.81	2154.23	180.46	1158.43	8.65	
INDI 450	INDI 450 PLS 1		Esophagus	II	1797.94	
5264.97	2511.45	*0.83	12.57	*2.755	11.72	3019.36
4304.34	1.08	1052.18	104.91	578.03	13.18	
INDI 452	INDI 452 PLS 1		Colorectum	II	*147.82	
472.95	2200.74	*0.83	22.81	*2.755	17.54	1,079.5
1956	1.17	2075.01	120.79	800.63	9.01	
INDI 453	INDI 453 PLS 1		Breast	I	*147.82	
1036.86	1134.9	6.83	31.80	*2.755	14.08	6237.27
*325.95	0.77	2897.15	*14.345	990.72	6.77	
INDI 454	INDI 454 PLS 1		Breast	III	*147.82	
1149.97	948.31	15.75	18.79	31.79	9.63	2,468.3
8161.17	1.8	876.94	225.41	668.91	8.05	
INDI 455	INDI 455 PLS 1		Breast	II	*147.82	
1685.33	1752.26	5.6	23.70	*2.755	10.08	720.0

Table4.txt

*325.95	1.02	1099.07	175.38	530.23	5.48		
INDI 456	INDI 456 PLS 1		Colorectum	II	*147.82		
560.46	596.15	28.13	3.39	491.12	*1.372	3,493.0	
1955.7	1.7	1382.41	217.11	*21.901	12.63		
INDI 457	INDI 457 PLS 1		Esophagus	II	5986.73		
3693.14	4970.74	21.92	13.43	55.15	22.82	3,584.6	
9225.61	1.99	970.29	309.69	1596.48	15.31		
INDI 458	INDI 458 PLS 1		Breast	III	*147.82		
867.39	3189.86	24.95	46.88	250.07	19.12	5,406.4	
21058	1.28	1131.95	190.23	385.95	23.34		
INDI 459	INDI 459 PLS 1		Breast	II	1059.74		
11586.41	3113.15	6.83	27.22	32.47	18.54	*75.938	
194407.31	1.17	2228.83	217.11	1019.48	10.4		
INDI 460	INDI 460 PLS 1		Breast	III	*147.82		
2137.18	1452.76	20.02	11.09	19.01	11.87	490.93	
*325.95	2.55	2253.77	303.44	818.68	4.9		
INDI 461	INDI 461 PLS 1		Colorectum	III	*147.82		
785.87	1796.85	*0.83	7.32	*2.755	13.19	7,231.7	
2734.67	1.01	1197.84	194.95	800.63	7.29		
INDI 462	INDI 462 PLS 1		Breast	III	1200.69		
7249.36	3087.61	2759.3	172.48	471.50	27.71	209,102.0	
**245954.599	2.05	4200.57	233.44	1047.9	15.53		
INDI 463	INDI 463 PLS 1		Colorectum	II	*147.82		
1282.05	1206.45	18.75	4.06	39.56	7.32	21,051.1	
2639.08	1.61	1679.44	284.02	385.95	7.21		
INDI 464	INDI 464 PLS 1		Liver	III	5135.34		
773.34	2831.24	855.37	107.96	123.01	12.17	190,437.5	
3669.08	1.24	2169.13	104.91	398.28	18.14		
INDI 465	INDI 465 PLS 1		Esophagus	II	*147.82		
1382.77	1495.55	27.34	8.23	26.66	12.61	6,735.5	
*325.95	1.17	1278.1	104.91	480.48	9.85		
INDI 466	INDI 466 PLS 1		Colorectum	II	*147.82		
6360.32	1991.43	*0.83	7.28	35.86	10.88	3,095.2	
*325.95	1.03	3511.55	*14.345	593.59	5.75		
INDI 467	INDI 467 PLS 1		Colorectum	II	1786.6		
920.72	753.16	7.14	10.25	*2.755	17.21	3918.15	
*325.95	1.57	1356.29	199.56	373.44	36.01		
INDI 468	INDI 468 PLS 1		Colorectum	II	1615.92		
1093.41	1005.83	6.83	14.05	16.53	11.43	7,822.7	
3484.98	1.56	2278.75	233.44	1279.43	11.8		
INDI 469	INDI 469 PLS 1		Breast	III	1581.65		
3370.32	2138.07	15.44	25.11	*2.755	12.66	1576.53	
*325.95	1.2	1240.29	113.13	220.08	14.89		
INDI 470	INDI 470 PLS 1		Colorectum	III	*147.82		
1118.54	2222.25	*0.83	8.24	*2.755	18.48	2,584.8	
*325.95	1.81	795.41	95.97	541	10.08		
INDI 471	INDI 471 PLS 1		Breast	III	*147.82		
363.70	1179.63	*0.83	13.03	*2.755	8.56	1410.34	

Table4.txt

1955.70	1.61	534.35	190.23	170.07	5.95		
INDI 472	INDI 472 PLS 1		Colorectum	II	3231.59		
3622.75	2407.1	25.42	14.10	*2.755	16.52	8,040.3	
*325.95	1.51	1256.82	277.29	598.73	6.21		
INDI 473	INDI 473 PLS 1		Breast	III	*147.82		
698.16	1846.8	45.02	32.21	*2.755	*1.372	698.7	
20766	1.08	1798.15	199.56	265.58	8.94		
INDI 474	INDI 474 PLS 1		Breast	II	*147.82		
917.58	2184.62	10.88	34.31	*2.755	14.08	7014.30	
2924.55	1.52	2154.23	225.41	629.22	7.31		
INDI 475	INDI 475 PLS 1		Liver	III	*147.82		
926.99	2313.71	7.77	19.18	*2.755	14.31	1,162.8	
*325.95	2.42	1487.28	199.56	491.72	11.89		
INDI 476	INDI 476 PLS 1		Esophagus	II	3365.32		
3290.53	3450.36	*0.83	25.42	*2.755	14.13	1,826.9	
11860	1.12	2409.21	*14.345	818.68	11.85		
INDI 477	INDI 477 PLS 1		Colorectum	III	*147.82		
2952.76	1388.56	24.15	5.08	*2.755	9.67	1379.01	
*325.95	0.95	1413.34	*14.345	321.47	3.73		
INDI 478	INDI 478 PLS 1		Breast	II	3198.16		
2612.64	2068.29	*0.83	23.03	*2.755	16.5	2,680.3	
*325.95	1.38	1735.06	199.56	446.06	8.28		
INDI 479	INDI 479 PLS 1		Breast	III	*147.82		
2746.05	1111.63	23.19	9.83	43.90	10.08	1,433.9	
3299.59	0.83	907.26	199.56	132.89	4.6		
INDI 480	INDI 480 PLS 1		Breast	III	*147.82		
1452.05	1766.53	14.97	12.67	55.80	12.05	1773.94	
*325.95	0.94	1415.72	113.13	422.46	4.85		
INDI 482	INDI 482 PLS 1		Liver	II	108284.29		
1697.95	211.14	*0.83	20.24	39.89	8.82	3,342.8	
3113	0.91	1841.96	86.07	410.44	9.99		
INDI 483	INDI 483 PLS 1		Colorectum	II	*147.82		
1395.36	1195.73	*0.83	6.99	*2.755	12.72	*75.938	
*325.95	1.08	1645.66	170.15	791.55	9.53		
INDI 484	INDI 484 PLS 1		Colorectum	II	*138.956		
1270.15	4069.31	*0.815	7.98	*2.744	25.13	675.5	
*323.192	1.36	2003.11	*14.413	821.48	3.85		
INDI 485	INDI 485 PLS 1		Esophagus	III	3491.78		
1331.28	2382.61	*0.816	7.46	*2.737	15.92	2,474.4	
*331.366	0.72	2057.55	*14.107	614.19	3.43		
INDI 487	INDI 487 PLS 1		Breast	II	3743.59		
1002.76	1015.09	5.45	11.19	*2.737	18.97	813.65	
*331.366	0.75	654.36	*14.107	2116.75	3.87		
INDI 488	INDI 488 PLS 1		Breast	III	1218.96		
2174.92	851.58	*0.831	23.39	*2.782	18.24	908.12	
*325.874	0.66	1233.04	228.84	1091.53	6.03		
INDI 489	INDI 489 PLS 1		Breast	II	*137.024		
1758.08	1054.45	7.03	14.97	*2.782	13.52	6,618.8	

Table4.txt

*325.874	0.71	2363.74	189.5	347.47	4.01	INDI 490	INDI 490 PLS 1
Breast	III	1703.14	1961.97	4358.56	308.89	22.39	39.23
24.63	5,876.0	*325.874	0.75	3419.83	120.99	1091.53	5.86
INDI 491	INDI 491 PLS 1	Lung	I	1425.93	441.16	1114.83	6.08
15.80	*2.782	15.71	938.89	*325.874	0.79	1708.11	*14.53
1115.81	9.41	INDI 492	INDI 492 PLS 1	Lung	I	5958.7	2132.28
1537.79	*0.831	10.90	*2.782	*1.36	794.20	*325.874	0.83
1544.45	100.18	1004.46	7.06	INDI 493	INDI 493 PLS 1	Breast	II
2058.19	5637.11	374.39	*0.831	27.74	*2.782	14.7	1664.00
*325.874	0.57	1797.56	100.18	398.13	4.07	INDI 494	INDI 494 PLS 1
Lung	III	*137.024	1045.01	2472.02	13.76	29.68	*2.782
13.07	45,376.4	*325.874	0.76	1637.39	120.99	641.2	10
INDI 495	INDI 495 PLS 1	Lung	I	*137.024	4357.56	1507.38	6.4
49.48	18.59	22.13	1549.28	*325.874	0.74	2265.81	159.59
1940.62	4.03	INDI 497	INDI 497 PLS 1	Lung	II	1485.43	756.49
621.15	8.32	13.21	31.64	11.85	2366.48	2815.65	0.76
2198.12	200.1	1029.69	8.51	INDI 498	INDI 498 PLS 1	Colorectum	II
1503.63	860.62	2977.23	*0.815	7.73	*2.744	15.13	823.5
*323.192	0.7	2030.9	179.41	1368.46	4.14	INDI 499	INDI 499 PLS 1
Lung	I	1434.39	1563.21	933.16	4.99	7.76	*2.782
*1.36	1251.45	*325.874	0.63	2025.55	152.8	1029.69	6.58
INDI 501	INDI 501 PLS 1	Colorectum	III	3069.7	1143.74	6481.12	*0.815
19.94	*2.744	46.49	684.06	*323.192	0.64	2303.89	*14.413
959.98	3.74	INDI 502	INDI 502 PLS 1	Colorectum	III	5616.93	733.73
1036.91	*0.815	14.56	*2.744	26.36	3,163.0	*323.192	0.68
2156.43	*14.413	400.66	6.57	INDI 503	INDI 503 PLS 1	Lung	I
1276.03	865.00	581.22	*0.831	22.85	*2.782	14.37	1924.61
*325.874	0.72	1655.99	100.18	832.3	6.07	INDI 504	INDI 504 PLS 1
Breast	III	*137.024	806.54	1458.51	5.14	11.67	*2.782
13.47	682.72	2389.58	0.8	737.87	262.26	1079.3	5.52
INDI 505	INDI 505 PLS 1	Lung	II	*137.024	6193.41	552.21	*0.831
15.81	*2.782	18.2	474.5	*325.874	0.71	1018.61	100.18
2996.68	6.56	INDI 506	INDI 506 PLS 1	Colorectum	I	*145.246	1194.55
3462.32	*0.826	23.65	*2.756	44.77	543.74	*327.082	0.95
1081.31	151.16	928.31	9.35	INDI 507	INDI 507 PLS 1	Lung	II
7850.82	1149.97	1170.61	*0.831	5.05	*2.782	15.63	2,770.1

Table4.txt

*325.874	0.7	2074.27	120.99	*79.85	4.45		
INDI 508	INDI 508 PLS 1		Colorectum	III	905.9		
1820.76	1906.33	*0.826	15.07	*2.756	28.38	472.44	
*327.082	0.67	2283.03	126.77	749.51	6.54		
INDI 511	INDI 511 PLS 1		Colorectum	III	*145.246		
1517.49	1701.29	*0.826	15.08	*2.756	20.03	487.8	
*327.082	0.83	2167.73	104.23	724.47	4.14		
INDI 512	INDI 512 PLS 1		Breast	II	*137.024		
957.01	2406.39	13.25	12.22	*2.782	20.32	545.17	
*325.874	0.7	1831.14	120.99	1121.84	5.14		
INDI 513	INDI 513 PLS 1		Lung	I	2528.84		
1800.51	881.88	9.29	69.60	19.85	15.32	2646.54	
1955.25	0.62	1540.73	178.21	245.76	10.33		
INDI 514	INDI 514 PLS 1		Stomach	I	*137.024		
898.44	1592.02	*0.831	6.44	*2.782	11.63	950.5	
*325.874	0.86	959.51	*14.53	1837.02	4.28		
INDI 515	INDI 515 PLS 1		Colorectum	III	1848.54		
1257.07	1568.48	*0.826	18.91	*2.756	34.82	1,492.2	
*327.082	0.71	683.6	112.33	305.43	4.67		
INDI 516	INDI 516 PLS 1		Pancreas	II	920		
2351.35	1960.39	14.44	5.10	627.86	24.22	2,557.1	
*315.949	0.68	1890.23	154.78	1335.79	4.26		
INDI 517	INDI 517 PLS 1		Breast	III	*137.024		
2894.29	2655.64	*0.831	25.47	*2.782	17.55	1079.41	
*325.874	0.76	2613.21	111.22	846.12	6.27		
INDI 518	INDI 518 PLS 1		Colorectum	III	1716.98		
5538.12	3611.54	*0.826	10.31	*2.756	34.61	1,192.1	
*327.082	0.87	2888.57	95.29	1169.17	5.97		
INDI 519	INDI 519 PLS 1		Lung	I	5020.97		
1377.33	1000.89	*0.831	45.11	*2.782	13.22	1,511.4	
*325.874	0.76	1140.57	100.18	818.38	6.37		
INDI 521	INDI 521 PLS 1		Colorectum	II	1195.65		
1203.47	2484.76	*0.826	11.07	*2.756	34.14	626.3	
*327.082	0.83	2132.07	151.16	640.68	3.88		
INDI 522	INDI 522 PLS 1		Lung	I	2067.53		
2349.94	3090.3	*0.831	12.76	*2.782	16.22	*77.625	
*325.874	0.89	2590.47	87.18	1029.69	6.92		
INDI 523	INDI 523 PLS 1		Colorectum	I	2202.18		
7846.46	2435.1	8.93	19.46	49.54	44.36	2,798.0	
*327.082	0.74	1437.19	112.33	984.98	5.21		
INDI 524	INDI 524 PLS 1		Lung	III	2266.26		
1141.56	2342.72	12.92	15.74	19.85	15.76	697.44	
8995.64	0.91	893.02	489.89	1528.6	7.74		
INDI 525	INDI 525 PLS 1		Colorectum	I	*145.246		
1634.89	3991.44	*0.826	27.21	*2.756	35.74	756.8	
*327.082	0.96	2467.08	112.33	882.01	4.28		
INDI 526	INDI 526 PLS 1		Esophagus	III	1615.09		
2448.28	3409.96	5.14	33.82	*2.782	17.86	34275.61	

Table4.txt

*325.874	0.65	2018.06	100.18	656.8	5.45		
INDI 527	INDI 527 PLS 1		Colorectum	III	*145.246		
1061.06	1797.18	*0.826	10.39	*2.756	24.89	*76.193	
*327.082	0.91	1607.16	*14.2	973.74	5.15		
INDI 528	INDI 528 PLS 1		Colorectum	II	1027.61		
2034.86	4611.46	*0.826	11.57	*2.756	54.52	562.6	
*327.082	0.74	2187.57	*14.2	1450.77	4.9		
INDI 529	INDI 529 PLS 1		Colorectum	I	*145.246		
1342.14	2644.87	*0.826	9.23	*2.756	20.8	1,544.7	
*327.082	0.76	1391.02	104.23	*83.65	4.42		
INDI 530	INDI 530 PLS 1		Breast	I	*137.024		
590.15	1164.03	7.35	12.79	*2.782	12.61	682.72	
*325.874	0.64	1284.86	200.1	509.03	6.51		
INDI 532	INDI 532 PLS 1		Lung	I	*137.024		
1242.49	1536.1	5.14	20.98	*2.782	16.55	1,223.1	
*325.874	0.81	2228.19	120.99	846.12	4.57		
INDI 533	INDI 533 PLS 1		Pancreas	II	1356.49		
1982.24	3170.34	*0.817	97.70	88.85	30.72	3296.32	
3972.46	0.85	1564.57	84.9	846.1	8.42		
INDI 534	INDI 534 PLS 1		Stomach	III	855.1		
1550.52	1337.9	*0.831	4.55	*2.782	14.83	*77.625	
*325.874	0.66	2051.78	100.18	873.43	7.53		
INDI 535	INDI 535 PLS 1		Lung	I	*137.024		
1504.01	2374.53	5.77	9.28	*2.782	18.13	10,476.5	
*325.874	0.76	1218.24	*14.53	543.47	7.37		
INDI 537	INDI 537 PLS 1		Ovary	I	2276.34		
3664.28	675.82	5.11	4.35	*2.624	14.22	*76.03	
2203.21	0.72	1064.32	145.03	517.5	6.05		
INDI 538	INDI 538 PLS 1		Lung	III	2668.01		
1221.45	1062.59	*0.831	22.38	21.53	22.98	6,944.8	
*325.874	0.82	1136.88	*14.53	473.45	3.09		
INDI 539	INDI 539 PLS 1		Colorectum	II	2067.39		
2932.80	2093.09	*0.826	13.94	*2.756	38.28	2,054.3	
*327.082	0.88	3330.19	112.33	945.45	8.06		
INDI 540	INDI 540 PLS 1		Breast	II	1099.1		
2021.54	2116.03	6.4	7.94	22.80	14.37	1,119.0	
*325.874	1.08	3450.7	100.18	1004.46	6.35		
INDI 541	INDI 541 PLS 1		Breast	II	*137.024		
540.40	1147.61	*0.831	32.35	*2.782	17.35	1411.30	
*325.874	0.6	1935.74	120.99	832.3	5.65		
INDI 544	INDI 544 PLS 1		Colorectum	III	*145.246		
1743.59	1104.84	*0.826	5.78	*2.756	26.19	1,447.6	
*327.082	0.77	1417.94	161.87	450.95	5.95		
INDI 545	INDI 545 PLS 1		Lung	I	*137.024		
1040.82	1931.6	*0.831	16.14	*2.782	17.2	3,742.1	
*325.874	1.03	1678.32	120.99	991.73	5.19		
INDI 546	INDI 546 PLS 1		Lung	II	*137.024		
515.56	3215.95	5.14	31.45	*2.782	19.16	1,150.9	

Table4.txt

*325.874	0.82	2548.82	*14.53	1646.18	7.87		
INDI 547	INDI 547 PLS 1		Stomach	III	2578.31		
1453.31	1955.86	*0.831	23.95	*2.782	15.37	1,047.9	
*325.874	0.85	2352.43	*14.53	1720.76	7.39		
INDI 548	INDI 548 PLS 1		Breast	II	5871.66		
5950.28	5148.67	6.24	44.71	*2.782	20.39	1,968.8	
*325.874	1.08	3667.38	*14.53	1620.96	10.52		
INDI 549	INDI 549 PLS 1		Lung	III	*137.024		
3221.53	4232.61	5.77	7.83	*2.782	21.62	606.19	
*325.874	1.38	1730.46	100.18	886.94	7.84		
INDI 550	INDI 550 PLS 1		Lung	III	*137.024		
735.66	1742.11	5.14	28.41	23.22	14.7	1629.84	
*325.874	1.28	1229.34	*14.53	818.38	5.75		
INDI 551	INDI 551 PLS 1		Colorectum	II	*145.246		
915.07	1136.17	*0.826	7.85	*2.756	28.21	1,711.5	
*327.082	0.83	1942.73	95.29	1132.2	6.28		
INDI 555	INDI 555 PLS 1		Colorectum	II	*145.246		
1934.51	2702.86	*0.826	5.10	*2.756	26.73	5,581.2	
*327.082	0.8	1611.04	95.29	6143.61	3.82		
INDI 558	INDI 558 PLS 1		Colorectum	I	*147.82		
2285.99	4468.14	6.21	11.83	20.06	29.85	1,278.0	
*325.95	1.52	2243.79	134.8	578.03	5.69		
INDI 559	INDI 559 PLS 1		Breast	III	3209.3		
2355.70	1479.5	6.52	9.26	*2.755	12.86	1,786.1	
2252	0.94	1014.72	190.23	434.33	4.57		
INDI 560	INDI 560 PLS 1		Colorectum	I	1165.6		
2358.87	3312.55	*0.83	11.49	*2.755	13.72	842.37	
*325.95	1.62	1323.08	120.79	2754.5	8.81		
INDI 561	INDI 561 PLS 1		Breast	III	*147.82		
986.63	281.27	*0.83	13.27	*2.755	*1.372	1,034.4	
*325.95	1.34	1000.68	86.07	764.01	4.66		
INDI 562	INDI 562 PLS 1		Colorectum	I	1012.37		
5524.73	2892.92	*0.83	3.80	*2.755	11.47	1,505.0	
2543.03	1.29	2858.33	159.22	1055.95	7.2		
INDI 564	INDI 564 PLS 1		Colorectum	I	*147.82		
5609.29	3009.26	*0.83	9.16	*2.755	9.31	*75.938	
*325.95	1.36	1010.04	*14.345	932.08	7.31		
INDI 565	INDI 565 PLS 1		Breast	III	23124.6		
2631.69	2446.66	*0.83	4.39	*2.755	11.96	930.3	
2925	1.25	1458.62	*14.345	398.28	3.76		
INDI 566	INDI 566 PLS 1		Breast	II	*147.82		
867.39	694.95	5.29	7.17	*2.755	11.24	583.22	
*325.95	1.42	2020.76	147.5	629.22	4.93		
INDI 567	INDI 567 PLS 1		Colorectum	II	*147.82		
**10000.597	5403.35	7.77	6.08	27.00	19.45	47,542.6	
1955.7	1.44	1275.73	86.07	786.99	8.33		
INDI 568	INDI 568 PLS 1		Breast	II	*147.82		
1307.22	1566.85	*0.83	3.15	*2.755	11.47	989.56	

Table4.txt

*325.95	2.18	1444.31	159.22	535.63	5.65		
INDI 569	INDI 569 PLS 1		Breast	III	*147.82		
8993.64	1565.07	*0.83	5.97	*2.755	13.14	846.0	
2349.47	1.34	1439.54	225.41	629.22	4.4		
INDI 570	INDI 570 PLS 1		Colorectum	II	*147.82		
6353.76	5497.27	15.6	5.83	*2.755	16.19	524.86	
*325.95	2.43	1221.41	190.23	480.48	5.12		
INDI 571	INDI 571 PLS 1		Breast	III	*147.82		
1074.56	1673.81	*0.83	4.22	*2.755	11.18	600.53	
*325.95	1.4	1391.92	134.8	649.2	4.16		
INDI 572	INDI 572 PLS 1		Colorectum	II	*147.82		
785.87	955.51	*0.83	7.36	*2.755	7.32	504.46	
*325.95	1.18	369.34	134.8	1119.49	3.35		
INDI 573	INDI 573 PLS 1		Colorectum	I	*147.82		
1093.41	1474.15	*0.83	4.63	*2.755	*1.372	748.58	
*325.95	1.3	459.26	104.91	668.91	4.38		
INDI 574	INDI 574 PLS 1		Colorectum	III	928.93		
839.17	481.58	*0.83	9.78	*2.755	6.94	*75.938	
*325.95	1.49	335.89	170.15	698.02	4.36		
INDI 575	INDI 575 PLS 1		Breast	II	940.89		
939.54	1260.05	*0.83	19.91	*2.755	20.21	922.9	
*325.95	1.28	1458.62	180.46	562.29	6.35		
INDI 577	INDI 577 PLS 1		Breast	I	1524.42		
735.74	564.87	5.9	12.90	17.24	17.13	3483.84	
4572.73	1.2	734.88	190.23	588.42	6.28		
INDI 578	INDI 578 PLS 1		Breast	I	*147.82		
1871.59	1030.96	*0.83	6.14	*2.755	10.85	1,216.3	
4033.71	1.02	1164.87	170.15	360.76	3.46		
INDI 579	INDI 579 PLS 1		Breast	I	*147.82		
1036.86	2802.24	102.9	17.30	18.65	9.19	2793.98	
3112.82	1.06	1706.02	104.91	678.68	7.86		
INDI 581	INDI 581 PLS 1		Colorectum	II	3131.3		
1975.87	2914.71	*0.83	30.92	*2.755	10.5	3,575.4	
1955.7	1.01	1155.46	*14.345	279.99	6.32		
INDI 582	INDI 582 PLS 1		Colorectum	II	*147.82		
773.34	1995	*0.83	5.64	23.55	10.29	307,683.1	
*325.95	1.42	1518.37	86.07	398.28	11.53		
INDI 583	INDI 583 PLS 1		Colorectum	II	*147.82		
1011.74	2376.55	*0.83	10.88	*2.755	8.47	4390.63	
*325.95	1.7	1961.77	113.13	608.97	30.24		
INDI 584	INDI 584 PLS 1		Colorectum	II	*147.82		
2266.99	789.44	*0.83	15.32	*2.755	12.29	2,412.6	
6825.06	1.19	830.34	159.22	567.56	22.74		
INDI 585	INDI 585 PLS 1		Esophagus	III	*147.82		
1439.45	3415.4	9.17	32.84	39.89	16.32	2,344.3	
13264.5	1.06	2097.26	134.8	279.99	17.03		
INDI 586	INDI 586 PLS 1		Liver	III	3075.57		
4389.52	4595.43	60.62	17.49	22.16	17.31	642.4	

Table4.txt

*325.95	1.12	688.32	185.41	524.8	3.83		
INDI 587	INDI 587 PLS 1		Colorectum	II	*147.82		
1963.23	2012.87	8.7	11.33	*2.755	28.07	3139.93	
*325.95	1.11	1075.62	104.91	2084.34	8.95		
INDI 588	INDI 588 PLS 1		Breast	III	2091.58		
279.55	1299.34	*0.83	13.86	*2.755	10.47	993.28	
*325.95	0.89	879.28	159.22	220.08	5.87		
INDI 589	INDI 589 PLS 1		Breast	II	*147.82		
651.19	1490.2	6.21	8.80	*2.755	8.99	1640.59	
4750.51	1.16	890.93	241.24	265.58	10.99		
INDI 591	INDI 591 PLS 1		Colorectum	II	964.29		
14137.98	2533.36	4.88	12.47	*2.715	8.71	2,745.2	
*312.793	2.15	1461.11	136.9	783.88	6.34		
INDI 592	INDI 592 PLS 1		Breast	II	*157.823		
1186.21	2114.61	*0.803	13.53	26.20	13.24	1,582.4	
1969.27	0.7	1348.46	136.9	525.92	7.68		
INDI 593	INDI 593 PLS 1		Breast	II	5498.88		
1996.57	6601.21	*0.803	7.91	35.88	14.61	4664.83	
19350.78	1.27	1910.94	187.1	711.31	9.57		
INDI 594	INDI 594 PLS 1		Colorectum	III	*157.823		
2005.41	1738.26	*0.803	3.98	*2.715	13.47	1,059.3	
*312.793	1.13	1759.83	88.71	408.3	7.19		
INDI 595	INDI 595 PLS 1		Esophagus	II	*157.823		
4522.14	1616.6	10.04	7.91	31.22	12.84	827.0	
31071.18	0.76	1133.07	260.68	141.32	8.94		
INDI 596	INDI 596 PLS 1		Breast	III	*157.823		
781.20	876	5.65	11.31	18.94	9.46	1727.12	
2337.96	0.87	797.96	291.04	510.48	3.83		
INDI 597	INDI 597 PLS 1		Breast	II	*157.823		
1540.09	1949.88	*0.803	13.31	*2.715	12.84	786.38	
*312.793	0.76	443.09	171.97	305.58	9.96		
INDI 598	INDI 598 PLS 1		Colorectum	II	*157.823		
680.26	1761	*0.803	7.02	*2.715	12.34	3,279.3	
1969.27	1.68	904.47	115.42	816.75	6.08		
INDI 599	INDI 599 PLS 1		Colorectum	II	*157.823		
1053.00	1469.04	*0.803	7.62	17.43	11.95	27378.02	
3069.79	0.98	696.46	171.97	797.62	13.88		
INDI 600	INDI 600 PLS 1		Colorectum	II	*157.823		
1025.46	1243.64	7.21	5.95	*2.715	12.08	1,457.5	
1969.27	1.12	1852.54	232.68	613.18	6.26		
INDI 601	INDI 601 PLS 1		Breast	III	2840.2		
377.48	2134.45	4.88	164.45	181.80	12.64	3,015.0	
99452.06	0.77	1040.78	136.9	283.94	5.28		
INDI 602	INDI 602 PLS 1		Colorectum	II	*157.823		
688.18	1925	7.21	5.37	*2.715	*1.372	3,055.3	
3433.43	1.44	1168.86	376.66	283.94	6.5		
INDI 603	INDI 603 PLS 1		Breast	III	*157.823		
427.46	1558	15.54	30.56	26.20	12.76	9343.74	

Table4.txt

*312.793	0.67	1654.72	171.97	395.05	7.08		
INDI 604	INDI 604 PLS 1		Breast	II	*157.823		
1127.73	1778.52	*0.803	3.30	*2.715	12.26	533.7	
3614.76	0.94	1310.03	291.04	84.84	8.5		
INDI 605	INDI 605 PLS 1		Colorectum	II	*157.823		
1130.51	401.53	22.31	10.42	*2.715	15.17	706.05	
1969.27	1.01	619.69	201.12	671.38	12.89		
INDI 606	INDI 606 PLS 1		Breast	II	*157.823		
483.13	2550.06	*0.803	16.00	*2.715	15.46	1827.83	
2153.88	1.09	1266.33	214.27	865.39	5.42		
INDI 607	INDI 607 PLS 1		Breast	II	*157.823		
2174.05	748.3	7.21	3.75	*2.715	11.04	*75	
*312.793	0.85	1567.73	136.9	913.28	5.18		
INDI 608	INDI 608 PLS 1		Colorectum	II	*157.823		
513.79	1705.1	*0.803	5.61	*2.715	8.02	4,920.7	
1876.76	1.19	627.99	226.7	3297.36	6.84		
INDI 609	INDI 609 PLS 1		Colorectum	II	*157.823		
861.86	2710.51	4.88	15.29	39.00	12.26	6,163.2	
13753.05	1.44	1010.85	214.27	965.7	16.72		
INDI 610	INDI 610 PLS 1		Colorectum	II	*157.823		
612.06	539.32	5.39	6.81	*2.715	*1.372	921.39	
2521.55	2.09	*27.581	318.81	395.05	10.34		
INDI 611	INDI 611 PLS 1		Colorectum	II	2887.94		
2575.70	1554.57	*0.803	5.78	*2.715	10.3	5281.79	
2153.88	1.56	1288.15	364.92	714.14	12.44		
INDI 612	INDI 612 PLS 1		Colorectum	II	*157.823		
1058.52	273.14	*0.803	4.23	*2.715	9.2	798.53	
2704.70	1.53	981.05	271.14	682.86	7.95		
INDI 613	INDI 613 PLS 1		Breast	II	*157.823		
387.43	393.13	5.9	4.70	21.22	13.2	806.6	
*312.793	1.27	784.34	214.27	860.02	11.68		
INDI 614	INDI 614 PLS 1		Colorectum	II	*157.823		
1400.25	1797.83	*0.803	7.91	*2.715	16.59	1,386.9	
2613.18	1.45	1387.07	271.14	1399.12	20.06		
INDI 615	INDI 615 PLS 1		Colorectum	II	*157.823		
1278.70	839.88	*0.803	3.76	*2.715	10.52	2,622.1	
1969.27	2.15	1299.08	115.42	1192.81	15.06		
INDI 617	INDI 617 PLS 1		Colorectum	III	*157.823		
2575.70	3183.73	*0.803	5.47	*2.715	10.94	734.03	
*312.793	1.59	1269.96	155.42	535.12	6.96		
INDI 618	INDI 618 PLS 1		Colorectum	III	1025.73		
1902.57	1416.4	*0.803	6.98	97.36	8.64	2,079.0	
4696.88	1.34	780.94	88.71	1919.36	10.6		
INDI 619	INDI 619 PLS 1		Breast	II	*157.823		
1208.57	921.86	*0.803	3.61	*2.715	8.64	*75	
*312.793	0.85	1547.05	136.9	312.7	4.75		
INDI 620	INDI 620 PLS 1		Colorectum	II	*157.823		
6995.37	3547.17	*0.803	4.49	*2.715	19.49	5315.95	

Table4.txt

1969.27	1.15	2100.2	115.42	171.4	5.73	
INDI 621	INDI 621 PLS 1		Colorectum	II	*157.823	
1727.60	1303.63	*0.803	17.76	*2.715	8.79	3340.86
*312.793	1.01	1554.56	155.42	223.78	4.78	
INDI 622	INDI 622 PLS 1		Liver	III	43779.36	
5141.16	2350.85	6.95	7.74	*2.715	12.68	10,872.1
4337	1.01	1530.17	155.42	547.33	8.2	
INDI 623	INDI 623 PLS 1		Breast	III	*157.823	
2779.03	1001.73	133.24	10.49	34.32	12.08	762.2
6482.74	0.99	1115.23	171.97	595.42	11.52	
INDI 624	INDI 624 PLS 1		Colorectum	II	*140.254	
1583.05	3134.87	*0.835	5.95	*2.794	27.83	*77.894
*328.815	1.05	585	136.53	1210.95	7.65	
INDI 625	INDI 625 PLS 1		Colorectum	II	*157.823	
1124.96	1527.12	*0.803	8.62	21.22	9.2	827.0
3614.76	1.4	861.33	207.8	816.75	10.66	
INDI 626	INDI 626 PLS 1		Colorectum	II	*157.823	
2515.31	3154.87	6.55	16.70	248.03	9.59	246,925.4
3614.76	1.82	691.42	271.14	2260.07	15.28	
INDI 627	INDI 627 PLS 1		Breast	II	*157.823	
284.44	2060.67	5.13	14.81	*2.715	9.89	2715.58
*312.793	2.73	150.48	352.86	886.76	9.55	
INDI 628	INDI 628 PLS 1		Colorectum	II	*157.823	
727.89	2812.06	*0.803	5.75	29.67	12.26	1008.82
*312.793	1.27	1242.75	291.04	1417.87	8.42	
INDI 629	INDI 629 PLS 1		Breast	I	*157.823	
135.21	1030.72	*0.803	10.95	21.22	7.5	1457.47
*312.793	1.57	679.69	226.7	728.23	8.06	
INDI 630	INDI 630 PLS 1		Breast	I	*157.823	
733.21	1672.05	*0.803	8.15	18.56	7.68	690.13
*312.793	1.08	1168.86	249.83	501.16	6.79	
INDI 631	INDI 631 PLS 1		Colorectum	II	*157.823	
1990.69	1910.8	*0.803	5.04	*2.715	14.58	12,657.8
5055.63	0.99	1926.58	226.7	636.63	9.18	
INDI 632	INDI 632 PLS 1		Colorectum	II	10404.07	
1791.55	3166.41	10.18	12.77	44.09	33.51	2,154.5
6483	1.87	784.34	413.79	280.29	20.38	
INDI 633	INDI 633 PLS 1		Colorectum	II	*157.823	
651.31	1157.75	*0.803	5.72	*2.715	*1.372	7,004.1
2887.44	0.9	423.79	201.12	659.86	7.38	
INDI 635	INDI 635 PLS 1		Colorectum	II	1565.62	
977.45	4881.67	*0.835	2.59	*2.794	29.08	*77.894
2235.86	1.6	1892.48	184.28	978.23	6.84	
INDI 636	INDI 636 PLS 1		Liver	III	*157.823	
861.86	902.84	32.12	7.24	*2.715	7.76	892.5
*312.793	0.94	821.87	115.42	996.77	7.88	
INDI 637	INDI 637 PLS 1		Breast	III	*157.823	
377.48	1340.5	8.01	21.66	22.75	9.46	4510.64

Table4.txt

5055.63	0.73	659.63	238.53	200.08	5.01		
INDI 638	INDI 638 PLS 1		Breast	I	*157.823		
554.95	515.95	5.13	7.37	*2.715	9.59	*75	
*312.793	1.22	871.66	136.9	298.42	7.28		
INDI 639	INDI 639 PLS 1		Liver	II	270818.88		
3199.48	3172.18	6.42	12.44	202.88	18.64	4,303.3	
5055.63	0.69	2603.5	384.32	805.84	10.8		
INDI 640	INDI 640 PLS 1		Colorectum	II	1119.86		
1245.40	4094.83	*0.835	7.81	*2.794	22.64	6,140.5	
4810.03	1.76	1535.06	230.22	*74.45	11.51		
INDI 641	INDI 641 PLS 1		Breast	III	990.48		
2395.00	182.92	5.39	15.88	25.05	10.41	1,887.8	
*312.793	0.99	1414.76	291.04	84.84	11.08		
INDI 643	INDI 643 PLS 1		Colorectum	II	1017.91		
1847.75	3647.31	*0.835	4.87	*2.794	18.95	2,983.5	
2627.86	1.27	1588.46	175.65	4135.49	10.93		
INDI 644	INDI 644 PLS 1		Colorectum	I	1587.36		
1618.68	5010.57	*0.835	13.11	*2.794	27.45	912.76	
3533.32	1.39	1995.84	192.57	964.55	4.43		
INDI 645	INDI 645 PLS 1		Liver	III	**99634.823		
2733.37	2992.17	5.13	7.81	*2.715	17.99	1,768.2	
2796.12	1.48	*27.581	260.68	99.75	23.57		
INDI 646	INDI 646 PLS 1		Breast	II	1685.86		
1462.86	1240.32	*0.803	21.62	35.88	9.65	851.46	
2704.70	0.84	720	88.71	1323.4	9.22		
INDI 647	INDI 647 PLS 1		Colorectum	III	1132.83		
905.13	5567.25	*0.835	12.24	*2.794	44.04	29915.23	
7758.3	1.14	1780.43	112.47	471.48	7.39		
INDI 648	INDI 648 PLS 1		Colorectum	III	*140.254		
2772.48	2535.98	23.64	4.56	207.39	12.67	27,548.3	
162084.89	3.87	1941.88	480.52	555.18	6.62		
INDI 649	INDI 649 PLS 1		Colorectum	III	*140.254		
856.82	4675.17	12.97	5.55	*2.794	19.49	8447.92	
*328.815	2.27	935.79	266.56	3202.77	10.06		
INDI 650	INDI 650 PLS 1		Colorectum	III	*140.254		
674.96	3568.68	6.06	1.71	18.38	23.06	1,635.6	
*328.815	0.69	822.61	125.04	908.83	3.06		
INDI 651	INDI 651 PLS 1		Colorectum	III	1251.74		
901.10	1702.63	*0.835	4.08	17.73	49.31	1219.27	
*328.815	1.27	2054.38	157.18	2991.11	14.19		
INDI 654	INDI 654 PLS 1		Colorectum	II	*140.254		
1709.62	3685.32	*0.835	4.24	*2.794	40.51	1194.55	
*328.815	1	918.34	166.64	431.93	18.36		
INDI 655	INDI 655 PLS 1		Colorectum	II	*140.254		
925.23	1726.04	7.26	2.85	*2.794	27.39	*77.894	
*328.815	1.21	1419.64	184.28	894.65	5.72		
INDI 656	INDI 656 PLS 1		Breast	III	7958.52		
1003.48	1375.84	9.36	33.52	*2.715	11.81	892.50	

Table4.txt

*312.793	0.92	1339.29	115.42	323.3	4.22		
INDI 657	INDI 657 PLS 1		Colorectum	II	*140.254		
2099.59	2012.87	12.12	11.07	211.24	13.15	102,115.2	
3790.07	0.71	1370.92	200.57	411.49	4.78		
INDI 658	INDI 658 PLS 1		Colorectum	I	*140.254		
1934.42	2375.01	9.31	30.35	*2.794	27.58	1764.61	
1972.89	0.35	1499.51	223.11	706.82	6.29		
INDI 659	INDI 659 PLS 1		Breast	II	*157.823		
669.72	551.06	5.65	4.05	18.94	9.59	549.1	
2338	0.74	580.01	249.83	319.78	5.64		
INDI 660	INDI 660 PLS 1		Colorectum	II	*140.254		
2959.39	2296.05	*0.835	3.16	*2.794	24.98	1,362.4	
*328.815	1.23	735.9	98.38	865.95	14.57		
INDI 661	INDI 661 PLS 1		Liver	III	*157.823		
1669.67	1443.53	5.65	20.63	23.51	8.1	734.0	
5771	0.66	1319.16	260.68	276.63	4.96		
INDI 662	INDI 662 PLS 1		Breast	I	*157.823		
2533.41	2190.5	*0.803	5.87	20.46	10.19	3146.54	
3976.53	0.94	863.05	226.7	645.37	9.88		
INDI 663	INDI 663 PLS 1		Esophagus	II	*157.823		
7594.14	3692.82	6.16	8.23	*2.715	13.04	5,706.8	
3795.79	0.6	2659.93	187.1	127.89	9.5		
INDI 664	INDI 664 PLS 1		Breast	I	*157.823		
1838.21	929.8	*0.803	5.01	*2.715	9.07	666.33	
3976.53	0.82	745.32	155.42	150.08	4.05		
INDI 665	INDI 665 PLS 1		Esophagus	III	1820.38		
1287.14	2431.7	6.95	9.16	212.62	8.49	183,408.1	
*312.793	1.06	981.05	146.45	411.6	11.48		
INDI 666	INDI 666 PLS 1		Breast	II	*157.823		
274.81	486.95	5.39	13.65	*2.715	7.11	1546.52	
*312.793	0.78	935.7	226.7	276.63	2.46		
INDI 667	INDI 667 PLS 1		Breast	II	1645.08		
1844.05	2925.6	*0.803	8.77	*2.715	12.21	3238.30	
*312.793	0.8	1809.93	155.42	485.51	5.93		
INDI 668	INDI 668 PLS 1		Breast	III	1614.69		
1287.14	2710.51	*0.803	22.36	*2.715	11.14	24867.67	
2153.88	0.89	2266.71	115.42	1202.61	6.88		
INDI 669	INDI 669 PLS 1		Liver	III	**99634.823		
1180.63	2394.9	*0.803	17.08	*2.715	12.13	3,927.0	
4517.16	0.89	2013.01	155.42	472.89	3.93		
INDI 670	INDI 670 PLS 1		Colorectum	III	3597.73		
1360.09	1179.71	*0.826	15.45	120.83	24.32	170,479.1	
7666.56	0.69	2806.93	95.29	1407	4.77		
INDI 671	INDI 671 PLS 1		Lung	I	975.04		
669.07	1914.29	*0.831	17.02	*2.782	12.81	5282.07	
*325.874	0.95	1240.45	*14.53	846.12	4.85		
INDI 672	INDI 672 PLS 1		Breast	II	*137.024		
1415.31	1660.07	*0.831	11.59	*2.782	13.27	908.12	

Table4.txt

*325.874	1.68	1514.74	166.06	985.34	4.65		
INDI 673	INDI 673 PLS 1		Breast	II	9636.03		
1673.29	2224.69	10.27	31.91	*2.782	20.22	1,403.0	
*325.874	1.14	2959.34	200.1	1017.11	8.22		
INDI 674	INDI 674 PLS 1		Lung	I	4436.25		
2392.69	2088.08	5.46	11.83	*2.782	18.87	3,427.0	
*325.874	1.21	1678.32	120.99	1631.07	7.21		
INDI 675	INDI 675 PLS 1		Colorectum	III	*145.246		
5476.12	4829.46	77.28	14.02	*2.756	35.33	952.9	
*327.082	0.84	2745.88	95.29	2318.86	8.14		
INDI 677	INDI 677 PLS 1		Colorectum	II	2722.56		
884.22	3378.51	*0.826	4.08	18.20	12.11	616.6	
2396.41	1.35	1077.51	198.86	*83.65	6.08		
INDI 678	INDI 678 PLS 1		Colorectum	III	*145.246		
1752.66	2768.92	*0.826	9.57	29.13	31.97	29,535.4	
*327.082	0.71	2410.91	218.84	798.65	4.32		
INDI 679	INDI 679 PLS 1		Colorectum	II	1080.33		
1007.86	1908.87	*0.826	5.96	*2.756	19.08	1015.32	
*327.082	0.72	1805.61	161.87	984.98	4.05		
INDI 681	INDI 681 PLS 1		Lung	II	1367.1		
931.90	1389.7	13.93	31.77	*2.782	16.8	2156.62	
*325.874	0.94	1262.65	178.21	1636.11	5.47		
INDI 682	INDI 682 PLS 1		Colorectum	III	1082.37		
1819.42	2455.89	5.55	5.51	*2.781	23.97	4,441.9	
*327.606	0.7	1111.99	*15.64	1181.88	5.4		
INDI 683	INDI 683 PLS 1		Colorectum	II	*166.572		
1473.10	1593.81	*0.824	8.39	*2.781	28.8	1187.91	
*327.606	0.86	1416.74	*15.64	724	5.41		
INDI 684	INDI 684 PLS 1		Liver	III	1545.57		
2243.18	2741.66	*0.831	22.06	*2.782	17.59	*77.625	
2604	0.65	1760.27	166.06	966.04	6.14		
INDI 685	INDI 685 PLS 1		Colorectum	III	*166.572		
2308.80	3077.75	*0.824	21.32	*2.781	28.89	2442.12	
*327.606	1.02	1722.6	*15.64	2144.34	6.67		
INDI 686	INDI 686 PLS 1		Pancreas	II	1195.94		
2014.84	2962.71	55.59	28.81	674.89	18.68	1,805.1	
2203.21	0.85	1757.19	197.94	707.23	6.09		
INDI 687	INDI 687 PLS 1		Lung	III	*137.024		
4044.19	3989.33	50.86	51.94	*2.782	15.37	*77.625	
4461.54	0.92	922.57	100.18	1256.6	4.03		
INDI 688	INDI 688 PLS 1		Colorectum	II	3468.12		
1056.34	2103.15	*0.824	15.75	*2.781	25.03	1,301.1	
*327.606	0.85	2022.45	*15.64	724	4.52		
INDI 690	INDI 690 PLS 1		Lung	III	1738.71		
2191.98	2222.93	41.83	14.64	*2.782	*1.36	3326.83	
10016.75	0.98	3215.87	138.02	1222.13	6.94		
INDI 691	INDI 691 PLS 1		Lung	I	914.54		
982.14	1641.33	5.77	16.74	19.01	13.71	577.4	

Table4.txt

4259.89	1.08	1629.95	312.65	1175.44	9.16	
INDI 692	INDI 692 PLS 1		Colorectum	III	2326.29	
1016.23	3737.38	8.68	30.19	19.76	24.91	18359.27
2786.53	1.17	1128.09	*14.319	646.74	10.95	
INDI 693	INDI 693 PLS 1		Lung	III	8876.44	
2452.56	1083.78	9.62	10.00	19.01	16.26	*77.625
11482.78	1.14	1444.22	*14.53	1740.39	6.14	
INDI 694	INDI 694 PLS 1		Lung	I	*137.024	
1749.59	1431.61	*0.831	7.58	*2.782	13.17	1,071.5
2603.54	1.12	3466.14	237.63	832.3	4.68	
INDI 695	INDI 695 PLS 1		Pancreas	II	1231.9	
2651.21	3534.9	5.97	177.76	17.36	33.01	1247.04
3780.79	0.75	555.82	112.06	1114.12	6.5	
INDI 696	INDI 696 PLS 1		Lung	II	*137.024	
990.52	1943.73	7.67	6.44	*2.782	17.97	1,494.6
*325.874	0.85	2594.26	189.5	839.22	8.09	
INDI 697	INDI 697 PLS 1		Breast	II	4621.21	
9101.36	1836.61	10.6	39.22	*2.782	13.71	1,867.5
16299.76	1.44	3319.66	254.31	8126.49	4.36	
INDI 698	INDI 698 PLS 1		Ovary	III	2478.13	
2351.35	2782.84	105.92	17.09	47.65	23.98	*76.03
*315.949	0.73	1625.01	99.23	867.44	5.06	
INDI 699	INDI 699 PLS 1		Pancreas	II	960.01	
1248.49	4398.23	5.4	6.73	42.00	37.22	2,201.5
*315.949	1.34	1846.99	105.8	689.84	6.31	
INDI 700	INDI 700 PLS 1		Lung	III	1864.75	
2157.86	1750.68	7.03	16.48	*2.782	14.83	8,422.4
*325.874	0.72	1470.19	152.8	1379.4	7.39	
INDI 701	INDI 701 PLS 1		Colorectum	II	1431.41	
2112.60	1898.63	*0.817	23.70	*2.624	20.54	2,106.1
*315.949	0.86	937.56	145.03	802.73	5.31	
INDI 702	INDI 702 PLS 1		Lung	II	1349.07	
1797.39	2736.58	*0.817	21.68	*2.624	24.69	770.9
2203.21	0.99	1023.08	99.23	851.45	9.17	
INDI 703	INDI 703 PLS 1		Lung	I	1027.8	
4017.14	1179.93	*0.817	34.26	*2.624	27.29	1717.45
3684.57	1.13	1258.39	99.23	612.29	4.89	
INDI 704	INDI 704 PLS 1		Breast	II	*137.024	
2396.96	2163.28	7.03	20.65	25.74	11.18	1,111.1
1955.25	0.84	700.91	210.13	378.25	3.45	
INDI 706	INDI 706 PLS 1		Lung	I	1268.18	
1459.65	5838.09	5.83	19.16	33.92	38.46	722.7
*315.949	0.7	1451.33	189.9	292.7	7.72	
INDI 708	INDI 708 PLS 1		Colorectum	III	1087.66	
1197.54	4235	*0.835	11.26	*2.794	43.94	83,595.9
*328.815	0.81	2525.63	98.38	714.78	3.04	
INDI 709	INDI 709 PLS 1		Colorectum	II	1742.64	
2582.60	2019.54	*0.817	5.20	*2.624	30.99	802.2

Table4.txt

*315.949	1.1	1800.25	112.06	1534.98	5.98						
INDI 710	INDI 710 PLS 1		Colorectum	III	11516.96						
1408.72	6067.84	5.69	15.74	19.38	50	1,905.8					
*315.949	0.88	1458.39	84.9	1807.78	4.71						
INDI 711	INDI 711 PLS 1		Breast	III	*137.024						
1082.77	367.08	10.93	22.00	*2.782	20.63	11,612.3					
5259.02	1.59	1455.35	237.63	846.12	5.46						
INDI 712	INDI 712 PLS 1		Breast	I	*137.024						
1647.87	2070.63	*0.831	14.61	*2.782	11.85	474.5					
*325.874	1.3	1984.37	100.18	775.92	10.61						
INDI 713	INDI 713 PLS 1		Breast	II	825.79						
2089.67	1827.99	*0.831	5.33	*2.782	17.04	*77.625					
*325.874	0.95	1496.17	100.18	702.58	5.08						
INDI 714	INDI 714 PLS 1		Breast	III	*137.024						
1461.76	2943.46	*0.831	36.90	*2.782	25.57	847.1					
*325.874	0.95	2503.43	*14.53	1279.34	9.49						
INDI 715	INDI 715 PLS 1		Breast	III	*137.024						
673.23	1955.86	98.43	68.17	*2.782	13.81	6,975.2					
127666	1.28	970.59	189.5	293.02	8.75						
INDI 716	INDI 716 PLS 1		Colorectum	III	2540.54						
2763.11	2687.63	*0.817	25.15	*2.624	32.5	1,284.6					
7652	0.87	1861.39	112.06	730.15	6.71						
INDI 717	INDI 717 PLS 1		Breast	I	*137.024						
1491.33	3137.58	*0.831	23.59	*2.782	14.51	635.2					
*325.874	0.83	1551.88	*14.53	900.35	7.23						
INDI 718	INDI 718 PLS 1		Colorectum	II	*140.254						
1610.76	2873	*0.835	17.65	*2.794	38.57	1,261.9					
*328.815	0.55	2072.41	125.04	784.54	4.78						
INDI 720	INDI 720 PLS 1		Colorectum	III	1238.34						
1507.77	2238.23	*0.835	12.19	*2.794	26.17	2,416.5					
*328.815	0.51	1428.51	175.65	1383.66	3.55						
INDI 721	INDI 721 PLS 1		Breast	II	1858.45						
1805.18	2511.45	*0.824	22.77	*2.781	26.46	507.36					
*327.606	0.96	2153.85	*15.64	578.25	3.82						
INDI 722	INDI 722 PLS 1		Breast	I	6430.66						
2679.86	2358.02	7.35	29.20	82.55	27.15	1611.84					
4111.76	0.96	3053.98	173.16	911.88	3.54						
INDI 723	INDI 723 PLS 1		Ovary	III	*166.572						
2732.22	2275.45	134.63	140.67	*2.781	26.86	670.1					
10617.8	0.74	2255.06	*15.64	1000.61	2.42						
INDI 724	INDI 724 PLS 1		Colorectum	II	*140.254						
585.56	3320.23	*0.835	11.95	*2.794	17.36	611.50					
*328.815	0.72	1905.95	125.04	807.13	3.22						
INDI 725	INDI 725 PLS 1		Colorectum	II	*140.254						
1253.38	3582.23	*0.835	11.32	*2.794	28.52	872.76					
*328.815	0.81	1490.62	*14.391	894.65	5.2						
INDI 726	INDI 726 PLS 1		Colorectum	I	*140.254						
885.01	2096.61	8.21	10.45	*2.794	33.46	2,005.4					

Table4.txt

*328.815	0.6	2235.02	166.64	769.3	4.5		
INDI 729	INDI 729	PLS 1	Colorectum	II	1638.46		
1309.14	2926.31	*0.835	17.41	*2.794	39.21	680.9	
*328.815	0.69	1758.06	112.47	1045.34	6.96		
INDI 731	INDI 731	PLS 1	Pancreas	II	*166.572		
1548.96	2239.58	15.11	27.42	387.15	26.61	1825.47	
2061.47	0.94	2167.02	132.93	1110.67	7.2		
INDI 732	INDI 732	PLS 1	Colorectum	III	16503.63		
1132.04	784.14	6.1	14.04	19.24	11.08	3,911.2	
*327.606	0.75	2272.7	*15.64	765.63	3.97		
INDI 734	INDI 734	PLS 1	Pancreas	II	1815.12		
1644.97	3661.32	20.33	33.97	63.00	23.5	*76.03	
3199	1.05	1472.51	84.9	935.4	2.47		
INDI 735	INDI 735	PLS 1	Pancreas	II	3539.18		
1314.07	3658.57	6.41	8.74	67.04	26.09	2,813.4	
2805	1.1	3345.63	99.23	1423.78	7.32		
INDI 736	INDI 736	PLS 1	Lung	III	*126.474		
1735.72	3510.18	*0.817	13.91	*2.624	32.91	1,084.3	
*315.949	1.09	2122.26	99.23	213.92	3.55		
INDI 737	INDI 737	PLS 1	Stomach	I	*137.024		
1175.19	2075.87	11.59	29.75	*2.782	8.28	816.79	
*325.874	0.9	2624.58	*14.53	859.82	5.46		
INDI 740	INDI 740	PLS 1	Pancreas	II	2398.56		
1525.09	1791.4	21.46	20.98	*2.624	28.18	702.1	
10111	0.9	1771.53	209.57	1152.24	4.94		
INDI 741	INDI 741	PLS 1	Pancreas	III	2079.72		
3462.58	10114.38	22.44	41.85	286.51	58.51	4,661.1	
4068	1.25	4089.88	248.77	775.14	8.49		
INDI 742	INDI 742	PLS 1	Breast	II	1319.48		
1117.18	2513.85	*0.817	6.23	*2.624	34.82	882.9	
*315.949	0.82	1265.36	84.9	707.23	5.68		
INDI 743	INDI 743	PLS 1	Stomach	II	*137.024		
1011.47	1903.92	5.77	17.39	20.27	13.32	704.82	
*325.874	0.92	2277.1	*14.53	702.58	3.22		
INDI 745	INDI 745	PLS 1	Pancreas	II	*166.572		
2584.69	10130.78	8.05	28.94	365.70	46.11	971.9	
*327.606	0.65	2458.79	*15.64	*78.14	5.61		
INDI 746	INDI 746	PLS 1	Colorectum	III	*140.254		
1993.46	2702.84	5.01	5.84	26.51	31.49	5,865.9	
*328.815	0.73	1874.53	157.18	865.95	9.81		
INDI 747	INDI 747	PLS 1	Colorectum	III	*140.254		
1997.39	3290.63	6.32	7.30	*2.794	29.57	1,100.2	
*328.815	1.1	1508.39	112.47	1045.34	7.66		
INDI 749	INDI 749	PLS 1	Colorectum	III	*140.254		
949.34	3966.07	12.26	2.81	*2.794	32.72	524.9	
6072.08	0.76	944.51	237.15	1084.62	7.41		
INDI 750	INDI 750	PLS 1	Colorectum	III	*140.254		
3696.18	4602.86	*0.835	6.11	*2.794	29.08	3327.08	

Table4.txt

3275.77	0.91	1820.73	125.04	2351.07	10.66		
INDI 751	INDI 751 PLS 1		Colorectum	III	*140.254		
1958.04	3726.08	*0.835	8.16	*2.794	28.65	1,072.5	
2235.86	1.27	1150.38	166.64	2492.23	8.67		
INDI 752	INDI 752 PLS 1		Colorectum	III	*140.254		
1245.40	1674.04	*0.835	7.98	*2.794	33.18	1,696.0	
*328.815	0.61	874.78	192.57	1032.08	9.87		
INDI 753	INDI 753 PLS 1		Esophagus	III	*157.823		
5758.10	2755.57	*0.803	5.80	*2.715	6.91	2,116.7	
4696.88	1.33	1503.98	187.1	642.46	18.25		
INDI 754	INDI 754 PLS 1		Breast	III	1851.84		
279.62	1233.68	*0.803	17.39	*2.715	9.65	1127.11	
*312.793	0.44	686.39	115.42	261.84	2.97		
INDI 755	INDI 755 PLS 1		Esophagus	III	*157.823		
4273.07	2215.89	*0.803	14.22	*2.715	8.02	3,376.9	
2704.7	0.71	1732.96	115.42	347.67	3.99		
INDI 756	INDI 756 PLS 1		Breast	II	1426.09		
1978.91	1233.68	*0.803	20.27	*2.715	10.68	1627.39	
*312.793	0.86	2266.71	88.71	711.31	10.85		
INDI 757	INDI 757 PLS 1		Breast	II	*157.823		
452.68	542.25	4.88	7.11	16.67	8.18	2359.69	
*312.793	0.63	1342.96	155.42	254.35	4.04		
INDI 758	INDI 758 PLS 1		Colorectum	II	*140.254		
4386.52	2306.57	*0.835	16.12	*2.794	43.19	1,703.6	
*328.815	0.74	3047.96	98.38	1412.38	6.96		
INDI 759	INDI 759 PLS 1		Breast	III	*157.823		
1270.26	2121.82	*0.803	11.67	*2.715	9.07	958.72	
*312.793	0.67	1233.71	88.71	381.68	4.3		
INDI 760	INDI 760 PLS 1		Liver	III	**99634.823		
3503.82	5268.16	5.9	14.04	*2.715	10.41	2854.53	
3886.20	0.43	1040.78	201.12	447.37	11.58		
INDI 761	INDI 761 PLS 1		Colorectum	II	*140.254		
2624.26	3805.01	*0.835	7.12	*2.794	30.6	3,251.4	
*328.815	0.77	1370.92	*14.391	509.49	6.93		
INDI 762	INDI 762 PLS 1		Esophagus	II	*157.823		
1428.68	1300.28	*0.803	8.98	*2.715	*1.372	794.47	
1969.27	0.65	730.12	136.9	574.51	11.68		
INDI 763	INDI 763 PLS 1		Colorectum	I	968.15		
1348.93	3126.83	*0.835	14.18	24.55	24.71	929.52	
*328.815	0.98	1045.07	*14.391	346.94	6.93		
INDI 764	INDI 764 PLS 1		Colorectum	II	*140.254		
2526.62	3301.39	7.67	7.95	*2.794	36.15	2,285.5	
*328.815	0.64	1722.29	136.53	490.66	5.8		
INDI 765	INDI 765 PLS 1		Colorectum	I	*140.254		
4628.73	5309.16	5.53	15.89	47.96	20.25	764.4	
*328.815	0.78	2171.71	112.47	*74.45	7.96		
INDI 766	INDI 766 PLS 1		Breast	II	*157.823		
894.34	1407.93	5.39	5.86	*2.715	11.04	884.27	

Table4.txt

*312.793	0.69	720	136.9	269.26	4.45		
INDI 767	INDI 767	PLS 1	Colorectum	II	1238.34		
1005.53	2396.09	*0.835	13.38	*2.794	31.08	20,381.1	
*328.815	0.69	1561.75	*14.391	714.78	5.9		
INDI 768	INDI 768	PLS 1	Colorectum	II	*140.254		
820.54	2225.1	*0.835	5.49	*2.794	20.25	1613.04	
3918.16	1.23	1154.78	175.65	1283.76	13.28		
INDI 769	INDI 769	PLS 1	Colorectum	II	*140.254		
430.20	3382.2	*0.835	4.64	*2.794	26.94	649.2	
*328.815	1.8	922.7	125.04	581.74	6.86		
INDI 770	INDI 770	PLS 1	Colorectum	II	*140.254		
569.27	3108.07	*0.835	3.10	21.62	23.83	1,311.9	
4301.36	1.18	1137.2	175.65	1247.61	7.91		
INDI 771	INDI 771	PLS 1	Liver	II	22322.18		
1383.22	2940.8	*0.803	6.42	17.43	15.83	1,654.5	
*312.793	0.71	2230.37	187.1	1098.51	9.96		
INDI 772	INDI 772	PLS 1	Colorectum	II	*140.254		
1523.63	2652.45	*0.835	8.21	18.38	22	627.17	
2887.77	1.27	649.53	184.28	1557.48	7.91		
INDI 773	INDI 773	PLS 1	Colorectum	II	*140.254		
2040.65	3791.39	*0.835	6.12	*2.794	33.58	1,730.2	
*328.815	0.83	3186.4	*14.391	1850.09	5.67		
INDI 774	INDI 774	PLS 1	Colorectum	I	871.14		
1539.48	3576.81	*0.835	2.25	*2.794	34.32	1,051.9	
3790.07	1.11	418.31	112.47	1789.36	23.7		
INDI 775	INDI 775	PLS 1	Liver	II	**99634.823		
2947.09	4970.33	6.16	6.46	*2.715	9.71	1,273.3	
2887	0.6	277.81	171.97	1325.78	14.92		
INDI 776	INDI 776	PLS 1	Esophagus	II	4777.43		
1116.63	855.56	11.29	3.89	19.70	12.76	5140.01	
13059.34	1.29	1284.51	499.76	1118.54	10.69		
INDI 777	INDI 777	PLS 1	Colorectum	II	*140.254		
1476.04	3821.36	*0.835	5.93	*2.794	34.26	1,413.3	
2627.86	1.42	2117.52	200.57	908.83	9.57		
INDI 778	INDI 778	PLS 1	Liver	II	191825.44		
899.77	985.68	*0.803	10.77	*2.715	*1.372	1,690.7	
7192.21	0.76	1584.68	300.55	1045.44	5.13		
INDI 779	INDI 779	PLS 1	Colorectum	II	*140.254		
1468.11	5838.45	*0.835	2.84	*2.794	44.04	561.8	
*328.815	1.44	753.22	112.47	250.33	9.52		
INDI 780	INDI 780	PLS 1	Colorectum	II	*140.254		
1317.10	2417.18	*0.835	7.14	23.57	21.72	1,703.6	
*328.815	2.01	1588.46	215.81	957.67	7.29		
INDI 781	INDI 781	PLS 1	Colorectum	II	*140.254		
836.67	2896.98	*0.835	6.52	*2.794	23.89	555.6	
2888	1.38	1370.92	200.57	865.95	11.11		
INDI 782	INDI 782	PLS 1	Colorectum	III	1486.77		
3440.76	4697.44	12.26	15.36	*2.794	40.61	27,188.4	

Table4.txt

13401.61	1.21	2027.36	215.81	1929.6	7.58		
INDI 783	INDI 783	PLS 1	Colorectum	III	*140.254		
2170.27	4864.89	*0.835	13.99	*2.794	27.58	3,018.3	
*328.815	0.61	1075.75	*14.391	1210.95	3.44		
INDI 784	INDI 784	PLS 1	Stomach	I	1956.22		
4296.56	517.31	11.59	29.98	19.01	13.86	900.5	
3442	1.06	1819.95	262.26	1175.44	7.38		
INDI 785	INDI 785	PLS 1	Colorectum	I	*140.254		
1101.65	722.01	*0.835	2.16	*2.794	33.12	2,490.9	
*328.815	0.62	1811.77	*14.391	633.19	5.11		
INDI 786	INDI 786	PLS 1	Liver	I	**100010.334		
2209.04	2482.68	*0.831	5.23	*2.782	36	1,119.0	
3442.41	1.55	2841.14	100.18	804.34	10.86		
INDI 787	INDI 787	PLS 1	Breast	II	1135.56		
3375.30	5007.69	*0.824	9.38	*2.781	36.18	927.52	
*327.606	0.78	2804	*15.64	779.33	4.44		
INDI 788	INDI 788	PLS 1	Colorectum	II	*140.254		
1594.93	5027.41	*0.835	11.43	*2.794	31.61	20,037.4	
*328.815	0.91	1767	*14.391	730.55	3.42		
INDI 789	INDI 789	PLS 1	Breast	II	*166.572		
1226.72	2547.86	*0.824	27.15	*2.781	23.65	517.31	
*327.606	1.3	2013.71	115.58	516.17	5.27		
INDI 790	INDI 790	PLS 1	Breast	II	*166.572		
980.67	1330.92	6.1	13.01	36.93	21.81	804.06	
*327.606	0.74	1739.9	*15.64	*78.14	5.44		
INDI 791	INDI 791	PLS 1	Breast	III	*166.572		
1667.55	1715.3	*0.824	6.42	*2.781	43.08	3139.31	
*327.606	0.86	2405.47	132.93	975.56	11.13		
INDI 792	INDI 792	PLS 1	Stomach	I	1425.93		
113.86	2452.49	5.77	258.76	*2.782	16.55	1047.90	
*325.874	1.13	2814.49	152.8	873.43	8.87		
INDI 793	INDI 793	PLS 1	Breast	II	6764.26		
2403.91	2153.39	*0.824	8.99	17.78	27.93	1,554.3	
*327.606	0.69	991.5	*15.64	1726.98	4.54		
INDI 794	INDI 794	PLS 1	Breast	II	*166.572		
2698.90	4228.37	*0.824	14.39	*2.781	36.06	554.05	
*327.606	0.85	413.18	*15.64	695.76	4.8		
INDI 795	INDI 795	PLS 1	Breast	II	3621.85		
2318.31	650.02	*0.824	14.47	*2.781	20.34	1509.36	
*327.606	0.72	3619.19	161.07	*78.14	4.26		
INDI 797	INDI 797	PLS 1	Stomach	II	5393.21		
1775.05	1817.67	5.77	16.08	*2.782	18.46	2,552.4	
*325.874	0.86	2115.52	152.8	746.99	8.94		
INDI 798	INDI 798	PLS 1	Ovary	II	*166.572		
2917.91	1751.97	10.64	19.97	*2.781	23.48	645.9	
3561.45	0.82	1476.9	285.18	911.88	5.92		
INDI 799	INDI 799	PLS 1	Stomach	II	1615.09		
334.09	3274.4	*0.831	8.68	*2.782	11.35	*77.625	

Table4.txt

*325.874	0.73	2548.82	120.99	1054.63	2.93	INDI 800	INDI 800 PLS 1
Liver	II	40391.09	5928.20	1203.56	6.72	19.56	*2.782
14.83	1,999.8	*325.874	0.88	4426.4	120.99	269.88	7.65
INDI 801	INDI 801 PLS 1	Stomach	I	3241.89	811.26	1295.77	*0.816
25.42	17.01	14.86	1,137.4	*319.819	0.58	2195.84	129.61
778.56	5.18	INDI 802	INDI 802 PLS 1	Pancreas	II	1410.48	3008.40
2229.05	*0.824	14.68	99.78	25.65	854.5	*327.606	0.82
2592.65	105.47	667.1	7.61	INDI 803	INDI 803 PLS 1	Esophagus	II
1443.75	1635.80	857.25	*0.816	19.59	21.92	17.7	1,481.5
3880.89	0.55	1250.96	289.56	831.88	7.59	INDI 805	INDI 805 PLS 1
Colorectum	II	1094.07	1879.28	1726.04	*0.835	9.85	*2.794
23.76	936.25	*328.815	0.6	927.06	136.53	1058.51	6.79
INDI 806	INDI 806 PLS 1	Colorectum	II	*140.254	864.88	2002.42	*0.835
6.91	*2.794	30.3	*77.894	*328.815	0.82	944.51	125.04
1018.75	4.25	INDI 808	INDI 808 PLS 1	Colorectum	III	*140.254	929.25
677.98	*0.835	10.95	*2.794	28.02	*77.894	*328.815	0.54
*33.46	136.53	991.83	5.23	INDI 809	INDI 809 PLS 1	Colorectum	III
*140.254	609.98	2958.33	5.53	11.40	*2.794	23.83	1977.85
*328.815	1.26	1668.7	257.05	776.93	8.16	INDI 812	INDI 812 PLS 1
Ovary	II	3550.69	1786.19	1969.95	25.12	10.62	42.89
26.36	567.5	*327.606	0.7	2718.31	*15.64	637.99	2.5
INDI 814	INDI 814 PLS 1	Stomach	I	*159.986	2161.28	1410.31	6.68
19.42	534.15	9.49	1093.75	2725.41	0.92	468.78	206.36
1539.19	8.06	INDI 815	INDI 815 PLS 1	Colorectum	II	*140.254	2815.34
2254	*0.835	8.17	*2.794	33.81	19,767.1	*328.815	0.67
922.7	147.18	581.74	6.87	INDI 816	INDI 816 PLS 1	Colorectum	II
4141.88	784.22	2012.87	7.13	3.75	*2.794	27.71	754.72
*328.815	0.55	249.46	321.69	1148.62	4.8	INDI 817	INDI 817 PLS 1
Liver	III	1637.93	3503.40	1063.93	6.31	31.20	*2.689
13.14	1,750.3	*319.819	0.52	2771.22	92.7	800.05	9.95
INDI 818	INDI 818 PLS 1	Ovary	III	*166.572	2204.21	2893.84	337.91
122.41	25.83	40.37	1,001.7	6091.44	1.33	844.35	161.07
5010.71	5.4	INDI 819	INDI 819 PLS 1	Breast	III	*166.572	1065.80
841.27	*0.824	59.52	18.14	31.81	1,724.2	3005.26	0.92
1744.23	*15.64	*78.14	3.01	INDI 821	INDI 821 PLS 1	Colorectum	III
*140.254	751.89	2112.32	9.17	4.05	*2.794	27.58	916.11

Table4.txt

*328.815	0.51	1005.68	166.64	451.91	4.73		
INDI 822	INDI 822 PLS 1		Colorectum	II	1738.7		
4043.05	4539.38	*0.824	16.78	*2.781	39	1,757.8	
*327.606	0.83	3652.08	*15.64	492.2	4.95		
INDI 823	INDI 823 PLS 1		Breast	II	*166.572		
2741.74	3363.01	*0.824	13.82	*2.781	29.17	2315.36	
*327.606	1.45	1983.16	*15.64	709.94	7.54		
INDI 824	INDI 824 PLS 1		Esophagus	II	3292.47		
1187.48	1548.12	*0.816	10.07	78.67	19.26	946.4	
*319.819	0.54	6714.14	195.4	1138.49	5.39		
INDI 825	INDI 825 PLS 1		Colorectum	III	*140.254		
1277.28	1892.74	*0.835	7.85	*2.794	30.42	1,938.7	
*328.815	0.84	1928.4	98.38	1032.08	5.42		
INDI 826	INDI 826 PLS 1		Colorectum	II	*140.254		
1895.04	1414.66	*0.835	3.25	*2.794	27.83	2,232.9	
*328.815	0.72	1829.69	98.38	509.49	4.07		
INDI 827	INDI 827 PLS 1		Colorectum	III	*140.254		
1400.61	2873	8.62	9.38	*2.794	22.29	1,427.9	
*328.815	0.6	2036.36	*14.391	1173.74	3.32		
INDI 828	INDI 828 PLS 1		Breast	II	*166.572		
1155.71	1279.9	*0.824	14.08	*2.781	32.26	1945.32	
*327.606	0.81	2088.06	115.58	652.6	4.39		
INDI 829	INDI 829 PLS 1		Colorectum	III	*140.254		
707.38	1757.26	*0.835	12.75	*2.794	37.51	946.34	
*328.815	0.67	342.02	161.97	674.58	5.14		
INDI 830	INDI 830 PLS 0		Breast	II	3119.96		
1795.69	2283.9	*0.824	21.08	*2.781	27.15	632.2	
*327.606	0.85	2525.62	*15.64	364.94	4.75		
INDI 831	INDI 831 PLS 1		Breast	I	3669.49		
3156.08	4878.94	8.62	13.38	*2.781	36.79	1230.59	
*327.606	0.7	4330.46	*15.64	1496.16	4.73		
INDI 832	INDI 832 PLS 1		Breast	II	*166.572		
980.67	2487.92	*0.824	6.67	*2.781	24.82	832.8	
*327.606	0.73	1283.68	*15.64	459.55	5.32		
INDI 833	INDI 833 PLS 1		Breast	I	3729.26		
5175.06	4773.93	*0.824	8.79	*2.781	30.47	1,277.5	
*327.606	0.74	2193.4	*15.64	813.19	8.16		
INDI 835	INDI 835 PLS 1		Colorectum	III	*140.254		
1177.58	1303.39	*0.835	8.40	*2.794	19.26	1,229.9	
*328.815	0.56	1415.21	200.57	714.78	4.44		
INDI 837	INDI 837 PLS 1		Colorectum	II	1402.3		
1594.93	4814.58	*0.835	13.73	*2.794	32.08	1768.43	
*328.815	0.77	2621.4	112.47	1331.22	6.83		
INDI 838	INDI 838 PLS 1		Colorectum	III	*140.254		
1077.65	644.28	*0.835	16.80	*2.794	33.75	592.8	
*328.815	0.89	308.27	166.64	908.83	9.33		
INDI 839	INDI 839 PLS 1		Breast	II	*166.572		
1748.22	2296.58	*0.824	11.52	*2.781	29.55	1988.55	

Table4.txt

*327.606	0.87	2290.36	*15.64	*78.14	3.69		
INDI 840	INDI 840 PLS 0		Breast	II	*166.572		
990.13	1889.36	*0.824	3.72	*2.781	32.26	869.01	
*327.606	0.76	2092.44	*15.64	467.79	4.31		
INDI 841	INDI 841 PLS 1		Colorectum	III	847.42		
3518.21	5193.4	*0.835	3.39	*2.794	50.37	8,213.9	
*328.815	0.81	2827.31	*14.391	1167.48	8.94		
INDI 842	INDI 842 PLS 1		Breast	I	*166.572		
2285.03	1051.84	*0.824	19.84	*2.781	27.59	1,501.2	
*327.606	0.81	1253.64	*15.64	*78.14	3.88		
INDI 843	INDI 843 PLS 1		Esophagus	I	*159.986		
894.44	1102.48	*0.816	13.92	*2.689	13.83	1827.31	
*319.819	0.49	1327.41	137.42	734.88	6.61		
INDI 844	INDI 844 PLS 1		Stomach	I	7963.52		
1831.74	3280.95	*0.816	7.70	*2.689	21.59	2,281.5	
3027	0.64	1967.42	*13.517	678.86	5.38		
INDI 846	INDI 846 PLS 1		Colorectum	II	*168.118		
2660.15	2800.57	*0.845	13.42	*2.915	9.3	39289.21	
*347.375	*0.107	832.75	105.39	*76.56	4.95		
INDI 847	INDI 847 PLS 1		Liver	III	**100101.482		
1223.67	1596.14	5.61	9.14	37.73	9.58	1,463.9	
6835.48	*0.107	2528.27	217.27	546.51	8		
INDI 848	INDI 848 PLS 1		Colorectum	II	1426.36		
1095.47	1951.6	*0.845	4.52	92.00	12.01	1309.54	
*347.375	1.4	1619.57	127.5	833.58	6.41		
INDI 849	INDI 849 PLS 1		Colorectum	II	*168.118		
1086.94	1406.34	5.34	5.75	*2.915	15.31	713.46	
2203.03	*0.107	1553.52	191.89	1038.51	11.25		
INDI 850	INDI 850 PLS 1		Esophagus	II	*168.118		
2094.46	1435.32	6.97	109.91	*2.915	7.71	778.4	
12715.32	*0.107	978.25	170.56	489.11	7.49		
INDI 853	INDI 853 PLS 1		Esophagus	II	1798.81		
3036.10	1739.82	*0.845	7.33	48.06	7.19	1,386.4	
15471.84	*0.107	1518.58	*15.378	313.08	12.04		
INDI 854	INDI 854 PLS 1		Colorectum	II	*168.118		
1817.34	2137.46	5.74	15.64	*2.915	13.71	3780.79	
2895.27	*0.107	2299.89	162.85	281.14	14.67		
INDI 855	INDI 855 PLS 1		Colorectum	II	2830.21		
4311.92	2509.68	*0.845	24.30	*2.915	10.51	1,126.0	
2668.03	1.99	1070.42	146.25	646.28	9.33		
INDI 856	INDI 856 PLS 1		Breast	III	1101.09		
597.86	2204.78	*0.82	3.84	23.05	14.63	1543.01	
2786.53	0.81	798.44	156.31	532.3	11.13		
INDI 857	INDI 857 PLS 1		Breast	III	*132.09		
758.27	1452.1	*0.82	28.54	30.37	9.24	1,653.4	
*327.917	0.57	1309.03	169.09	305.85	4.57		
INDI 858	INDI 858 PLS 1		Breast	I	2548.88		
1246.96	2824.49	7.12	11.99	*2.74	17.16	1118.21	

Table4.txt

*327.917	1.02	1546.84	108.45	779.98	10.51	
INDI 859	INDI 859 PLS 1		Esophagus	II	*132.09	
8167.48	1705.01	*0.82	*0.23	*2.74	16.87	*73.577
*327.917	0.74	976.04	*14.319	568.94	18.7	
INDI 860	INDI 860 PLS 1		Breast	I	*132.09	
867.12	3842.41	*0.82	4.22	*2.74	22.09	1402.20
*327.917	0.92	616.8	85.91	699.49	5.11	
INDI 861	INDI 861 PLS 1		Liver	II	1288.64	
2903.49	2910.7	*0.82	12.18	*2.74	13.67	836.2
2087.27	1.15	495.98	85.91	298.95	12.74	
INDI 862	INDI 862 PLS 1		Pancreas	II	2062.31	
2898.86	2517.87	*0.824	16.98	*2.781	22.09	768.4
2252	2.24	1223.61	173.16	355.91	7.39	
INDI 864	INDI 864 PLS 1		Liver	III	**99798.215	
1072.04	2828.49	17.78	12.31	*2.74	12.85	*73.577
*327.917	1.3	1052.62	85.91	507.58	7.84	
INDI 865	INDI 865 PLS 1		Breast	III	*168.118	
1330.76	1154.88	*0.845	3.96	*2.915	*1.372	683.78
*347.375	*0.107	1193.63	127.5	1136.85	6.75	
INDI 867	INDI 867 PLS 1		Esophagus	II	2154.08	
4931.50	724.98	*0.845	10.10	*2.915	14.36	1,184.9
7798.77	*0.107	1565.17	127.5	608.82	11.79	
INDI 868	INDI 868 PLS 1		Liver	III	166472.07	
1524.07	482.25	5.61	108.54	*2.915	7.28	1,441.7
24959.33	*0.107	1662.35	234.63	1546.04	15.47	
INDI 870	INDI 870 PLS 1		Breast	II	3796.42	
1604.58	1818.22	*0.82	18.34	*2.74	11.29	474.0
*327.917	1.36	230.61	108.45	412.53	5.7	
INDI 872	INDI 872 PLS 1		Breast	III	*132.09	
5027.69	1978.72	*0.82	4.43	*2.74	18.57	1,910.4
*327.917	1.15	1330.13	85.91	463.73	5.25	
INDI 873	INDI 873 PLS 1		Breast	III	2737.7	
804.36	912.01	7.43	23.76	*2.74	16.66	937.33
*327.917	0.99	738.5	85.91	305.85	5.18	
INDI 875	INDI 875 PLS 1		Breast	II	*132.09	
2527.34	2147.66	*0.82	4.44	*2.74	15.55	744.99
*327.917	1.17	964.03	108.45	682	5.19	
INDI 876	INDI 876 PLS 1		Breast	II	*132.09	
2475.01	2346.92	*0.82	6.10	*2.74	8.35	1552.16
*327.917	1.17	798.44	85.91	1182.01	5.99	
INDI 877	INDI 877 PLS 1		Breast	I	*132.09	
3467.97	2926.76	*0.82	10.21	*2.74	18.42	5,012.7
3238	1.36	2066.17	180.93	699.49	8.9	
INDI 878	INDI 878 PLS 1		Breast	III	*132.09	
2203.30	3452.8	13.7	15.09	43.95	22.48	840.4
*327.917	1.07	759.7	202.5	346.63	6.14	
INDI 879	INDI 879 PLS 1		Breast	II	*132.09	
597.86	3261.69	*0.82	16.14	*2.74	15.85	2043.31

Table4.txt

*327.917	1.24	2693.85	85.91	2022.96	7.3	
INDI 880	INDI 880 PLS 1		Breast	II	*132.09	
1207.22	3067.61	*0.82	5.38	*2.74	17	878.12
*327.917	1.77	1586.13	108.45	785.67	6.74	
INDI 881	INDI 881 PLS 1		Breast	II	*132.09	
1956.43	1650.45	*0.82	10.83	*2.74	18.19	663.5
4541.78	1.26	1304.81	108.45	1113.69	9.82	
INDI 882	INDI 882 PLS 1		Breast	II	1244.3	
624.34	1607.61	5.23	4.18	*2.74	19.14	591.36
*327.917	1.26	898.42	264.59	791.34	4.28	
INDI 883	INDI 883 PLS 1		Breast	II	*132.09	
1828.38	2555.13	*0.82	11.75	17.28	19.83	728.6
*327.917	1.81	1330.13	85.91	1150.58	5.61	
INDI 884	INDI 884 PLS 1		Breast	II	*132.09	
2505.77	4884.25	72.6	5.56	*2.74	16.07	*73.577
*327.917	0.75	1283.78	*14.319	457.39	8.41	
INDI 885	INDI 885 PLS 1		Breast	II	*132.09	
1828.38	1845.59	15.27	10.21	75.17	13.37	1005.68
*327.917	1.16	1036.42	*14.319	431.87	5.38	
INDI 886	INDI 886 PLS 1		Breast	II	*132.09	
1589.97	1186.59	6.17	15.00	21.82	14.91	753.22
*327.917	1.04	1455.95	85.91	127.67	5.19	
INDI 887	INDI 887 PLS 1		Breast	III	*132.09	
6858.12	2626.77	*0.82	19.29	317.41	22.61	5528.10
*327.917	0.86	1378.92	108.45	213.19	7.35	
INDI 888	INDI 888 PLS 1		Pancreas	II	2190.21	
1394.16	2834.58	20.49	32.20	1004.95	32.96	2,339.8
2606	0.73	2437.66	84.9	1016.4	6.18	
INDI 889	INDI 889 PLS 1		Colorectum	II	3066.13	
981.17	3648.19	*0.819	13.60	*2.688	24	6,637.5
4071	1.11	2399.04	237.68	3313.78	3.24	
INDI 892	INDI 892 PLS 1		Stomach	I	*130.232	
2066.21	1801.63	8.02	17.97	25.82	14.37	881.49
*1033.785	1.13	1715.64	*13.973	869.48	8.11	
INDI 893	INDI 893 PLS 1		Pancreas	II	2004.23	
1996.73	4636.63	5.4	32.82	38.76	52.23	*76.03
2405.70	0.94	2071.3	123.81	1254.55	9.83	
INDI 896	INDI 896 PLS 1		Lung	I	2776.32	
1248.49	2443.38	6.26	24.01	*2.624	12.76	1,033.4
2606	0.78	2805.58	154.78	1740.23	5.24	
INDI 897	INDI 897 PLS 1		Breast	III	2776.32	
1750.23	2410.88	*0.817	28.82	*2.624	34.72	3,525.7
*315.949	0.82	1402.01	99.23	575.14	5.85	
INDI 898	INDI 898 PLS 1		Breast	I	7017.03	
1891.66	5198.39	7.87	6.58	*2.624	38.7	2,019.7
*315.949	1.33	1440.75	123.81	1006.42	7.96	
INDI 899	INDI 899 PLS 1		Breast	I	7346.28	
2842.50	2589.83	*0.817	7.48	*2.624	32.19	1741.28

Table4.txt

*315.949	1.05	2660.04	84.9	1094.86	6.07	
INDI 902	INDI 902 PLS 1		Breast	III	6680.42	
1314.07	3425.1	7.73	39.20	27.46	28.57	890.0
10716	0.92	1948.01	164.08	*71.31	5.83	
INDI 903	INDI 903 PLS 1		Breast	I	6932.41	
1270.35	3427.85	*0.817	25.75	*2.624	25.17	997.20
*315.949	0.76	1710.65	112.06	666.37	5.39	
INDI 905	INDI 905 PLS 1		Esophagus	II	*166.572	
3303.80	3662.77	*0.824	8.90	*2.781	28.42	1,246.2
2630.59	0.91	1489.79	*15.64	337.6	16.59	
INDI 907	INDI 907 PLS 1		Esophagus	II	*166.572	
3089.38	2098.97	*0.824	6.16	*2.781	18.15	677.1
*327.606	0.8	974.25	*15.64	578.25	4.04	
INDI 908	INDI 908 PLS 1		Esophagus	II	*166.572	
4081.23	1723.44	5.01	6.05	*2.781	19.73	2,556.7
4928.08	0.77	1839.57	*15.64	*78.14	6.9	
INDI 909	INDI 909 PLS 1		Esophagus	II	*166.572	
6959.88	1256.44	*0.824	16.24	19.97	31.28	1,035.4
2252.24	0.91	1223.61	132.93	833.26	15.02	
INDI 911	INDI 911 PLS 1		Esophagus	II	*166.572	
2061.64	2381.37	7.49	24.57	*2.781	30.28	4292.87
*327.606	1.9	1796.2	*15.64	866.33	3.31	
INDI 913	INDI 913 PLS 1		Esophagus	III	1768.45	
1843.16	1021.38	*0.824	15.27	*2.781	22.54	931.20
2630.59	1.46	1468.3	147.81	492.2	5.26	
INDI 915	INDI 915 PLS 1		Breast	II	1112.06	
966.26	4595.75	5.23	17.26	*2.74	8.5	836.2
*327.917	0.73	1385.31	202.5	774.29	6.89	
INDI 917	INDI 917 PLS 1		Liver	III	*132.09	
7732.06	2818.48	*0.82	20.39	*2.74	14.35	878.1
*327.917	0.63	499.65	*14.319	734.21	5.27	
INDI 919	INDI 919 PLS 1		Breast	II	*132.09	
1094.45	2248.16	*0.82	18.39	27.94	18.8	*73.577
*327.917	0.74	849.19	85.91	734.21	8.95	
INDI 920	INDI 920 PLS 1		Ovary	III	2221.5	
1757.35	1564.81	18.41	23.12	*2.74	16.79	671.6
*327.917	0.58	1689.67	*14.319	690.76	5.24	
INDI 921	INDI 921 PLS 1		Breast	II	*132.09	
3480.80	3644.99	6.8	32.01	*2.74	16.91	1,267.9
4114.33	0.67	2239.35	126.63	312.72	5.38	
INDI 922	INDI 922 PLS 1		Breast	II	1200.09	
2997.73	1994.41	*0.82	15.12	*2.74	9.79	*73.577
*327.917	0.67	2310.48	*14.319	213.19	7.49	
INDI 923	INDI 923 PLS 1		Esophagus	I	1738.4	
2224.53	2265.92	*0.82	44.46	*2.74	23.61	736.8
*327.917	0.85	2447.1	*14.319	892.13	6.38	
INDI 924	INDI 924 PLS 1		Breast	III	*132.09	
1727.85	2628.76	*0.82	12.76	*2.74	12.74	687.8

Table4.txt

*327.917	0.74	1641.04	85.91	485.76	3.72		
INDI 926	INDI 926 PLS 1		Breast	II	*132.09		
988.43	2416.2	*0.82	3.79	*2.74	16.24	671.6	
*327.917	0.61	707.82	*14.319	227.91	4.71		
INDI 927	INDI 927 PLS 1		Breast	II	3311.13		
6524.83	2183.11	*0.82	16.92	*2.74	9.65	1,971.9	
*327.917	0.66	2750.86	85.91	292.01	5.15		
INDI 928	INDI 928 PLS 1		Stomach	II	114364.32		
2475.01	3792.95	5.23	10.41	21.41	27.76	2,192.0	
3680.07	1.01	234.12	212.46	1300.96	8.04		
INDI 929	INDI 929 PLS 1		Stomach	II	1333.1		
1689.58	2778.46	9.94	30.66	*2.74	14.16	*73.577	
*327.917	0.79	755.84	*14.319	292.01	7.88		
INDI 930	INDI 930 PLS 1		Stomach	II	*132.09		
2505.77	2072.94	*0.82	24.98	*2.74	20.19	1,492.8	
*327.917	0.84	878.68	*14.319	1033.78	15.55		
INDI 931	INDI 931 PLS 1		Ovary	III	*132.09		
1005.10	2732.49	25.47	17.29	*2.74	18.04	869.7	
*327.917	0.74	1814.81	85.91	1192.44	6.88		
INDI 932	INDI 932 PLS 1		Ovary	III	1944.2		
2254.91	1888.62	48.28	22.05	*2.74	17.68	1,783.5	
2087.27	0.76	1566.46	85.91	708.2	3.38		
INDI 933	INDI 933 PLS 1		Esophagus	III	*132.09		
1128.16	2025.81	*0.82	10.28	*2.74	13.37	886.5	
*327.917	0.74	*27.606	180.93	802.66	5.11		
INDI 935	INDI 935 PLS 1		Esophagus	I	829.99		
555.72	1833.86	*0.82	4.60	*2.74	13.27	945.8	
*327.917	0.84	1024.3	108.45	457.39	4.41		
INDI 936	INDI 936 PLS 1		Ovary	I	*132.09		
1792.82	3009.19	*0.82	13.22	*2.74	18.61	2,254.8	
*327.917	0.86	3030.32	*14.319	808.31	8.23		
INDI 937	INDI 937 PLS 1		Esophagus	III	*132.09		
1301.11	1675.77	25.63	4.35	26.32	9.79	*73.577	
*327.917	0.86	751.98	169.09	587.08	5.99		
LCR 588	LCR 588 PLS1		Normal	NA	2003.87		
957.85	2674.11	12.5	20.62	20.76	24.22	803.13	
*334.48	0.83	2207.1	127.59	772.37	10.08		
LCR 589	LCR 589 PLS1		Normal	NA	1477.71		
955.15	2298.18	5.43	4.30	*2.724	44.68	686.29	
*334.48	0.86	1100.17	132.13	581.32	26.01		
LCR 590	LCR 590 PLS1		Normal	NA	*152.33		
1267.35	3851.64	8.93	15.40	*2.724	26.89	*71.073	
*334.48	0.74	988.31	108.13	755.99	4.85		
LCR 591	LCR 591 PLS1		Normal	NA	*152.33		
395.10	3761.8	*0.814	24.18	*2.724	34.4	2040.86	
*334.48	0.69	2577.19	85.72	462.56	7.56		
LCR 592	LCR 592 PLS1		Normal	NA	2782.15		
759.62	3411.16	*0.814	10.49	*2.724	24.47	432.26	

Table4.txt

*334.48	1.26	*27.566	210.9	961.21	8.06		
LCR 593	LCR 593 PLS1		Normal	NA	*152.33		
828.82	4429.71	8.63	6.71	*2.724	36.81	899.80	
*334.48	0.72	2506.05	197.6	979.4	7.79		
LCR 594	LCR 594 PLS1		Normal	NA	*152.33		
1292.30	5105.37	*0.814	*0.233	*2.724	19.85	467.51	
*334.48	0.82	1875.69	85.72	976.38	3.71		
LCR 595	LCR 595 PLS1		Normal	NA	*152.33		
680.45	3740.68	5.43	15.89	27.39	14.7	1302.73	
*334.48	0.94	1875.69	*14.286	337.04	7.9		
LCR 596	LCR 596 PLS1		Colorectum	I	*152.33		
159.97	4318.06	6.12	4.59	33.23	21.45	2412.11	
2431.46	1.31	832.59	183.67	477.91	8.77		
LCR 597	LCR 597 PLS1		Normal	NA	*152.33		
1971.39	1512.99	*0.814	11.66	*2.724	28.77	458.6	
*334.48	1.39	1401.74	97.39	918.3	5.71		
LCR 599	LCR 599 PLS1		Normal	NA	3164.21		
1708.22	3519.12	*0.814	12.39	*2.724	20.66	1,732.4	
*334.48	0.84	2960.81	85.72	450.94	4.6		
LCR 600	LCR 600 PLS1		Normal	NA	1228.17		
930.84	2616.6	*0.814	15.25	*2.724	22.86	579.46	
*334.48	0.87	1769.1	85.72	602.69	4.93		
LCR 601	LCR 601 PLS1		Normal	NA	*152.33		
221.14	1111.34	*0.814	16.91	*2.724	18.65	695.9	
*334.48	1.1	350.37	145.14	252.09	5.72		
LCR 602	LCR 602 PLS1		Normal	NA	*152.33		
1209.28	2100.2	*0.814	14.67	*2.724	44.44	744.26	
*334.48	1.05	2193.28	97.39	1100.97	6.34		
LCR 603	LCR 603 PLS1		Normal	NA	1373.78		
947.04	5027.65	*0.814	12.46	27.99	31.7	470.47	
*334.48	1.02	1088.08	*14.286	616.8	3.1		
LCR 604	LCR 604 PLS1		Normal	NA	3093.96		
938.94	3232.35	*0.814	11.72	*2.724	23.91	506.29	
*334.48	0.76	370.06	97.39	581.32	8.71		
LCR 605	LCR 605 PLS1		Normal	NA	*152.33		
278.96	2006.52	*0.814	8.69	*2.724	26.17	*71.073	
*334.48	0.96	255.12	97.39	462.56	3.24		
LCR 606	LCR 606 PLS1		Normal	NA	*152.33		
264.40	2360.76	8.63	8.40	*2.724	21.17	*71.073	
*334.48	1.05	711.77	183.67	306.65	5.16		
LCR 607	LCR 607 PLS1		Normal	NA	*152.33		
581.31	2355.54	*0.814	4.73	*2.724	21.78	*71.073	
*334.48	1.25	1197.78	190.72	366.56	7.59		
LCR 608	LCR 608 PLS1		Normal	NA	*152.33		
3099.81	2951.57	14.54	14.32	*2.724	22.43	635.57	
3112.88	0.79	1255.43	247.88	383.09	11.15		
LCR 610	LCR 610 PLS1		Normal	NA	*152.33		
604.67	2167.9	*0.814	11.28	*2.724	17.53	567.13	

Table4.txt

*334.48	1.09	1764.68	145.14	139.51	5.31	
LCR 611	LCR 611 PLS1		Normal	NA	*152.33	
615.08	3614.02	*0.814	3.61	28.80	23.44	699.09
*334.48	1.04	1267.85	136.56	893.5	5.04	
LCR 612	LCR 612 PLS1		Normal	NA	*152.33	
675.20	5000.87	*0.814	3.73	*2.724	43.69	933.62
*334.48	0.97	1589.86	168.99	630.8	16.92	
LCR 613	LCR 613 PLS1		Normal	NA	*152.33	
2040.57	3032.85	*0.814	14.72	*2.724	19.5	443.95
*334.48	0.74	952.84	168.99	2116.01	6.45	
LCR 614	LCR 614 PLS1		Normal	NA	*152.33	
871.65	3434.85	5.43	14.30	21.96	20.37	974.54
*334.48	1.45	2019.67	253.7	500.64	8.26	
LCR 616	LCR 616 PLS1		Normal	NA	1373.78	
4161.04	4872.42	*0.814	13.65	*2.724	28.68	2136.51
*334.48	0.84	5067.37	118.15	1121.29	8.72	
LCR 617	LCR 617 PLS1		Normal	NA	*152.33	
481.06	3487.51	*0.814	9.77	*2.724	52.02	754.01
*334.48	1.36	1096.13	210.9	4649.5	8.92	
LCR 618	LCR 618 PLS1		Normal	NA	*152.33	
529.70	3492.78	9.22	9.58	*2.724	29.41	1237.76
*334.48	1.09	2299.71	145.14	759.27	7.14	
LCR 619	LCR 619 PLS1		Normal	NA	2954.5	
427.79	1575.25	*0.814	4.35	*2.724	20.77	*71.073
*334.48	0.99	861.4	91.69	297.79	5.33	
LCR 620	LCR 620 PLS1		Normal	NA	*152.33	
400.12	1788.15	14.54	4.61	*2.724	64.02	548.73
*334.48	1.23	851.78	183.67	795.13	7.17	
LCR 621	LCR 621 PLS1		Normal	NA	2477.69	
1470.93	2214.79	*0.814	12.71	*2.724	23.07	591.84
3372.63	0.64	1992.51	*14.286	836.84	8.83	
LCR 622	LCR 622 PLS1		Normal	NA	*152.33	
990.35	2355.54	5.43	3.76	17.15	23.96	789.97
*334.48	1.48	945	118.15	470.25	11.75	
LCR 623	LCR 623 PLS1		Normal	NA	*152.33	
944.34	265.4	8.33	16.16	*2.724	36.73	2241.09
*334.48	0.79	1043.96	297.53	332.76	2.52	
LCR 624	LCR 624 PLS1		Normal	NA	1829.96	
764.93	2128.84	*0.814	10.63	*2.724	26.84	1130.98
*334.48	1.21	1294.84	*14.286	685.84	4.83	
LCR 625	LCR 625 PLS1		Normal	NA	*152.33	
1805.10	2389.45	*0.814	15.36	*2.724	29	441.0
*334.48	1.13	1729.44	197.6	1277.01	10.23	
LCR 626	LCR 626 PLS1		Normal	NA	*152.33	
844.86	5570.59	*0.814	7.73	*2.724	18.72	1335.46
*334.48	0.78	696.92	85.72	1062.92	4.74	
LCR 627	LCR 627 PLS1		Normal	NA	*152.33	
1039.28	3997.15	*0.814	10.37	*2.724	28.81	*71.073

Table4.txt

*334.48	1.57	1624.54	108.13	752.7	8.44		
LCR 628	LCR 628 PLS1		Normal	NA	*152.33		
791.49	2175.71	*0.814	4.59	*2.724	21.45	776.85	
*334.48	1.42	1707.48	153.37	991.47	4.29		
LCR 629	LCR 629 PLS1		Normal	NA	1023.44		
4194.81	7198.46	*0.814	4.70	*2.724	38.71	744.3	
*334.48	1.69	3730.94	85.72	985.44	9.45		
LCR 630	LCR 630 PLS1		Normal	NA	*152.33		
1645.78	4597.46	6.78	11.19	18.75	37.86	984.8	
*334.48	0.77	1210.09	136.56	899.72	4.62		
LCR 631	LCR 631 PLS1		Normal	NA	*152.33		
1645.78	2089.79	9.79	16.27	*2.724	41.59	876.26	
*334.48	0.77	1542.41	176.43	319.79	5.12		
LCR 632	LCR 632 PLS1		Normal	NA	4702.79		
863.60	2269.51	*0.814	4.11	*2.724	32.43	1088.82	
*334.48	1.07	1880.16	108.13	630.8	6.19		
LCR 633	LCR 633 PLS1		Normal	NA	*152.33		
2086.80	2512.11	*0.814	9.07	17.15	23.28	692.69	
*334.48	0.82	6476.03	85.72	1132.84	4.66		
LCR 634	LCR 634 PLS1		Normal	NA	4144.23		
882.39	3817.28	*0.814	15.41	23.37	27.7	667.18	
*334.48	0.78	1134.56	140.9	545.13	9.88		
LCR 635	LCR 635 PLS1		Normal	NA	*152.33		
*12.797	2925.37	*0.814	13.50	*2.724	17.15	461.59	
*334.48	1	*27.566	*14.286	*23.506	5.86		
LCR 636	LCR 636 PLS1		Normal	NA	*152.33		
1583.54	5212.7	*0.814	5.92	16.75	26.99	1,357.4	
*334.48	0.78	3577.49	153.37	3234.51	7.68		
LCR 637	LCR 637 PLS1		Normal	NA	*152.33		
565.78	1163.12	*0.814	9.87	*2.724	37.28	518.35	
*334.48	1.03	462.68	161.31	852.7	14.82		
LCR 638	LCR 638 PLS1		Normal	NA	1359.07		
1143.21	927.57	8.63	21.25	*2.724	21.67	1040.03	
2431.46	0.72	1326.12	204.33	1876.1	7.71		
LCR 639	LCR 639 PLS1		Normal	NA	*152.33		
1259.04	3687.88	*0.814	2.45	*2.724	20.71	715.16	
*334.48	1.73	769.85	97.39	1285.32	11.19		
LCR 640	LCR 640 PLS1		Normal	NA	*152.33		
478.51	3156.18	*0.814	20.98	*2.724	36.37	2040.86	
*334.48	1.18	1450.47	85.72	552.43	7.6		
LCR 641	LCR 641 PLS1		Normal	NA	*152.33		
*12.797	4076.61	17.44	14.61	*2.724	26.56	503.29	
5011.79	1.29	*27.566	419.04	*23.506	4.9		
LCR 642	LCR 642 PLS1		Normal	NA	2116.26		
733.15	5489.72	*0.814	3.67	*2.724	19.5	836.22	
*334.48	1.23	1902.53	85.72	729.53	7.18		
LCR 643	LCR 643 PLS1		Normal	NA	*152.33		
1066.55	1990.91	*0.814	16.61	*2.724	20.08	1152.19	

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*334.48	0.94	2855.99	145.14	1098.06	5.86		
LCR 644	LCR 644 PLS1		Normal	NA	947.91		
2133.11	3915.11	*0.814	11.80	*2.724	39.01	783.41	
*334.48	0.97	1942.92	102.86	1876.1	9.32		
LCR 645	LCR 645 PLS1		Normal	NA	*152.33		
1994.43	2016.92	*0.814	17.24	*2.724	20.08	524.40	
*334.48	0.93	1924.95	153.37	188.2	5.08		
LCR 646	LCR 646 PLS1		Normal	NA	3076.45		
1702.53	5376.64	*0.814	4.30	*2.724	25.08	*71.073	
*334.48	1.12	962.67	127.59	1307.4	7.75		
LCR 647	LCR 647 PLS1		Normal	NA	2386.2		
638.55	3872.79	*0.814	8.06	*2.724	34.15	*71.073	
*334.48	1.12	493.79	97.39	1434.79	9.58		
LCR 648	LCR 648 PLS1		Normal	NA	1560.48		
638.55	3077.44	*0.814	3.96	*2.724	20.31	579.46	
*334.48	0.96	847.93	118.15	470.25	4.01		
LCR 649	LCR 649 PLS1		Normal	NA	*152.33		
240.29	2303.39	*0.814	4.38	*2.724	18.9	1273.78	
*334.48	1.13	2087.86	145.14	949.01	8.63		
LCR 650	LCR 650 PLS1		Normal	NA	*152.33		
834.16	1126.87	10.35	11.72	38.46	11.26	1659.79	
4910.34	1.8	1512.36	241.98	746.1	5.78		
LCR 652	LCR 652 PLS1		Normal	NA	*152.33		
607.27	2402.49	*0.814	5.70	*2.724	16.56	*71.073	
*334.48	0.71	505.98	*14.286	315.43	7.34		
LCR 653	LCR 653 PLS1		Normal	NA	*152.33		
1061.09	4365.89	8.03	10.73	*2.724	49.21	*71.073	
*334.48	0.76	1128.48	153.37	519.33	11.11		
LCR 654	LCR 654 PLS1		Normal	NA	*152.33		
586.50	2402.49	*0.814	18.28	*2.724	26.41	545.68	
*334.48	1.39	2033.27	*14.286	742.8	11.99		
LCR 655	LCR 655 PLS1		Normal	NA	*152.33		
680.45	2836.32	*0.814	26.89	*2.724	35.37	1138.04	
*334.48	1.09	1092.1	85.72	651.62	9.28		
LCR 658	LCR 658 PLS1		Normal	NA	*152.33		
1611.81	4397.8	*0.814	4.08	*2.724	29.27	500.29	
*334.48	1.07	1882.39	*14.286	493.1	7.78		
LCR 659	LCR 659 PLS1		Normal	NA	2019.85		
860.92	1590.82	*0.814	13.83	*2.724	18.47	*71.073	
*334.48	1.1	192.03	168.99	454.82	3.6		
LCR 660	LCR 660 PLS1		Normal	NA	*152.33		
1668.46	2162.69	*0.814	9.97	*2.724	20.08	1064.37	
*334.48	1.34	1760.27	*14.286	973.35	6.14		
LCR 661	LCR 661 PLS1		Normal	NA	*152.33		
2272.57	2538.23	*0.814	14.01	*2.724	24.98	789.97	
*334.48	0.95	1080.03	85.72	415.46	6.08		
LCR 662	LCR 662 PLS1		Normal	NA	*152.33		
1546.87	2533.01	*0.814	13.62	*2.724	35.13	482.35	

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*334.48	1.02	1607.18	*14.286	588.47	19.55		
LCR 663	LCR 663 PLS1		Normal	NA	1359.07		
1896.69	3192.94	*0.814	6.18	*2.724	14.12	449.8	
*334.48	0.87	2416.51	85.72	1321.14	4.54		
LCR 665	LCR 665 PLS1		Normal	NA	3145.72		
2972.63	4722.06	*0.808	13.57	*2.749	26	466.98	
*324.366	0.96	685.06	*14.148	399.63	5.82		
LCR 666	LCR 666 PLS1		Normal	NA	6246.67		
1565.05	358.48	*0.808	40.56	18.15	64.8	1925.96	
*324.366	1.32	2228.36	159.22	2056.72	4.86		
LCR 667	LCR 667 PLS1		Normal	NA	*149.188		
5596.48	1854.72	6.13	9.40	*2.749	27.09	719.23	
*324.366	1.04	4171.77	150.55	230.38	6.36		
LCR 668	LCR 668 PLS1		Normal	NA	*149.188		
739.01	4756.67	*0.808	20.33	*2.749	21.66	975.49	
*324.366	1.2	1762.48	141.53	429.86	7.22		
LCR 670	LCR 670 PLS1		Normal	NA	*149.188		
2975.72	2481.11	*0.808	13.53	*2.749	29.93	520.28	
*324.366	1.37	1847.11	202.26	761.98	7.07		
LCR 671	LCR 671 PLS1		Normal	NA	1208.28		
1015.45	538.64	*0.808	22.10	*2.749	28.29	1878.27	
*324.366	1.48	1887.66	159.22	414.85	3.13		
LCR 672	LCR 672 PLS1		Normal	NA	*149.188		
4575.64	2898.04	*0.808	16.46	31.04	14.17	1582.53	
*324.366	1.7	229.11	111.64	409.8	9.63		
LCR 673	LCR 673 PLS1		Normal	NA	*149.188		
2137.94	2704.97	6.13	5.83	24.27	28.68	1048.20	
*324.366	1.45	2804.92	219.91	596.54	7.17		
LCR 674	LCR 674 PLS1		Normal	NA	*149.188		
1044.50	2325.54	*0.808	7.84	*2.749	21.36	1037.74	
*324.366	1.3	970.39	183.53	378.96	4.27		
LCR 675	LCR 675 PLS1		Normal	NA	*149.188		
2050.31	3965.69	*0.808	3.68	*2.749	36.99	883.71	
*324.366	1.07	409.52	111.64	1158.43	4.56		
LCR 676	LCR 676 PLS1		Normal	NA	2386.17		
2609.78	2739.02	*0.808	11.11	*2.749	79.33	2123.34	
*324.366	1.51	869.92	*14.148	843.18	10.76		
LCR 677	LCR 677 PLS1		Normal	NA	1471.25		
1767.82	2085.6	*0.808	15.65	*2.749	18.14	1104.35	
*324.366	1.23	1623.01	154.93	217.48	4.6		
LCR 678	LCR 678 PLS1		Normal	NA	*149.188		
1161.11	3011.77	*0.808	7.05	*2.749	60.85	1189.76	
*324.366	1.18	681.51	*14.148	325.15	6.42		
LCR 679	LCR 679 PLS1		Normal	NA	*147.076		
3318.90	324.45	*0.792	18.40	*2.747	24.9	523.16	
*323.745	1.09	2648.89	163.47	696.28	5.48		
LCR 680	LCR 680 PLS1		Normal	NA	4859.55		
767.56	4920.51	5.26	6.52	18.02	40.3	1,023.3	

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*323.745	1.25	989.83	106.34	720.08	10.49		
LCR 681	LCR 681 PLS1		Normal	NA	3001.45		
1313.65	1849.1	25.51	8.30	*2.749	24.6	2416.55	
*324.366	1.55	1916.14	183.53	478.44	3.77		
LCR 682	LCR 682 PLS1		Normal	NA	2243.27		
1199.15	2761.72	*0.808	29.30	*2.749	18.76	1027.31	
*324.366	1.07	799.42	111.64	429.86	4.82		
LCR 683	LCR 683 PLS1		Normal	NA	*149.188		
1651.35	1677.77	*0.808	13.15	*2.749	19.14	*76.613	
*324.366	1.2	1423.36	132.09	217.48	4.22		
LCR 684	LCR 684 PLS1		Normal	NA	1491.49		
2174.26	2158.92	*0.808	14.28	*2.749	48.63	*76.613	
*324.366	0.92	402.65	88.14	255.36	12.1		
LCR 685	LCR 685 PLS1		Normal	NA	1451		
4062.23	2827.02	*0.808	23.13	41.45	71.49	6030.66	
*324.366	1.16	2076.27	141.53	302.62	4.24		
LCR 686	LCR 686 PLS1		Normal	NA	*149.188		
1131.90	3228.16	*0.808	9.99	*2.749	35.28	502.38	
*324.366	1.98	1380.85	88.14	204.27	7.56		
LCR 687	LCR 687 PLS1		Normal	NA	*149.188		
2753.94	1492.83	*0.808	9.00	20.27	25.07	1578.71	
*324.366	1.34	1135.61	100.38	357.83	5.82		
LCR 688	LCR 688 PLS1		Normal	NA	*149.188		
1702.07	1436.88	*0.808	20.92	36.83	40.07	1,044.7	
*324.366	1.49	1273.55	127.19	444.65	4.43		
LCR 689	LCR 689 PLS1		Normal	NA	*149.188		
1015.45	4097.65	4.99	6.59	*2.749	35.12	568.69	
*324.366	1.66	871.73	*14.148	291.09	4.75		
LCR 690	LCR 690 PLS1		Normal	NA	*149.188		
1416.87	3905.49	5.56	30.18	27.54	42.7	1093.78	
*324.366	1.74	2272.5	111.64	681.28	9.97		
LCR 691	LCR 691 PLS1		Normal	NA	*149.188		
1624.54	2512.25	*0.808	6.90	20.51	22.87	887.08	
*324.366	1.69	999.85	*14.148	622.45	5.71		
LCR 692	LCR 692 PLS1		Normal	NA	*149.188		
2877.02	2365.11	*0.808	18.37	17.68	50.59	5826.48	
*324.366	1.68	2513.06	*14.148	1304.97	12.44		
LCR 693	LCR 693 PLS1		Normal	NA	2960.28		
1108.56	2032.05	5.56	25.50	*2.749	49.65	735.34	
*324.366	1.36	2327.4	100.38	347.07	4.25		
LCR 694	LCR 694 PLS1		Normal	NA	2182.09		
4258.17	1504.02	*0.808	7.79	22.86	20.11	712.80	
*324.366	1.5	2230.45	191.17	384.17	5.02		
LCR 697	LCR 697 PLS1		Normal	NA	2816.36		
727.59	1431.29	*0.808	6.03	*2.749	22.47	599.4	
*324.366	1.24	724.18	159.22	816.48	13.56		
LCR 698	LCR 698 PLS1		Normal	NA	1793.24		
2599.57	2408.55	5.26	70.21	38.24	63.3	2371.10	

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2637.28	0.62	1202.17	127.42	1077.26	9.46	
LCR 699	LCR 699 PLS1		Normal	NA	4207.44	
2473.54	3534.35	*0.792	15.22	19.17	28.47	723.72
2320.19	0.82	2096.1	113.68	973.17	5.52	
LCR 700	LCR 700 PLS1		Normal	NA	1642.89	
1036.32	5352.12	9.44	13.01	27.98	47.52	1450.51
10293.21	0.96	1728.49	283.74	1015.27	35.81	
LCR 701	LCR 701 PLS1		Normal	NA	3629.18	
632.39	2871.58	6.98	20.12	*2.747	28.34	539.39
2637.28	1.2	1247.73	204.18	333.81	9.05	
LCR 702	LCR 702 PLS1		Normal	NA	3928.82	
1677.21	2322.78	5.95	10.11	*2.747	67.58	1649.97
*323.745	1.13	1615.84	376.13	3995.43	5.9	
LCR 703	LCR 703 PLS1		Normal	NA	2090.42	
3012.79	1453.66	*0.808	7.17	19.57	35.79	568.69
*324.366	1.6	1567.78	159.22	4459.79	9	
LCR 704	LCR 704 PLS1		Normal	NA	11636.84	
1098.52	4027.82	11.58	66.85	*2.747	48.63	2,616.3
3661	2.13	993.86	421.52	708.21	9.29	
LCR 705	LCR 705 PLS1		Normal	NA	5830.13	
2151.03	1416.34	*0.792	13.48	32.93	25.13	1,038.1
2213	0.56	2010.87	213.49	344.18	6.09	
LCR 706	LCR 706 PLS1		Normal	NA	*147.076	
3638.83	3212.96	*0.792	17.88	31.78	19.98	1089.97
*323.745	1.38	4334.73	204.18	864.86	9.29	
LCR 707	LCR 707 PLS1		Normal	NA	1431.34	
2453.08	2143.59	4.92	49.27	*2.747	22.09	1585.60
*323.745	0.73	2485.07	184.61	461.12	5.59	
LCR 709	LCR 709 PLS1		Normal	NA	*149.188	
2222.74	1750.75	*0.808	13.69	*2.749	36.76	1795.46
*324.366	2.41	2597.27	209.44	2156.5	3.1	
LCR 710	LCR 710 PLS1		Normal	NA	*149.188	
2041.26	2291.63	5.85	7.85	*2.749	34.49	958.3
*324.366	1.79	754.55	183.53	1131.61	9.28	
LCR 711	LCR 711 PLS1		Normal	NA	1978.16	
1180.13	1466.48	*0.792	20.99	*2.747	41.28	1344.94
*323.745	0.76	945.56	98.61	2977.3	6.77	
LCR 712	LCR 712 PLS1		Normal	NA	*149.188	
1594.78	2591.56	*0.808	12.72	*2.749	24.79	1822.97
*324.366	0.75	1977.44	*14.148	1014.6	5.82	
LCR 713	LCR 713 PLS1		Normal	NA	*149.188	
1621.56	5114.97	*0.808	22.37	44.90	17	3,706.2
*324.366	1.24	1526.57	88.14	793.31	6.24	
LCR 714	LCR 714 PLS1		Normal	NA	4289.43	
2466.10	4126.36	*0.808	20.29	*2.749	33.61	917.47
*324.366	1.16	2754.32	100.38	902.99	8.68	
LCR 715	LCR 715 PLS1		Normal	NA	4574.88	
1074.14	3512.51	6.64	32.43	*2.747	44.11	972.02

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2213.19	0.91	757.05	213.49	1444.48	14.98		
LCR 716	LCR 716 PLS1		Normal	NA	*147.076		
1254.04	2658.48	8.73	31.89	*2.747	41.4	885.32	
3256.64	1.1	1864.37	356.97	1144.66	6.28		
LCR 717	LCR 717 PLS1		Normal	NA	1858.22		
1380.88	2467.58	8.73	23.37	40.51	52.74	1788.39	
*323.745	1.15	1899.71	174.27	528.89	8.12		
LCR 718	LCR 718 PLS1		Normal	NA	9343.19		
1476.04	2009.51	*0.808	14.91	*2.749	23.65	777.59	
*324.366	2.07	3126.48	191.17	1971.17	4.82		
LCR 719	LCR 719 PLS1		Normal	NA	*149.188		
1743.90	2634.08	*0.808	13.15	*2.749	22.52	593.24	
*324.366	1.06	2592.94	*14.148	1204.78	4.18		
LCR 720	LCR 720 PLS1		Normal	NA	986.02		
3285.53	445.64	*0.808	28.09	*2.749	34.17	2475.33	
*324.366	1.11	1307.9	132.09	1269.79	4.94		
LCR 721	LCR 721 PLS1		Normal	NA	*149.188		
733.30	2549.07	33.07	8.25	17.20	40.07	1302.07	
*324.366	1.17	1070.25	*14.148	487.91	6.04		
LCR 722	LCR 722 PLS1		Normal	NA	*149.188		
1681.18	3276.62	*0.808	8.40	*2.749	50.12	709.60	
*324.366	1.77	296.9	*14.148	1042.6	5.04		
LCR 723	LCR 723 PLS1		Normal	NA	*149.188		
1812.74	1972.9	*0.808	6.04	20.04	35.4	1076.20	
*324.366	1.46	1650.75	*14.148	1276.21	7.58		
LCR 724	LCR 724 PLS1		Normal	NA	2280.41		
2208.83	2408.55	6.86	24.73	19.96	19.07	1298.13	
*309.784	0.52	3370.01	95.83	1808.57	5.44		
LCR 725	LCR 725 PLS1		Normal	NA	4069.65		
523.86	2175.85	*0.808	24.22	*2.749	53.44	2492.18	
*324.366	1.59	1552.06	191.17	1339.78	7.57		
LCR 726	LCR 726 PLS1		Normal	NA	1664.26		
902.34	1203.14	*0.792	6.14	*2.747	30.94	1434.77	
*323.745	0.93	2291.3	194.57	344.18	4.3		
LCR 727	LCR 727 PLS1		Normal	NA	1978.16		
998.63	1171.62	*0.792	22.10	*2.747	18.97	1387.76	
*323.745	0.57	1142.45	113.68	107.3	4.95		
LCR 728	LCR 728 PLS1		Normal	NA	*147.076		
3620.65	2039.53	*0.792	25.04	*2.747	31.44	*72.617	
2213.19	0.93	*26.698	208.87	399.32	17.58		
LCR 729	LCR 729 PLS1		Normal	NA	4476.46		
1177.40	792.49	4.92	43.15	17.64	23.33	2384.11	
*323.745	0.77	1888.65	98.61	1559.28	6.54		
LCR 730	LCR 730 PLS1		Normal	NA	*149.188		
827.77	4169.43	*0.808	4.90	*2.749	29.81	*76.613	
*324.366	1.11	1536.37	*14.148	827.96	3.73		
LCR 731	LCR 731 PLS1		Normal	NA	1934.43		
1087.68	1416.34	*0.792	6.50	*2.747	28.81	*72.617	

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*323.745	0.66	837.87	98.61	1107.77	4.24		
LCR 732	LCR 732 PLS1		Normal	NA	1504.93		
754.46	1582.75	*0.792	44.46	*2.747	31.11	1187.68	
*323.745	0.72	1504.4	140.17	727.95	4.81		
LCR 733	LCR 733 PLS1		Normal	NA	7269.66		
911.25	1896.91	5.99	12.37	25.67	21.41	1567.27	
2005.08	1.08	2264.08	159.22	986.29	4.81		
LCR 734	LCR 734 PLS1		Normal	NA	3724.69		
2211.72	2245.16	7.68	7.81	*2.747	26.71	1310.09	
3660.51	1.65	1030.27	194.57	842.62	5.99		
LCR 736	LCR 736 PLS1		Normal	NA	*149.188		
3316.62	1894.09	*0.808	13.31	22.39	29.55	2151.87	
*324.366	1.5	1544.21	246.4	877.02	3.92		
LCR 737	LCR 737 PLS1		Normal	NA	1632.22		
2070.36	3539.81	5.77	23.47	16.87	82.53	1067.66	
3052.15	1.44	921.51	106.34	184.86	6.03		
LCR 738	LCR 738 PLS1		Normal	NA	*149.188		
3378.86	2707.81	*0.808	15.25	*2.749	26.37	2500.62	
*324.366	1.33	2800.51	100.38	429.86	8.64		
LCR 739	LCR 739 PLS1		Normal	NA	*149.188		
1603.71	1784.45	*0.808	11.84	*2.749	24.37	1305.73	
*324.366	1.25	3112.91	167.59	384.17	3.33		
LCR 740	LCR 740 PLS1		Normal	NA	*149.188		
1743.90	2475.45	8.02	17.48	25.44	38.62	1409.10	
*324.366	1.3	2658.1	111.64	*21.339	5.5		
LCR 741	LCR 741 PLS1		Normal	NA	*149.188		
1731.94	736.6	*0.808	13.77	*2.749	57.65	1027.31	
*324.366	1.07	1668.62	167.59	722.09	15		
LCR 742	LCR 742 PLS1		Normal	NA	1430.76		
6005.58	2418.85	6.13	17.30	32.20	19.3	614.90	
3640.15	2.93	6565.33	226.72	4475.33	8.36		
LCR 743	LCR 743 PLS1		Normal	NA	*149.188		
1375.53	6590.95	*0.808	13.49	25.91	49.45	1791.53	
2181.48	1.58	1928.37	183.53	267.48	13.22		
LCR 745	LCR 745 PLS1		Normal	NA	1132.13		
5798.06	1725.78	5.95	25.76	31.40	22.9	744.44	
2637.28	1.03	16244.26	194.57	3957.22	7.51		
LCR 746	LCR 746 PLS1		Normal	NA	2478.16		
3920.45	2963.42	*0.808	5.65	*2.749	32.89	2196.88	
*324.366	1.06	2251.46	111.64	1080.62	4.55		
LCR 747	LCR 747 PLS1		Normal	NA	*147.076		
1458.63	3174.93	*0.792	48.18	*2.747	55.59	4709.15	
*323.745	0.65	3952.85	113.68	339.01	8.49		
LCR 749	LCR 749 PLS1		Normal	NA	2263.67		
1520.51	3359.33	6.28	36.89	19.09	25.82	1062.18	
2005.08	1.15	1742.43	233.4	2091.07	5.77		
LCR 750	LCR 750 PLS1		Normal	NA	931.71		
691.87	2920.23	*0.792	16.39	*2.747	30.82	2956.53	

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*323.745	0.71	229.73	113.68	1236.67	7.27		
LCR 751	LCR 751 PLS1		Normal	NA	3063.8		
2558.47	3621.8	5.95	14.78	*2.747	31.61	1049.13	
2320.19	0.89	2494.38	272.25	923.2	10.86		
LCR 752	LCR 752 PLS1		Normal	NA	1337.48		
886.38	3997.55	4.92	9.26	*2.747	34.28	964.73	
2845.75	1.05	721.83	222.52	296.56	9.2		
LCR 753	LCR 753 PLS1		Normal	NA	3688.83		
3663.09	2715.05	*0.792	8.32	*2.747	23.47	716.84	
*323.745	0.67	1952.93	163.47	743.6	4.94		
LCR 754	LCR 754 PLS1		Normal	NA	1610.91		
1813.08	2515.92	7.85	14.98	*2.747	20.18	648.75	
*323.745	1.09	1331.14	248.24	339.01	3.64		
LCR 755	LCR 755 PLS1		Normal	NA	5218.29		
462.35	2243.61	*0.808	6.98	*2.749	20.84	890.44	
*324.366	1.77	685.06	327.82	846.97	5.76		
LCR 757	LCR 757 PLS1		Normal	NA	*149.188		
3229.62	2384.91	*0.808	7.25	54.07	47.06	1949.90	
*324.366	2.11	378.68	100.38	1011.08	14.75		
LCR 758	LCR 758 PLS1		Normal	NA	*149.188		
605.50	1666.55	*0.808	25.31	52.47	17.06	2627.88	
*324.366	1.32	1133.74	159.22	664.69	4.45		
LCR 759	LCR 759 PLS1		Normal	NA	1934.43		
532.72	4475.32	*0.792	24.67	19.17	40.26	2414.54	
*323.745	1.7	1398.39	113.68	647.75	6.98		
LCR 760	LCR 760 PLS1		Normal	NA	2913.08		
1629.33	1395.25	*0.792	11.08	*2.747	25.31	*72.617	
5030.98	0.79	2222.84	194.57	923.2	6.73		
LCR 761	LCR 761 PLS1		Normal	NA	1275.39		
2853.31	1487.6	*0.792	2.44	*2.747	21.75	1490.00	
6536.67	0.8	2569.06	174.27	622.99	11.15		
LCR 762	LCR 762 PLS1		Normal	NA	*149.188		
2201.52	4344.74	*0.808	12.99	*2.749	46.57	538.33	
*324.366	1.74	2924.54	150.55	854.52	9.41		
LCR 763	LCR 763 PLS1		Normal	NA	*149.188		
819.15	1750.75	*0.808	19.18	*2.749	25.54	*76.613	
*324.366	1.26	3315.54	150.55	1175.07	4.06		
LCR 764	LCR 764 PLS1		Normal	NA	*149.188		
2017.13	4083.3	*0.808	4.64	17.68	27.27	544.37	
*324.366	2.55	2167.68	88.14	1191.61	26.06		
LCR 765	LCR 765 PLS1		Normal	NA	*149.188		
2341.19	2314.23	*0.808	4.43	*2.749	21.87	2,378.9	
*324.366	1.37	1849.13	122.16	1314.5	7.11		
LCR 766	LCR 766 PLS1		Normal	NA	2855.4		
2523.29	2575.06	*0.792	16.64	*2.747	29.59	1045.44	
*323.745	0.62	861.68	194.57	165.1	3.64		
LCR 768	LCR 768 PLS1		Normal	NA	4921.76		
1904.19	4317.5	*0.792	23.35	24.54	36.67	5365.09	

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*323.745	0.71	837.87	174.27	493.17	11.68		
LCR 769	LCR 769 PLS1		Normal	NA	1101.74		
*13.395	2403.18	9.08	18.29	*2.747	29.46	1256.25	
*323.745	0.79	*26.698	231.31	*21.526	6.92		
LCR 770	LCR 770 PLS1		Normal	NA	3239.02		
1177.40	2333.5	7.33	9.34	*2.747	25.77	2092.63	
*323.745	1	1564.25	174.27	465.75	4.74		
LCR 771	LCR 771 PLS1		Normal	NA	1198.17		
1854.71	3805.23	*0.808	27.12	42.60	58.99	1261.97	
*324.366	2.05	3169.51	*14.148	*21.339	21.73		
LCR 772	LCR 772 PLS1		Normal	NA	1248.71		
870.90	2438.66	*0.808	21.28	*2.749	25.31	1682.45	
*324.366	1.55	801.22	*14.148	267.48	8.36		
LCR 773	LCR 773 PLS1		Normal	NA	*149.188		
2338.15	2136.36	*0.808	5.40	21.92	17.63	461.14	
*324.366	1.49	1552.06	141.53	1426.81	8.61		
LCR 774	LCR 774 PLS1		Normal	NA	7072.51		
3031.34	1585.24	*0.808	28.34	*2.749	22.87	*76.613	
*324.366	1.18	3324.72	100.38	183.77	7.28		
LCR 775	LCR 775 PLS1		Normal	NA	*149.188		
1207.94	2898.04	15.03	19.41	36.83	34.25	1041.23	
6975.85	2.61	2190.66	400.85	419.88	6.26		
LCR 776	LCR 776 PLS1		Normal	NA	*149.188		
1196.22	1922.23	*0.808	18.57	*2.749	24.22	1933.93	
*324.366	1.23	2467.97	88.14	714	4.37		
LCR 777	LCR 777 PLS1		Normal	NA	2603.55		
875.75	2411.23	5.26	13.97	16.87	55.48	7377.64	
2845.75	0.86	302.79	239.88	349.32	13.59		
LCR 778	LCR 778 PLS1		Normal	NA	1358.26		
343.70	2360.29	7.33	54.87	27.21	18.61	2054.62	
4255.21	1.14	735.51	213.49	759.14	6.7		
LCR 779	LCR 779 PLS1		Normal	NA	2580.82		
2874.06	1943.64	5.26	72.03	42.03	21.36	1438.70	
3459.38	0.76	1368.91	309.41	680.24	4.26		
LCR 780	LCR 780 PLS1		Normal	NA	2490.17		
1403.05	2774.38	8.03	25.20	20.33	29.03	1426.92	
1997.01	0.91	1463.98	309.41	318.04	4.72		
LCR 781	LCR 781 PLS1		Normal	NA	7604.41		
1711.08	3534.35	4.92	31.44	23.77	36.27	779.22	
*323.745	1.49	1917.42	98.61	930.4	10.83		
LCR 782	LCR 782 PLS1		Normal	NA	*149.188		
5713.11	538.64	*0.808	10.95	47.66	22.96	1083.22	
*324.366	1.26	1706.45	150.55	891.9	5.78		
LCR 783	LCR 783 PLS1		Normal	NA	*149.188		
905.48	2122.25	7	7.68	28.94	27	*76.613	
*324.366	1.32	1571.72	226.72	1014.6	4.31		
LCR 784	LCR 784 PLS1		Normal	NA	*149.188		
2047.29	1353.05	*0.808	12.67	*2.749	19.74	5,714.9	

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*324.366	0.85	1353.91	88.14	587.81	6.99		
LCR 785	LCR 785 PLS1		Normal	NA	*149.188		
1681.18	1604.86	*0.808	19.87	*2.749	19.68	2530.19	
*324.366	1.98	1832.95	*14.148	846.97	4.85		
LCR 786	LCR 786 PLS1		Normal	NA	*149.188		
1544.25	2915.1	*0.808	18.47	*2.749	36.91	2921.34	
*324.366	1.04	1700.47	*14.148	547.83	6.29		
LCR 812	LCR 812 PLS1		Pancreas	II	1110.21		
1700.18	5671.74	5.46	8.28	829.35	11.29	5,550.7	
6146.18	1.01	3291.27	281.53	607.1	5.61		
LCR 814	LCR 814 PLS1		Pancreas	II	1695.51		
2356.29	3139.22	4.83	34.86	25.57	68.72	2,620.2	
*313.835	1.15	3205.65	162.22	254.37	9.26		
NL 918	NL PLS 918		Normal	NA	*126.474		
3001.22	7204.71	*0.817	36.52	*2.624	51.7	1,693.7	
*315.949	0.88	1717.8	105.8	562.54	3.14		
NL 919	NL PLS 919		Normal	NA	867.44		
2604.27	6107.1	*0.817	36.17	*2.624	30.99	1587.54	
2904.45	0.78	1468.98	181.6	213.92	2.64		
NL 920	NL PLS 920		Normal	NA	*140.254		
1828.03	9739.63	*0.835	9.03	*2.794	19.26	1362.41	
*328.815	0.6	2330.16	112.47	*74.45	2.78		
NL 921	NL PLS 921		Normal	NA	*140.254		
1511.74	4974.1	*0.835	21.19	*2.794	37.45	1244.08	
*328.815	0.61	1664.24	112.47	*74.45	2.58		
NL 922	NL PLS 922		Normal	NA	*140.254		
1847.75	1295.64	*0.835	6.91	*2.794	28.59	2,132.4	
*328.815	0.63	1977.85	98.38	*74.45	2.31		
NL 923	NL PLS 923		Normal	NA	*140.254		
1476.04	2910.31	10.7	37.38	*2.794	34.48	2,482.6	
*328.815	0.54	1879.02	171.2	471.48	5.34		
NL 924	NL PLS 924		Normal	NA	*140.254		
528.47	5535.97	*0.835	5.51	21.29	31.61	1946.49	
*328.815	0.57	1588.46	125.04	275.97	5.49		
NL 925	NL PLS 925		Normal	NA	*140.254		
812.48	5128.61	*0.835	13.47	*2.794	47.09	1,818.4	
*328.815	0.62	2420.97	136.53	223.36	5.05		
NL 930	NL PLS 930		Normal	NA	*132.958		
1507.42	4137.04	*0.824	21.88	54.56	23.1	1428.04	
*327.347	0.57	1089.27	136.7	372.71	4.45		
NL 931	NL PLS 931		Normal	NA	*132.958		
1327.46	1647.12	*0.824	30.68	*2.717	22.07	2249.87	
*327.347	1.06	2969.01	*15.284	739.46	3.11		
NL 932	NL PLS 932		Normal	NA	*132.958		
1081.60	3238.93	*0.824	20.31	*2.717	25.45	1870.61	
*327.347	0.55	1363.58	181.13	591.45	6.11		
NL 938	NL PLS 938		Normal	NA	1820.88		
1281.05	1395.62	*0.797	24.71	*2.636	12.94	*71.888	

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*320.985	0.67	1766.41	93.06	1027.02	3.04		
NL 939	NL PLS 939		Normal	NA	2796.31		
1146.13	215.18	*0.797	20.75	*2.636	7.92	1,542.0	
*320.985	0.65	764.72	141.28	350.47	3.74		
NL 940	NL PLS 940		Normal	NA	1820.88		
2588.22	3476.35	*0.797	8.77	*2.636	16.63	1734.11	
*320.985	0.51	2083.46	101.92	1032.47	0.36		
NL 941	NL PLS 941		Normal	NA	*131.746		
666.79	2387.31	*0.797	4.67	*2.636	14.75	1890.62	
*320.985	0.61	1585.67	*13.953	1908.72	4.83		
NL 942	NL PLS 942		Normal	NA	2520.63		
271.12	930.22	10.48	14.53	24.73	*1.372	774.99	
5600.29	0.66	1209.79	367.15	*75.36	2.27		
NL 943	NL PLS 943		Normal	NA	*131.746		
2281.85	3175.39	*0.797	7.27	*2.636	11.5	1078.59	
*320.985	0.61	2388.42	*13.953	*75.36	6.96		
NL 944	NL PLS 944		Normal	NA	*132.958		
2619.80	4199.71	6.13	45.70	*2.717	33.59	2,731.4	
2043	0.73	3285.13	204.69	1240.67	5.2		
NL 945	NL PLS 945		Normal	NA	*132.958		
680.96	2011.04	*0.824	8.47	*2.717	18.01	2543.45	
*327.347	0.88	3651.78	167.9	942.01	6.16		
NL 946	NL PLS 946		Normal	NA	*132.958		
1512.16	4113.2	*0.824	17.67	*2.717	35.46	1,276.7	
*327.347	0.58	3048.96	167.9	703.63	3.92		
NL 947	NL PLS 947		Normal	NA	*132.958		
1735.05	1777.13	11.89	20.65	19.41	35.65	2826.23	
*327.347	0.58	1903.26	210.11	652.22	7.16		
NL 948	NL PLS 948		Normal	NA	*132.958		
2039.04	3296.72	*0.824	11.58	*2.717	26.41	1,165.2	
*327.347	0.52	1862.61	*15.284	344.42	3.23		
NL 949	NL PLS 949		Normal	NA	*132.958		
1982.00	2169.04	*0.824	16.77	*2.717	21.95	944.1	
*327.347	0.61	1275.94	91.71	372.71	3.05		
NL 950	NL PLS 950		Normal	NA	1186.44		
1336.92	2727.96	*0.824	21.38	*2.717	22.62	1,520.2	
*327.347	0.55	1696.32	136.7	159.19	2.73		
NL 951	NL PLS 951		Normal	NA	*132.958		
1341.66	1951.53	*0.824	4.56	*2.717	20.95	1257.98	
*327.347	0.6	2021.09	153.27	511.8	4.76		
NL 952	NL PLS 952		Normal	NA	*132.958		
2105.60	2511.86	*0.824	40.50	*2.717	19.99	670.68	
*327.347	0.5	3001.91	117.07	519.98	6.4		
NL 964	NL PLS 964		Normal	NA	*157.823		
762.50	507.22	*0.803	12.17	*2.715	13.55	754.11	
*312.793	0.71	1201.22	226.7	843.87	2.84		
NL 965	NL PLS 965		Normal	NA	1329.61		
840.27	1618.33	*0.803	18.89	*2.715	8.18	3641.94	

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*312.793	0.71	911.4	*14.785	510.48	2.6		
NL 1160	NL PLSA 1160		Normal	NA	1156		
2703.73	2305.41	*0.82	3.75	*2.74	15.72	2019.48	
*327.917	0.71	1475.33	*14.319	513.79	2.54		
NL 1163	NL PLSA 1163		Normal	NA	*132.09		
1834.31	3107.95	*0.82	11.15	*2.74	22.96	1,722.9	
*327.917	0.68	1121.94	*14.319	220.58	2.8		
NL 1164	NL PLSA 1164		Normal	NA	*132.09		
498.26	2014.03	*0.82	16.50	*2.74	17.8	1303.51	
*327.917	0.67	1559.92	149.48	373.27	5.3		
NL 1165	NL PLSA 1165		Normal	NA	*132.09		
1292.54	3363.21	5.55	8.53	*2.74	18.42	1192.70	
*327.917	0.79	1077	126.63	305.85	4.87		
NL 1166	NL PLSA 1166		Normal	NA	*147.076		
1057.92	2931.05	*0.792	11.67	*2.747	19.12	582.00	
*323.745	0.54	2015.34	98.61	1275.35	6.13		
NL 1167	NL PLSA 1167		Normal	NA	2198.77		
1325.59	1363.62	*0.792	10.11	16.87	20.92	906.85	
*323.745	0.46	2350.95	152.14	423.47	3.25		
NL 1168	NL PLSA 1168		Normal	NA	2740.52		
5080.71	1535.16	*0.792	17.83	*2.747	21.46	1,180.1	
*323.745	0.35	2145.72	127.42	1239.91	3.86		
NL 1169	NL PLSA 1169		Normal	NA	1696.38		
870.45	1566.88	6.29	13.43	*2.747	19.63	549.2	
*323.745	0.35	1566.4	140.17	484.09	3.2		
NL 1170	NL PLSA 1170		Normal	NA	911.97		
2989.92	2036.87	*0.792	11.28	16.87	26.89	2079.94	
*323.745	0.58	2114.12	194.57	1447.55	5.01		
NL 1171	NL PLSA 1171		Normal	NA	*147.076		
1439.15	1847.89	*0.792	20.38	16.87	54.87	786.21	
*323.745	0.75	1060.73	152.14	409.04	3.19		
NL 1172	NL PLSA 1172		Normal	NA	*147.076		
4443.66	1813.35	6.64	8.61	*2.747	25.09	1,233.3	
*323.745	1.05	*26.698	127.42	930.4	0.89		
NL 1173	NL PLSA 1173		Normal	NA	*147.076		
1531.17	3090.82	*0.792	4.24	*2.747	17.03	878.16	
*323.745	0.82	1026.22	127.42	418.68	4.09		
NL 1174	NL PLSA 1174		Normal	NA	*147.076		
1708.26	1500.81	*0.792	14.19	*2.747	18.14	1180.10	
*323.745	0.57	1672.01	152.14	484.09	3.76		
NL 1175	NL PLSA 1175		Normal	NA	*147.076		
1036.32	3202.09	*0.792	10.18	*2.747	25.27	1,747.5	
*323.745	0.43	1419.5	127.42	812.62	2.33		
NL 1176	NL PLSA 1176		Normal	NA	*147.076		
2365.57	1079.83	*0.792	5.87	*2.747	23.37	1521.74	
*323.745	0.59	1339.52	140.17	743.6	5.76		
NL 1177	NL PLSA 1177		Normal	NA	*147.076		
865.14	839.38	*0.792	8.14	*2.747	25.13	1356.59	

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*323.745	0.53	1502.27	184.61	1313.61	5.84		
NL 1178	NL PLSA 1178		Normal	NA	*147.076		
609.25	2804.06	*0.792	11.80	*2.747	21.27	1,650.0	
*323.745	0.49	1466.11	140.17	951.87	2.77		
NL 1179	NL PLSA 1179		Normal	NA	2490.17		
2467.69	2111.56	*0.792	29.15	*2.747	28.68	1164.99	
*323.745	0.5	1506.53	213.49	502.19	4.16		
NL 1180	NL PLSA 1180		Normal	NA	*147.076		
568.31	4160.08	*0.792	6.71	*2.747	30.48	1290.81	
*323.745	0.72	1986.32	174.27	905.12	4.6		
NL 1181	NL PLSA 1181		Normal	NA	*147.076		
1196.52	1778.84	*0.792	4.72	*2.747	32.65	5,319.1	
*323.745	0.45	1615.84	*14.348	307.37	3.71		
NL 1182	NL PLSA 1182		Normal	NA	*147.076		
1620.89	2143.59	*0.792	16.92	*2.747	20.48	993.94	
*323.745	0.95	798.35	140.17	1435.28	2.5		
NL 1183	NL PLSA 1183		Normal	NA	*147.076		
1756.35	1962.27	4.92	5.72	*2.747	27.55	1796.59	
*323.745	0.53	2410.89	174.27	474.95	3.96		
NL 1184	NL PLSA 1184		Normal	NA	2108.4		
1624.93	2087.48	*0.797	8.86	*2.636	16.28	1288.80	
*320.985	0.6	2671.94	148.44	458.54	2.67		
NL 1185	NL PLSA 1185		Normal	NA	1049.45		
1921.46	1246.47	*0.797	18.78	*2.636	15.17	1139.44	
*320.985	0.78	1574.04	118.51	2455.19	4.34		
NL 1186	NL PLSA 1186		Normal	NA	2542.11		
720.83	1280.39	*0.797	13.36	*2.636	11.2	1377.90	
*320.985	0.77	2192.72	83.72	885.23	5.01		
NL 1187	NL PLSA 1187		Normal	NA	938.03		
653.27	2419.08	*0.797	2.70	*2.636	11.9	1062.12	
*320.985	0.67	1388.52	93.06	491.56	2.35		
NL 1188	NL PLSA 1188		Normal	NA	*131.746		
693.81	368.76	8.65	3.63	*2.636	6.95	1323.14	
*320.985	0.72	8995.68	175.42	1122.87	2.91		
NL 1189	NL PLSA 1189		Normal	NA	1187.44		
1442.91	2692.32	*0.797	17.57	*2.636	14.05	2876.84	
*320.985	0.7	3698.47	133.92	591.62	3.32		
NL 1190	NL PLSA 1190		Normal	NA	6007.15		
1031.42	3866.16	*0.797	13.87	*2.636	11.2	1,444.8	
*320.985	0.72	1983.34	*13.953	*75.36	2.86		
NL 1191	NL PLSA 1191		Normal	NA	1083.51		
1496.85	2550.98	*0.797	14.70	*2.636	15.6	*71.888	
*320.985	0.56	1731.35	118.51	350.47	3.54		
NL 1192	NL PLSA 1192		Normal	NA	943.52		
666.79	1884.11	*0.797	7.55	*2.636	10.57	529.46	
*320.985	0.64	1898.17	162.23	458.54	6.56		
NL 1193	NL PLSA 1193		Normal	NA	1551.35		
1409.19	791.31	*0.797	9.04	*2.636	8.9	824.15	

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*320.985	0.62	1072.11	162.23	*75.36	3.72		
NL 1194	NL PLSA 1194		Normal	NA	4548.56		
1692.34	1066.68	*0.797	12.97	*2.636	13.7	3454.35	
*320.985	0.63	1183.93	*13.953	775.11	3.48		
NL 1195	NL PLSA 1195		Normal	NA	2218.22		
2035.99	2442.97	6.19	27.55	*2.636	13.86	3719.63	
*320.985	0.77	3042.25	83.72	244.16	5.04		
NL 1196	NL PLSA 1196		Normal	NA	862.07		
1817.02	3314.54	*0.797	5.38	*2.636	16.77	*71.888	
*320.985	0.62	1842.48	93.06	723.4	6.75		
NL 1197	NL PLSA 1197		Normal	NA	1926.54		
504.57	3064.56	8.87	13.19	*2.636	11.9	2321.80	
*320.985	0.72	1434.8	110.38	*75.36	3.93		
NL 1198	NL PLSA 1198		Normal	NA	1939.86		
673.54	1863.22	*0.797	14.48	*2.636	9.88	*71.888	
*320.985	0.59	1745.95	*13.953	1158.97	2.93		
NL 1199	NL PLSA 1199		Normal	NA	830.05		
1631.68	1560.13	*0.797	5.99	*2.636	7.72	553.40	
*320.985	0.75	986.38	93.06	*75.36	2.26		
NL 1200	NL PLSA 1200		Normal	NA	*131.746		
2002.31	1947.04	*0.797	5.10	*2.636	9.62	2037.41	
*320.985	0.97	2552.3	101.92	775.11	2.71		
NL 1201	NL PLSA 1201		Normal	NA	1906.61		
2362.66	1893.62	*0.797	4.67	*2.636	22.39	498.67	
*320.985	0.73	1854.2	*13.953	627.72	2.96		
NL 1202	NL PLSA 1202		Normal	NA	1187.44		
1031.42	1829.11	*0.797	5.98	*2.636	*1.372	1178.52	
*320.985	0.65	1221.29	83.72	458.54	3.61		
NL 1203	NL PLSA 1203		Normal	NA	3746.81		
254.19	1431.93	5.97	27.42	16.07	12.33	741.72	
*320.985	0.59	1218.41	110.38	723.4	2.45		
NL 1204	NL PLSA 1204		Normal	NA	2259.79		
1742.89	1776.26	*0.797	20.13	*2.636	14.48	1372.12	
*320.985	0.64	2972.72	83.72	591.62	2.27		
NL 1205	NL PLSA 1205		Normal	NA	*131.746		
1496.85	1472.04	*0.797	6.71	*2.636	9.17	1,661.5	
2488	0.6	977.82	148.44	379.01	3.32		
NL 1206	NL PLSA 1206		Normal	NA	1293.86		
599.21	2991.82	*0.797	24.10	*2.636	10.69	1288.80	
*320.985	0.5	2433.04	133.92	458.54	3.22		
NL 1207	NL PLSA 1207		Normal	NA	*131.746		
741.10	2623.48	4.89	19.88	*2.636	15.63	948.29	
*320.985	0.46	1112.2	148.44	310.33	4.27		
NL 1208	NL PLSA 1208		Normal	NA	*131.746		
909.92	1538.03	*0.797	16.77	*2.636	12.98	648.67	
*320.985	0.55	1524.66	83.72	255.81	0.94		
NL 1209	NL PLSA 1209		Normal	NA	2442.28		
734.35	1298.3	*0.797	14.38	*2.636	13.44	811.15	

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*320.985	0.61	1452.18	*13.953	244.16	3.07		
NL 1210	NL PLSA 1210		Normal	NA	*131.746		
1847.34	3912.24	*0.797	6.55	*2.636	13.34	1,100.6	
*320.985	0.68	1915.78	*13.953	676.47	5.36		
NL 1211	NL PLSA 1211		Normal	NA	1729.76		
1065.16	3232.16	*0.797	36.32	17.59	10.45	762.16	
*320.985	0.89	2039.26	*13.953	*75.36	3.83		
NL 1212	NL PLSA 1212		Normal	NA	2238.98		
855.91	1874.61	*0.797	5.44	*2.636	7.17	570.27	
*320.985	0.47	1813.2	*13.953	*75.36	3.5		
NL 1213	NL PLSA 1213		Normal	NA	*131.746		
795.13	2070.08	*0.797	10.52	*2.636	14.11	832.0	
*320.985	0.65	1186.8	83.72	1107.21	5.04		
NL 1214	NL PLSA 1214		Normal	NA	889		
2177.45	1495.82	*0.797	17.30	*2.636	15.54	2312.08	
*320.985	0.56	1839.55	*13.953	743.02	5.66		
NL 1215	NL PLSA 1215		Normal	NA	*131.746		
430.18	500.32	*0.797	6.69	*2.636	*1.372	706.22	
2283.48	0.73	1072.11	200.36	350.47	3.8		
NL 1216	NL PLSA 1216		Normal	NA	*131.746		
687.06	1619.3	*0.797	2.78	*2.636	12.61	2,138.7	
*320.985	0.58	1492.75	148.44	641.85	4.56		
NL 1217	NL PLSA 1217		Normal	NA	*131.746		
1968.62	3179.59	*0.797	10.02	*2.636	12.67	921.6	
*320.985	0.6	1959.83	*13.953	648.85	3.69		
NL 1218	NL PLSA 1218		Normal	NA	1032.52		
1813.65	511.47	*0.797	33.06	*2.636	14.36	2221.81	
*320.985	0.53	1783.95	93.06	1496.7	3.51		
NL 1219	NL PLSA 1219		Normal	NA	3385.48		
1088.78	4256.2	5.1	7.50	*2.636	13.44	764.7	
*320.985	1.36	3723.11	*13.953	2444.93	3.96		
NL 1220	NL PLSA 1220		Normal	NA	2855.32		
1142.76	2023.78	*0.797	4.77	*2.636	12.81	980.54	
*320.985	0.48	1865.92	*13.953	*75.36	5.81		
NL 1221	NL PLSA 1221		Normal	NA	*131.746		
1267.56	967.97	*0.797	12.75	*2.636	10.37	916.26	
*320.985	0.65	2936.5	*13.953	330.73	3.45		
NL 1222	NL PLSA 1222		Normal	NA	*133.814		
239.05	834.98	5.77	13.81	*2.745	10.39	655.04	
2573.12	0.74	1362.87	243.51	548.95	3.06		
NL 1223	NL PLSA 1223		Normal	NA	*133.814		
1485.55	2541.95	*0.83	5.04	*2.745	18.88	1028.88	
*328.934	0.71	1668.16	84.68	873.8	3.95		
NL 1224	NL PLSA 1224		Normal	NA	*133.814		
2008.83	956.88	*0.83	27.53	*2.745	18.03	811.69	
*328.934	0.65	987.14	150.94	463.08	6.1		
NL 1225	NL PLSA 1225		Normal	NA	*133.814		
518.99	346.47	6.84	7.90	*2.745	10.33	587.67	

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2124.39	0.63	864.15	218.53	406.53	2.12		
NL 1226	NL PLSA 1226		Normal	NA	*131.746		
1267.56	2058.49	5.32	20.63	*2.636	15.6	769.86	
*320.985	0.49	1510.15	*13.953	662.74	6.68		
NL 1227	NL PLSA 1227		Normal	NA	*131.746		
2002.31	2814.64	*0.797	11.43	*2.636	15.66	1918.54	
*320.985	0.85	618.02	141.28	289.19	4.9		
NL 1228	NL PLSA 1228		Normal	NA	*131.746		
1742.89	1096.37	*0.797	5.17	*2.636	15.02	1477.04	
*320.985	0.68	1376.96	83.72	523.43	2.2		
NL 1229	NL PLSA 1229		Normal	NA	*131.746		
1274.31	1470.21	5.1	7.05	*2.636	*1.372	913.60	
*320.985	0.71	1457.97	148.44	1054.11	2.59		
NL 1230	NL PLSA 1230		Normal	NA	*131.746		
1409.19	4055.66	4.89	5.80	*2.636	15.6	1,268.9	
*320.985	0.73	1684.67	235	406.44	4.9		
NL 1231	NL PLSA 1231		Normal	NA	*131.746		
1840.60	2186.61	*0.797	9.22	*2.636	10.29	1195.35	
*320.985	0.69	1000.65	93.06	491.56	4.52		
NL 1232	NL PLSA 1232		Normal	NA	*131.746		
805.26	2716.7	*0.797	7.71	*2.636	10.29	2062.63	
*320.985	0.64	1731.35	*13.953	775.11	5.46		
NL 1233	NL PLSA 1233		Normal	NA	960.04		
423.41	1314.44	*0.797	8.95	*2.636	*1.372	1530.11	
*320.985	0.58	1608.93	118.51	1401.44	2.86		
NL 1234	NL PLSA 1234		Normal	NA	*131.746		
3062.75	262.53	*0.797	11.00	*2.636	14.75	932.2	
*320.985	0.57	1195.42	*13.953	569.38	4.3		
NL 1235	NL PLSA 1235		Normal	NA	1246.26		
1479.99	2907.08	*0.797	12.14	*2.636	14.29	2,183.4	
*320.985	0.54	1469.56	83.72	867.41	3.68		
NL 1236	NL PLSA 1236		Normal	NA	*131.746		
896.42	2044.98	*0.797	4.19	*2.636	9.44	1,172.9	
*320.985	0.48	1014.93	110.38	340.67	2.44		
NL 1237	NL PLSA 1237		Normal	NA	*131.746		
494.43	1634.14	*0.797	3.45	*2.636	11.08	929.57	
*320.985	0.65	1842.48	101.92	*75.36	3.9		
NL 1238	NL PLSA 1238		Normal	NA	6559.32		
1381.41	4319.23	*0.83	25.35	17.59	23.91	1303.10	
*328.934	0.71	2038.23	98.45	296.89	3.46		
NL 1239	NL PLSA 1239		Normal	NA	*133.814		
455.65	2856.7	*0.83	19.86	*2.745	15.46	1222.02	
*328.934	0.65	1374.4	110.68	620.4	3.59		
NL 1240	NL PLSA 1240		Normal	NA	1617.53		
1251.50	1922.53	*0.83	15.87	*2.745	15.8	*74.812	
*328.934	0.83	1293.85	110.68	878.24	3.1		
NL 1241	NL PLSA 1241		Normal	NA	*133.814		
819.04	4202.93	*0.83	43.72	*2.745	21.26	1569.50	

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*328.934	0.69	2302.78	*14.113	689.1	4.33		
NL 1242	NL PLSA 1242		Normal	NA	4580.53		
493.63	769.42	*0.83	8.91	*2.745	17.46	551.85	
*328.934	0.68	1270.91	121.83	674.59	2.82		
NL 1243	NL PLSA 1243		Normal	NA	*133.814		
1345.65	2487.95	*0.83	9.94	*2.745	11.15	541.67	
*328.934	0.58	1612.53	167.92	693.92	3.04		
NL 1244	NL PLSA 1244		Normal	NA	*133.814		
4050.72	4492.93	*0.83	13.24	*2.745	17.22	*74.812	
*328.934	0.95	1907.18	*14.113	774.1	3.04		
NL 1245	NL PLSA 1245		Normal	NA	*133.814		
2136.94	1456.73	*0.83	5.81	*2.745	17.11	825.2	
*328.934	0.73	1437.96	84.68	559.34	3.5		
NL 1246	NL PLSA 1246		Normal	NA	*133.814		
137.04	109.44	6.84	10.15	*2.745	8.9	670.74	
2349.40	0.64	418.28	198.16	185.72	4.25		
NL 1247	NL PLSA 1247		Normal	NA	*133.814		
1514.87	4386.63	6.04	22.80	*2.745	15.93	1037.28	
*328.934	0.76	1709.26	84.68	1103.62	2.44		
NL 1248	NL PLSA 1248		Normal	NA	*133.814		
1287.19	3297.8	*0.83	5.83	*2.745	22.04	750.0	
*328.934	0.83	1583.31	*14.113	1012.2	5.03		
NL 1249	NL PLSA 1249		Normal	NA	*131.746		
1523.82	1549.07	*0.797	3.80	*2.636	9.79	452.02	
*320.985	0.85	1106.47	*13.953	613.41	5.13		
NL 1250	NL PLSA 1250		Normal	NA	1608.13		
1692.34	1161.37	10.25	11.68	*2.636	19.47	2106.94	
*320.985	0.63	2927.45	126.34	627.72	3.75		
NL 1251	NL PLSA 1251		Normal	NA	4565.36		
3140.14	937.07	7.74	20.79	16.07	12.19	782.72	
*320.985	0.58	2942.54	141.28	330.73	2.93		
NL 1252	NL PLSA 1252		Normal	NA	*131.746		
1274.31	2176.86	5.21	5.92	*2.636	9.92	1139.44	
*320.985	0.59	1527.56	155.41	546.66	2.6		
NL 1253	NL PLSA 1253		Normal	NA	*131.746		
663.41	653.72	*0.797	10.44	*2.636	*1.372	579.96	
3208.81	0.76	795.86	235	569.38	2.64		
NL 1254	NL PLSA 1254		Normal	NA	2301.56		
866.04	704.74	5.1	17.80	*2.636	12.54	1328.89	
*320.985	0.56	1140.87	93.06	*75.36	3.88		
NL 1255	NL PLSA 1255		Normal	NA	798.94		
1131.04	NA	20.25	5.11	18.60	NA	*71.628	
*322.249	0.67	1024.11	83.39	534.89	3.89		
NL 1256	NL PLSA 1256		Normal	NA	*133.157		
320.93	NA	*0.803	8.10	*2.713	NA	442.27	
*322.249	0.62	1553.5	87.56	523.64	8.2		
NL 1257	NL PLSA 1257		Normal	NA	*133.157		
2931.23	NA	11.54	9.95	*2.713	NA	521.24	

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*322.249	0.62	1172.89	*13.899	267.83	1.94		
NL 1258	NL PLSA 1258		Normal	NA	*133.157		
3199.54	NA	*0.803	6.16	21.26	NA	*71.628	
*322.249	0.52	1052.11	91.61	756.76	4.55		
NL 1259	NL PLSA 1259		Normal	NA	*133.157		
1527.60	NA	*0.803	8.54	*2.713	NA	1276.52	
*322.249	0.58	1002.16	99.4	398.26	8.74		
NL 1260	NL PLSA 1260		Normal	NA	*133.157		
1313.48	NA	*0.803	4.51	*2.713	NA	899.38	
*322.249	0.67	1445.25	*13.899	640.06	6.27		
NL 1291	NL PLSA 1291		Normal	NA	*127.973		
1148.45	669.1	*0.805	28.41	*2.369	16.47	781.59	
*322.135	0.89	757.07	164.29	869.3	4.17		
NL 1292	NL PLSA 1292		Normal	NA	*127.973		
1091.92	1624.24	*0.805	16.31	*2.369	15.95	893.91	
*322.135	0.61	1710.47	121.5	414.21	3.46		
NL 1293	NL PLSA 1293		Normal	NA	*127.973		
807.71	1173.66	10.81	3.84	*2.369	16.47	1091.44	
*322.135	0.64	1391.7	237.61	212.09	4.93		
NL 1294	NL PLSA 1294		Normal	NA	939.65		
1555.73	1993.82	7.16	27.18	*2.369	17.37	*75.427	
*322.135	0.75	1476.01	224.92	119.92	6.7		
NL 1295	NL PLSA 1295		Normal	NA	*133.814		
819.04	999.57	*0.83	6.91	*2.745	10.33	808.99	
*328.934	0.59	1091.47	150.94	1168.48	2.6		
NL 1296	NL PLSA 1296		Normal	NA	*133.814		
2242.20	1085.1	*0.83	3.52	*2.745	17.88	*74.812	
*328.934	0.64	557.19	104.72	371.26	2.97		
NL 1297	NL PLSA 1297		Normal	NA	*133.814		
1102.54	395.42	*0.83	4.33	*2.745	14.58	*74.812	
*328.934	0.59	989.95	*14.113	296.89	3.88		
NL 1298	NL PLSA 1298		Normal	NA	*133.814		
1635.58	2718.22	*0.83	7.53	*2.745	17.99	*74.812	
*328.934	0.68	1374.4	141.81	829	4.51		
NL 1299	NL PLSA 1299		Normal	NA	*133.814		
1121.94	2242.48	5.77	9.13	*2.745	14.21	950.98	
*328.934	0.61	1208	159.62	986.77	3.61		
NL 1300	NL PLSA 1300		Normal	NA	*133.814		
569.81	1962.18	10.07	12.10	23.67	18.48	782.11	
*328.934	0.58	1111.3	183.56	698.72	2.62		
NL 1301	NL PLSA 1301		Normal	NA	*133.814		
1769.59	2858.71	*0.83	15.10	*2.745	17.73	*74.812	
*328.934	0.6	797.6	110.68	635.33	0.25		
NL 1302	NL PLSA 1302		Normal	NA	3161.55		
925.10	1137.7	*0.83	5.83	*2.745	16.01	665.50	
*328.934	0.67	880.85	167.92	645.22	1.74		
NL 1303	NL PLSA 1303		Normal	NA	925.88		
557.09	951.06	*0.83	19.36	*2.745	16.55	739.38	

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*328.934	0.68	3049.46	98.45	334.79	2.33		
NL 1304	NL PLSA 1304		Normal	NA	*133.814		
364.20	1517.68	*0.83	23.27	*2.745	10.86	*74.812	
*328.934	0.69	2122.06	183.56	527.94	4.75		
NL 1305	NL PLSA 1305		Normal	NA	*133.814		
6012.14	1999.88	*0.83	20.48	32.36	19.91	1721.15	
*328.934	0.62	2164.09	98.45	277.3	2.87		
NL 1306	NL PLSA 1306		Normal	NA	*133.814		
430.37	1661.49	6.3	6.11	*2.745	12.25	647.2	
*328.934	0.6	1732.79	132.15	468.61	3.69		
NL 1307	NL PLSA 1307		Normal	NA	*133.814		
2674.36	2282.33	6.3	5.57	*2.745	14.03	458.8	
*328.934	0.64	2152.07	110.68	615.39	3.65		
NL 1308	NL PLSA 1308		Normal	NA	*133.814		
1329.41	2354.13	*0.83	9.86	*2.745	15.93	1,545.5	
*328.934	0.68	3512.15	84.68	*20.74	2.43		
NL 1309	NL PLSA 1309		Normal	NA	*133.814		
1257.99	1553.1	*0.83	6.78	18.70	15.03	508.79	
*328.934	0.65	1618.37	98.45	283.88	3.5		
NL 1310	NL PLSA 1310		Normal	NA	*133.814		
3570.40	982.1	5.24	4.28	*2.745	15.72	*74.812	
2721.62	1	2549.09	211.92	5090.66	3.06		
NL 1311	NL PLSA 1311		Normal	NA	*133.814		
1661.71	3374.57	4.98	4.46	*2.745	11.43	1482.72	
*328.934	0.79	3844.34	141.81	579.94	2.63		
NL 1312	NL PLSA 1312		Normal	NA	*133.814		
1576.83	1689.12	5.24	7.68	*2.745	20.32	*74.812	
*328.934	0.57	1513.39	110.68	659.96	3.58		
NL 1313	NL PLSA 1313		Normal	NA	*133.814		
2992.19	2101.18	*0.83	13.65	*2.745	10.92	471.22	
*328.934	1.11	1472.74	198.16	574.82	4.13		
NL 1314	NL PLSA 1314		Normal	NA	*133.814		
411.44	1600.37	5.24	9.87	*2.745	18.48	928.90	
*328.934	0.79	*28.66	159.62	334.79	2.5		
NL 1315	NL PLSA 1315		Normal	NA	*133.814		
1423.69	1833.4	*0.83	18.63	*2.745	14.98	*74.812	
*328.934	0.57	864.15	98.45	564.52	6.98		
NL 1316	NL PLSA 1316		Normal	NA	*133.814		
9079.93	1663.46	*0.83	7.78	*2.745	12.46	639.40	
*328.934	0.58	2748.64	121.83	517.33	*0.004		
NL 1317	NL PLSA 1317		Normal	NA	*133.814		
480.96	2206.63	5.77	3.90	*2.745	15.5	582.53	
*328.934	0.71	1316.82	84.68	640.29	1.93		
NL 1318	NL PLSA 1318		Normal	NA	1380.96		
1063.76	2300.28	*0.83	10.35	*2.745	9.7	686.49	
*328.934	0.58	1600.84	*14.113	590.15	2.37		
NL 1319	NL PLSA 1319		Normal	NA	*133.814		
1012.11	1574.76	*0.83	24.78	*2.745	15.29	556.95	

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*328.934	0.65	1709.26	159.62	689.1	4.29		
NL 1320	NL PLSA 1320		Normal	NA	*133.814		
684.56	642.66	*0.83	6.29	*2.745	10.08	702.29	
*328.934	0.73	1762.24	171.94	559.34	4.62		
NL 1321	NL PLSA 1321		Normal	NA	*133.814		
1782.68	1215.76	*0.83	4.27	*2.745	16.38	731.41	
*328.934	0.7	1898.28	121.83	429.46	5.03		
NL 1322	NL PLSA 1322		Normal	NA	*133.814		
909.01	2051.51	*0.83	8.55	*2.745	14.49	*74.812	
*328.934	0.58	903.15	110.68	429.46	5.18		
NL 1323	NL PLSA 1323		Normal	NA	*133.814		
960.52	1184.51	5.77	17.50	17.59	14.62	697.0	
*328.934	0.67	736.94	183.56	703.51	4.28		
NL 1324	NL PLSA 1324		Normal	NA	*133.814		
774.14	1446.91	*0.83	10.30	*2.745	9.83	*74.812	
*328.934	0.86	1562.89	183.56	640.29	4.17		
NL 1325	NL PLSA 1325		Normal	NA	*133.814		
1021.79	440.77	*0.83	6.88	*2.745	6.8	*74.812	
3894	0.72	864.15	211.92	322.33	4.08		
NL 1326	NL PLSA 1326		Normal	NA	*133.814		
1989.13	2234.51	7.24	10.85	*2.745	20.05	1,690.6	
*328.934	0.62	981.52	190.98	708.29	7.38		
NL 1327	NL PLSA 1327		Normal	NA	*133.814		
1426.95	3025.62	5.24	9.30	*2.745	14.4	*74.812	
*328.934	0.64	2116.06	218.53	463.08	5.41		
NL 1328	NL PLSA 1328		Normal	NA	868.85		
1123.64	2814.03	*0.83	13.05	*2.72	23.08	904.2	
*334.715	0.96	891.87	*14.229	340.04	6.47		
NL 1329	NL PLSA 1329		Normal	NA	1105.39		
1595.10	1527.06	*0.83	6.39	*2.72	17.62	490.87	
*334.715	0.84	1540.42	*14.229	264.56	3.01		
NL 1330	NL PLSA 1330		Normal	NA	*139.248		
543.66	2457.33	*0.83	19.68	*2.72	11.02	1,325.6	
*334.715	0.69	1254.56	*14.229	*76.98	2.74		
NL 1331	NL PLSA 1331		Normal	NA	1961.52		
1055.16	2847.87	*0.83	7.45	*2.72	9.87	1876.89	
*334.715	1.07	653.06	136.77	*76.98	4.96		
NL 1332	NL PLSA 1332		Normal	NA	1387.15		
802.46	2911.65	*0.83	21.31	*2.72	19.33	1308.48	
*334.715	1.06	1436.53	127.8	450.18	5.25		
NL 1333	NL PLSA 1333		Normal	NA	*139.248		
995.35	1757.05	*0.83	17.84	*2.72	14.53	1487.04	
*334.715	0.64	1824.74	*14.229	365.71	2.7		
NL 1334	NL PLSA 1334		Normal	NA	*139.248		
5597.97	2431.68	*0.83	5.04	51.33	13.28	1434.80	
*334.715	0.94	1466.17	97.32	666.65	4.78		
NL 1335	NL PLSA 1335		Normal	NA	*139.248		
1183.68	3344.72	*0.83	19.72	*2.72	17.79	1589.56	

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*334.715	0.85	1528.03	*14.229	*76.98	4.93		
NL 1336	NL PLSA 1336		Normal	NA	*139.248		
1832.90	2768.28	*0.83	8.37	*2.72	20.05	1,007.2	
*334.715	0.75	2311.82	108.22	495.47	4.87		
NL 1337	NL PLSA 1337		Normal	NA	*139.248		
3185.75	2203.57	*0.83	8.30	*2.72	20.12	*74.234	
*334.715	1.02	1397.08	85.37	581.18	5.93		
NL 1338	NL PLSA 1338		Normal	NA	1488.89		
1940.61	2676.93	*0.83	11.19	*2.72	23.79	818.91	
*334.715	0.77	2013.74	108.22	1431.37	5.91		
NL 1339	NL PLSA 1339		Normal	NA	1521.06		
288.06	2129.13	*0.83	18.85	*2.72	14.81	966.3	
*334.715	0.82	1915.26	91.5	*76.98	2.97		
NL 1340	NL PLSA 1340		Normal	NA	2494.9		
1115.08	2849.86	*0.83	16.76	*2.72	14.15	598.55	
*334.715	0.8	2815.16	*14.229	560.29	4.14		
NL 1341	NL PLSA 1341		Normal	NA	*139.248		
978.28	1273.69	*0.83	5.46	*2.72	11.28	*74.234	
*334.715	0.68	976.67	108.22	*76.98	2.31		
NL 1342	NL PLSA 1342		Normal	NA	2913.77		
751.61	2565.99	8.12	9.13	39.14	12.92	1023.56	
*334.715	0.82	998.51	97.32	414.89	2.75		
NL 1343	NL PLSA 1343		Normal	NA	953.69		
1824.17	2504.71	*0.83	2.89	*2.72	16.43	1619.08	
*334.715	0.83	1607.44	*14.229	*76.98	2.92		
NL 1344	NL PLSA 1344		Normal	NA	953.69		
521.29	3181.8	*0.83	15.56	*2.72	16.95	1771.11	
*334.715	0.69	1520.6	85.37	632.06	3.85		
NL 1345	NL PLSA 1345		Normal	NA	1540.44		
1873.62	3322.56	*0.83	22.90	*2.72	17.58	1,317.0	
*334.715	0.63	2322.08	*14.229	402.84	2.9		
NL 1346	NL PLSA 1346		Normal	NA	*139.248		
1545.97	3658.21	*0.83	16.98	*2.72	20.21	6472.69	
*334.715	0.77	3169.72	*14.229	*76.98	3.16		
NL 1347	NL PLSA 1347		Normal	NA	*139.248		
2532.95	1071.63	*0.83	9.19	*2.72	16.25	1699.25	
*334.715	0.97	1722.08	190.43	779.92	6.3		
NL 1348	NL PLSA 1348		Normal	NA	1093.52		
859.06	2635.29	*0.83	9.29	*2.72	14.07	760.98	
*334.715	0.83	1550.34	118.32	326.89	2.25		
NL 1349	NL PLSA 1349		Normal	NA	908.19		
873.23	2376.5	*0.83	33.20	*2.72	15.33	952.8	
*334.715	0.77	1890.08	*14.229	285.98	3.3		
NL 1350	NL PLSA 1350		Normal	NA	2612.85		
1206.58	1793.9	5.78	10.60	*2.72	14.4	1440.59	
*334.715	0.99	1054.4	97.32	738.33	6.95		
NL 1351	NL PLSA 1351		Normal	NA	3262.18		
462.69	1606.14	*0.83	6.48	*2.72	9.75	1789.16	

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*334.715	0.72	1525.55	102.88	489.91	3.96	
NL 1352	NL PLSA 1352		Normal	NA	874.44	
1476.70	3268.21	*0.83	9.86	22.56	11.38	*74.234
*334.715	0.85	2204.35	85.37	908.03	5.66	
NL 1353	NL PLSA 1353		Normal	NA	1751.06	
610.91	2907.67	*0.83	12.41	*2.72	11.59	2282.90
*334.715	1.5	1384.76	97.32	738.33	6.6	
NL 1354	NL PLSA 1354		Normal	NA	*139.248	
819.43	1185.84	*0.83	9.85	*2.72	14.57	1,111.7
*334.715	0.88	1654.72	85.37	*76.98	3.98	
NL 1355	NL PLSA 1355		Normal	NA	2349.46	
1551.75	2152.62	*0.83	10.64	*2.72	18.13	575.79
*334.715	0.89	1849.84	85.37	271.78	6.35	
NL 1356	NL PLSA 1356		Normal	NA	*139.248	
2391.56	1774.5	*0.83	3.54	*2.72	19	*74.234
*334.715	0.82	508.8	145.32	606.85	5.54	
NL 1357	NL PLSA 1357		Normal	NA	1081.68	
2098.26	1891.05	*0.83	5.62	*2.72	15.56	923.07
*334.715	0.74	597.74	145.32	306.73	4.3	
NL 1358	NL PLSA 1358		Normal	NA	3930.57	
802.46	1519.36	13.49	10.55	*2.72	18.61	1161.81
*334.715	0.71	1565.22	*14.229	249.86	4.81	
NL 1359	NL PLSA 1359		Normal	NA	2135.62	
2107.04	1275.6	5.32	7.50	*2.72	12.56	888.2
*334.715	0.75	1446.41	108.22	352.97	8.08	
NL 1360	NL PLSA 1360		Normal	NA	1201.53	
1035.21	3831.1	*0.83	11.56	*2.72	16.73	782.0
*334.715	0.76	1463.7	*14.229	916.58	3.26	
NL 1361	NL PLSA 1361		Normal	NA	*139.248	
1212.31	2867.79	*0.83	16.44	*2.72	16.55	535.6
*334.715	0.54	1654.72	85.37	983.75	5.26	
NL 1362	NL PLSA 1362		Normal	NA	5162.77	
1763.16	2062.63	*0.83	27.60	16.61	17.58	1,181.4
*334.715	0.66	850.77	97.32	234.78	4.85	
NL 1363	NL PLSA 1363		Normal	NA	1579.4	
1882.35	2117.38	*0.83	16.99	*2.72	18.9	1741.10
*334.715	0.66	2003.62	85.37	829.51	4.95	
NL 1364	NL PLSA 1364		Normal	NA	1954.63	
1006.73	2595.68	*0.83	8.62	31.74	14.28	1139.50
*334.715	0.67	633.82	85.37	*76.98	3.52	
NL 1365	NL PLSA 1365		Normal	NA	*139.248	
3233.53	1394.38	5.55	4.44	*2.72	13.51	824.21
*334.715	0.6	1667.18	*14.229	420.86	4.67	
NL 1366	NL PLSA 1366		Normal	NA	*139.248	
1737.04	1963.1	*0.83	19.38	20.87	14.69	1018.08
*334.715	0.65	1789.63	97.32	365.71	5.92	
NL 1367	NL PLSA 1367		Normal	NA	1906.62	
1252.42	1782.26	*0.83	26.55	17.47	13.68	1240.43

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*334.715	0.67	1940.47	97.32	299.88	5.43		
NL 1368	NL PLSA 1368		Normal	NA	1592.44		
983.97	1525.14	*0.83	5.56	*2.72	14.97	560.68	
*334.715	1.05	1059.26	*14.229	484.32	5.82		
NL 1369	NL PLSA 1369		Normal	NA	841.02		
822.26	3449.63	*0.83	5.14	*2.72	17.55	2,609.7	
*334.715	0.92	3159.05	85.37	326.89	4.92		
NL 1370	NL PLSA 1370		Normal	NA	3604.41		
734.69	1848.28	*0.83	10.15	16.32	12.97	1568.96	
*334.715	1.04	1318.35	91.5	414.89	5.7		
NL 1371	NL PLSA 1371		Normal	NA	1081.68		
1049.46	2333.2	*0.83	9.66	20.30	13.72	1411.68	
*334.715	1.02	1779.61	136.77	326.89	2.13		
NL 1372	NL PLSA 1372		Normal	NA	*139.248		
2344.52	1413.58	*0.83	6.16	*2.72	15.13	535.62	
*334.715	1.24	2388.9	*14.229	*76.98	3.92		
NL 1373	NL PLSA 1373		Normal	NA	2135.62		
1641.40	2768.28	*0.83	22.72	18.03	16.06	1498.70	
*334.715	1.02	2173.74	85.37	784.49	3.36		
NL 1374	NL PLSA 1374		Normal	NA	*139.248		
1664.57	1434.71	*0.83	27.80	*2.72	8.77	2282.90	
*334.715	0.75	1707.09	97.32	285.98	3.13		
NL 1375	NL PLSA 1375		Normal	NA	*139.248		
1574.86	1577.19	*0.83	9.41	*2.72	11.84	724.4	
*334.715	0.72	2386.33	*14.229	340.04	4.14		
NL 1376	NL PLSA 1376		Normal	NA	*139.248		
1069.41	1758.99	*0.83	6.76	*2.72	9.15	1059.23	
*334.715	0.7	1466.17	118.32	890.84	5.13		
NL 1377	NL PLSA 1377		Normal	NA	*139.248		
1470.94	2031.38	5.78	9.40	*2.72	18	988.07	
*334.715	0.92	1822.23	168.99	*76.98	5.64		
NL 1378	NL PLSA 1378		Normal	NA	*139.248		
329.46	1098.24	*0.83	13.21	*2.72	11.18	636.7	
*334.715	1.44	2092.33	145.32	426.79	4.65		
NL 1379	NL PLSA 1379		Normal	NA	*139.248		
368.21	1285.16	*0.83	18.30	*2.72	17.3	*74.234	
*334.715	0.73	703.62	153.51	426.79	4.96		
NL 1380	NL PLSA 1380		Normal	NA	2687.28		
1243.82	1557.9	*0.83	4.25	*2.72	18.07	1251.73	
*334.715	0.73	2453.34	*14.229	384.47	4.07		
NL 1381	NL PLSA 1381		Normal	NA	*139.248		
630.56	2595.68	*0.83	9.20	*2.72	18.41	1735.11	
*334.715	1.02	1127.46	118.32	*76.98	6.17		
NL 1382	NL PLSA 1382		Normal	NA	*141.842		
1354.68	1462.18	*0.827	7.00	20.14	13.13	2375.10	
*336.559	0.76	1802.53	106.2	681.87	4.67		
NL 1383	NL PLSA 1383		Normal	NA	*141.842		
1781.21	3942.71	*0.827	20.09	*2.767	13.68	3652.22	

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*336.559	0.59	1797.58	*14.082	519.24	4.13		
NL 1384	NL PLSA 1384		Normal	NA	2701.01		
989.11	3066.97	*0.827	11.95	*2.767	12.77	1918.02	
*336.559	0.54	3225.07	*14.082	719.26	5.5		
NL 1385	NL PLSA 1385		Normal	NA	*141.842		
1315.11	1179.22	7.61	13.00	*2.767	13.21	514.80	
*336.559	1.44	1056.32	152.56	*78.12	7.24		
NL 1386	NL PLSA 1386		Normal	NA	*141.842		
1621.46	1170.05	*0.827	7.92	*2.767	12.59	*72.188	
*336.559	0.6	2257.39	*14.082	673.46	3.13		
NL 1387	NL PLSA 1387		Normal	NA	*141.842		
2355.94	1724.22	*0.827	18.70	*2.767	*1.372	468.53	
*336.559	0.72	2188.76	*14.082	418.33	3.15		
NL 1388	NL PLSA 1388		Normal	NA	*141.842		
2840.06	2142.21	*0.827	4.02	*2.767	11.09	636.57	
*336.559	0.75	1270.44	97	*78.12	3.35		
NL 1389	NL PLSA 1389		Normal	NA	*141.842		
766.59	1585.67	5.18	4.12	*2.767	11.04	674.56	
*336.559	0.61	1175.76	97	413.31	5.34		
NL 1390	NL PLSA 1390		Normal	NA	*141.842		
1575.92	2775.88	4.96	4.43	*2.767	16.8	1532.57	
*336.559	0.98	1189.91	106.2	377.56	4.54		
NL 1391	NL PLSA 1391		Normal	NA	1245.95		
2073.56	2549.1	*0.827	23.46	17.87	13.72	796.57	
*336.559	0.72	1872.07	*14.082	533.07	4.87		
NL 1392	NL PLSA 1392		Normal	NA	*141.842		
1428.28	2338.6	*0.827	21.67	*2.767	14.68	928.1	
*336.559	0.54	2797.11	106.2	755.96	2.39		
NL 1393	NL PLSA 1393		Normal	NA	*141.842		
1964.45	4091.8	5.18	102.98	*2.767	19.07	1355.83	
*336.559	0.76	1095.97	97	677.67	7.93		
NL 1394	NL PLSA 1394		Normal	NA	*141.842		
1264.30	2758.82	*0.827	3.61	30.99	11.82	1418.46	
*336.559	0.65	2697.91	87.1	1004.81	2.82		
NL 1395	NL PLSA 1395		Normal	NA	*141.842		
1309.46	1877.98	*0.827	3.82	*2.767	15.1	847.56	
*336.559	0.65	1426.05	*14.082	698.58	3.61		
NL 1396	NL PLSA 1396		Normal	NA	*141.842		
1269.94	2760.72	*0.827	25.65	*2.767	10.24	609.7	
*336.559	0.62	745.7	87.1	569.31	3.56		
NL 1397	NL PLSA 1397		Normal	NA	*139.248		
1120.79	3011.51	*0.83	10.12	*2.72	13.59	*74.234	
*334.715	0.89	1443.94	97.32	*76.98	4.66		
NL 1398	NL PLSA 1398		Normal	NA	1165.24		
644.60	660.56	*0.83	16.40	*2.72	16.43	1816.30	
*334.715	0.73	1983.39	91.5	*76.98	5.23		
NL 1399	NL PLSA 1399		Normal	NA	*139.248		
949.85	2015.76	*0.83	12.36	*2.72	12.56	969.04	

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*334.715	0.79	1644.76	91.5	847.23	5.64		
NL 1400	NL PLSA 1400		Normal	NA	2093.49		
554.85	2433.65	*0.83	5.61	*2.72	10.21	3256.08	
*334.715	0.8	1980.86	*14.229	671.53	4.9		
NL 1401	NL PLSA 1401		Normal	NA	2225.14		
818.77	1632.28	*0.797	10.77	25.24	12.26	2286.21	
*320.985	0.61	2039.26	141.28	406.44	2.91		
NL 1402	NL PLSA 1402		Normal	NA	*131.746		
1355.24	4256.2	5.97	5.32	*2.636	15.72	881.81	
*320.985	0.81	1708	141.28	598.93	5.47		
NL 1403	NL PLSA 1403		Normal	NA	*131.746		
896.42	3160.7	*0.797	8.24	*2.636	8.81	*71.888	
*320.985	0.94	1851.27	110.38	1567.13	3.65		
NL 1404	NL PLSA 1404		Normal	NA	2204.41		
1901.25	1576.73	*0.797	6.80	*2.636	12.19	759.60	
*320.985	0.75	1397.19	110.38	424.19	3.99		
NL 1405	NL PLSA 1405		Normal	NA	1112.13		
1038.17	1273.24	6.41	4.92	*2.636	15.05	1,899.9	
*320.985	0.61	1948.08	141.28	475.2	3.49		
NL 1406	NL PLSA 1406		Normal	NA	1665.44		
1001.05	1150.79	4.89	7.97	*2.636	15.08	520.0	
*320.985	0.84	1371.18	148.44	926.1	3.74		
NL 1407	NL PLSA 1407		Normal	NA	*131.746		
768.12	418.39	*0.797	5.06	*2.636	12.15	*71.888	
*320.985	0.91	2615.06	141.28	538.98	2.13		
NL 1408	NL PLSA 1408		Normal	NA	938.03		
1786.69	1787.56	*0.797	12.15	*2.636	*1.372	638.76	
*320.985	0.72	1789.8	*13.953	762.36	4.82		
NL 1409	NL PLSA 1409		Normal	NA	808.88		
1230.46	1262.52	*0.797	21.93	*2.636	14.48	698.66	
*320.985	0.54	1658.43	101.92	849.38	3.88		
NL 1410	NL PLSA 1410		Normal	NA	*131.746		
3173.78	3853.02	9.1	16.62	*2.636	14.05	991.3	
*320.985	0.69	1504.35	*13.953	982.86	5.63		
NL 1411	NL PLSA 1411		Normal	NA	1526.3		
1024.67	3510.62	*0.797	13.95	*2.636	9.7	*71.888	
*320.985	0.67	2237.1	83.72	920.32	4.07		
NL 1412	NL PLSA 1412		Normal	NA	*131.746		
531.62	1399.24	5.32	1.94	*2.636	*1.372	*71.888	
3312.07	0.5	969.27	259.31	768.75	3.01		
NL 1413	NL PLSA 1413		Normal	NA	982.19		
1146.13	2835.13	7.07	9.30	*2.636	13.08	1,619.4	
*320.985	0.54	2065.77	110.38	*75.36	4.01		
NL 1414	NL PLSA 1414		Normal	NA	*131.746		
1597.97	1479.35	*0.797	3.65	*2.636	6.89	503.38	
*320.985	0.72	1244.3	*13.953	*75.36	2.65		
NL 1425	NL PLSA 1425		Normal	NA	1886.13		
904.42	1726.04	*0.83	11.54	*2.72	17.41	1,229.1	

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*334.715	0.8	2001.09	97.32	365.71	4.17		
NL 1426	NL PLSA 1426		Normal	NA	*139.248		
465.48	1617.73	*0.83	7.02	*2.72	16.66	*74.234	
*334.715	2.54	1360.14	145.32	920.84	3.82		
NL 1427	NL PLSA 1427		Normal	NA	4179.94		
437.63	2859.82	*0.83	22.75	*2.72	20.55	1,246.1	
*334.715	0.7	1694.61	123.13	*76.98	6.98		
NL 1428	NL PLSA 1428		Normal	NA	863.26		
898.75	957.85	5.32	8.72	*2.72	14.89	1059.23	
*334.715	1.15	1814.7	234.83	249.86	4.39		
NL 1429	NL PLSA 1429		Normal	NA	835.49		
310.13	1555.97	*0.83	8.62	*2.72	21.18	1,001.7	
*334.715	0.81	2217.12	*14.229	967.14	5.18		
NL 1430	NL PLSA 1430		Normal	NA	*139.248		
1635.61	2730.52	*0.83	4.28	*2.72	21.83	955.49	
*334.715	1.17	1293.8	118.32	*76.98	6.4		
NL 1431	NL PLSA 1431		Normal	NA	1717.69		
622.13	1982.6	9.56	13.11	*2.72	17.16	1,302.8	
*334.715	0.83	1587.57	*14.229	1008.43	7.8		
NL 1432	NL PLSA 1432		Normal	NA	1865.71		
757.26	1838.56	*0.83	11.66	*2.72	13.51	456.4	
*334.715	0.9	1779.61	108.22	581.18	3.98		
NL 1433	NL PLSA 1433		Normal	NA	982.41		
1046.61	2621.43	*0.83	10.51	*2.72	16.4	1122.82	
*334.715	0.86	1852.36	113.35	438.55	2.81		
NL 1434	NL PLSA 1434		Normal	NA	*139.248		
884.57	1229.73	*0.83	10.32	*2.72	13.11	1153.44	
*334.715	0.71	1764.59	*14.229	719.52	5.06		
NL 1435	NL PLSA 1435		Normal	NA	1129.23		
667.09	1803.6	*0.83	8.09	*2.72	15.99	818.9	
2132	0.7	1639.78	118.32	450.18	6.47		
NL 1436	NL PLSA 1436		Normal	NA	1105.39		
647.41	345.43	9.32	3.74	*2.72	14.15	1175.79	
*334.715	0.86	1764.59	252.14	352.97	2.67		
NL 1437	NL PLSA 1437		Normal	NA	930.87		
2145.07	984.36	*0.83	10.34	*2.72	10.27	*74.234	
*334.715	0.83	429.47	113.35	825.06	2.67		
NL 1438	NL PLSA 1438		Normal	NA	*139.248		
459.91	2354.85	*0.83	31.21	*2.72	17.23	1040.00	
*334.715	0.91	2097.4	*14.229	*76.98	2.72		
NL 1439	NL PLSA 1439		Normal	NA	1858.91		
881.73	2090	*0.83	30.39	*2.72	17.93	1504.53	
*334.715	0.72	1193.38	*14.229	313.51	3.71		
NL 1440	NL PLSA 1440		Normal	NA	1592.44		
700.87	1425.1	*0.83	2.08	*2.72	11.07	1,472.5	
*334.715	0.66	1017.94	85.37	455.95	3.98		
NL 1441	NL PLSA 1441		Normal	NA	*139.248		
1563.30	528.24	*0.83	5.59	*2.72	14.65	734.9	

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*334.715	0.6	1293.8	*14.229	340.04	4.86		
NL 1442	NL PLSA 1442		Normal	NA	*139.248		
354.36	367.46	*0.83	5.83	*2.72	9.63	750.5	
*334.715	0.6	1729.57	91.5	*76.98	2.74		
NL 1443	NL PLSA 1443		Normal	NA	*133.814		
1410.68	1801.74	*0.83	10.80	*2.745	15.72	1,181.8	
*328.934	0.55	1874.55	91.79	296.89	6.94		
NL 1444	NL PLSA 1444		Normal	NA	*133.814		
1316.41	1639.79	4.98	20.02	*2.745	13.46	516.35	
*328.934	0.66	1134	211.92	579.94	2.31		
NL 1445	NL PLSA 1445		Normal	NA	*133.814		
1466.01	1900.73	*0.83	4.34	20.37	10.2	587.7	
*328.934	0.61	1131.16	98.45	93.07	2.39		
NL 1482	NL PLSA 1482		Normal	NA	931.28		
908.79	1815	*0.807	11.78	*2.707	10.21	661.8	
*327.937	1.19	1656.38	104.41	1061.43	5.11		
NL 1483	NL PLSA 1483		Normal	NA	*130.362		
888.35	1728.04	*0.807	5.72	21.45	8.3	541.2	
*327.937	1.02	1514.21	*14.112	1032.37	5.16		
NL 1484	NL PLSA 1484		Normal	NA	*130.362		
1553.45	2739.11	*0.807	14.91	*2.707	7.68	1167.30	
*327.937	1.27	1460.13	104.41	1077.91	3.95		
NL 1485	NL PLSA 1485		Normal	NA	*130.362		
694.37	1824.89	*0.807	9.79	18.54	7.8	952.20	
*327.937	0.82	1127.81	98.12	1421.29	10.91		
NL 1486	NL PLSA 1486		Normal	NA	951.37		
684.44	931.99	*0.807	3.47	*2.707	10.21	461.8	
*327.937	0.99	1227.94	175.8	669.98	6.03		
NL 1487	NL PLSA 1487		Normal	NA	*130.362		
622.76	2390.93	*0.807	5.98	*2.707	8.67	753.81	
*327.937	1.27	1004.97	91.56	764.88	7.39		
NL 1488	NL PLSA 1488		Normal	NA	*130.362		
341.72	1231.01	*0.807	7.82	*2.707	7.5	*74.728	
*327.937	0.85	1034.13	*14.112	960.56	5.12		
NL 1489	NL PLSA 1489		Normal	NA	1648.48		
729.24	2051.08	*0.807	12.98	*2.707	*1.371	*74.728	
*327.937	1.27	1508.2	121.93	1126.82	5.75		
NL 1490	NL PLSA 1490		Normal	NA	*130.362		
1184.17	2932.31	*0.807	3.01	*2.707	*1.371	*74.728	
*327.937	1.08	877.21	*14.112	873.55	4.23		
NL 1491	NL PLSA 1491		Normal	NA	*130.362		
1178.90	1274.78	*0.807	12.46	*2.707	8.83	1001.54	
*327.937	1.68	1616.92	91.56	1174.99	4.96		
NL 1492	NL PLSA 1492		Normal	NA	*130.362		
829.86	3090.03	*0.807	27.76	*2.707	11.49	600.82	
*327.937	0.82	1157.19	*14.112	736.87	10.63		
NL 1493	NL PLSA 1493		Normal	NA	*130.362		
598.27	1212.31	*0.807	45.52	*2.707	*1.371	522.6	

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*327.937	1.09	675.68	104.41	1198.82	7.74		
NL 1494	NL PLSA 1494		Normal	NA	1372.89		
1055.88	2169.06	*0.807	20.34	*2.707	8.41	461.83	
*327.937	1.47	1022.46	*14.112	640.59	9.38		
NL 1495	NL PLSA 1495		Normal	NA	*130.362		
1016.94	3211.15	*0.807	24.60	21.86	8.46	889.6	
*327.937	1.33	1629.05	116.28	2195.92	9.3		
NL 1496	NL PLSA 1496		Normal	NA	*130.362		
2385.89	2567.48	*0.807	8.62	34.09	11.07	516.5	
*327.937	1.1	1562.46	147.98	1376.33	5.04		
NL 1497	NL PLSA 1497		Normal	NA	2271.2		
1071.50	1834.78	*0.807	5.54	*2.707	13.18	941.7	
*327.937	0.97	718.71	*14.112	960.56	8.67		
NL 1498	NL PLSA 1498		Normal	NA	*130.362		
527.89	1227.89	8.27	16.10	*2.707	8.03	727.25	
*327.937	1	1042.89	116.28	969.1	6.02		
NL 1499	NL PLSA 1499		Normal	NA	1478.19		
1348.71	3360.61	*0.807	27.87	17.71	*1.371	*74.728	
*327.937	1.1	1790.71	104.41	1284.79	13.01		
NL 1500	NL PLSA 1500		Normal	NA	*130.362		
2309.18	1448.67	*0.807	5.96	*2.707	11.42	*74.728	
*327.937	0.72	2235.9	84.67	1167.01	8.06		
NL 1501	NL PLSA 1501		Normal	NA	1103.54		
1569.75	3397.27	*0.807	3.64	*2.707	10.55	2,470.1	
*327.937	0.67	1849.1	*14.112	951.98	4.09		
NL 1502	NL PLSA 1502		Normal	NA	*130.362		
736.74	2577.93	*0.807	13.67	*2.707	*1.371	566.13	
*327.937	1.3	1367.42	91.56	1596.41	8.96		
NL 1503	NL PLSA 1503		Normal	NA	*130.362		
1221.12	981.85	*0.807	11.68	*2.707	8.78	455.84	
*327.937	0.77	1394.28	*14.112	891.19	5.1		
NL 1504	NL PLSA 1504		Normal	NA	801.89		
2471.44	1602.83	*0.807	43.63	*2.707	9.78	632.7	
*327.937	0.82	504.14	*14.112	947.69	5.76		
NL 1505	NL PLSA 1505		Normal	NA	3519.77		
1006.58	2480.66	6.1	21.20	32.48	7.86	2,164.1	
*327.937	0.65	1732.56	104.41	951.98	2.72		
NL 1506	NL PLSA 1506		Normal	NA	2149.22		
1184.17	2619.81	5.57	10.75	30.86	15.76	1,564.8	
*327.937	0.38	1769.26	*14.112	1138.93	5.88		
NL 1507	NL PLSA 1507		Normal	NA	*130.362		
908.79	3222.04	*0.807	10.69	*2.707	*1.371	3157.36	
*327.937	0.72	1784.58	110.45	1122.77	4.4		
NL 1508	NL PLSA 1508		Normal	NA	*130.362		
376.36	1589.9	*0.807	6.92	*2.707	12.18	*74.728	
*327.937	0.73	842.52	192.89	1019.83	5.47		
NL 1509	NL PLSA 1509		Normal	NA	*130.362		
1189.44	1932.49	*0.807	11.64	*2.707	16.64	*74.728	

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*327.937	0.58	1514.21	*14.112	869.12	7.17		
NL 1510	NL PLSA 1510		Normal	NA	2687.24		
1100.20	1184.33	*0.807	8.45	*2.707	11.19	*74.728	
*327.937	0.78	1322.77	*14.112	1476.8	11.86		
NL 1511	NL PLSA 1511		Normal	NA	1083.1		
867.95	2581.41	*0.807	15.39	*2.707	9.41	*74.728	
*327.937	1.17	1641.19	104.41	1057.29	2.63		
NL 1512	NL PLSA 1512		Normal	NA	1648.48		
797.00	1894.31	*0.807	12.05	*2.707	*1.371	1008.63	
*327.937	0.87	1104.34	104.41	1261.55	2.41		
NL 1513	NL PLSA 1513		Normal	NA	*130.362		
1042.88	2421.93	*0.807	33.85	30.05	15.92	*74.728	
*327.937	0.77	1616.92	91.56	899.96	3.68		
NL 1514	NL PLSA 1514		Normal	NA	*130.362		
608.06	307.85	*0.807	5.03	*2.707	*1.371	*74.728	
*327.937	0.79	575.52	91.56	679.68	2.35		
NL 1515	NL PLSA 1515		Normal	NA	2619.19		
1629.67	1688.87	8.82	17.52	23.51	8.3	2134.81	
*327.937	0.68	1445.13	*14.112	899.96	6.58		
NL 1516	NL PLSA 1516		Normal	NA	*130.362		
741.74	1606.07	*0.807	7.80	*2.707	8.93	*74.728	
*327.937	0.82	1133.68	91.56	1077.91	6.51		
NL 1517	NL PLSA 1517		Normal	NA	*130.362		
1783.26	2247.16	*0.807	17.20	*2.707	12.82	566.13	
*327.937	0.83	1034.13	*14.112	1073.79	14.63		
NL 1518	NL PLSA 1518		Normal	NA	1022.07		
944.69	1445.48	5.3	13.42	23.51	9.27	*74.728	
*327.937	0.82	1698.99	184.47	746.25	15.43		
NL 1519	NL PLSA 1519		Normal	NA	*130.362		
776.86	1202.97	*0.807	13.63	*2.707	*1.371	461.83	
*327.937	0.92	761.82	91.56	828.89	6.16		
NL 1520	NL PLSA 1520		Normal	NA	*130.362		
1921.65	3463.45	*0.807	10.12	21.45	12.35	1270.81	
*327.937	0.97	1604.8	104.41	1118.72	6.65		
NL 1521	NL PLSA 1521		Normal	NA	*130.362		
949.83	777.05	*0.807	5.21	*2.707	*1.371	*74.728	
*327.937	0.72	727.33	192.89	801.68	5.06		
NL 1522	NL PLSA 1522		Normal	NA	*130.362		
496.67	1719.87	*0.807	11.76	*2.707	12.79	*74.728	
*327.937	1.05	923.56	91.56	873.55	6.24		
NL 1523	NL PLSA 1523		Normal	NA	1383.38		
603.16	2836.3	*0.807	3.97	*2.707	*1.371	747.15	
*327.937	0.93	1729.5	116.28	1044.86	3.74		
NL 1524	NL PLSA 1524		Normal	NA	*130.362		
1079.32	1641.71	*0.807	4.86	*2.707	13.09	600.82	
*327.937	0.82	952.59	253.64	864.68	4.97		
NL 1525	NL PLSA 1525		Normal	NA	*130.362		
3691.29	6723.23	*0.807	28.43	52.42	14.02	578.7	

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*327.937	0.79	2175.98	147.98	951.98	10.21		
NL 1526	NL PLSA 1526		Normal	NA	*130.362		
719.26	1997.49	5.43	13.70	*2.707	*1.371	*74.728	
*327.937	0.78	1436.15	116.28	1167.01	4.83		
NL 1527	NL PLSA 1527		Normal	NA	*130.362		
300.66	1285.76	*0.807	18.32	18.54	*1.371	1,300.7	
*327.937	0.93	1328.72	104.41	846.85	3.62		
NL 1528	NL PLSA 1528		Normal	NA	*130.362		
1300.70	1033.54	5.04	31.66	*2.707	10.87	547.4	
*327.937	0.81	504.14	*14.112	750.92	9.93		
NL 1529	NL PLSA 1529		Normal	NA	1268.5		
771.83	1930.82	*0.807	16.33	16.87	13.12	1,498.8	
*327.937	0.71	1406.23	104.41	727.45	12.83		
NL 1530	NL PLSA 1530		Normal	NA	6938.81		
898.56	1630.36	*0.807	12.26	18.96	8.3	486.0	
*327.937	0.77	1424.17	166.86	1077.91	5.26		
NL 1531	NL PLSA 1531		Normal	NA	3566.84		
518.27	762.34	*0.807	20.55	*2.707	*1.371	844.9	
*327.937	0.69	1319.8	91.56	533.61	2.1		
NL 1532	NL PLSA 1532		Normal	NA	*130.362		
822.27	1369.26	*0.807	5.73	*2.707	10.47	566.1	
*327.937	0.68	756.07	*14.112	590.5	7.13		
NL 1533	NL PLSA 1533		Normal	NA	*147.7		
581.90	1053.57	6.68	8.61	26.00	11.76	1,216.0	
2035	1.49	815.91	295.1	1078.2	6.69		
NL 1534	NL PLSA 1534		Normal	NA	1417.02		
1913.34	1148.02	*0.83	19.41	22.89	26.33	880.9	
*339.24	1.28	1710.98	*15.72	1296.18	16.21		
NL 1535	NL PLSA 1535		Normal	NA	1982.85		
1003.81	2028.19	5.96	42.78	16.32	13.15	1177.15	
*339.24	1.31	2549.02	*15.72	1201.35	4.74		
NL 1536	NL PLSA 1536		Normal	NA	*147.7		
1937.20	1859.46	*0.83	20.67	*2.72	29.36	1,245.2	
*339.24	1.85	2061.47	*15.72	1144.57	14.73		
NL 1537	NL PLSA 1537		Normal	NA	*147.7		
2080.31	3009.22	*0.83	8.52	24.46	14.66	1274.46	
*339.24	1.33	2127.2	*15.72	975.31	4.65		
NL 1538	NL PLSA 1538		Normal	NA	1126.57		
1758.17	3950.71	5.22	19.88	19.67	11.9	2006.17	
*339.24	1.89	1530.47	94.3	1303.95	10.69		
NL 1539	NL PLSA 1539		Normal	NA	*147.7		
7286.22	4002.7	15.12	19.04	22.89	28.45	1085.45	
*339.24	1.6	3851.78	*15.72	1193.3	8.03		
NL 1540	NL PLSA 1540		Normal	NA	1928.4		
1590.92	2778.71	*0.83	9.40	*2.72	25.24	504.11	
*339.24	1.95	1200.57	94.3	1391.99	9.41		
NL 1541	NL PLSA 1541		Normal	NA	1337.36		
961.74	1231.27	*0.83	12.77	24.46	8.13	740.8	

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2035	2.67	299.3	230.18	1692.47	17		
NL 1542	NL PLSA 1542		Normal	NA	*147.7		
1572.99	2677.48	7.65	22.61	*2.72	20.6	1,362.7	
*339.24	1.81	2931.84	94.3	1217.36	13.16		
NL 1543	NL PLSA 1543		Normal	NA	1417.02		
1033.85	2603.63	5.22	23.55	19.67	14.21	1,143.3	
*339.24	1.42	1181.17	94.3	601.16	6.45		
NL 1544	NL PLSA 1544		Normal	NA	4262.92		
829.37	1132.9	*0.83	16.05	27.52	8.67	639.60	
*339.24	1.57	1142.44	94.3	1119.87	5.52		
NL 1545	NL PLSA 1545		Normal	NA	2366.93		
1063.88	1371.53	6.68	5.07	47.22	23.17	1560.89	
*339.24	1.46	2046.34	220.67	568.65	6.85		
NL 1546	NL PLSA 1546		Normal	NA	*147.7		
1501.24	2440.77	6.68	14.39	*2.72	16.37	956.48	
*339.24	1.45	2289.84	*15.72	1241.23	9.79		
NL 1547	NL PLSA 1547		Normal	NA	2366.93		
1057.87	1863.29	10.49	45.05	18.02	9.05	2047.23	
*339.24	2.18	2376.74	94.3	684.53	7.19		
NL 1548	NL PLSA 1548		Normal	NA	3702.41		
1273.79	2825.51	*0.83	9.89	*2.72	12.35	763.94	
*339.24	1.44	2592.95	189.11	1082.4	5.87		
NL 1549	NL PLSA 1549		Normal	NA	*147.7		
1123.90	3596.37	*0.83	24.54	53.75	13.91	1461.45	
*339.24	1.69	2167.74	94.3	601.16	4.65		
NL 1550	NL PLSA 1550		Normal	NA	16406.21		
642.36	4074.79	6.2	16.34	*2.72	19.55	862.03	
*339.24	1.39	2681.08	*15.72	568.65	12.49		
NL 1551	NL PLSA 1551		Normal	NA	2174.27		
1519.18	3264.45	*0.83	23.70	22.89	14.88	1530.99	
*339.24	1.94	1666.33	*15.72	1189.28	5.47		
NL 1552	NL PLSA 1552		Normal	NA	4917.37		
2110.12	1947.6	6.68	7.46	16.32	11.48	667.05	
2035.45	1.93	1186.02	210.71	1296.18	6.32		
NL 1553	NL PLSA 1553		Normal	NA	1819.84		
1471.34	2359.54	5.22	16.66	*2.72	13.99	*77.35	
*339.24	1.5	1676.25	*15.72	881.42	8.26		
NL 1554	NL PLSA 1554		Normal	NA	3716.7		
1501.24	2421.42	*0.83	15.33	*2.72	13.44	685.41	
*339.24	1.5	1701.05	*15.72	1361.64	8.26		
NL 1555	NL PLSA 1555		Normal	NA	*147.7		
829.37	2016.67	5.22	28.42	*2.72	11.43	612.26	
*339.24	1.38	1278.31	94.3	724.65	4.42		
NL 1556	NL PLSA 1556		Normal	NA	4888.12		
1339.68	1080	*0.83	8.19	*2.72	18.72	956.48	
*339.24	1.7	1644.04	*15.72	1099.12	4.87		
NL 1557	NL PLSA 1557		Normal	NA	1074.27		
1572.99	1148.02	15.12	9.02	49.85	22.12	759.30	

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*339.24	1.86	607.08	*15.72	1241.23	9.64		
NL 1558	NL PLSA 1558		Normal	NA	*147.7		
2050.50	2553.17	*0.83	12.18	*2.72	14.51	956.48	
*339.24	1.58	2502.6	*15.72	1221.36	10.06		
NL 1559	NL PLSA 1559		Normal	NA	*147.7		
1782.05	2043.56	*0.83	30.15	29.02	15.12	526.5	
*339.24	0.73	1530.47	164.42	1909.62	6.04		
NL 1560	NL PLSA 1560		Normal	NA	*147.7		
1782.05	1424.7	5.22	16.77	*2.72	21.2	947.00	
*339.24	1.33	1770.66	*15.72	1241.23	8.05		
NL 1561	NL PLSA 1561		Normal	NA	1205.32		
1644.70	243.59	*0.83	8.04	*2.72	8.67	937.5	
*339.24	1.5	1950.7	*15.72	679.45	6.76		
NL 1562	NL PLSA 1562		Normal	NA	*147.7		
1123.90	2553.17	8.6	15.49	19.67	12.17	791.85	
4316.53	1.7	2109.48	405.13	568.65	14.35		
NL 1563	NL PLSA 1563		Normal	NA	4089.77		
3089.44	2825.51	*0.83	32.67	*2.72	24.69	589.57	
*339.24	1.38	1715.95	*15.72	1448.17	5.98		
NL 1564	NL PLSA 1564		Normal	NA	*147.7		
943.71	1197.2	*0.83	11.40	20.49	13.91	1,496.2	
*339.24	1.37	2021.13	*15.72	524.05	4.89		
NL 1565	NL PLSA 1565		Normal	NA	1738.72		
955.73	1634.03	*0.83	21.71	*2.72	12.17	985.00	
*339.24	1.46	995.39	164.42	783.15	11.48		
NL 1566	NL PLSA 1566		Normal	NA	*147.7		
835.39	1897.76	5.71	6.95	26.00	7.99	539.94	
2452.42	1.65	1483.73	322.68	1809.18	3.71		
NL 1567	NL PLSA 1567		Normal	NA	*147.7		
702.75	1415.2	*0.83	5.58	*2.72	13.75	*77.35	
*339.24	1.5	1108.6	134.68	876.84	8.62		
NL 1568	NL PLSA 1568		Normal	NA	2339.33		
1135.90	1371.53	7.17	18.08	45.88	14.36	1,620.9	
13499	1.61	1012.21	116.54	1292.29	4.58		
NL 1569	NL PLSA 1569		Normal	NA	1996.48		
1495.26	1405.7	9.08	18.59	33.42	11.53	2067.80	
2850.45	1.92	1244.26	280.31	940	8.3		
NL 1570	NL PLSA 1570		Normal	NA	3247.53		
1267.80	1493.12	*0.83	8.86	*2.72	17.22	876.14	
*339.24	1.91	1895.53	*15.72	1528.97	4.31		
NL 1571	NL PLSA 1571		Normal	NA	3545.52		
1207.87	2743.65	*0.83	25.36	24.46	15.85	1362.70	
*339.24	1.38	2213.45	*15.72	1027.29	5.33		
NL 1572	NL PLSA 1572		Normal	NA	*147.7		
684.64	1932.26	6.93	7.94	*2.72	22.52	1090.26	
*339.24	1.27	1082.05	*15.72	802.25	8.08		
NL 1573	NL PLSA 1573		Normal	NA	2242.94		
672.57	299.47	*0.83	40.36	24.46	11.67	777.88	

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*339.24	1.34	1740.8	*15.72	1078.2	4.61		
NL 1574	NL PLSA 1574		Normal	NA	*147.7		
787.19	2155.09	*0.83	6.76	37.68	12.7	713.03	
*339.24	1.43	863.63	*15.72	417.22	8.15		
NL 1575	NL PLSA 1575		Normal	NA	*147.7		
1201.87	1748.54	7.41	42.12	26.00	12.95	3906.71	
*339.24	1.48	1224.83	*15.72	512.65	5.16		
NL 1576	NL PLSA 1576		Normal	NA	*147.7		
1075.89	2162.79	*0.83	4.82	*2.72	12.39	909.14	
2035.45	1.56	1651.47	*15.72	1065.57	8.27		
NL 1577	NL PLSA 1577		Normal	NA	*147.7		
1225.85	2972.03	6.68	25.06	*2.72	18.38	1157.78	
*339.24	2.03	2198.2	*15.72	1140.47	4.16		
NL 1578	NL PLSA 1578		Normal	NA	6338.55		
1399.54	2827.46	*0.83	24.89	*2.72	19.17	1466.40	
*339.24	1.71	2500.03	*15.72	1514.41	6.02		
NL 1579	NL PLSA 1579		Normal	NA	1792.77		
654.45	898.98	11.89	24.23	*2.72	11.24	1481.28	
*339.24	1.53	1419.94	94.3	714.71	9.86		
NL 1580	NL PLSA 1580		Normal	NA	1443.65		
853.45	2332.49	10.02	12.25	*2.72	20.03	1177.15	
*339.24	3.74	1990.92	248.05	1433.28	3.45		
NL 1581	NL PLSA 1581		Normal	NA	1901.22		
6030.73	2593.92	8.13	10.49	*2.72	14.51	1,873.4	
*339.24	1.65	2494.88	94.3	1403.3	9.93		
NL 1582	NL PLSA 1582		Normal	NA	*147.7		
149.31	1704.62	7.65	37.38	37.68	14.25	1630.91	
*339.24	1.66	1380.78	*15.72	1444.45	17.21		
NL 1583	NL PLSA 1583		Normal	NA	*147.7		
1216.86	2936.82	9.55	14.56	36.27	15.09	539.94	
*339.24	1.83	1920.59	*15.72	535.34	14.94		
NL 1584	NL PLSA 1584		Normal	NA	8542.93		
1063.88	2263	6.68	15.33	18.02	13.56	504.11	
*339.24	1.92	1444.45	134.68	899.61	5.26		
NL 1585	NL PLSA 1585		Normal	NA	*147.7		
1090.89	2749.49	*0.83	15.73	16.32	21.37	1284.24	
*339.24	1.8	1473.9	*15.72	1433.28	5.82		
NL 1586	NL PLSA 1586		Normal	NA	2811.58		
793.22	2070.46	*0.83	11.47	*2.72	20.08	495.19	
*339.24	1.71	1611.88	*15.72	332.39	6.82		
NL 1587	NL PLSA 1587		Normal	NA	1537.11		
1159.90	2677.48	*0.83	13.50	34.85	18.94	2726.78	
*339.24	1.75	1562.5	*15.72	931.09	9.59		
NL 1588	NL PLSA 1588		Normal	NA	*147.7		
1489.28	1668.36	8.36	7.11	*2.72	9.88	2641.96	
*339.24	1.76	1843	*15.72	1319.44	10.57		
NL 1589	NL PLSA 1589		Normal	NA	*147.7		
472.85	2720.28	7.65	24.14	*2.72	11.14	*77.35	

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3604.40	1.65	858.86	264.68	913.16	11.84		
NL 1590	NL PLSA 1590		Normal	NA	4961.28		
859.47	4542.25	*0.83	18.68	*2.72	12.65	*77.35	
*339.24	1.41	1424.84	94.3	684.53	6.48		
NL 1591	NL PLSA 1591		Normal	NA	5196.03		
1243.83	816.19	*0.83	6.09	*2.72	11.67	740.76	
*339.24	2.02	1845.5	134.68	1052.87	7.28		
NL 1592	NL PLSA 1592		Normal	NA	2839.56		
1626.77	1263.46	*0.83	25.03	*2.72	16.5	1,357.8	
*339.24	1.46	1995.95	164.42	1010.09	6.53		
NL 1593	NL PLSA 1593		Normal	NA	*147.7		
290.30	2147.39	6.2	15.07	*2.72	10.48	1042.28	
*339.24	1.72	110.11	264.68	658.95	6.81		
NL 1594	NL PLSA 1594		Normal	NA	1337.36		
1357.64	3109.19	7.65	38.31	*2.72	16.69	*77.35	
*339.24	1.67	2655.12	*15.72	4998.47	7.45		
NL 1595	NL PLSA 1595		Normal	NA	1537.11		
1345.67	2584.21	*0.83	34.17	21.30	19.87	1254.94	
*339.24	1.9	1968.29	*15.72	1209.37	9.41		
NL 1596	NL PLSA 1596		Normal	NA	*147.7		
612.14	1895.85	5.22	21.02	26.00	14.98	504.11	
*339.24	2.34	916.24	94.3	1148.66	7.83		
NL 1597	NL PLSA 1597		Normal	NA	*147.7		
600.04	1769.56	5.22	20.80	22.89	9.36	815.18	
*339.24	2.23	1021.83	210.71	1384.43	13.97		
NL 1598	NL PLSA 1598		Normal	NA	1982.85		
1832.79	2454.32	*0.83	8.02	*2.72	11.14	*77.35	
*339.24	1.95	2051.38	94.3	1069.79	4.84		
NL 1599	NL PLSA 1599		Normal	NA	1792.77		
1024.84	2051.24	*0.83	11.32	*2.72	9.42	*77.35	
*339.24	1.83	1639.09	*15.72	1197.33	7.46		
NL 1600	NL PLSA 1600		Normal	NA	*147.7		
1441.43	2901.64	*0.83	31.11	19.67	22.66	3801.32	
*339.24	1.33	1402.8	280.31	585	7.48		
NL 1601	NL PLSA 1601		Normal	NA	3120.47		
1531.14	3066.04	5.22	6.38	30.50	18.32	2139.96	
*339.24	1.14	1520.62	335.64	1035.85	6.2		
NL 1602	NL PLSA 1602		Normal	NA	*147.7		
1291.77	2062.77	5.22	22.80	16.32	13.36	1186.85	
2035.45	2.04	1351.45	164.42	601.16	10.25		
NL 1603	NL PLSA 1603		Normal	NA	2297.98		
1847.71	1670.27	6.2	31.69	*2.72	19.55	1148.11	
*339.24	1.64	2231.25	94.3	1260.97	3.81		
NL 1604	NL PLSA 1604		Normal	NA	3205.14		
1453.39	4686.33	*0.83	61.79	*2.72	19.65	5460.88	
*339.24	1.56	1785.61	94.3	1425.81	8.67		
NL 1605	NL PLSA 1605		Normal	NA	2160.55		
1423.48	2309.32	*0.83	8.19	25.23	12.7	1167.46	

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*339.24	1.35	508.04	*15.72	1311.71	6.9		
NL 1606	NL PLSA 1606		Normal	NA	*147.7		
1261.81	1531.17	6.2	20.96	16.32	9.54	1148.11	
*339.24	1.89	1496.02	134.68	1010.09	8.69		
NL 1607	NL PLSA 1607		Normal	NA	1231.65		
1859.64	1717.98	15.58	12.13	*2.72	12.52	1186.85	
*339.24	1.67	2041.29	264.68	1418.32	5.91		
NL 1608	NL PLSA 1608		Normal	NA	3176.89		
2062.43	232.42	*0.83	6.69	*2.72	22.8	843.26	
*339.24	1.5	1745.78	94.3	704.71	9.57		
NL 1609	NL PLSA 1609		Normal	NA	4610.45		
1970.19	1694.63	5.94	11.26	18.38	14.98	*72.188	
*336.559	0.69	2860.01	87.1	731.57	9.39		
NL 1610	NL PLSA 1610		Normal	NA	2056.28		
2350.17	1794.56	*0.827	27.83	20.39	18.55	509.62	
*336.559	0.9	2398	*14.082	398.13	16.75		
NL 1611	NL PLSA 1611		Normal	NA	*141.842		
2119.57	1905.82	*0.827	12.20	*2.767	14.87	*72.188	
*336.559	0.6	2588.8	101.68	1073.27	5.36		
NL 1612	NL PLSA 1612		Normal	NA	1108.62		
1844.12	2990.65	*0.827	11.46	*2.767	12.59	604.34	
*336.559	0.58	2902.03	*14.082	706.88	4.56		
NL 1613	NL PLSA 1613		Normal	NA	1343.57		
2825.52	2032.24	*0.827	5.06	*2.767	16.2	*72.188	
*336.559	0.74	2387.73	87.1	447.99	7.3		
NL 1614	NL PLSA 1614		Normal	NA	*141.842		
822.02	703.14	*0.827	9.88	24.87	10.18	762.92	
*336.559	0.96	1249.07	184.57	881.65	6.43		
NL 1615	NL PLSA 1615		Normal	NA	*141.842		
667.22	1414.33	*0.827	33.64	16.86	14.64	847.56	
*336.559	0.69	1862.12	130.87	739.73	9.48		
NL 1616	NL PLSA 1616		Normal	NA	*141.842		
3832.12	475.84	5.39	17.15	70.35	26.86	445.71	
*336.559	1.38	2398	*14.082	1273.34	71.16		
NL 1617	NL PLSA 1617		Normal	NA	*141.842		
617.74	2332.97	6.16	19.22	*2.767	18.41	1603.13	
2678.49	0.76	1409.19	*14.082	1083.94	14.83		
NL 1618	NL PLSA 1618		Normal	NA	3361.09		
1904.25	1118.72	5.83	9.10	*2.767	24.65	*72.188	
*336.559	0.89	2640.69	*14.082	979.16	8.45		
NL 1619	NL PLSA 1619		Normal	NA	*141.842		
1884.20	2181.41	*0.827	7.58	*2.767	15.67	*72.188	
*336.559	0.83	2833.78	106.2	1192.04	10.27		
NL 1620	NL PLSA 1620		Normal	NA	1607.48		
922.13	1408.81	*0.827	7.11	*2.767	16.2	609.7	
*336.559	0.94	1921.93	*14.082	1030.22	6.48		
NL 1621	NL PLSA 1621		Normal	NA	1736.84		
2407.95	1922.54	*0.827	24.03	*2.767	11.3	1,551.8	

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*336.559	0.94	1748.12	*14.082	1108.68	10.14		
NL 1622	NL PLSA 1622		Normal	NA	*141.842		
1467.98	3316.1	*0.827	14.50	*2.767	9.42	729.55	
*336.559	0.85	1455	87.1	780.08	11.99		
NL 1623	NL PLSA 1623		Normal	NA	2083.45		
888.71	2194.49	*0.827	7.17	*2.767	19.3	*72.188	
*336.559	0.72	2387.73	*14.082	819.68	18.68		
NL 1624	NL PLSA 1624		Normal	NA	*141.842		
722.36	2103.03	*0.827	7.01	*2.767	17.93	583.0	
*336.559	0.71	1979.47	*14.082	1378.92	15.06		
NL 1625	NL PLSA 1625		Normal	NA	1505.68		
913.77	1957.84	*0.827	13.77	24.87	9.42	620.41	
*336.559	0.64	1306.16	130.87	279.15	7.37		
NL 1626	NL PLSA 1626		Normal	NA	940.86		
601.28	1737.17	*0.827	13.31	*2.767	10.59	1281.40	
*336.559	0.78	500.42	196.33	639.43	13.88		
NL 1627	NL PLSA 1627		Normal	NA	*141.842		
399.85	2927.8	*0.827	18.72	19.89	12.68	572.43	
*336.559	0.66	783.83	87.1	560.33	10.69		
NL 1628	NL PLSA 1628		Normal	NA	1185.79		
822.02	2181.41	*0.827	7.51	*2.767	10.42	527.80	
*336.559	0.78	1033.07	*14.082	1478.49	5.84		
NL 1629	NL PLSA 1629		Normal	NA	*141.842		
2151.22	418.85	*0.827	36.68	*2.767	12.77	2065.95	
*336.559	0.87	3522.81	97	1519.52	10.33		
NL 1630	NL PLSA 1630		Normal	NA	*141.842		
1151.67	2342.35	*0.827	23.49	*2.767	14.45	631.18	
*336.559	0.78	1684.08	*14.082	1044.64	11.14		
NL 1631	NL PLSA 1631		Normal	NA	*141.842		
1106.73	1998.74	*0.827	17.64	*2.767	15.13	768.5	
*336.559	0.95	1149.88	*14.082	1015.73	8.6		
NL 1632	NL PLSA 1632		Normal	NA	*141.842		
950.02	596.91	*0.827	12.78	*2.767	10.98	847.56	
2288.36	1.21	1265.69	165.88	452.86	11.52		
NL 1633	NL PLSA 1633		Normal	NA	2521.83		
944.44	1425.37	*0.827	8.87	*2.767	12.21	824.83	
*336.559	0.72	1844.71	*14.082	858.6	3.98		
NL 1634	NL PLSA 1634		Normal	NA	*141.842		
2901.18	2082.53	4.96	12.65	*2.767	16.9	561.87	
*336.559	0.91	1450.17	*14.082	1212.55	26.22		
NL 1635	NL PLSA 1635		Normal	NA	*141.842		
736.18	1713.12	*0.827	5.69	*2.767	16.2	*72.188	
*336.559	0.74	1074.96	178.49	372.35	4.3		
NL 1636	NL PLSA 1636		Normal	NA	5396.23		
2703.47	2662.33	*0.827	11.41	*2.767	16.8	696.5	
*336.559	1.27	2219.23	87.1	1041.05	6.82		
NL 1637	NL PLSA 1637		Normal	NA	*141.842		
3070.22	1772.34	*0.827	16.71	*2.767	13.97	1468.96	

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*336.559	1.56	2408.26	*14.082	723.37	20.57		
NL 1638	NL PLSA 1638		Normal	NA	1325.14		
546.54	1517.44	*0.827	4.22	*2.767	14.09	*72.188	
*336.559	0.87	1738.25	165.88	1293.37	9.55		
NL 1639	NL PLSA 1639		Normal	NA	*141.842		
560.21	346.99	*0.827	11.90	*2.767	12.77	*72.188	
*336.559	0.82	1916.94	106.2	569.31	4.82		
NL 1640	NL PLSA 1640		Normal	NA	1221.8		
705.80	1939.25	*0.827	9.89	*2.767	17.87	1,015.8	
*336.559	0.75	1684.08	97	438.18	9.68		
NL 1641	NL PLSA 1641		Normal	NA	*141.842		
1467.98	1794.56	*0.827	4.44	*2.767	9.68	609.69	
*336.559	1.04	2873.13	114.85	1933.66	7.62		
NL 1642	NL PLSA 1642		Normal	NA	1543.68		
3462.09	1894.69	*0.827	11.41	*2.767	18.81	535.62	
*336.559	1.23	3380.2	*14.082	1273.34	7.53		
NL 1643	NL PLSA 1643		Normal	NA	*141.842		
1337.71	3176	*0.827	17.11	*2.767	17.18	633.87	
*336.559	0.7	2578.44	*14.082	324.21	10.91		
NL 1644	NL PLSA 1644		Normal	NA	1185.79		
2110.94	1920.68	*0.827	7.33	*2.767	12.77	922.3	
*336.559	1.14	2014.59	*14.082	1122.72	6.83		
NL 1645	NL PLSA 1645		Normal	NA	*141.842		
1496.36	2518.96	*0.827	20.57	*2.767	12.49	699.2	
*336.559	0.92	2077.49	*14.082	1157.57	3.65		
NL 1646	NL PLSA 1646		Normal	NA	1138.17		
716.84	1824.21	*0.827	13.95	*2.767	12.77	*72.188	
*336.559	0.74	3065.64	*14.082	956.98	9.03		
NL 1647	NL PLSA 1647		Normal	NA	*141.842		
1490.68	1364.67	*0.827	24.57	*2.767	12.45	1250.63	
*336.559	0.76	1595.88	*14.082	505.29	6.55		
NL 1648	NL PLSA 1648		Normal	NA	1021.07		
634.22	2707.71	5.07	5.93	*2.767	16.9	535.6	
*336.559	0.92	1829.81	*14.082	613.48	14.31		
NL 1649	NL PLSA 1649		Normal	NA	*141.842		
4173.99	2370.48	7.16	6.59	*2.767	19.95	2,800.2	
*336.559	0.8	2234.49	*14.082	486.46	7.73		
NL 1650	NL PLSA 1650		Normal	NA	*141.842		
1388.63	1652.13	*0.827	22.34	*2.767	11.72	*72.188	
*336.559	0.72	1681.62	*14.082	1073.27	6.28		
NL 1651	NL PLSA 1651		Normal	NA	*141.842		
694.77	3950.54	*0.827	9.34	*2.767	15.57	853.27	
*336.559	0.96	1583.68	123.05	1044.64	7.22		
NL 1652	NL PLSA 1652		Normal	NA	*141.842		
2729.61	3264.22	*0.827	18.58	19.13	12.72	1500.70	
*336.559	0.63	3230.41	127	1051.83	7.81		
NL 1653	NL PLSA 1653		Normal	NA	1915.01		
1550.33	884.32	7.16	10.18	22.88	13.04	639.3	

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2824	0.74	2506.07	282.42	457.71	6	
NL 1654	NL PLSA 1654		Normal	NA	*141.842	
1575.92	1967.13	*0.827	46.13	*2.767	11.82	1162.22
*336.559	0.61	2007.06	*14.082	739.73	12.73	
NL 1655	NL PLSA 1655		Normal	NA	16512.36	
1329.23	2136.61	6.27	7.21	*2.767	14.13	1072.12
2678.49	2.04	977.53	234.28	2252.69	6.5	
NL 1656	NL PLSA 1656		Normal	NA	2056.28	
810.92	2346.1	11.06	14.21	*2.767	11.3	483.86
*336.559	0.97	2072.45	172.26	*78.12	8.14	
NL 1657	NL PLSA 1657		Normal	NA	906.95	
1168.54	2088.12	*0.827	7.05	23.38	15.71	2735.51
*336.559	0.72	940.71	*14.082	927.12	10.66	
NL 1658	NL PLSA 1658		Normal	NA	*141.842	
2402.17	1679.84	*0.827	16.69	*2.767	12.59	2,575.2
*336.559	0.58	1664.43	*14.082	755.96	6.69	
NL 1659	NL PLSA 1659		Normal	NA	2090.26	
271.16	3638.68	*0.827	31.95	*2.767	13.93	1,213.9
*336.559	0.88	2770.96	*14.082	551.3	8.52	
NL 1660	NL PLSA 1660		Normal	NA	*141.842	
672.73	4017.17	*0.827	19.05	*2.767	21.33	3959.21
*336.559	0.92	1327.65	87.1	1588.07	7.27	
NL 1661	NL PLSA 1661		Normal	NA	*141.842	
565.68	464.82	6.05	6.10	*2.767	10.76	468.53
2092.79	0.64	1349.18	218.56	919.6	8.34	
NL 1662	NL PLSA 1662		Normal	NA	2686.57	
997.49	1333.43	*0.827	36.92	*2.767	15.02	836.18
*336.559	1.17	2362.11	*14.082	635.13	5.95	
NL 1663	NL PLSA 1663		Normal	NA	*141.842	
913.77	3000.18	*0.827	4.87	*2.767	12.06	2219.45
*336.559	0.48	1882.03	*14.082	747.86	7.12	
NL 1664	NL PLSA 1664		Normal	NA	1620.32	
656.22	2662.33	5.18	6.87	*2.767	21.5	593.67
*336.559	1.52	2077.49	*14.082	630.83	10.84	
NL 1665	NL PLSA 1665		Normal	NA	*141.842	
4926.21	2028.52	7.61	6.97	*2.767	21.6	2,785.8
*336.559	0.55	2356.98	*14.082	457.71	4.87	
NL 1666	NL PLSA 1666		Normal	NA	*141.842	
1402.79	1570.91	*0.827	36.17	*2.767	14.05	*72.188
*336.559	0.8	1882.03	*14.082	1073.27	5.25	
NL 1667	NL PLSA 1667		Normal	NA	*141.842	
716.84	3198.99	*0.827	9.73	*2.767	17.25	847.56
*336.559	1.01	1735.78	106.2	1058.99	4.46	
NL 1668	NL PLSA 1668		Normal	NA	*141.842	
2266.47	3160.67	*0.827	23.15	*2.767	13.72	2089.68
*336.559	0.38	3493.15	114.85	723.37	7.5	
NL 1669	NL PLSA 1669		Normal	NA	1736.84	
1502.03	992.32	6.71	9.77	19.39	10.76	682.76

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2678.49	0.66	2578.44	286.95	505.29	8.77		
NL 1701	NL PLSA 1701		Normal	NA	2254.19		
3781.59	4612.17	8.62	24.92	21.20	18.09	2024.99	
*332.479	1.48	*30.173	118.75	1088.63	7.33		
NL 1702	NL PLSA 1702		Normal	NA	1600.12		
3193.60	3203.93	*0.833	15.02	*2.733	27.85	650.36	
*332.479	1.18	3115.57	118.75	923.5	10.33		
NL 1703	NL PLSA 1703		Normal	NA	5305.31		
1094.80	2425.33	6.66	9.23	18.42	17.16	982.59	
1994.88	1.21	1554.55	185.29	391.29	15.56		
NL 1704	NL PLSA 1704		Normal	NA	4500.37		
1449.40	2362.3	*0.833	2.24	*2.733	17.75	1222.04	
*332.479	1.37	2231.3	240.18	659.24	4.99		
NL 1705	NL PLSA 1705		Normal	NA	1200.48		
2016.95	3508.48	5.25	31.65	*2.733	23.37	675.33	
*332.479	1.22	1001.09	176.07	765.99	8.98		
NL 1706	NL PLSA 1706		Normal	NA	1121.29		
1105.81	2181.29	*0.833	10.93	*2.733	11.15	545.35	
*332.479	1.4	725.4	102.9	939.86	4.78		
NL 1707	NL PLSA 1707		Normal	NA	*131.507		
947.33	2407.06	*0.833	6.81	*2.733	7.52	*77.963	
*332.479	1.22	1087.89	155.91	695.39	6.81		
NL 1708	NL PLSA 1708		Normal	NA	*131.507		
1807.34	3172.69	*0.833	8.68	*2.733	15.49	697.26	
*332.479	1.16	2439.35	155.91	644	5.39		
NL 1709	NL PLSA 1709		Normal	NA	*131.507		
2193.35	1944.45	7.31	21.94	33.05	16.13	949.94	
*332.479	0.95	1937.92	194.06	811.95	4.43		
NL 1710	NL PLSA 1710		Normal	NA	3918.26		
615.38	1484.88	*0.833	6.37	*2.733	13.78	694.13	
*332.479	1.05	510.7	247.07	851.5	5.36		
NL 1711	NL PLSA 1711		Normal	NA	*131.507		
1674.69	921.29	6.02	3.12	*2.733	11.37	600.72	
*332.479	1.42	1691.19	83.33	336.46	4.81		
NL 1712	NL PLSA 1712		Normal	NA	*131.507		
1460.72	1865.86	*0.833	8.91	*2.733	12.17	1128.02	
*332.479	1.48	1703.55	118.75	794.81	9.82		
NL 1713	NL PLSA 1713		Normal	NA	1843.17		
1506.12	2875.07	*0.833	19.08	*2.733	12.17	*77.963	
*332.479	1.73	1256.55	118.75	993.78	5.51		
NL 1714	NL PLSA 1714		Normal	NA	946.05		
5556.32	3301.44	*0.833	5.21	*2.733	10.61	1208.54	
*332.479	0.55	2288.42	83.33	1073.01	9.71		
NL 1715	NL PLSA 1715		Normal	NA	*131.507		
1149.96	5708.31	*0.833	13.41	22.76	14.48	878.62	
2589.23	0.84	2001.83	144.71	369.66	8.83		
NL 1716	NL PLSA 1716		Normal	NA	*131.507		
3887.84	2332.53	*0.833	8.29	*2.733	13.03	1378.95	

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*332.479	1.3	1138.48	83.33	659.24	3.41		
NL 1717	NL PLSA 1717		Normal	NA	1439.48		
1824.72	4623.3	*0.833	22.64	*2.733	14.69	824.02	
*332.479	1.13	1617.45	102.9	419.56	3.28		
NL 1718	NL PLSA 1718		Normal	NA	*131.507		
834.21	3031.03	*0.833	4.82	*2.733	8.25	478.36	
*332.479	0.93	1480.23	185.29	355.02	6.35		
NL 1719	NL PLSA 1719		Normal	NA	*131.507		
1580.18	2945.18	*0.833	10.75	*2.733	14.41	*77.963	
*332.479	1.09	1544.46	102.9	789.07	4.49		
NL 1720	NL PLSA 1720		Normal	NA	5127.7		
1012.60	3070.66	*0.833	4.40	*2.733	21.64	1141.38	
*332.479	1.35	2800.46	102.9	871.07	4.5		
NL 1721	NL PLSA 1721		Normal	NA	*131.507		
1497.60	3025.87	*0.833	12.74	19.61	17.4	930.4	
*332.479	1.26	1895.57	102.9	713.24	8.14		
NL 1722	NL PLSA 1722		Normal	NA	*131.507		
1720.71	3151.89	*0.833	9.22	*2.733	9.95	*77.963	
*332.479	1.27	2354.74	118.75	340.2	5.49		
NL 1723	NL PLSA 1723		Normal	NA	2043.16		
649.19	2350.72	5	12.83	*2.733	24.63	814.43	
*332.479	0.91	1510.26	83.33	546.78	6.47		
NL 1724	NL PLSA 1724		Normal	NA	1130.08		
561.15	1067.99	5.5	4.88	*2.733	14.79	2,091.7	
1995	1.03	329.06	233.1	*92.89	4.77		
NL 1725	NL PLSA 1725		Normal	NA	171255.75		
23665.88	1241.58	*0.833	10.72	*2.733	14.27	*77.963	
*332.479	0.89	1486.22	102.9	1251.26	4.86		
NL 1726	NL PLSA 1726		Normal	NA	*131.507		
1191.50	593.19	*0.833	13.49	*2.733	11.71	1437.69	
*332.479	0.98	1392.92	176.07	956.14	8.18		
NL 1727	NL PLSA 1727		Normal	NA	*131.507		
2102.02	3765.81	*0.833	4.67	*2.733	16.93	*77.963	
*332.479	1.5	2687.98	132.45	969.63	5.03		
NL 1728	NL PLSA 1728		Normal	NA	2985.13		
1577.32	4604.75	*0.833	16.27	25.48	46.21	2,817.6	
*332.479	1.04	1034.14	83.33	873.85	17.75		
NL 1729	NL PLSA 1729		Normal	NA	998.52		
1738.00	4434.83	*0.833	8.27	22.76	18.84	3191.78	
*332.479	1.16	1013.92	125.81	1078.22	7.05		
NL 1730	NL PLSA 1730		Normal	NA	*131.507		
901.37	1461.68	*0.833	3.62	*2.733	8.53	551.5	
*332.479	0.93	1195.28	118.75	362.37	5.5		
NL 1731	NL PLSA 1731		Normal	NA	841.32		
2571.42	2852.9	*0.833	6.79	*2.733	18.71	885.08	
*332.479	1.57	3063.71	144.71	575.53	7.75		
NL 1732	NL PLSA 1732		Normal	NA	*131.507		
1166.56	1557.91	5.63	13.46	18.82	9.45	*77.963	

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*332.479	1.58	505.99	218.3	553.21	4.74		
NL 1733	NL PLSA 1733		Normal	NA	*131.507		
1319.81	1845.09	8.62	6.24	*2.733	7.77	484.42	
*332.479	1.34	1732.47	155.91	376.91	4.79		
NL 1734	NL PLSA 1734		Normal	NA	*131.507		
1194.28	2522.01	*0.833	24.11	21.20	11.15	*77.963	
*332.479	3.36	2135.37	210.52	419.56	3.06		
NL 1735	NL PLSA 1735		Normal	NA	*131.507		
4262.03	3724.78	*0.833	6.60	18.82	20.14	788.92	
*332.479	1.58	1605.23	*13.888	945.29	7.99		
NL 1736	NL PLSA 1736		Normal	NA	3263.06		
1188.73	1713.28	5.25	7.74	*2.733	10.61	1098.04	
*332.479	0.8	1993.28	194.06	559.62	4.47		
NL 1737	NL PLSA 1737		Normal	NA	3282.36		
925.67	3824.82	*0.833	5.82	*2.733	21.83	1114.68	
*332.479	1.65	2923.27	132.45	1129.96	3.99		
NL 1738	NL PLSA 1738		Normal	NA	*131.507		
1125.10	2461.93	*0.833	7.22	18.82	7.26	551.5	
*332.479	0.56	1460.28	83.33	904.29	6.09		
NL 1739	NL PLSA 1739		Normal	NA	858.76		
1600.18	2311.07	*0.833	12.84	*2.733	10.75	490.49	
*332.479	1.31	2290.63	*13.888	1320.33	3.24		
NL 1740	NL PLSA 1740		Normal	NA	*131.507		
1543.10	1776.63	*0.833	6.08	20.01	9.55	551.5	
*332.479	0.52	1769.81	102.9	789.07	7.85		
NL 1741	NL PLSA 1741		Normal	NA	806.46		
3098.65	3231.74	*0.833	6.71	*2.733	12.21	619.29	
*332.479	1.05	164.43	83.33	647.06	9.79		
NL 1742	NL PLSA 1742		Normal	NA	884.93		
1089.30	3304.93	*0.833	9.24	*2.733	14.34	1,358.3	
*332.479	1.28	1980.47	194.06	713.24	4.97		
NL 1743	NL PLSA 1743		Normal	NA	*131.507		
2128.50	2656.3	*0.833	8.18	*2.733	10.89	*77.963	
*332.479	1.16	1842.93	102.9	412.55	4.52		
NL 1744	NL PLSA 1744		Normal	NA	*131.507		
3089.48	1786.16	*0.833	3.42	*2.733	16.56	1698.13	
*332.479	0.98	1931.55	102.9	1030.99	10.42		
NL 1745	NL PLSA 1745		Normal	NA	2635.41		
2084.39	3138.04	*0.833	12.43	*2.733	19.3	493.52	
*332.479	0.81	2470.69	*13.888	845.89	6.85		
NL 1746	NL PLSA 1746		Normal	NA	3311.33		
2562.42	642.83	6.27	5.66	*2.733	29.15	4011.70	
2654.31	0.92	1202.9	260.35	1007.12	13.59		
NL 1747	NL PLSA 1747		Normal	NA	1626.99		
2867.14	2545.43	*0.833	12.67	*2.733	11.07	644.14	
1994.88	1.13	2284.02	176.07	*92.89	4.27		
NL 1748	NL PLSA 1748		Normal	NA	*131.507		
449.31	1918.74	*0.833	5.64	*2.733	9.65	631.70	

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*332.479	2.07	1633.77	132.45	1474.2	0.91		
NL 1749	NL PLSA 1749		Normal	NA	*131.507		
2087.33	2996.64	*0.833	14.80	*2.733	11.33	681.59	
*332.479	1.43	2205.04	102.9	546.78	2.38		
NL 1750	NL PLSA 1750		Normal	NA	1332.98		
1726.47	1947.66	*0.833	13.69	*2.733	11.76	533.12	
*332.479	1.09	1765.65	166.31	294.42	5.35		
NL 1751	NL PLSA 1751		Normal	NA	*131.507		
3963.03	3462.68	*0.833	6.22	*2.733	11.76	*77.963	
*332.479	1.25	1687.07	118.75	628.65	4.66		
NL 1752	NL PLSA 1752		Normal	NA	*131.507		
1056.36	2900.69	*0.833	3.97	*2.733	9.8	*77.963	
*332.479	0.92	3051.95	150.42	328.94	7.21		
NL 1753	NL PLSA 1753		Normal	NA	*131.507		
952.75	826.09	6.79	9.64	20.41	10	2047.17	
1994.88	1.19	2341.44	285.25	556.42	5.87		
NL 1754	NL PLSA 1754		Normal	NA	*131.507		
1089.30	2004.09	5.76	12.50	*2.733	14.1	*77.963	
*332.479	0.82	1542.44	102.9	823.31	7.06		
NL 1755	NL PLSA 1755		Normal	NA	911.11		
1144.43	1626.71	*0.833	5.51	*2.733	9.9	650.36	
*332.479	1.14	2642.38	155.91	384.12	5.81		
NL 1756	NL PLSA 1756		Normal	NA	*131.507		
2755.11	3020.71	*0.833	19.97	*2.733	13.22	1385.84	
*332.479	1.28	2018.95	118.75	1036.27	4.87		
NL 1757	NL PLSA 1757		Normal	NA	4157.45		
1714.95	1562.59	6.79	13.93	18.82	18.87	982.6	
*332.479	1.01	953.79	194.06	569.18	6.82		
NL 1758	NL PLSA 1758		Normal	NA	3563.93		
7351.58	1415.43	12.63	11.02	*2.733	10.43	*77.963	
*332.479	1.05	2027.52	132.45	1109.35	4.07		
NL 1759	NL PLSA 1759		Normal	NA	*131.507		
2311.76	2657.98	*0.833	21.22	*2.733	13.22	613.10	
*332.479	1.34	2488.64	83.33	806.25	7.23		
NL 1760	NL PLSA 1760		Normal	NA	*131.507		
1050.88	329.34	*0.833	4.72	*2.733	9.5	*77.963	
*332.479	0.84	1071.15	155.91	575.53	4.87		
NL 1761	NL PLSA 1761		Normal	NA	*131.507		
6055.07	2382.18	*0.833	10.00	*2.733	18.48	709.8	
*332.479	0.72	2535.9	83.33	591.3	7.35		
NL 1762	NL PLSA 1762		Normal	NA	*131.507		
2514.48	3696.29	*0.833	4.00	*2.733	11.67	846.45	
*332.479	2.4	2042.54	118.75	656.2	6.34		
NL 1763	NL PLSA 1763		Normal	NA	1430.59		
2897.50	2832.46	*0.833	12.05	*2.733	12.09	*77.963	
*332.479	1.29	3106.13	218.3	546.78	5.48		
NL 1764	NL PLSA 1764		Normal	NA	*131.507		
1305.80	1917.13	*0.833	12.12	*2.733	19.19	687.9	

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*332.479	0.76	1954.91	83.33	514.28	3.23		
NL 1765	NL PLSA 1765		Normal	NA	*131.507		
2586.43	1944.45	*0.833	5.16	*2.733	15.42	989.14	
*332.479	1.38	1013.92	102.9	597.58	6.7		
NL 1766	NL PLSA 1766		Normal	NA	*131.507		
1111.32	1529.89	*0.833	11.22	19.61	10.98	644.1	
*332.479	0.84	722	194.06	376.91	4.95		
NL 1767	NL PLSA 1767		Normal	NA	*131.507		
2478.58	3503.19	*0.833	12.72	*2.733	13.11	*77.963	
*332.479	1.87	2385.84	83.33	467.67	5.04		
NL 1768	NL PLSA 1768		Normal	NA	*131.507		
1015.33	1929.98	5	7.24	*2.733	7.77	594.55	
*332.479	1.07	2094.24	273.05	309.91	4.21		
NL 1769	NL PLSA 1769		Normal	NA	*131.507		
1100.31	1765.52	*0.833	16.34	*2.733	14.27	472.31	
*332.479	0.97	1984.74	102.9	725.06	3.45		
NL 1770	NL PLSA 1770		Normal	NA	*131.507		
933.79	1196.35	*0.833	4.64	*2.733	13.63	827.22	
*332.479	1.45	3382.6	83.33	*92.89	2.87		
NL 1771	NL PLSA 1771		Normal	NA	*131.507		
1155.49	2686.66	*0.833	3.29	*2.733	13.18	490.49	
2654.31	1.2	1609.3	194.06	487.82	2.84		
NL 1772	NL PLSA 1772		Normal	NA	1033.55		
3071.14	4414.59	*0.833	9.08	*2.733	10.33	594.55	
*332.479	1.08	2018.95	83.33	585.01	4.37		
NL 1773	NL PLSA 1773		Normal	NA	806.46		
1361.93	3136.31	*0.833	3.22	*2.733	11.11	606.91	
*332.479	1.23	1254.63	185.29	540.33	18.02		
NL 1774	NL PLSA 1774		Normal	NA	806.46		
3950.49	3062.04	*0.833	11.33	*2.733	19.09	2605.46	
*332.479	0.97	2920.94	102.9	440.38	6.32		
NL 1775	NL PLSA 1775		Normal	NA	*131.507		
1067.33	3089.64	*0.833	5.73	*2.733	12.61	606.91	
*332.479	1.16	1597.1	118.75	713.24	4.69		
NL 1776	NL PLSA 1776		Normal	NA	*131.507		
3004.00	2493.61	*0.833	11.21	*2.733	14.48	722.42	
*332.479	1.17	206.97	*13.888	760.19	6.39		
NL 1777	NL PLSA 1777		Normal	NA	*127.973		
1065.09	1289.06	*0.805	7.75	*2.369	16.3	504.26	
*322.135	1.22	1339.65	*13.379	494.31	4.27		
NL 1778	NL PLSA 1778		Normal	NA	1677.86		
1218.76	1829.08	5.36	6.52	*2.369	40.82	881.77	
*322.135	1.56	897.66	164.29	389.1	5.3		
NL 1779	NL PLSA 1779		Normal	NA	*127.973		
1311.20	2334.61	*0.805	11.93	*2.369	26.76	511.71	
*322.135	1.73	1966.52	90.59	1082.51	4.28		
NL 1780	NL PLSA 1780		Normal	NA	*127.973		
1739.28	2994.38	*0.805	11.07	*2.369	7.72	519.17	

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*322.135	1.03	1053.57	90.59	752.15	2.7		
NL 1781	NL PLSA 1781		Normal	NA	*127.973		
3299.13	3669.87	*0.805	7.53	*2.369	21.67	694.98	
*322.135	1.29	2296.13	90.59	869.3	1.92		
NL 1782	NL PLSA 1782		Normal	NA	*127.973		
1102.67	3111.73	*0.805	8.59	*2.369	17.13	*75.427	
*322.135	1.23	876.65	*13.379	785.31	5.04		
NL 1783	NL PLSA 1783		Normal	NA	1776.7		
716.28	1117.89	*0.805	19.30	*2.369	30.2	602.32	
*322.135	1.09	2231.03	*13.379	532.64	2.09		
NL 1784	NL PLSA 1784		Normal	NA	*127.973		
836.61	1377.58	*0.805	13.01	*2.369	20.97	2276.33	
2667.75	0.97	1449.7	237.61	232.78	6.1		
NL 1785	NL PLSA 1785		Normal	NA	*127.973		
1385.01	207.28	*0.805	11.25	*2.369	20.57	1502.97	
*322.135	1.88	887.14	282.92	3788.93	2.33		
NL 1786	NL PLSA 1786		Normal	NA	1062.41		
1876.69	3097.79	*0.805	10.03	*2.369	28.04	910.1	
*322.135	1.26	1241.96	90.59	791.88	2.3		
NL 1787	NL PLSA 1787		Normal	NA	*127.973		
679.94	1144.82	8.98	13.50	*2.369	27.11	*75.427	
*322.135	2.39	539.26	121.5	389.1	2.71		
NL 1788	NL PLSA 1788		Normal	NA	*127.973		
1633.38	2677.94	*0.805	8.81	*2.369	23.31	*75.427	
*322.135	3.44	929.28	90.59	1527.44	13.84		
NL 1789	NL PLSA 1789		Normal	NA	*127.973		
979.57	2901.16	*0.805	7.09	*2.369	20.03	519.17	
*322.135	3.82	1633.58	90.59	613.7	3.46		
NL 1790	NL PLSA 1790		Normal	NA	*127.973		
2701.77	2428.51	*0.805	15.37	*2.369	24.27	1158.58	
*322.135	1.27	1421.59	181.5	691.08	5.01		
NL 1791	NL PLSA 1791		Normal	NA	1382.01		
1237.75	2703.56	5.72	33.07	*2.369	21.61	549.20	
*322.135	1.41	1130.93	*13.379	804.97	3.35		
NL 1792	NL PLSA 1792		Normal	NA	*127.973		
2397.71	3647.62	*0.805	9.54	*2.369	22.77	749.92	
*322.135	0.67	2018.11	*13.379	824.45	3.18		
NL 1793	NL PLSA 1793		Normal	NA	*127.973		
6327.48	1612.66	21.22	14.45	*2.369	21.42	1494.19	
*322.135	1.97	717.68	312.94	1264.92	4.48		
NL 1794	NL PLSA 1794		Normal	NA	*127.973		
374.88	2948.74	*0.805	13.46	*2.369	23.48	583.26	
*322.135	1.58	527.66	121.5	*24.873	4.21		
NL 1795	NL PLSA 1795		Normal	NA	1995.98		
6034.70	2297.06	*0.768	17.23	*2.652	27.6	*73.544	
*302.743	1.54	1828.15	96.04	893.18	4.04		
NL 1796	NL PLSA 1796		Normal	NA	*123.336		
1429.10	1865.65	*0.768	14.85	*2.652	26.41	809.97	

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*302.743	0.95	1749.86	111.67	2278.07	2.13		
NL 1797	NL PLSA 1797		Normal	NA	*123.336		
1378.68	2362.5	9.97	2.52	*2.652	16.58	*73.544	
*302.743	0.85	1413.47	87.79	744.12	4.46		
NL 1798	NL PLSA 1798		Normal	NA	1256.98		
2027.41	2523.74	*0.768	19.93	*2.652	30.07	*73.544	
*302.743	1.36	492.6	96.04	998.65	4.91		
NL 1799	NL PLSA 1799		Normal	NA	*123.336		
562.52	3601.42	6.54	35.04	19.88	21.63	2138.40	
*302.743	1.05	464.97	119.13	871.49	3.92		
NL 1800	NL PLSA 1800		Normal	NA	*123.336		
1683.29	2922.26	*0.768	12.71	22.62	22.3	833.44	
*302.743	1.05	1108.97	147.17	1222.83	22.91		
NL 1801	NL PLSA 1801		Normal	NA	2794.77		
3388.13	4176.8	*0.768	13.29	*2.652	21.9	3169.21	
*302.743	1.39	1787.93	103.98	2132.97	2.23		
NL 1802	NL PLSA 1802		Normal	NA	4100.92		
647.15	2028.84	*0.768	10.66	*2.652	31.25	*73.544	
*302.743	1.59	1214.4	115.43	315.21	3.87		
NL 1803	NL PLSA 1803		Normal	NA	*123.336		
1683.29	1995.42	*0.768	11.98	*2.652	26.96	545.66	
*302.743	0.8	3514.25	96.04	744.12	1.95		
NL 1804	NL PLSA 1804		Normal	NA	740.02		
2538.98	2473.05	*0.768	17.69	23.17	29.29	3320.75	
*302.743	1.15	2263.78	*13.922	1039.58	3.04		
NL 1805	NL PLSA 1805		Normal	NA	1687.72		
2713.88	460.12	*0.768	39.76	*2.652	22.57	1788.23	
*302.743	1.87	1159.65	100.04	1197.35	5.27		
NL 1806	NL PLSA 1806		Normal	NA	*123.336		
1490.91	2465.54	*0.768	4.10	*2.652	19.9	*73.544	
*302.743	1.06	1559.63	147.17	755.7	3.66		
NL 1807	NL PLSA 1807		Normal	NA	*123.336		
910.21	1688.16	*0.768	1.63	*2.652	19.9	*73.544	
*302.743	1.06	1256.16	119.13	293.02	2.92		
NL 1808	NL PLSA 1808		Normal	NA	1041.01		
1112.37	1595.9	*0.768	15.09	*2.652	16.21	1058.20	
*302.743	0.79	765.97	96.04	347.36	1.84		
NL 1809	NL PLSA 1809		Normal	NA	*123.336		
1019.13	2019.55	*0.768	15.15	16.60	18.97	483.65	
*302.743	1.21	2213.61	87.79	525.16	2.17		
NL 1810	NL PLSA 1810		Normal	NA	*123.336		
4581.44	2325.09	*0.768	*0.22	*2.652	19.9	*73.544	
*302.743	1.37	1848.31	*13.922	418.17	5.33		
NL 1811	NL PLSA 1811		Normal	NA	*123.336		
2128.83	2019.55	*0.768	15.13	17.14	17.9	2,302.4	
*302.743	0.93	993.68	*13.922	914.66	3.77		
NL 1812	NL PLSA 1812		Normal	NA	*123.336		
2429.91	883.5	*0.768	4.18	*2.652	16.67	1461.91	

Table4.txt

*302.743	0.83	1204.94	*13.922	529.6	3.8	NL 1813	NL PLSA 1813
Normal	NA	*123.336	557.26	2159.03	*0.768	7.55	*2.652
19.59	506.38	*302.743	0.8	1485.3	*13.922	456.51	2.95
NL 1814	NL PLSA 1814	Normal	NA	*123.336	1353.53	2326.96	6.8
2.43	17.14	18.81	*73.544	*302.743	1.16	1108.97	96.04
577.56	5.07	NL 1815	NL PLSA 1815	Normal	NA	*123.336	1139.90
1828.63	*0.768	3.41	*2.652	21.07	450.10	*302.743	1.27
1256.16	*13.922	493.6	2.73	NL 1816	NL PLSA 1816	Normal	NA
*123.336	583.62	1991.7	*0.768	3.56	*2.652	13.73	*73.544
*302.743	0.94	1775.89	*13.922	1617.24	2.21	NL 1817	NL PLSA 1817
Normal	NA	936.15	1041.01	1708.47	*0.768	16.85	*2.652
24.63	655.8	*302.743	0.98	2430.44	*13.922	712.89	2.89
NL 1818	NL PLSA 1818	Normal	NA	*123.336	1206.18	2580.14	*0.768
30.77	*2.652	23.09	728.00	*302.743	0.85	2184.44	*13.922
900.36	8.68	NL 1819	NL PLSA 1819	Normal	NA	1679.96	2424.03
2270.91	7.85	34.47	*2.652	19.67	673.05	*302.743	0.7
2575.78	*13.922	293.02	4.04	NL 1820	NL PLSA 1820	Normal	NA
*123.336	392.76	1774.99	*0.768	2.94	*2.652	14.82	*73.544
*302.743	1.15	1049.27	126.39	293.02	1.8	NL 1821	NL PLSA 1821
Normal	NA	*123.336	866.88	2270.91	*0.768	9.58	*2.652
23.09	*73.544	*302.743	1.08	1616.72	*13.922	860.57	7.39
NL 1822	NL PLSA 1822	Normal	NA	*123.336	165.53	1965.73	*0.768
12.87	*2.652	15.82	638.70	*302.743	1.01	1959.91	*13.922
275.93	3.01	NL 1823	NL PLSA 1823	Normal	NA	*123.336	2059.24
1743.57	*0.768	7.91	*2.652	23.53	1145.77	*302.743	1.24
1415.4	140.4	555.97	4.66	NL 1824	NL PLSA 1824	Normal	NA
*123.336	557.26	1806.43	*0.768	8.06	*2.652	26.41	2257.67
*302.743	0.94	898.18	*13.922	484.44	3.15	NL 1825	NL PLSA 1825
Normal	NA	*123.336	1356.33	1776.84	*0.768	15.28	*2.652
26.36	*73.544	*302.743	0.62	811	*13.922	336.78	1.89
NL 1826	NL PLSA 1826	Normal	NA	*123.336	2785.35	2446.79	*0.768
12.54	*2.652	20.93	*73.544	*302.743	0.91	869.02	179.24
615.63	1.42	NL 1827	NL PLSA 1827	Normal	NA	833.57	1328.42
1978.71	*0.768	6.18	*2.652	20.2	809.97	*302.743	1.13
1612.78	133.47	502.7	3.59	NL 1828	NL PLSA 1828	Normal	NA
*123.336	1468.41	3246.66	*0.768	13.05	*2.652	23.59	*73.544

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*302.743	1.41	1506.76	96.04	681.1	5.08		
NL 1829	NL PLSA 1829		Normal	NA	*123.336		
1062.93	2351.27	*0.768	8.83	*2.652	22.96	*73.544	
*302.743	0.72	773.15	*13.922	628.11	3.91		
NL 1830	NL PLSA 1830		Normal	NA	*123.336		
4932.87	5983.29	*0.768	3.09	*2.652	29.34	870.32	
*302.743	1.3	2424.07	*13.922	1266.9	6.31		
NL 1831	NL PLSA 1831		Normal	NA	5676.12		
1502.17	1651.24	*0.768	4.00	*2.652	27.12	1,353.2	
6363	1.73	1146.48	*13.922	1413.6	7.42		
NL 1832	NL PLSA 1832		Normal	NA	*123.336		
753.84	2435.54	*0.768	1.76	*2.652	16.11	*73.544	
*302.743	0.7	1103.35	107.86	827.45	4.1		
NL 1833	NL PLSA 1833		Normal	NA	*123.336		
1082.14	2971.68	*0.768	5.10	*2.652	26.19	452.31	
*302.743	1.06	1015.88	103.98	1662.33	5.4		
NL 1834	NL PLSA 1834		Normal	NA	*123.336		
764.56	2099.47	*0.768	21.56	*2.652	20.2	*73.544	
*302.743	1.11	273.08	*13.922	935.94	2.36		
NL 1835	NL PLSA 1835		Normal	NA	*123.336		
1054.71	2647.93	*0.768	21.88	*2.652	22.1	1044.25	
*302.743	0.98	1917.16	*13.922	437.51	8.65		
NL 1836	NL PLSA 1836		Normal	NA	*123.336		
1065.67	1135.73	*0.768	9.39	*2.652	21.97	*73.544	
*302.743	1.28	1090.27	166.74	1039.58	9.38		
NL 1837	NL PLSA 1837		Normal	NA	*123.336		
1785.92	3909.28	*0.768	3.20	*2.652	29.63	1604.04	
*302.743	1.35	2629.65	147.17	1187.75	7.28		
NL 1838	NL PLSA 1838		Normal	NA	*123.336		
416.08	659.75	*0.768	11.98	*2.652	15.63	1,002.7	
*302.743	0.73	901.83	147.17	511.73	3.73		
NL 1839	NL PLSA 1839		Normal	NA	*123.336		
578.34	2627.21	*0.768	6.12	*2.652	26.41	*73.544	
*302.743	1.01	1880.66	*13.922	1229.16	5.73		
NL 1840	NL PLSA 1840		Normal	NA	*123.336		
7531.68	1987.99	*0.768	8.19	*2.652	21.83	643.58	
*302.743	0.72	1371.01	*13.922	511.73	4.29		
NL 1841	NL PLSA 1841		Normal	NA	1112.1		
509.97	1762.05	*0.768	7.70	*2.652	24.93	*73.544	
*302.743	1.47	1199.26	*13.922	1878.24	5.17		
NL 1842	NL PLSA 1842		Normal	NA	*123.336		
1538.82	1802.73	*0.768	10.21	*2.652	24.93	1183.05	
*302.743	0.99	1951.75	*13.922	357.81	4.61		
NL 1843	NL PLSA 1843		Normal	NA	*123.336		
1200.65	2071.57	*0.768	4.85	*2.652	21.9	465.68	
*302.743	1.78	1715.92	*13.922	594.6	4.06		
NL 1844	NL PLSA 1844		Normal	NA	1147.99		
1322.84	2356.89	*0.768	13.83	*2.652	22.5	529.39	

Table4.txt

*302.743	1.81	1524.35	111.67	573.27	2.14		
NL 1845	NL PLSA 1845		Normal	NA	*123.336		
1929.33	1117.34	*0.768	20.50	*2.652	24.27	576.23	
*302.743	0.82	1723.89	*13.922	1341.05	3.6		
NL 1846	NL PLSA 1846		Normal	NA	*123.336		
1558.58	2918.46	7.06	17.58	*2.652	27.28	538.67	
*302.743	1.15	1321.07	*13.922	827.45	3.91		
NL 1847	NL PLSA 1847		Normal	NA	*123.336		
5194.49	2700.75	*0.768	3.14	*2.652	20.93	*73.544	
*302.743	1.07	2118.06	87.79	564.64	2.11		
NL 1848	NL PLSA 1848		Normal	NA	*123.336		
610.05	1610.65	*0.768	8.84	*2.652	11.2	*73.544	
*302.743	0.82	1378.71	133.47	805.07	4.71		
NL 1849	NL PLSA 1849		Normal	NA	*123.336		
1723.14	1815.68	*0.768	21.38	*2.652	25.28	445.7	
*302.743	0.88	2377.45	*13.922	293.02	7.55		
NL 1850	NL PLSA 1850		Normal	NA	*123.336		
1197.88	3780.3	*0.768	19.88	*2.652	24.69	862.38	
*302.743	1.55	2105.66	*13.922	812.56	5.46		
NL 1851	NL PLSA 1851		Normal	NA	*123.336		
1519.08	2893.79	*0.768	6.95	*2.652	21.76	538.67	
*302.743	1.35	2385.91	*13.922	623.96	4.94		
NL 1852	NL PLSA 1852		Normal	NA	*123.336		
3916.14	3334.98	*0.768	25.71	17.69	27.55	648.46	
*302.743	0.97	1169.06	96.04	673.06	3.92		
NL 1853	NL PLSA 1853		Normal	NA	*123.336		
1142.66	1649.39	*0.768	6.30	*2.652	18.16	*73.544	
*302.743	0.75	321.77	111.67	357.81	3.86		
NL 1854	NL PLSA 1854		Normal	NA	*123.336		
2184.08	1492.69	*0.768	2.42	*2.652	16.39	501.81	
*302.743	0.79	664.26	119.13	988.31	7.17		
NL 1855	NL PLSA 1855		Normal	NA	1198.61		
1197.88	2267.18	*0.768	6.10	*2.652	24.87	*73.544	
*302.743	1.42	1025.14	103.98	1139.23	3.94		
NL 1856	NL PLSA 1856		Normal	NA	*123.336		
775.30	1891.58	*0.768	9.18	*2.652	22.03	604.85	
*302.743	0.86	1430.89	122.78	555.97	3.74		
NL 1857	NL PLSA 1857		Normal	NA	*123.336		
3187.83	3770.56	*0.768	8.94	*2.652	28.89	668.11	
*302.743	1.43	2328.9	*13.922	790.01	4.44		
NL 1858	NL PLSA 1858		Normal	NA	*123.336		
641.84	1041.9	*0.768	1.74	*2.652	19.52	*73.544	
*302.743	1.19	1019.58	153.81	1194.16	4.63		
NL 1859	NL PLSA 1859		Normal	NA	*123.336		
4264.45	3093.61	*0.768	6.79	*2.652	25.62	851.83	
*302.743	1.22	3004.4	*13.922	782.44	4.56		
NL 1860	NL PLSA 1860		Normal	NA	*123.336		
1010.93	1448.49	*0.768	15.99	*2.652	19.75	*73.544	

Table4.txt

*302.743	1.32	1481.41	87.79	484.44	6.62		
NL 1861	NL PLSA 1861		Normal	NA	*123.336		
2701.98	2612.14	*0.768	18.34	*2.652	17.99	626.55	
*302.743	1.33	1317.24	*13.922	1298	3.24		
NL 1862	NL PLSA 1862		Normal	NA	*123.336		
853.37	2550.05	*0.768	7.69	*2.652	19.29	*73.544	
*302.743	1.84	1727.89	*13.922	856.91	4.76		
NL 1863	NL PLSA 1863		Normal	NA	*123.336		
2773.43	2657.36	*0.768	6.76	*2.652	22.7	*73.544	
*302.743	1.4	1664.22	*13.922	1848.79	4.75		
NL 1864	NL PLSA 1864		Normal	NA	*123.336		
1401.07	2293.32	*0.768	8.46	*2.652	22.57	461.21	
*302.743	2.42	2242.85	*13.922	1119.59	1.83		
NL 1865	NL PLSA 1865		Normal	NA	*123.336		
1906.32	4206.45	*0.768	11.92	*2.652	26.85	1276.17	
*302.743	0.84	2432.57	*13.922	656.86	5.76		
NL 1866	NL PLSA 1866		Normal	NA	*123.336		
1683.29	2151.58	*0.768	4.93	*2.652	25.39	768.7	
*302.743	1.09	852.66	*13.922	525.16	4.32		
NL 1867	NL PLSA 1867		Normal	NA	*123.336		
802.16	1069.51	*0.768	31.17	*2.652	13.73	*73.544	
2320.11	1.45	1086.53	173.04	1690.26	4.34		
NL 1868	NL PLSA 1868		Normal	NA	*123.336		
1112.37	1606.96	*0.768	21.21	*2.652	25.1	638.70	
*302.743	1.27	1206.83	*13.922	677.08	2.87		
NL 1869	NL PLSA 1869		Normal	NA	*123.336		
583.62	1708.47	*0.768	15.13	*2.652	17.65	1264.43	
*302.743	1.04	1838.23	119.13	154.46	4.21		
NL 1870	NL PLSA 1870		Normal	NA	*123.336		
312.88	685.72	*0.768	8.57	*2.652	24.09	*73.544	
*302.743	2.04	1225.77	*13.922	5070.86	1.99		
PANC 669	PANC 669 PLS 1		Pancreas	II	*144.477		
1265.44	2977.95	*0.803	16.61	204.20	21.28	2,313.2	
*324.823	0.99	1199.41	261.85	1604.13	8.32		
PANC 670	PANC 670 PLS 1		Pancreas	II	4033.39		
1075.54	1036.63	6.78	4.87	26.48	14.02	595.93	
1948.94	0.54	1075.47	288.93	724.15	1.44		
PANC 671	PANC 671 PLS 1		Pancreas	II	921.94		
1116.19	2452.33	6.78	51.07	145.76	24.96	10,179.9	
5013	0.57	2252.97	261.85	1543.96	6.45		
PANC 672	PANC 672 PLS 1		Pancreas	II	4045.8		
899.69	4707.2	*0.803	27.84	259.77	20.14	698.7	
*324.823	0.43	3490.58	*16.814	490.7	5.36		
PANC 673	PANC 673 PLS 1		Pancreas	II	2416.71		
1099.25	2337.59	*0.803	8.36	25.75	41.66	*75.547	
1949	0.79	2014.92	178.35	771.16	5.21		
PANC 674	PANC 674 PLS 1		Pancreas	II	1264.58		
1279.03	3967.26	17.35	21.25	139.00	20.56	9,295.3	

Table4.txt

1949	0.81	1668.78	231.87	1045.15	3.65		
PANC 675	PANC 675 PLS 1		Pancreas	II	4841.94		
1065.38	1711.44	12.16	23.80	730.04	12.4	12,380.4	
4087	0.63	1900.93	288.93	582.5	11.55		
PANC 676	PANC 676 PLS 1		Pancreas	II	*144.477		
1472.88	2396.02	*0.803	7.16	112.68	41.94	2,563.1	
*324.823	0.95	1823.1	156.71	597.24	2.83		
PANC 677	PANC 677 PLS 1		Pancreas	II	1656.32		
2012.63	3536.6	25.28	30.80	316.30	30.53	4,840.3	
*324.823	0.78	2677.24	131.71	400.16	5.47		
PANC 678	PANC 678 PLS 1		Pancreas	II	7999.16		
1913.31	3584.05	*0.803	15.65	*2.727	20.46	1423.81	
*324.823	1.03	4563.1	178.35	328.93	5.86		
PANC 679	PANC 679 PLS 1		Pancreas	II	*144.477		
256.14	3666.7	8.25	12.20	54.25	25.15	628.80	
*324.823	0.68	1717.69	131.71	997.62	3.56		
PANC 680	PANC 680 PLS 1		Pancreas	II	2810.21		
1408.21	4248.42	7.6	13.14	53.21	25.15	1,278.5	
1949	1.04	2090.23	409.12	589.88	2.16		
PANC 757	PANC 757 PLS 1		Pancreas	II	*141.604		
1066.71	6808.96	7.5	4.61	156.20	20.19	1793.79	
*319.113	0.71	587.4	106.95	*75.2	2.37		
PANC 758	PANC 758 PLS 1		Pancreas	II	1606.51		
1466.86	7084.71	5.1	13.13	490.69	24.21	68801.67	
*319.113	0.72	1700.86	261.66	494.82	3.21		
PANC 759	PANC 759 PLS 1		Pancreas	II	*141.604		
558.97	6696.45	7.5	8.97	101.63	38.41	5464.39	
*319.113	0.67	2616.87	*15.991	2334.43	20.51		
PANC 760	PANC 760 PLS 1		Pancreas	II	*141.604		
662.45	1502.95	*0.822	9.68	*2.733	19.14	3601.31	
4397.67	0.59	1059.45	175.46	*75.2	14.64		
PANC 761	PANC 761 PLS 1		Pancreas	II	1947.39		
716.98	3729.66	19.2	22.12	72.17	25.6	1207.91	
*319.113	0.53	917.15	202.87	1239.35	2.3		
PANC 762	PANC 762 PLS 1		Pancreas	II	*141.604		
940.89	4611.54	9.53	25.78	2159.22	27.34	15,443.4	
*319.113	2.29	2278.14	189.54	1295.6	4.38		
PANC 764	PANC 764 PLS 1		Pancreas	II	8545.31		
968.23	5044.91	9.19	23.10	211.05	30.76	551.5	
*319.113	0.61	1134.7	356.92	513.2	4.83		
PANC 765	PANC 765 PLS 1		Pancreas	II	*141.604		
1524.50	5539.94	13.22	26.01	983.42	58.65	12,251.4	
2325.42	0.79	2998.98	160.48	2433.31	23.56		
PANC 766	PANC 766 PLS 1		Pancreas	I	4450.92		
9672.24	1343.62	19.36	14.49	33.77	34.43	2,070.4	
*319.113	0.73	1574.35	144.35	1752.13	1.6		
PANC 767	PANC 767 PLS 1		Pancreas	II	*141.604		
1823.98	3773.44	*0.822	20.63	40.07	28.25	568.2	

Table4.txt

*319.113	0.61	1946.2	126.71	555.16	*0.004		
PANC 768	PANC 768 PLS 1		Pancreas	II	1580.51		
1510.77	2940.24	*0.822	19.92	*2.733	41.7	1876.38	
*319.113	1.28	1607.83	126.71	555.16	2.53		
PANC 769	PANC 769 PLS 1		Pancreas	II	*141.604		
1867.98	7543.33	*0.822	25.92	40.54	20.66	729.09	
*319.113	1.28	1602.67	106.95	292.57	0.32		
PANCA 1001	PANCA 1001 PLS 1		Pancreas	II	1422.46		
1202.66	379.12	17.8	25.25	114.95	31.77	938.11	
5391.04	1.34	1026.89	281.23	482.7	3.41		
PANCA 1004	PANCA 1004 PLS 1		Pancreas	II	*138.33		
1225.77	1558.16	10.11	34.12	396.56	22.39	6,795.8	
6270	1.96	3256.06	175.17	585.88	3.69		
PANCA 1005	PANCA 1005 PLS 1		Pancreas	II	3164.66		
1441.48	2658.85	31.04	43.98	51.62	65.96	2460.96	
2349.29	1.94	3240.21	236.37	688.73	3.32		
PANCA 1006	PANCA 1006 PLS 1		Pancreas	II	10155.54		
1090.99	2430.93	21.14	45.76	955.34	109.23	1,876.0	
4778	2.23	2370.01	240.17	1255.94	15.71		
PANCA 1008	PANCA 1008 PLS 1		Pancreas	II	1213.43		
1641.85	744.84	7.77	23.61	20.51	40.28	1,172.4	
*341.473	1.94	2940.45	145.52	791.91	4.54		
PANCA 1009	PANCA 1009 PLS 1		Pancreas	II	1259.86		
11995.13	1345.03	29.03	48.99	2168.59	40.2	8,246.0	
6270	1.58	1821.18	342.09	520.5	2.23		
PANCA 1010	PANCA 1010 PLS 1		Pancreas	I	2103.29		
3559.62	6904.68	*0.83	38.70	17.82	6.86	748.40	
*322.664	0.67	3023.24	207.33	1182.14	6.62		
PANCA 1011	PANCA 1011 PLS 1		Pancreas	II	4402.97		
3186.20	7115.7	22.24	33.59	367.04	33.77	2,297.0	
4087	0.69	4862.17	242.65	1139.01	6.24		
PANCA 1012	PANCA 1012 PLS 1		Pancreas	II	5490.65		
1289.30	3426.09	7.12	37.21	106.32	51.19	1382.40	
2981.99	1.18	2640.97	148.9	1536.41	5.85		
PANCA 1013	PANCA 1013 PLS 1		Pancreas	III	1826.89		
185.81	859.87	10.17	16.13	166.49	18.97	482.6	
4385	0.95	1838.07	298.47	808.2	5.4		
PANCA 1014	PANCA 1014 PLS 1		Pancreas	II	2355.36		
1904.69	8629.35	13.15	28.59	*2.764	68	7,747.4	
1917	1.16	3320.56	207.33	4003.08	7.36		
PANCA 1015	PANCA 1015 PLS 1		Pancreas	III	1024.76		
1170.81	3496	6.24	21.11	214.54	20.41	825.73	
3309.35	1.39	2016.53	183.93	402	7.43		
PANCA 1016	PANCA 1016 PLS 1		Pancreas	I	3041.93		
456.21	728.85	5.79	71.94	29.08	39.24	4032.96	
3469.20	0.87	1972.28	214.72	175.77	4.83		
PANCA 1018	PANCA 1018 PLS 1		Pancreas	II	4337.27		
2021.41	8390.89	86.09	29.67	349.93	44.53	3,361.7	

Table4.txt

2982	1.42	3004.16	347.74	1177.38	16.28		
PANCA 1020	PANCA 1020 PLS 1		Pancreas	II	6472.92		
891.69	3105.43	24.27	42.98	44.18	28.18	1,740.5	
8087	1.22	932.52	387.76	306.81	7.42		
PANCA 1022	PANCA 1022 PLS 1		Pancreas	II	*139.05		
403.52	11256.12	7.56	15.82	57.32	25.61	1,207.8	
6454	1.07	2085.47	280.74	*28.11	3.78		
PANCA 1024	PANCA 1024 PLS 1		Pancreas	II	5101.61		
1636.36	2058.01	*0.83	21.82	*2.764	31.54	1299.31	
*322.664	0.65	1485.9	167.07	745.7	2.91		
PANCA 1025	PANCA 1025 PLS 1		Pancreas	III	4600.96		
1387.24	6916.79	126.45	38.60	453.17	34.19	3,435.4	
2643	0.83	1671.68	167.07	680.9	5.7		
PANCA 1028	PANCA 1028 PLS 1		Pancreas	III	3307.88		
1575.85	4580.97	34.07	11.47	75.09	34.26	1,027.7	
*322.664	0.86	2630.34	191.95	460.36	13.08		
PANCA 1030	PANCA 1030 PLS 1		Pancreas	II	4337.27		
2826.24	5500.47	23.46	51.12	42.31	34.14	*77.788	
4237	0.82	2477.09	268.47	474.46	6.97		
PANCA 1031	PANCA 1031 PLS 1		Pancreas	II	1348.2		
2105.45	5647.59	11.45	20.86	885.17	45.58	5127.96	
2814.01	0.78	1624.48	214.72	857.85	7.8		
PANCA 1034	PANCA 1034 PLS 1		Pancreas	II	2385.3		
970.23	1722.52	17.78	28.33	56.17	23.44	2598.10	
6721.89	0.79	1963.14	542.98	797	3.65		
PANCA 1036	PANCA 1036 PLS 1		Pancreas	II	11113.1		
1877.89	3900.6	9.31	23.35	*2.764	36.32	1207.82	
2814.01	0.73	2556.57	228.99	984.72	12.35		
PANCA 1037	PANCA 1037 PLS 1		Pancreas	II	5780.98		
2452.76	3607.54	15.25	13.51	120.38	35.58	1,014.3	
2468	0.77	4050.67	268.47	626.58	7.07		
PANCA 1039	PANCA 1039 PLS 1		Pancreas	II	4717.07		
1423.92	5093.25	*0.833	23.83	221.40	44.83	1635.70	
*338.379	1.29	2348.86	183.93	421.51	7.54		
PANCA 1040	PANCA 1040 PLS 1		Pancreas	II	19555.82		
1362.87	3834.85	23.06	44.60	37.84	26.43	1,759.7	
7096	1.42	294.57	315.49	594.38	7.11		
PANCA 1042	PANCA 1042 PLS 1		Pancreas	II	1073.98		
5523.72	1883.91	*0.833	16.25	20.95	13.27	722.6	
*338.379	1.1	1729.96	125.85	1042.83	5.46		
PANCA 1043	PANCA 1043 PLS 1		Pancreas	II	5626.99		
1251.50	4933.72	6.68	6.39	171.84	53.55	3382.77	
*338.379	0.94	931.07	167.07	858.91	5.52		
PANCA 1044	PANCA 1044 PLS 1		Pancreas	II	3817.28		
3561.93	10869.84	11.45	43.82	57.32	54.06	2,527.4	
2814	0.92	1793.03	242.65	1510.79	11.92		
PANCA 1047	PANCA 1047 PLS 1		Pancreas	II	*154.335		
468.37	3500.61	9.52	23.30	68.31	10.64	1471.33	

Table4.txt

2106.36	1.52	1384.82	439.72	*76.52	6.13	
PANCA 1048	PANCA 1048	PLS 1	Pancreas	III	3073.04	
1632.19	9040.37	32.68	26.96	117.51	43.89	2492.13
*338.379	1.15	1254.2	167.07	613.35	6.71	
PANCA 1050	PANCA 1050	PLS 1	Pancreas	II	2415.29	
1682.48	4638.21	*0.833	10.87	123.90	27.8	1,067.9
2106	1.2	1532.99	148.9	884.91	9.24	
PANCA 1051	PANCA 1051	PLS 1	Pancreas	II	4667.25	
1704.03	2466.36	14.41	22.44	149.40	51.76	1,688.0
*338.379	1.69	2149.58	183.93	979.57	6.19	
PANCA 1052	PANCA 1052	PLS 1	Pancreas	II	1542.64	
3584.80	4120.61	7.34	37.46	*2.767	52.89	774.06
*338.379	0.85	951.6	183.93	1578.7	11.71	
PANCA 1053	PANCA 1053	PLS 1	Pancreas	II	*154.335	
3078.29	4583.04	8.29	23.47	1487.88	102.66	1,944.8
2406	2.38	1312.15	112.8	1215	17.43	
PANCA 1054	PANCA 1054	PLS 1	Pancreas	II	7639.81	
2114.12	8444.11	6.01	49.08	225.22	64.56	1212.37
7222.30	1.33	3251.23	183.93	1167.84	17.21	
PANCA 1055	PANCA 1055	PLS 1	Pancreas	II	*154.335	
423.92	2020.28	*0.833	18.13	19.52	10.07	519.13
*338.379	0.7	661.46	149.75	321.43	6.22	
PANCA 1056	PANCA 1056	PLS 1	Pancreas	II	5575.8	
8527.97	2036.6	43.71	12.45	76.70	62.53	1,702.3
39518	1.92	2185.61	679.56	6019.65	7.88	
PANCA 1057	PANCA 1057	PLS 1	Pancreas	II	4700.45	
1150.84	3735.93	*0.833	30.49	642.95	26.06	1522.40
*338.379	1.03	1786.57	106.53	306.81	1.79	
PANCA 1058	PANCA 1058	PLS 1	Pancreas	II	2611.59	
1862.17	7180.44	23.06	20.03	75.09	35.6	4572.63
*338.379	0.99	1631.92	128.97	728.27	7.26	
PANCA 1059	PANCA 1059	PLS 1	Pancreas	II	1683.86	
1571.14	3036.07	11.88	12.07	511.14	29.88	1855.86
*338.379	1.19	1174.77	199.75	488.38	8.27	
PANCA 1061	PANCA 1061	PLS 1	Pancreas	II	4353.68	
1456.24	2023.54	13.99	13.95	497.22	56.03	6,197.9
3782	1.47	3295.57	249.28	1704.97	15.06	
PANCA 1063	PANCA 1063	PLS 1	Pancreas	II	*154.335	
1222.75	7088.54	74.34	14.19	317.41	19.74	2308.63
*338.379	1	1567.65	105.91	743.8	3.03	
PANCA 1149	PANCA 1149	PLS 1	Pancreas	II	*147.076	
2488.16	1635.68	*0.792	14.18	44.30	37.92	1,553.6
*323.745	1.49	1347.91	174.27	178.36	6.72	
PANCA 1152	PANCA 1152	PLS 1	Pancreas	I	2066.02	
1193.78	4173.87	11.22	62.61	33.69	44.33	1,016.0
*323.745	0.58	2031	98.61	493.17	1.69	
PANCA 1153	PANCA 1153	PLS 1	Pancreas	II	1863.94	
1060.85	1833.86	5.55	4.29	189.15	21.96	811.15

Table4.txt

*327.917	0.83	336.71	*14.319	271	4.31		
PANCA 1155	PANCA 1155	PLS 1	Pancreas	II	*132.09		
2784.67	5110.97	40.09	22.23	*2.74	40.01	9,260.1	
*327.917	0.67	1512.09	*14.319	1300.96	4.55		
PANCA 1156	PANCA 1156	PLS 1	Pancreas	II	4189.16		
2413.63	2630.75	*0.82	12.91	226.44	33.01	2459.62	
*327.917	0.79	1134.25	*14.319	1202.86	20.98		
PAP 938	PAP 938	PLS 1	Ovary	III	*146.583		
3760.06	3170.67	519.78	23.25	29.69	17.59	945.6	
5138	1.07	2397.23	179.17	1628.42	19.49		
PAP 939	PAP 939	PLS 1	Ovary	III	3078.34		
5130.59	2235.8	269.12	53.37	20.94	10.94	1,793.9	
14386	1.4	1830.06	162.25	2199.96	6.57		
PAP 940	PAP 940	PLS 1	Ovary	III	*146.583		
3428.83	1502.85	178.88	338.84	26.60	16.17	444.8	
21501	0.8	1152.8	143.09	1272.89	11.31		
PAP 941	PAP 941	PLS 1	Ovary	III	*146.583		
603.16	1135.67	58.75	14.90	19.02	7.26	789.7	
3590	0.91	604.03	307.18	921.49	6.69		
PAP 944	PAP 944	PLS 1	Ovary	III	40359.14		
2629.64	2648.15	491.71	40.54	144.76	18.43	3,381.1	
*328.486	0.89	381.98	143.09	618.01	13.56		
PAP 945	PAP 945	PLS 1	Ovary	III	4997.93		
2914.26	1462.84	372.01	218.90	17.73	14.26	479.8	
3765	0.74	1658.68	120.42	1704.01	8.53		
PAP 946	PAP 946	PLS 1	Ovary	III	*146.583		
2112.97	2433.61	618.68	47.54	558.22	25.01	3,302.6	
1971	0.97	316.47	245.96	367.73	16.34		
PAP 947	PAP 947	PLS 1	Ovary	III	*146.583		
315.76	1657.41	9.21	12.01	17.73	21.92	653.7	
1971	0.95	1113.68	208.62	654.58	16.76		
PAP 949	PAP 949	PLS 1	Ovary	III	*146.583		
4315.56	1718.57	4.86	24.56	29.69	15.36	1,679.9	
1971	1.37	3604.65	*15.177	4570.53	7.47		
PAP 950	PAP 950	PLS 1	Ovary	III	1500.16		
1460.74	3882.74	3329.74	248.67	*2.74	7.91	1,489.8	
91223	1.78	1400.14	179.17	1622.98	19.34		
PAP 951	PAP 951	PLS 1	Ovary	III	1921.24		
1622.12	1072.46	37.57	28.80	*2.74	13.77	*73.577	
*327.917	0.82	1130.15	85.91	631.94	17.69		
PAP 953	PAP 953	PLS 1	Ovary	III	*146.583		
813.98	726.57	24.63	12.98	42.39	10.68	691.0	
2882	1.04	376.16	278.24	1767.97	5.79		
PAP 954	PAP 954	PLS 1	Ovary	III	*146.583		
1204.94	2568.03	**600.004	68.67	33.97	9	*73.835	
13465	1.14	*29.079	143.09	711.79	11.93		
PAP 955	PAP 955	PLS 1	Ovary	III	1398.1		
996.49	1737.7	177.69	8.19	43.58	15.79	451.7	

Table4.txt

*328.486	1.03	1144.09	143.09	1183.73	18.48		
PAP 956	PAP 956 PLS 1		Ovary	III	2357.46		
2405.94	880.92	59.52	15.94	*2.74	10.05	*73.835	
4798	0.86	1144.09	91.06	1922.22	6.85		
PAP 957	PAP 957 PLS 1		Ovary	III	*146.583		
1353.25	1890.97	7.76	18.48	*2.74	16.76	2,340.5	
*328.486	1.22	2231.68	91.06	1468.16	22.17		
PAP 959	PAP 959 PLS 1		Ovary	III	3649.47		
1647.11	2218.39	425.72	29.31	*2.74	36.02	736.3	
*328.486	1.27	559.71	120.42	1080.03	21.61		
PAP 961	PAP 961 PLS 1		Ovary	III	1603.12		
1914.09	979.82	253.84	52.20	98.83	23.63	5,926.2	
*328.486	0.82	887.03	*15.177	1308	13.89		
PAP 962	PAP 962 PLS 1		Ovary	III	37732.35		
679.58	2505.63	16.22	9.68	17.09	10.12	1,233.1	
*328.486	1.09	1391.19	91.06	2320.13	8.36		
PAP 974	PAP 974 PLS 1		Ovary	I	1418.44		
3162.93	1856.45	37.69	22.06	*2.74	15.89	1,029.2	
*328.486	0.99	1905.02	120.42	976.29	16.37		
PAPA 1330	PAPA 1330 PLS 1		Ovary	III	1222.17		
1361.24	417.68	470.04	201.12	*2.74	*1.35	*73.577	
2324	0.95	1123.99	*14.319	1060.55	69.52		
PAPA 1331	PAPA 1331 PLS 1		Ovary	III	*146.583		
4061.22	957.01	433.88	386.71	*2.74	*1.36	*73.835	
4112	0.69	976.07	*15.177	3158.64	6.7		
PAPA 1332	PAPA 1332 PLS 1		Ovary	I	*146.583		
1377.09	1285.84	5.58	4.20	*2.74	13.4	759.1	
*328.486	0.74	887.03	179.17	1153.54	14.17		
PAPA 1333	PAPA 1333 PLS 1		Ovary	III	*146.583		
1780.26	1200.29	523.47	316.48	113.11	14.77	472.73	
8513.73	0.68	997.42	162.25	406.23	3.45		
PAPA 1334	PAPA 1334 PLS 1		Ovary	III	*146.583		
5717.79	2098.69	318.93	22.10	*2.74	19.24	465.7	
23186	2.71	1848.75	143.09	1045.82	16.3		
PAPA 1335	PAPA 1335 PLS 1		Ovary	III	951.61		
2854.67	1396.19	11.05	10.23	*2.74	14	805.0	
*328.486	0.63	2311.74	*15.177	2042.34	7.78		
PAPA 1336	PAPA 1336 PLS 1		Ovary	I	*146.583		
3670.67	4076.83	14.37	7.23	*2.74	17.16	*73.835	
35886	1.64	1530.84	187.01	1924.8	14.01		
PAPA 1339	PAPA 1339 PLS 1		Ovary	I	1500.16		
2125.25	1278.24	2176.6	37.35	**2081.912	11.96	1,073.6	
4798	5.97	1656.38	307.18	927.99	8.54		
PAPA 1342	PAPA 1342 PLS 1		Ovary	III	7212.72		
1883.62	1221.2	379.12	63.58	72.26	14.82	*73.835	
2521	0.83	1128.87	132.32	868.95	10.75		
PAPA 1343	PAPA 1343 PLS 1		Ovary	III	1377.81		
1853.17	1196.49	176.09	**139.475	54.16	13.57	511.7	

Table4.txt

4456	1.28	541.67	91.06	908.44	12.57		
PAPA 1344	PAPA 1344 PLS 1		Ovary	III	2130.42		
1110.66	774.26	265.09	14.96	35.19	14.51	1,706.1	
*328.486	0.94	726.53	257.18	414.63	14.42		
PAPA 1345	PAPA 1345 PLS 1		Ovary	III	*146.583		
1046.15	310.04	56.83	88.65	*2.74	*1.36	*73.835	
7133	1.13	1035.99	120.42	2271.32	11.82		
PAPA 1346	PAPA 1346 PLS 1		Ovary	III	*146.583		
3530.52	831.42	918.76	**139.475	151.45	11.01	*73.835	
7052	0.81	186.75	91.06	632.72	2.83		
PAPA 1347	PAPA 1347 PLS 1		Ovary	I	*146.583		
1193.13	1459.03	535.16	14.97	1275.52	11.21	3,180.5	
2792	0.81	*29.079	179.17	1302.17	4.97		
PAPA 1348	PAPA 1348 PLS 1		Ovary	III	3350.8		
1629.00	728.48	549.33	147.53	27.84	8.43	*73.835	
5475	0.62	1413.58	120.42	4212.49	6.16		
PAPA 1349	PAPA 1349 PLS 1		Ovary	III	*146.583		
2586.04	1297.25	2235.26	**139.475	87.17	9.54	646.3	
15756	1.74	1567.2	143.09	1073.84	6.07		
PAPA 1350	PAPA 1350 PLS 1		Ovary	II	2346.58		
1904.94	1014.04	7.39	9.85	*2.74	12.56	1558.46	
*328.486	1.16	1214	*15.177	1540.65	5.47		
PAPA 1353	PAPA 1353 PLS 1		Ovary	I	*146.583		
1484.70	2096.76	24.82	10.30	42.39	14.92	914.00	
*328.486	3.05	1113.68	221.8	875.57	8.51		
PAPA 1354	PAPA 1354 PLS 1		Ovary	I	1337.33		
1607.90	852.37	5.58	9.80	*2.74	12.32	1,179.5	
*328.486	1.74	1702.42	234.2	573.21	19.76		
PAPA 1355	PAPA 1355 PLS 1		Ovary	III	*146.583		
1592.84	1044.45	30.48	8.48	*2.74	8.26	*73.835	
3590	0.73	499.81	91.06	650.95	8.67		
PAPA 1356	PAPA 1356 PLS 1		Ovary	II	*146.583		
5267.95	1445.69	1469.45	23.74	62.26	16.53	*73.835	
50659.05	1.24	2219.6	143.09	1033.29	6.69		
PAPA 1357	PAPA 1357 PLS 1		Ovary	III	*146.583		
3546.43	1493.32	1428.31	**139.475	37.90	13.78	*73.835	
3060	1.01	1750.98	208.62	715.32	12.84		

*Protein concentration below the limit of detection of the assay; value set as lower limit of detection
**Protein concentration above the limit of detection of the assay; value set as upper limit of detection
NA: Not available

G-CSF	GDF15	HE4	HGF	IL-6	IL-8	Kallikrein-6	Leptin	Mesothelin	Midkine	Myeloperoxidase	NSE	OPG

Table4.txt

OPN (pg/ml)	PAR (ng/ml)	Prolactin (pg/ml)	sEGFR (pg/ml)	sFas (pg/ml)	SHBG (pg/ml)	(pg/ml)
(pg/ml)	(ng/ml)	(pg/ml)	(ng/ml)	(ng/ml)		
*43.82	0.53	*642.952	377.26	*1.886	*1.373	5938.28
75826.61	14.29	315.23		14.22	12.04	0.47
56516.58	8852.96	11606.6	3284.17	*34.132	55.06	
*43.82	2.39	5779.11	659.68	21.28	29.82	3409.18
211751.33	32.57	260.56		23.88	23.25	0.34
61001.39	20782.58	14374.99	1911.81	*34.132	72.92	
*43.82	0.5	*642.952	329.07	*1.886	35.06	3338.6
2683.07	15.09	491.81		12.02	12.84	0.37
88896.24	7534.43	38375	1743.94	*34.132	173.78	
152.24	0.19	7819.17	266.66	15.3	15.89	3162.89
41859.78	16.52	230.45		6.49	22.79	*0.029
42549.61	4722.42	12072.51	1059.24	*34.132	29.47	
*43.82	0.3	*642.952	370.88	*1.886	*1.373	4442.46
100119.47	8.81	238.47		13.33	27.2	*0.029
24274.11	6945.9	23718.17	1736.92	*34.132	78.07	
*43.82	1.09	*642.952	269.99	*1.886	9.47	4845.57
6804.38	16.88	276.87		10.6	22.32	0.57
66920.22	9321.12	16602.78	1871.12	*34.132	251.78	
422.75	0.28	9276.09	246.56	*1.886	250.72	5123.27
25346.38	12.82	331.33		12.08	21.66	*0.029
53572.27	12378.98	22077.74	2704.94	5389.05	61.54	
*43.82	0.42	4701.46	312.81	*1.886	*1.373	5369.64
127507.81	21.4	216.77		8.42	15.58	*0.029
73727.23	4793.64	14294.39	1203.16	*34.132	207.62	
*43.82	0.14	6559.67	226.23	13.61	10.53	3060.7
28575.13	7.42	172.98		16.65	11.1	*0.029
41313.18	3057.66	34149.07	1683.93	*34.132	144.11	
*43.82	0.14	*642.952	205.65	*1.886	9.47	5617.59
13222.45	15.21	191.06		9.54	11.81	*0.029
55873.69	3804.41	32295.94	1949.59	*34.132	236.94	
*43.82	0.44	*642.952	358.09	*1.886	10.88	5754.98
126964.73	32.38	295.14		15.44	10.87	0.33
49915.81	10755.72	26147.85	1899.59	*34.132	125.95	
*43.82	0.33	4701.46	408.95	*1.886	*1.373	6281.47
50112.25	14.09	1357.7		13.14	46.86	0.39
44818.58	2307.6	10917.49	1853.87	*34.132	91.35	
463.34	0.38	*642.952	325.83	*1.886	9.29	4969.81
44504.42	17.77	274.39		76.86	45.03	*0.029
19598.92	6016.05	22781.25	1639.15	*34.132	28.49	
*43.82	2.08	*642.952	351.67	*1.886	*1.373	4394.61
102187.16	1.49	241.12		18.95	24.98	0.4
38244.16	6233.89	143071.71	429.59	*34.132	85.86	
*43.82	0.58	*642.952	212.54	*1.886	10.7	3668.5
4783.86	23.33	338.12		10.07	22.69	0.74

Table4.txt

32019.25	16444.34	17990.85	2585.99	*34.132	84.74				
*43.82	0.2	11146.85	299.72	*1.886	133.5	4744.28			
21580.74	9.73	261.83		23.49	24.17	*0.029			
41694.21	6470.56	26446.49	1801.28	3705.77	232.86				
*43.82	0.25	*642.952	233.03	*1.886	10.53	7945.8			
15779.86	4.37	213.99		18.76	21.47	*0.029			
34248.73	3892.01	31045.8	1399.04	*34.132	33.17				
138.48	0.33	*642.952	279.95	*1.886	25.01	6394.6			
24543.56	9.42	230.45		11.39	14.07	*0.029			
31969.37	9923.12	19489.58	2137.26	*34.132	71.03				
162.34	0.89	*642.952	415.25	*1.886	33.18	7117.39			
10706.52	9.7	284.24		15.08	8.88	*0.029			
81075.21	8126.61	19542.04	622.59	270.66	120.16				
185.28	0.16	*642.952	279.95	*1.886	21.34	2884.76			
125608.48	14.92	235.81		15.14	13.41	*0.029			
65374.68	8312.38	16854.58	2317.39	*34.132	63.93				
*43.82	0.31	*642.952	421.54	*1.886	*1.373	4064.76			
59629.28	16.34	108.22		11.89	20.03	*0.029			
54862.15	5528.15	38032.32	2011.12	*34.132	51.98				
*43.82	0.37	5779.11	198.72	*1.886	22.44	3766.32			
3295.05	24.68	826.44		7.65	10.38	*0.029			
92181.23	11174.03	11496.66	1680.93	*34.132	52.25				
*43.82	0.66	*642.952	520.74	*1.886	28.71	5058.88			
162648.18	27.83	310.56		12.12	8.1	0.52			
73545.84	9734.67	55189.55	2002.9	*34.132	76.49				
*43.82	0.45	4701.46	325.83	*1.886	11.24	4936.57			
34589.3	27.28	227.74		14.32	15.15	*0.029			
28230.8	10907.68	10418.15	2143.5	*34.132	87.36				
*43.82	0.32	*642.952	370.88	*1.886	13.73	6533.35			
39817.83	21.49	176.06		13.2	11.81	*0.029			
75268.97	5834.97	11262.65	1349.87	*34.132	32.8				
*43.82	0.39	*642.952	345.23	*1.886	24.27	4031.23			
7490.35	8.06	364.67		11.75	14.07	*0.029			
62916.67	13787.56	19043.38	1674.95	*34.132	79.42				
*43.82	0.27	*642.952	226.23	20.75	29.82	4121.72			
46338.18	13.17	222.29		8.55	7.56	*0.029			
49218.3	7682.14	28394.16	921.04	*34.132	51.29				
*43.82	0.16	6559.67	273.31	14.74	29.27	4365.46			
8941.34	12.98	202.68		7.22	15.89	*0.029			
45101.04	1624.8	11551.65	809.86	613.4	49.15				
*43.82	0.36	*642.952	293.15	*1.886	*1.373	3358.03			
47939.92	15.27	130.28		9.87	15.37	*0.029			
28843.86	6726.19	14025.42	1193.72	*34.132	137.22				
*43.82	0.18	4701.46	393.15	*1.886	*1.373	2273.05			
12683.08	9.7	166.76		14.19	17.45	*0.029			
90811.52	8535.74	9565.22	2261.61	*34.132	71.54				
*43.82	0.25	8310.74	184.77	11.32	9.82	1704.23			
47847.13	9.82	169.89		9.38	13.18	*0.029			

Table4.txt

39975.19	1740.08	114088.44	557.4	*34.132	65.05	
*43.82	0.12	*642.952	293.15	*1.886	12.66	4402.57
98257.84	12.13	768.37		13.14	10.62	*0.029
48239.82	9396.2	26394.56	3071.16	*34.132	48.33	
*43.82	0.57	*642.952	266.66	*1.886	34.31	3753.73
2683.07	11.8	199.8		9.67	14.51	*0.029
45571.29	7497.54	87118.19	1241.95	*34.132	204.66	
*43.82	0.33	*642.952	345.23	*1.886	38.07	3554.16
33825.55	9.94	185.13		11.42	18.66	0.4
36012.6	5097.22	7306.13	851.75	323.21	35.16	
*43.82	0.41	*642.952	184.77	*1.886	*1.373	2954.79
10955.28	14.08	191.06		6.32	16.62	*0.029
43875.22	4972.04	6349.47	1509	*34.132	47.95	
*43.82	0.28	*642.952	188.27	*1.886	8.76	4777.04
82194.51	8.95	162.02		22.63	16.73	*0.029
70688.39	6964.23	16775.1	2187.27	*34.132	62.63	
*43.82	0.48	15138.84	246.56	18.6	11.24	8181.02
26027.24	60.05	153.97		16.98	9.64	*0.029
25538.59	9471.33	22651.03	1611.39	*34.132	25.71	
*43.82	0.3	*642.952	587.65	*1.886	34.12	5816.8
41525.72	17.05	150.69		50.31	17.45	*0.029
35279.63	13555.14	14065.79	1221.11	513.19	44.54	
*43.82	1.11	*642.952	*27.259	*1.886	8.59	3936.31
3346.97	26.23	133.78		3.64	20.71	0.74
26113.26	4936.32	3370.16	868.77	*34.132	84.83	
*43.82	0.2	*642.952	259.98	*1.886	10.88	2961.81
7659.66	11.82	248.98		18.17	13.52	*0.029
20488.45	7534.43	11990.44	1775.09	*34.132	81.6	
*43.82	0.4	*642.952	325.83	*1.886	9.47	3693.5
123867.04	12.85	230.45		12.45	11.1	0.59
38099.33	6598.28	9607.38	2480.88	*34.132	53.03	
*43.82	1.69	5246.17	665.64	18.05	25.93	4129.51
54014.62	15.36	290.32		57.75	15.15	0.77
62096.25	11402.75	11524.16	1338.34	*34.132	69.22	
134.98	0.2	4701.46	377.26	*1.886	13.02	2716.3
61581.96	17.29	273.14		17.61	17.95	*0.029
35132.71	2510.57	34122.93	2016.26	*34.132	40.62	
*43.82	0.38	4142.95	249.92	*1.886	*1.373	4137.3
50933.86	11.98	157.21		35.84	25.79	0.3
29656.95	9847.71	14079.25	2197.71	*34.132	88.23	
258.89	0.18	*642.952	358.09	*1.886	22.25	4711.6
10211.5	23.68	271.9		81.99	23.8	*0.029
53572.27	10793.69	12645.33	2209.21	*34.132	65.22	
162.34	0.2	5246.17	312.81	*1.886	85.72	4302.1
45168.67	10.37	462.09		216.86	63.82	*0.029
31169.07	7719.11	10418.15	2335.34	2526.2	34.09	
*43.82	0.39	*642.952	289.86	*1.886	14.81	3029.99
35304.97	9.41	160.43		11.46	12.73	*0.029

Table4.txt

47586.16	3874.48	20432.58	1615.35	210.15	19.22	
*43.82	0.6	*642.952	358.09	14.74	*1.373	5369.64
11563.45	27.39	2052.28		63.2	10.02	*0.029
46697.26	5600.23	31071.82	1250.49	*34.132	39.96	
*43.82	2.34	7320.94	279.95	*1.886	21.7	3713.54
4865.49	16.92	291.53		30.2	30.55	0.3
117552.35	9659.37	27173.57	547.33	*34.132	187.09	
*43.82	0.15	*642.952	*27.259	*1.886	*1.373	3703.52
12931.85	9.58	144.04		16.13	10.14	*0.029
46228.54	4811.46	13134.11	1473.82	*34.132	146.75	
182.06	0.18	*642.952	296.44	*1.886	*1.373	2541.57
21502.86	14.03	163.61		20.43	12.96	*0.029
39543.61	9546.51	21438.63	2729.94	*34.132	58.1	
*12.46	0.33	*676.132	166.86	11.32	13.41	5280.53
13131.04	16.33	1211.47		2.89	7.66	0.28
30422.97	7065.34	17390.24	1997.64	2005.11	22.39	
100.72	1.15	*676.132	*27.292	*0.628	9.37	8376.85
98628.68	46.14	643.05		9.63	7.85	0.72
45896.1	14155.68	9941.77	3495.56	2218.49	27.98	
*12.46	0.29	*676.132	*27.292	*0.628	103.93	4720.47
14025.05	12.46	959.06		12.32	11.19	0.44
49894.78	7552.21	14213.81	772.68	1563.27	46.49	
379.95	0.3	*676.132	261.74	*0.628	*1.37	3615.49
39054.37	10.55	326.7		25.72	6.29	0.31
20095.65	5656.69	15193.88	1757.99	1147.97	14.81	
*12.46	0.26	*676.132	220.14	3.98	*1.37	5387.22
61763.77	17.8	254.25		11.83	8.4	0.31
29714.84	3199.86	16791.76	3027.7	921.34	8.97	
86.4	0.85	*676.132	166.86	6.08	9.68	6303.18
21774.89	51.5	695.16		19	8.31	0.43
58400.91	11915.85	28607.49	2610.65	1049.34	17.98	
*12.46	1.43	*676.132	301.57	39.67	298.93	4040.62
7262.69	44.06	1160.92		77.96	8.95	0.76
130703.62	23744.51	7469.56	2192.58	1185.35	28.13	
142	1.02	*676.132	208.67	*0.628	14.67	4842.78
1289.02	30.27	3588.75		22.19	3.66	0.71
40861.7	14232.08	30373.03	2718.47	1306.16	69.16	
*12.46	0.31	*676.132	275.19	*0.628	11.85	6022.49
18569.89	15.04	310.79		7.74	8.95	0.37
73136.49	5617.4	12934.3	986.02	1147.97	1.98	
144.68	0.72	*676.132	191.09	*0.628	11.53	2277.61
17493.33	16.93	485.74		7.2	8.86	0.56
49537.58	12663.61	14719.95	2258.64	782.1	60.36	
*12.46	0.33	*676.132	*27.292	*0.628	9.68	4483.64
3610.32	23.48	352.36		18.64	9.66	0.33
17798.77	10743.62	10502.05	3226.17	1517.64	41.46	
142	2.32	*676.132	317.1	4.83	29.28	5868.89
1482.38	29.23	565.31		30.83	7.28	0.56

Table4.txt

98302.54	10897.55	11380.85	1204.47	511.51	30.78	
264.09	0.11	*676.132	*27.292	*0.628	*1.37	3559.36
8114.82	15.32	618.96		11.85	6.69	0.18
23204.43	11647.11	10351.45	4428.47	679.94	31.22	
152.67	0.57	*676.132	*27.292	*0.628	8.45	5174.1
24941.05	20.37	459.87		11.33	9.48	0.82
52451.16	8891.01	143808.05	1729.06	591.29	38.98	
*12.46	0.63	*676.132	*27.292	*0.628	*1.37	3437.46
3019.28	10.77	266.05		17.35	7.08	0.29
54786.62	5105.85	8000.78	1602.8	983.15	105.49	
*12.46	0.34	*676.132	288.46	*0.628	9.68	5095.31
3296.59	11.37	1121.56		184.9	28.21	0.2
21297.99	2151.52	71518.03	2689.93	420.42	9.79	
*12.46	0.23	*676.132	*27.292	*0.628	*1.37	3741.24
4678.89	9.88	248.24		78.59	9.13	0.26
14033.22	6401.42	5870.77	3448.62	1185.35	25.32	
92.17	1.09	*676.132	*27.292	4.83	21.24	6539.67
1904.1	17.33	4062.06		5.74	7.37	0.32
79350.56	2029.51	7680.31	1067.31	1306.16	17.19	
*12.46	0.54	*676.132	*27.292	7.52	26.14	4268.26
256659.28	32.15	442.19		6.25	5.47	0.25
36729.01	10820.59	65090	1144.09	987.89	16.2	
*12.46	0.48	*676.132	*27.292	*0.628	*1.37	3824.19
19580.31	5.22	299.94		11.31	7.08	0.4
27811.88	6870.29	6303.25	2087.66	921.34	32.76	
*12.46	0.87	*676.132	*27.292	*0.628	11.53	2911.39
13293.79	29.77	459.87		58.99	8.22	0.45
44294.35	11781.5	7358.38	4557.81	1767.3	33.38	
293.09	0.43	*676.132	*27.292	*0.628	*1.37	4557.93
65548.31	19	271.85		8.27	6.49	0.24
38466.75	6792.22	15614.76	2650.27	921.34	53.4	
*12.46	0.46	*676.132	*27.292	*0.628	*1.37	9447.81
10801.08	10.82	337.09		4.15	4.37	0.23
43938.48	2838.59	10049.71	3167.01	1082.3	2.41	
144.68	0.88	*676.132	*27.292	*0.628	*1.37	6862.98
16799.36	39.64	391.5		6.52	2.91	0.35
98451.77	8852.3	69629.93	2684.97	660.33	45.31	
*12.46	0.57	*676.132	*27.292	*0.628	8.75	1490.62
19252.61	15.44	446.64		8.09	7.47	0.31
55481.52	13123.17	8033.85	1951.51	226.88	28.8	
*10.48	1.09	*623.86	207.92	*0.506	*4.627	11985.87
9828.36	61.08	683.58		20.81	11.34	0.78
94143.47	20959	124290.8	2605.02	*33.693	57.45	
*10.48	0.4	*623.86	*26.389	*0.506	*4.627	4083.65
8130.26	13.93	520.27		10.38	8.24	0.58
15126.05	11226.84	111039.59	2591.28	*33.693	172.9	
*10.48	0.69	*623.86	*26.389	3.48	*4.627	4286.73
7954.92	39.83	973.43		9.78	4.65	0.6

Table4.txt

54396.06	4074.68	31431.72	1121.94	*33.693	78.68	
*10.48	1.54	*623.86	171	*0.506	*4.627	9186.58
4876.59	47.96	355.59		11.61	4.65	0.58
95148.43	7002.44	34669.21	2420.07	*33.693	77.9	
*10.48	11.04	*623.86	213.93	*0.506	*4.627	4610.42
*417.822	8.9	933.6		12.98	9.52	0.33
47742.37	4402.56	88157.48	1370.84	*33.693	160.47	
67.47	0.54	*623.86	*26.389	*0.506	*4.627	4617.38
21340.78	31.89	253.23		8.37	5.81	0.56
46925.4	3729.42	25094.46	2133.31	*33.693	134.3	
44.18	0.82	*623.86	260.9	*0.506	*4.627	5350.87
29425.44	9.53	1224.06		8.3	5.81	0.31
52169.84	3427.6	103128.9	706.8	*33.693	29.58	
*10.48	0.65	*623.86	344.65	20.16	*4.627	2963.48
4967.45	16.38	255.52		14.16	3.39	0.45
56903.26	6808.03	9826.33	372.91	*33.693	33.91	
*10.48	0.92	*623.86	183.48	*0.506	37.01	7270.6
13172.35	41.6	285.06		11.08	9.83	0.41
81996.86	6121.73	7011.77	998.49	*33.693	51.85	
*10.48	0.69	*623.86	*26.389	*0.506	*4.627	7907.51
30859.71	27.68	1282.65		15	8.24	0.36
40274.02	5527.94	103644.32	1193.81	*33.693	41.3	
31.43	1.38	*623.86	201.87	63.29	36.16	3810.58
37779.38	31.65	697.01		15.28	10.44	1.1
129972.05	8114.77	23792.78	1275.78	*33.693	64.98	
*10.48	0.55	*623.86	*26.389	6.05	*4.627	4225.52
7407	11.3	383.51		14.35	13.05	0.54
53901.53	10931.33	51067.92	4592.95	*33.693	89.13	
*10.48	1.28	*623.86	*26.389	*0.506	35.3	7113.55
67875.46	31.32	504.07		8.98	6.18	0.84
38612.18	20302.66	17860.94	3038.19	*33.693	111.78	
*10.48	0.5	*623.86	*26.389	*0.506	*4.627	3883.34
9275.43	24.18	548.4		8.75	8.24	0.72
28352.05	7785.79	71838.75	1884.02	*33.693	108.35	
*10.48	0.87	*623.86	*26.389	6.86	*4.627	7416.71
4084.45	25.85	316.27		7.16	5.43	0.4
77518.74	8004.95	12939.3	505.27	*33.693	63.9	
*10.48	0.8	*623.86	164.7	*0.506	37.01	2954.2
18437.81	20.7	924.51		9.59	6.89	0.4
23806.57	18419.59	16367.87	2864.19	*33.693	168.89	
259.42	0.16	*623.86	177.26	17.36	*4.627	2574
5231.4	11.4	493.9		10.73	10.29	0.5
64573.21	6635.72	242232.89	467.09	*33.693	29.77	
*10.48	0.61	*623.86	249.33	*0.506	*4.627	7323.24
26884.12	28.55	1122.93		13.54	7.58	0.35
93883.3	8246.77	44551.91	2635.6	*33.693	27.3	
*10.48	0.3	*623.86	*26.389	*0.506	*4.627	6304.77
37988.4	24.18	576.28		10.98	5.81	0.48

Table4.txt

49302.98	11751.72	51884.88	1753.22	*33.693	57.33	
*10.48	0.82	*623.86	213.93	4.36	*4.627	3100.35
44372.05	27.85	639.11		17.4	6.18	0.41
13144.47	15752.13	133030.34	2240.92	*33.693	165.43	
*10.48	0.52	*623.86	213.93	4.36	*4.627	5958.45
4496.51	44.13	548.4		12.42	5.99	0.47
43038.92	8732.7	64057.18	1134.95	*33.693	107.84	
*10.48	0.77	*623.86	*26.389	*0.506	*4.627	3803.98
*417.822	15.1	225.36		9.33	7.24	0.63
81561.95	7632.78	31598.41	962.98	*33.693	148.82	
*10.48	1.18	*623.86	*26.389	*0.506	*4.627	4708.15
26311	12.98	298.51		10.13	5.05	0.69
49657.3	1928.34	15932.33	1086.96	*33.693	52.9	
*10.48	0.5	*623.86	*26.389	*0.506	*4.627	4523.67
77952.5	18.61	248.62		12.11	6.18	0.35
42967.33	5233.56	25606.03	850.43	*33.693	20.85	
109.3	3.57	*623.86	164.7	15.57	30.47	6170.79
18783.84	40.59	381.38		10.63	10.14	0.9
80223.13	17414.05	23655.26	2366.03	*33.693	144.7	
*10.48	0.46	6825.96	225.86	23.6	41.23	5227.54
24534.74	48.91	377.1		13.3	6.71	0.24
21882.99	11614.54	16945.85	324.07	*33.693	47.08	
*10.48	0.32	*623.86	*26.389	*0.506	*4.627	4324.26
10950.13	14.54	389.9		13.17	11.63	0.22
36503.67	9556.5	7324.07	3052.4	*33.693	155.81	
*10.48	2.48	*623.86	328.27	*0.506	*4.627	8316.63
27834.77	71.55	8858.12		78.86	4.25	2.95
143572.21	11500.37	22378.27	1885.45	*33.693	197.82	
*10.48	0.64	*623.86	*26.389	*0.506	*4.627	5471.43
2974.47	21.55	534.37		9.87	7.58	0.53
32825.27	13364.47	16349.76	3473.62	*33.693	155.01	
*10.48	0.87	*623.86	*26.389	*0.506	*4.627	4834.69
24182.36	17.91	481.65		13.26	5.81	0.55
56550.18	5359.51	30045.03	1224.1	*33.693	122.6	
128.77	0.88	*623.86	164.7	*0.506	*4.627	6079.48
79963.44	32.24	617.64		7.39	4.25	0.54
82722.47	19866.36	24581.65	1862.57	*33.693	64.45	
37.93	0.3	*623.86	*26.389	*0.506	*4.627	3542.66
16112.38	16.56	489.82		6.6	6.18	0.34
32379.48	8865.74	16999.88	1499.98	*33.693	130.83	
*10.48	0.64	4279.87	371.61	*0.506	48.21	4368.73
17183.81	15.49	746.5		16.11	10.14	0.72
71145.12	9065.7	48079.45	1022.72	*33.693	64.91	
50.23	0.69	*623.86	213.93	3.48	34.87	6957.75
14350.9	14.2	776.66		10.1	7.06	0.41
99530.71	4816.13	15421.86	804.9	*33.693	66.02	
*10.48	0.59	*623.86	*26.389	*0.506	*4.627	5913.27
24347.27	27.46	218.29		7.32	3.83	0.42

Table4.txt

51321.06	3069.19	12297.44	498.49	*33.693	79.53	
*10.48	0.7	4805.65	207.92	30.26	53.41	4003.2
3630.05	14.19	495.94		9.36	7.41	0.41
79825.71	4279.29	34272.1	678.16	*33.693	94.57	
172.5	0.31	*639.193	615.77	11.64	25.97	4503.76
18849.83	9.22	170.59		74.4	*0.751	0.29
107720.37	2655.7	22601.29	300.29	913.7	53.05	
1302.05	0.55	*639.193	736.31	34.47	123.63	1923.32
5824.79	9.58	373.68		203.03	85.49	0.34
162072.21	13234.47	34424.79	296.55	1221.9	39.68	
612.64	1.4	*639.193	1134.94	118.09	32.92	1579.14
29116.77	17.51	140.82		49.19	*0.751	0.46
270318.19	2667.4	6260.26	888.88	1244.59	44.22	
190.53	0.77	5936.13	427.97	59.08	20.57	5194.58
4975.92	15.83	182.48		22.31	*0.751	0.31
92854.43	1086.59	11195.83	646.07	1117.02	62.8	
61.85	0.68	*623.86	289.36	*0.506	*4.627	5737.43
233461.04	26.38	253.23		8.98	6.89	0.67
38901.81	6079.11	8712.12	2892.26	*33.693	82.84	
*10.48	0.33	*623.86	*26.389	*0.506	*4.627	4458.06
12707.1	15.86	215.93		6.76	8.57	0.43
38467.26	3628.51	10355.65	515.46	*33.693	82.6	
119.13	0.47	*623.86	*26.389	4.36	204.54	3478.1
98473.34	15.44	298.51		6.26	8.57	0.37
29453.87	3548	27944.67	1523.31	4834.29	36.41	
50.23	0.75	*623.86	158.34	*0.506	32.69	5019.24
96112.28	14.03	385.64		8.3	12.2	0.47
42931.54	10005.05	61562.84	2519.78	*33.693	58.39	
*10.48	0.82	*623.86	*26.389	*0.506	*4.627	5347.23
24860.31	12.62	234.71		11.92	9.83	0.75
72929.7	8114.77	113474.51	1586.79	*33.693	183.95	
*10.48	0.6	*623.86	*26.389	*0.506	*4.627	4855.88
29650.74	23.46	408.96		31.03	8.41	0.89
42645.06	17652.91	7324.07	3137.92	*33.693	100.39	
56.11	0.44	*623.86	*26.389	*0.506	*4.627	4499.47
16433.34	26.26	266.95		9.33	9.21	0.51
40129.84	8114.77	15275.53	2975.24	*33.693	172.33	
*10.48	0.34	4279.87	189.65	6.86	*4.627	5703.95
19068.42	24.01	253.23		13.11	9.83	0.27
65777.93	3749.63	27522.66	828.23	*33.693	63.56	
*10.48	0.34	*623.86	*26.389	*0.506	*4.627	4551.38
9479.74	28.7	253.23		4.54	5.43	0.3
22206.47	4857.7	18538.26	2080.63	*33.693	50.47	
*10.48	0.57	*623.86	*26.389	*0.506	*4.627	6117.47
15720.25	24.58	372.82		12.92	9.21	0.66
39335.75	6335.35	34437.61	1343.94	*33.693	42.07	
*10.48	0.14	*623.86	*26.389	*0.506	*4.627	3738.19
29260.84	20.18	230.04		4.47	3.61	0.23

Table4.txt

31932.63	1500.99	106868.96	1438.54	*33.693	115.15	
*37.3	0.2	*639.193	379.19	*0.68	11.67	7479.37
15997.47	20.42	1087.03		251.35	95.34	0.58
67901.16	1420.03	11701.29	426.83	1998.71	90.01	
*37.3	0.35	*639.193	1048.55	20.39	*1.36	4721.27
96591.86	16.93	4740.93		49.3	21.01	0.17
103022.16	1684.45	15233.98	627.67	1823.73	68.03	
654.84	0.31	*639.193	353.81	11.12	8.46	3585.36
21289.59	16.69	376.27		40.87	55.29	0.13
151104.83	1908.44	12424.87	2617.8	1162.73	81.82	
296.08	0.54	5204.4	366.59	21.91	17.28	4652.57
151228.49	26.19	521.75		22.11	81.55	0.29
45701.48	2737.73	9810.14	502.99	2259.09	34.2	
640.83	0.22	*639.193	227.4	14.23	13.94	5663.4
11017.24	13.66	519.59		55.25	34.31	0.17
57472.29	1885.9	28787.01	*39.613	2461.58	62.38	
135.25	0.13	*639.193	353.81	5.3	21.66	3516.24
28532.96	9.75	606.3		33.41	48.77	0.15
40074.25	2434.48	145833.88	533.26	1814.95	25.59	
*37.3	0.29	*639.193	211.5	*0.68	13.94	6946.78
56938.49	27.17	438.19		112.02	113.16	0.31
33980.17	2055.64	10401.77	1169.25	2483.06	51.8	
*37.3	0.39	*639.193	327.65	20.9	18.38	4542.38
349514.53	11.36	538.83		38.39	105.97	0.22
45455.96	887.56	12487.64	994.4	1298.89	57.89	
514.73	0.33	*639.193	1501.07	4.22	11.67	2431.37
81582.87	9.57	7390.04		82.5	42.76	0.2
78099.88	10116.98	53068.01	488.61	2029.21	47.63	
422.12	0.49	*639.193	327.65	14.23	9.35	5497.06
49944.32	8.26	302.14		16.92	85.49	0.35
52751.35	*132.654	14160.15	1389.75	913.7	48.96	
322.03	0.28	4438.36	397.76	18.35	15.62	1055.98
36908.42	7.8	633.67		91.41	119.49	0.24
218461.28	16036.24	44467.35	1596.69	1691.64	100.91	
246.14	1.13	*639.193	541.47	16.3	9.93	6338.79
39396.55	12.96	394.16		36.95	100.37	0.31
43736.19	1289.79	106934.95	1148.13	2129.18	27.65	
119.79	0.27	*639.193	403.88	4.76	18.93	2843.96
12246.83	24.88	1658.25		**20	176.97	0.32
93090.11	3487.67	13145.53	426.25	2272.05	86.46	
623.95	0.21	4438.36	250.34	22.42	8.16	10801.86
14228.67	18.61	901.06		27.22	71.14	0.19
61302.59	2796.49	54812.57	1585.72	2289.32	87.35	
479.3	0.52	*639.193	*26.646	*0.68	8.16	6833.77
6473.06	18.19	373.68		41.91	10.26	0.3
74100.63	2411.32	12299.26	503.59	1744.57	87.35	
*41.51	1.26	*1970.97	192.36	*16.134	61.37	2761.3
2156.08	20.19	631.76		13.78	5.98	0.64

Table4.txt

92865.73	7088.54	48963.5	1944.54	464.13	249.03	
*41.51	0.26	*1970.97	*27.42	*16.134	11.01	7007.89
39228.3	58.06	679.66		20.96	9.55	0.21
24017.12	3053.87	27504.43	4662.78	*33.371	212.85	
476.33	0.68	*639.193	584.35	41.67	28.39	4173.06
24094.97	15.51	158.22		276.48	7.77	0.37
73365.45	2702.54	12973.43	775.54	2198.53	21.35	
363.34	1.17	22122.73	1360.07	164.22	15.06	4572.12
6737.34	11.33	236.49		41.91	*0.751	0.86
255477.37	3998.12	27997.96	726.77	2401.38	39.32	
394.49	0.54	*639.193	508.47	82.31	14.5	1879.15
7408.66	9.68	259.41		123.99	*0.751	0.58
71351.98	4330.2	25363.17	743.16	1180.96	207.34	
890.3	1.39	*639.193	1156.25	225.56	35.04	3956.49
29138.73	16.68	205.04		140.63	*0.751	0.81
163373.59	3439.47	28690.22	2410.89	421.21	10.83	
*10.48	1	*623.86	392.89	*0.506	*4.627	5969.76
5231.4	28.1	2109.5		12.14	5.81	0.72
65104.56	2754.34	36139.02	668.66	*33.693	107.28	
*10.48	1.21	*623.86	255.13	10.01	*4.627	4855.88
17245.16	17.62	2577.56		15	6.89	0.67
80259.27	7545.49	7365.53	1226.74	*33.693	30.63	
*10.48	0.79	*623.86	*26.389	*0.506	*4.627	4617.38
6544.7	20.27	230.04		9.91	5.05	0.92
57609.44	4402.56	9786.93	1414.1	*33.693	110.38	
369.61	0.92	*639.193	594.89	158.36	39.28	3184.17
*412.805	23.43	278.17		179.24	*0.751	0.43
178099.97	4927.55	12644.48	968.46	744.03	84.52	
2114.54	1.75	5204.4	563.07	327.35	65.69	3533.51
3055.51	16.57	212.26		44.05	*0.751	0.3
26222.71	3535.95	50897.81	774.21	1080.34	73.43	
*37.3	0.54	*639.193	314.23	12.16	8.75	3264.03
3571.91	23.81	158.22		208.53	*0.751	0.22
69567.97	2318.94	8007.19	*39.613	*33.985	32.05	
1425.31	1.54	4438.36	2727.18	340.54	71.52	5368.34
3859.96	20.57	252.98		60.88	*0.751	0.64
186484.3	5053.05	11259.12	589.98	1384.46	36.37	
*37.3	0.09	*639.193	676.97	11.12	10.51	5267.62
9475.12	13.44	190.17		35.12	*0.751	0.14
79669.14	3985.88	51941.45	631.46	1244.59	50.52	
783.8	0.78	5936.13	397.76	77.01	32.92	1220.13
6473.06	4.31	1000.97		33.81	59.31	0.24
78137.15	10089.82	67150.39	578.16	1770.99	166.72	
523.51	1.25	4438.36	789.32	39.44	25.44	1774.39
15312.88	9.34	1508.21		22.93	30.59	0.53
85648.39	6792.04	13458.13	655.64	3628.85	66.24	
566.98	0.47	*639.193	177.87	19.37	*1.36	3747.2
*412.805	17.58	423.8		11.47	40.4	0.3

Table4.txt

41907.82	6519.88	31747.24	1346.61	2189.87	61.79			
535.17	2.72	5574.06	257.77	55.67	40.87	9782.85		
4118.84	46.86	319.44		9.97	24.89	0.42		
94192.71	2123.98	54431.53	374.33	1112.44	20.55			
1032.78	2.76	4438.36	391.61	161.41	56.44	2361.63		
*412.805	31.55	896.3		25.53	38.47	0.49		
171112.65	13767.43	25267.96	888.88	292.42	125.34			
*37.3	1.44	5936.13	300.56	24.95	35.04	4343.87		
3992.51	19.56	831.4		296.52	46.34	0.31		
46998.79	3379.33	18247.19	*39.613	2611.66	10.92			
840.05	0.36	*639.193	366.59	42.9	23.28	938.34		
2610.65	8.7	357.9		11.22	44.7	0.15		
50855.53	4852.42	26780.27	795.52	904.36	75.52			
*37.3	3.11	*639.193	286.61	7.44	17.28	9048.68		
*412.805	30.97	519.59		21.28	26.46	0.55		
120875.92	10484.37	28078.33	250.02	1673.97	69.94			
538.08	0.41	*639.193	250.34	11.64	*1.36	3582.47		
31674.86	22.63	226.28		9.21	40.87	0.19		
49943.56	2878.99	12613.12	941.3	3443.59	19.66			
783.8	3.13	5204.4	746.04	36.96	34.51	2200.25		
23988.92	26.49	1580.77		14.68	59.97	0.54		
103430.8	17964.81	28464.56	991.59	2560.27	91.4			
908.68	0.38	*639.193	300.56	62	12.81	1080.6		
11056.21	10.86	493.31		21.92	39.54	0.35		
42400.5	9561.93	22758.34	1024.03	1289.85	59.28			
289.53	0.31	5204.4	286.61	14.75	12.24	6250.32		
*412.805	35.93	428.63		22.34	211.81	0.23		
32605.53	1033.79	155178.45	2694.76	1518.66	17.26			
663.21	1.06	*639.193	227.4	24.7	15.62	2423		
*412.805	23.94	987.48		16.64	74.44	0.34		
52681.08	9117.78	19818.4	1232.4	1393.44	63.16			
*37.3	0.67	5574.06	366.59	16.81	12.81	1733.09		
*412.805	30.16	1095.56		18.44	166.96	0.36		
52470.3	7405.53	5495.18	1053.14	2440.09	29.12			
1593.5	0.89	*639.193	211.5	44.38	23.28	5249.34		
*412.805	44.09	553.52		25.84	71.14	0.28		
155312.13	1409.12	42454.64	479.67	763.06	56.69			
434.28	0.6	7984.19	327.65	7.44	20.02	4131.97		
6990.01	22.4	296.25		28.52	82.14	0.27		
30044.54	3596.39	44930.22	464.85	1629.72	54.22			
*37.3	1.51	4438.36	726.53	40.18	20.02	1937.13		
93343.55	17.67	158.22		145.58	*0.751	0.59		
139799.19	4441.54	3813.28	609.39	843.42	108.44			
176.14	1.59	*639.193	265.11	25.45	11.09	3648.84		
*412.805	10.34	201.38		56.8	*0.751	0.31		
148437.73	3863.69	11480.39	1795.57	672.22	12.03			
282.94	0.68	*639.193	300.56	15.78	17.83	6209.33		
*412.805	20.17	197.68		272.7	*0.751	0.3		

Table4.txt

64732.45	2644	77516.61	985.27	4182.36	32.64	341.22	0.81	15556.43	803.58
211.68	47.73	2383.93	13249.4	14.91	502.16	227.01	*0.751	0.44	
211068.5	6017.83	84328.83	431.47	233.82	52.95	446.37	0.99	*639.193	508.47
54.45	31.05	1810.21	10860.15	11.31	302.14	143.36	*0.751	0.61	
66097.67	1773.67	6771.85	745.13	*33.985	82.61	*37.3	0.46	*639.193	530.56
7.44	18.38	4400.03	*412.805	21.98	140.82	107.46	*0.751	0.27	
95537.81	2550.65	16538.87	1658.95	516.19	25.59	204.7	0.65	10484.95	1091.98
83.27	520.65	5319.46	3413.42	16.42	190.17	197.57	8.63	0.62	
250139.1	5787.65	16321.48	411.26	*33.985	22.74	*37.3	0.76	*639.193	1987.48
10.07	143.91	3892.4	23109.12	8.83	212.26	353.54	*0.751	0.57	
87875.17	8051.21	37248.1	479.07	1038.92	10.64	127.57	0.74	*639.193	474.63
22.93	12.24	1959.23	*412.805	9.86	272	14.9	11.19	0.24	
173004.05	4640.25	11543.54	694.23	1176.41	32.6	440.33	11.55	*639.193	942.08
14.23	30.79	979.39	8149.77	10.93	445.29	232.81	24.89	0.12	
74653.09	5634.76	455208.32	443.7	2995.24	174.76	256.28	0.6	4438.36	463.14
16.3	66.75	3576.71	2847.7	19.77	319.44	106.36	49.04	0.44	
70586.3	8051.21	7709.69	296.02	2782.52	12.66	115.86	1.66	*639.193	1057.27
68.8	68.34	2339.33	*412.805	18.47	262.59	108.73	*0.751	0.45	
174527.49	6688.21	16569.93	367.04	1660.71	14.35	*37.3	0.82	*639.193	1117.81
72.91	30.79	4913.29	4680.16	8.26	488.85	587.26	14.4	0.3	
93798.4	6481.1	11732.82	597.47	876.29	19.82	190.53	1.06	*639.193	1544.75
94.77	58.29	3753	*412.805	9.39	249.73	38.1	20.15	0.65	
110986.43	4802.4	5318.41	1056.7	461.46	9.98	850.68	0.74	*639.193	1004.59
47.83	74.44	1741.35	*412.805	27.07	302.14	234.65	26.46	0.35	
68697.39	8024.74	48869.3	748.43	791.52	11.71	261.19	4.34	*701.526	*26.487
19.68	40.82	468.46	2015.92	16.18	314.59	6.84	18.83	0.4	
133796.95	7903.11	226451.28	*39.516	2418.57	144.14	1231.6	1.15	*701.526	856.85
193.8	60.82	1901.1	14621.68	12.86	557.13	496.86	74.36	0.29	
85706.64	13082.18	66871.31	293.12	2054.75	42.17	392.17	1.52	9054.24	887.06
30.22	31.17	6356.89	4081.59	13.5	336.98	74.11	11.28	0.42	
213140.84	6718.69	14240.47	886.16	1885.36	14.37	981.84	0.85	*701.526	614.45
18.48	61.42	1913.39	2625.35	10.66	330.46	86.81	12.93	0.48	

Table4.txt

107281.37	7165.32	14137.81	714.58	875.27	127.08	
*35.8	1	*701.526	484.16	21.46	58.41	1950.36
1536.03	7.54	241.21		61.44	*0.692	0.32
58152.02	10372.4	14514.1	700.36	497.37	50.42	
274.21	0.8	*701.526	1238.45	52.74	187.94	1979.21
2625.35	22.69	194.2		172.43	*0.692	0.5
149389.02	5579.59	17512.81	889.15	3275.59	48.94	
*35.8	0.73	*701.526	627.22	38.78	288.71	3870.61
1257.47	15.38	187.57		286	10.42	0.4
104904.23	10290.48	7156.63	1484.2	1456.09	54.94	
153.2	4.52	5324.01	994.52	272.65	86.5	2542.78
3789.09	12.77	321.24		160.55	*0.692	0.81
108256.13	8112.48	21564.19	861.58	3495.25	65	
380.51	0.51	*701.526	1227.02	26.16	90.84	1622.7
4223.05	7.39	347.3		40.12	29.27	0.42
153701.25	12168.71	16339.33	1402.63	2129.14	54.77	
514.53	0.75	*701.526	1329.28	56.04	39.94	7016.5
3789.09	35.61	96.93		41.05	*0.692	0.4
231776.63	4085.32	26183.2	1838.09	1035.76	18.75	
*35.8	24.29	4209.16	1485.9	40.48	47.33	1270.75
2015.92	17.34	512.41		53.17	7.7	0.6
245532.25	15966.15	16475.51	300.79	1179.9	50.9	
*35.8	0.5	*701.526	2533.54	37.08	84.65	1399.21
1536.03	11.64	219.81		480.64	*0.692	0.44
237704.11	8160.84	19582.82	839.38	2608.88	82.11	
418.99	0.91	*701.526	470.83	43.85	29.44	5832.27
1536.03	12.68	134		16.35	*0.692	0.47
126493.58	2612.39	6587.43	798.27	587.63	28.04	
*35.8	1.45	*701.526	575.88	97.88	27.42	1512.16
2230.49	12.44	197.48		104.76	*0.692	0.61
131530.6	6147.37	4749.65	877.95	1291.17	63.7	
*35.8	0.67	*701.526	1249.86	45.52	183.37	1484.75
5741.06	5.51	159.96		166.8	*0.692	0.43
132895.87	5359.8	24118.94	440.35	382.62	23.07	
392.17	0.64	*701.526	276.42	6.71	12.47	1604.84
6082.22	14.23	180.84		161.04	10.42	0.53
107431	4564.4	34539.5	510.15	953.44	192.62	
*35.8	0.48	*701.526	575.88	*0.621	*1398	1210.18
8576.17	5.76	203.97		41.08	10.59	0.25
48644.38	5516.73	9739.32	713.16	558.9	128.7	
126.85	0.5	*701.526	1563.21	15.16	788	1516.09
266387.95	13.05	165.29		617.51	8.08	0.32
62302.62	10651.26	13829.64	1367.17	735.48	10.09	
*35.8	2.37	8533.8	1834.58	216.13	658.17	4197.62
6731.6	19.73	422.13		326.19	*0.692	0.96
177684.75	11391.78	17716.66	814.36	1109.88	10.05	
*35.8	1.24	4209.16	1519.11	38.78	481.12	3357.18
44627.42	15.47	284.55		309.78	15.13	0.37

Table4.txt

73247.24	12019.66	37859.83	812.9	612.26	8.85		
320.46	0.53	*701.526	1452.57	33.66	117.14	3552.87	
74270.45	14.06	292.87		48.97	12.61	0.61	
103654.11	11986.56	17750.63	1592.29	1567.48	24.68		
849.71	1.3	*701.526	470.83	63.7	30.59	1197	
2809.39	25.07	180.84		35.48	*0.692	0.6	
108180.97	1596.67	9878.64	812.9	899.95	154.78		
485.75	0.48	*701.526	1628.99	8.64	81.26	4803.75	
39671.95	11.5	200.74		87.05	29.52	0.71	
43707.89	7935.3	30420.37	726.72	669.75	16.98		
287.04	1.85	*701.526	170.8	11.78	13.02	1882.69	
2015.92	14.02	681.16		66.06	21.21	0.58	
5596.69	10897.72	883.71	864.55	231.28	36.78		
340.83	1.01	*701.526	1385.54	18.48	228.87	5674	
4890.92	27.02	134		308.39	8.08	0.44	
98277.49	6099.92	4786.1	936.51	998.71	13.24		
384.41	1.19	*701.526	396.38	33.95	15.79	1648.57	
10446.2	18.35	347.3		33.79	30.01	0.37	
125584.08	13632.39	17648.72	958.49	756.03	71.03		
*35.8	2.17	*701.526	232.14	46.64	26.56	1539.66	
5856.14	30.93	395.85		15.17	45.73	0.49	
72758.31	10831.96	11041.49	980.58	608.15	94.89		
415.19	0.83	*701.526	290.92	47.75	24.84	1841.9	
3713.77	16.28	471.58		23.37	41.83	0.4	
103178.43	12583.36	10521.65	315.65	891.72	62.78		
784.47	1.21	*701.526	333.74	25.58	20.29	5246.49	
1536.03	31.47	235.18		23.79	37.8	0.63	
88033.63	2240.64	9826.41	506.18	1146.95	40.89		
532.28	2.11	*701.526	802.02	22.05	13.57	1610.79	
102316.18	7.22	870.13		67.16	21.49	0.65	
164375.62	6941.77	158673.33	639.93	2096.08	39.61		
*35.8	1.71	*701.526	269.12	11.78	*1398	1496.49	
3637.49	34.35	271.86		8.45	19.68	0.42	
71693.89	5265.79	25777.02	1247.51	1906.01	70.83		
549.85	1.54	*701.526	261.79	16.67	13.57	4119.48	
9707.86	17.83	424.48		13.85	45.2	0.48	
48275.97	7005.59	26386.32	992.82	887.61	48.77		
234.55	2.71	*701.526	170.8	26.74	12.47	5805.35	
2015.92	22.15	280.35		13.35	43.14	0.53	
71360.8	3747.56	29707.51	686.91	563	30.62		
220.89	0.34	*701.526	1169.61	38.78	135.56	3613.99	
1257.47	15.61	267.58		47.99	13.25	0.28	
128241.82	9327.23	3404.34	2477.44	317.13	16.28		
*35.8	2.18	*701.526	3649.58	92.08	173.59	2133.07	
2230.49	18.35	513.49		205.18	10.25	0.66	
95212.93	10519.97	2784.23	1600.81	1641.76	11.14		
407.56	0.62	*701.526	575.88	12.4	315.29	1817.52	
39840.69	16.63	120.18		154.25	14.52	0.31	

Table4.txt

67889.33	8096.36	23611.45	348.88	480.96	43.21	
220.89	0.85	*701.526	4561.36	17.88	3294.37	1590.97
5326.48	5.56	221.37		187.69	16.2	0.62
231385.91	5093.73	22850.18	915.39	821.81	6.34	
437.84	1.05	6949.84	1519.11	42.73	129.18	3543.49
8116.08	21.83	261.82		299.6	8.82	0.45
111939.65	9783.57	4310.73	574.59	1015.18	3.91	
137.57	3.54	4770.23	1732.27	22.64	45.25	3301.76
2718.34	29.53	490.52		124.12	*0.692	0.45
233869.79	18630.8	31541.67	870.5	1583.98	126.33	
467.49	3.92	*701.526	677.89	51.91	43.77	1027.99
*155.532	25.67	321.24		51.02	14.2	0.66
150412.28	10897.72	4931.7	731.73	521.97	61.17	
115.86	1.19	*701.526	1283.99	196.29	47.03	1600.88
1257.47	8.77	470.46		108.78	7.7	0.31
215830.28	19947.76	34744.36	541.49	871.16	12.39	
574.18	0.82	*701.526	1053.4	22.64	31.46	2355.28
1786.06	19.29	488.31		78.92	8.45	0.35
171445.6	16845.51	19837	1169.13	813.58	15.76	
567.26	1.03	4490.68	6293.23	177.81	51.8	2671.65
82003.24	6.04	351.13		187.81	16.05	1.22
67889.33	7053.49	35188.45	980.58	961.67	3.06	
*35.8	1.05	*701.526	1123.36	49.42	27.13	4276.15
12780.9	17.07	205.58		28.6	14.83	0.66
72453.48	2537.74	9215.87	1070.82	439.97	9.05	
868.08	0.58	4770.23	1076.8	334.47	34.08	3419.78
4361.64	10.71	763.54		217.97	8.82	0.27
162987.94	4642	6943.53	513.46	1019.29	46.6	
*35.8	0.96	*701.526	*26.487	*0.621	*1398	1901.1
2432.91	10.91	177.44		97.63	9.9	0.6
46497.38	3472.71	30929.88	544.18	1089.29	80.96	
740.06	1.29	*701.526	3064.92	432.48	85.27	1529.83
4081.59	15.44	451.17		295.97	9.9	1.91
225208.72	6766.45	31201.73	1044.42	2191.14	14.55	
*35.8	0.45	*701.526	2395.46	23.82	329.01	5132.14
7639.44	8.76	295.62		511.7	65.8	0.33
122150.42	16676.15	65275.14	623.28	439.97	19.06	
256.81	1.01	*701.526	1100.12	5.4	44.66	2151.94
933.19	3.54	244.2		78.56	15.74	0.46
74229.54	10208.61	19853.95	1202.58	358.05	65.47	
299.7	0.79	*701.526	1158.08	*0.621	100.8	4466.72
1786.06	6.7	575.82		74.87	14.52	0.42
68542.01	14770.91	24541.87	1407.6	464.56	57.91	
274.21	1.36	*701.526	4834.41	88.64	31.17	3118.63
933.19	9.98	311.91		371.03	34.1	1.2
192469.35	25554.03	7828.92	1140.62	751.92	10.29	
137.57	0.56	*701.526	416.9	62.06	20.29	4424.45
19030.25	16.58	168.8		25.84	*0.692	0.42

Table4.txt

125295.59	2537.74	36933.73	658.07	604.05	59.27	
220.89	1.19	*701.526	4388.88	72.89	55.4	1274.55
39314.53	14.59	264.7		225.53	8.08	0.58
138276.24	17252.46	17818.57	1271.73	542.49	13.57	
388.3	1.74	6949.84	3485.51	45.25	59.61	2724.46
13376.65	10.54	242.71		426.6	13.57	0.4
115229.46	17269.43	70166.04	680.56	764.25	6.11	
162.32	1.01	*677.872	1073.29	19.6	27.75	1881.62
1671.07	24.51	353.09		135.06	10.02	0.89
141474.47	15103.6	24310.36	1925.53	1465.06	63.12	
791.42	0.8	*677.872	1370.31	59.66	36.78	3681.66
50454.43	13.72	208.89		106.46	13.75	0.49
113599.51	8025.5	5460.23	1914.63	1389.86	98.12	
599.67	1.35	*677.872	2791.4	158.6	40.52	4398.05
1203.32	16.8	1036.73		81.77	33.68	0.6
47352.5	16658.35	28119.65	1809.55	2593.39	103.92	
*12.832	0.53	*677.872	1145.05	57.07	17.48	5953.79
33511.75	9.02	545		237.6	53.31	0.53
38363.58	17242.57	8142.3	1884.38	1338.16	59.36	
*12.832	0.42	*677.872	1176.63	10.72	97.24	3132.74
2622	18.38	330.19		228.83	36.6	0.33
141823.16	18881.61	26538.92	1696.57	1333.46	94.56	
164.82	3.54	5007.58	1945.82	21.8	44.27	2171.88
3238.37	13.57	510.18		83.36	10.99	0.95
174463.68	17944.45	19827.78	1538.95	2659.24	61.56	
390.06	1.94	6827.94	2293.11	77.3	60.54	3924.67
35103.19	16.74	697.29		128.78	43.56	0.44
154494.31	10375.52	11317.09	1375.51	1450.96	38.48	
437.1	1.73	*677.872	490.36	73.44	23.79	7016.18
3485.89	38.29	168.09		45.11	8.83	0.6
121616	8082.58	25612.59	1988.6	2010.31	95.85	
563.37	1.15	*677.872	509.8	77.3	41.59	4696.66
6002.73	15.83	182.24		29.83	12.55	0.6
130896.25	8959.42	13194.81	311.87	1300.56	40.98	
213.72	0.24	*677.872	747.76	4.42	354.14	2364.84
21240.89	7.3	356.3		129.75	24.73	0.26
129753.02	10279.64	20443.63	1458.23	1164.25	53.72	
1677.11	0.79	4540.43	475.64	76.87	5229.77	2719.17
3834.86	15.5	251.54		18.17	11.63	0.47
23382.13	8272.96	15369.54	617.1	2010.31	68.53	
964.36	1.1	*677.872	460.79	33.2	64.92	2598.68
1203.32	13.51	439.11		19.95	13.46	1.01
104105.43	15705.5	14594.41	706.55	995.05	116.58	
218.5	2.59	*677.872	1184.5	109.37	57.81	5880.42
9053.98	55.87	766.38		123.35	19.27	1.63
227530.55	12916.1	9208.61	3277.87	4944.26	55.44	
220.88	1.18	*677.872	1662.45	34.51	24.58	4393.03
3485.89	15.47	348.26		48.96	9.35	0.81

Table4.txt

95406.71	12260.09	11037.49	1133.17	1653.06	73.35	569.45	0.35	5469.4	654.45
36.91	14.08	2501.58	4766.94	14.31	943.13	41.17	38.64	0.41	
81173.81	9896.39	48680.38	1326.06	1004.45	153.5	372.72	2.41	11152.32	2880.25
88.87	44.27	2171.88	39875.45	12.65	510.18	356.6	20.04	1.73	
177877.65	10663.33	18133.06	1515.17	3327.44	59.14	553.22	2	*677.872	1278.09
19.6	34.91	4310.38	90882.57	16.65	277.88	517.43	55.36	1.53	
133005.71	9973.01	4342.07	1330.76	2922.69	65.18	1032.39	0.71	*677.872	257.05
35.38	10.67	6938.82	4766.94	15.26	186.82	17.42	16.04	0.37	
70836.71	2147.03	17035.98	3571.88	1126.65	59.19	493.67	2.09	*677.872	357.88
137.85	24.58	2213.82	9238.41	16.32	335.17	30.06	4.37	0.49	
146349.34	8635.05	24961.28	1477.19	1004.45	103.19	919.8	1.18	*677.872	280.37
22.47	18.8	2817.59	907.29	3.85	168.09	30.69	22.55	0.43	
27952.26	2844.19	210008.73	933.53	473.17	74.6	1330.79	0.37	*677.872	336.29
25.32	15.12	2753.44	7008.31	7.99	126.56	31.72	46.24	0.18	
43923.09	11605.16	127365.37	3538.51	637.76	49.67	134.28	0.7	*677.872	257.05
5.78	46.16	2411.78	*121.197	14.97	589.62	48.07	17.95	0.35	
109926.15	15783.22	141532.6	2725.55	1718.87	134.12	390.06	0.97	*677.872	257.05
8.93	10.93	9678	10858.22	9.75	325.17	32.19	35.88	0.9	
18959.37	3139.41	162287.31	1108.79	1230.06	57.32	1244.54	0.28	4067.23	245.15
23.13	20.37	8222.35	1772.94	20.72	590.84	20.47	63.53	0.25	
43057.35	3194.87	124856.93	1581.81	1272.36	71.03	1300.98	0.56	*677.872	208.27
*0.661	16.7	1115.55	2695.56	6.78	456.04	6.14	39.74	0.32	
32799.55	5414.81	170929.23	1502.11	637.76	47.62	177.26	0.51	*677.872	*27.062
7.59	20.9	3292.54	907.29	18.74	398.13	23.78	22.31	0.52	
93750.82	4291.01	34173.93	1105.31	1389.86	52.04	37.93	0.22	*623.86	*26.389
3.03	*4.627	4955.12	34125.72	45.93	1094.74	16.42	3.83	0.23	
47067.54	7024.08	114547.01	866.54	*33.693	33.13	*10.48	0.96	*623.86	*26.389
*0.506	*4.627	3523.26	30978.84	13.04	381.38	7.49	3.39	0.44	
32899.46	1797.07	88385.17	428.33	*33.693	18.26	*10.48	2.31	4279.87	350.08
40.52	*4.627	3870.08	3863.4	50.47	1539.09	30.37	6.54	0.6	
71145.12	5485.78	25333.34	1151.9	*33.693	23.15	*10.48	0.59	*623.86	213.93
*0.506	*4.627	3823.78	18350.5	16.27	672.03	13.23	5.43	0.36	

Table4.txt

56055.85	4033.89	12901.69	1814.13	*33.693	49.96	
*10.48	1.16	5830.35	1034.05	38.62	*4.627	6034
19930.32	7.39	355.59		36.9	5.62	0.34
182230	9043.46	71788.39	654.46	*33.693	34.47	
*10.48	2.09	*623.86	371.61	14.85	360.15	4732.68
6474.14	37.45	1175.44		153.39	4.65	0.62
50896.49	4361.43	16222.89	454.85	*33.693	15.89	
*10.48	0.19	*623.86	189.65	*0.506	*4.627	3097.23
33583.46	13.44	196.85		13.64	5.99	0.21
23249.66	2327.78	12107.61	2723.17	*33.693	65.65	
*10.48	0.45	*623.86	*26.389	32.86	*4.627	4810.01
23150.49	21.59	385.64		*0.082	5.43	0.34
71787.1	3347.59	21475.25	1625.66	*33.693	29.98	
222.29	1.3	*623.86	317.26	3.48	58.52	3549.13
*417.822	34.99	307.41		15.4	6.36	0.61
47280.71	4054.28	16801.64	752.54	*33.693	84.82	
88.97	1.54	*623.86	237.65	13.02	51.02	2068.76
*417.822	14.35	471.39		13.05	5.43	0.44
89556.92	4774.59	15494.94	834.39	*33.693	83.89	
*10.48	0.36	*623.86	*26.389	*0.506	*4.627	4110.57
34901.37	16.22	276.03		15.28	5.05	0.4
87243.88	6015.22	31264.95	2649.39	*33.693	30.27	
*10.48	0.71	3743.16	*26.389	9.24	*4.627	4117.31
5231.4	14.08	469.33		16.02	11.63	0.61
47209.66	4733.09	176588.1	243.06	*33.693	40.97	
*10.48	0.47	*623.86	177.26	*0.506	38.29	5652.01
4295.01	18.7	871.44		8.98	5.43	0.28
139089.28	5107.94	11400.82	1463.06	*33.693	30.13	
*41.51	0.41	*1970.97	271.86	*16.134	10.5	4063.76
31317.73	20.92	648.8		17.71	12.39	0.21
37354.89	15634.7	15750.27	1589.73	*33.371	132.87	
*10.48	0.6	*623.86	*26.389	*0.506	*4.627	5180.63
*417.822	23.19	285.06		7.98	5.81	0.38
47635.86	1648.31	9232.35	1318.47	*33.693	65.65	
83.39	0.44	*673.809	335.34	*0.579	*1.378	7592.38
32742.96	46.24	245.85		11.27	10.16	0.42
49477.59	11209	22518.63	2013.66	2817.56	182.88	
138.8	0.86	4684.39	705.09	14.66	41.7	4718.7
102631.79	14.52	477.81		17.15	10.9	0.63
38156.54	8501.41	176095.2	1105.4	3315.93	46.66	
146.86	0.78	*673.809	197.43	3.48	14.44	8620.34
14050.95	62.1	528.1		8.77	6.52	0.4
81181.92	7432.06	82912.07	5583.96	2956.23	74.63	
34.3	1.18	*673.809	168.62	4.29	*1.378	5777.24
16696.46	20.31	619.23		7.21	9.78	0.49
70411.2	11443.07	25141.44	1442.7	1310.13	30.49	
*41.51	0.48	*1970.97	*27.42	*16.134	11.01	5725.86
1042.25	38.38	654.44		14.01	3.52	0.34

Table4.txt

40080.29	9273.62	13417.19	3469.64	*33.371	216.88	
*41.51	0.89	12729.83	*27.42	*16.134	20.32	6925.57
5343.35	29.75	457.8		4.93	4.81	0.76
55882.59	7646.94	13875.55	2620.2	*33.371	130.37	
*41.51	1.02	*1970.97	210.5	*16.134	12.05	6639.79
16692.44	25.92	1259.74		4.4	6.35	0.99
88883.49	5492.9	56940.58	1591.6	*33.371	113.57	
*10.51	0.75	*673.809	211.24	*0.579	8.83	7883.35
11107.11	42.39	739.52		9.13	5.84	0.57
43372.42	9750.07	20817.24	1650.88	2254.34	37.41	
142.85	1.06	*673.809	346.78	8.91	15.56	8147.06
14931.68	30.03	2343.09		11.18	7.39	0.59
51850.88	17966.3	39697.89	1926.57	2014.94	138.6	
*41.51	0.3	*1970.97	183.18	*16.134	8.97	3296.98
2604.15	17.83	825.1		5.61	8.09	0.17
45319.51	14790.99	14806.45	4811.68	*33.371	209.54	
*41.51	0.79	*1970.97	263.27	*16.134	12.57	7603.07
8365.7	44.49	526.02		9.04	5.6	0.33
107094.97	11063.31	27833.24	2176.65	*33.371	35.39	
*41.51	0.57	*1970.97	210.5	*16.134	21.96	4868.23
5817.21	23.46	2435.35		12.77	5.79	0.32
134757.67	13015.21	25734.47	3185.81	*33.371	133.39	
426.06	0.58	*673.809	659.39	*0.579	12.2	8620.34
14882.23	31.67	1992.24		57.38	12.66	0.42
59864.7	20768.38	177045.84	1748.14	1925.18	104.46	
*41.51	0.55	*1970.97	*27.42	*16.134	12.57	5891.88
35541.83	19.4	365.59		**20.02	6.89	0.39
20869.67	7732.75	12570.03	4628.35	*33.371	192.17	
*41.51	0.38	189497.53	*27.42	*16.134	8.97	5999.98
30868.86	17.6	287.23		4.23	5.4	0.34
71831.86	7217.5	8608	3787.94	*33.371	229.79	
*41.51	0.39	*1970.97	427.67	*16.134	20.59	3339.9
128365.2	16.69	1232.23		5.72	10.93	0.39
59923.23	31498.93	24095.57	6270.12	*33.371	94.63	
367.94	1.51	7338.12	312.05	14.66	16.12	10385.81
6189.73	48.38	569.06		8.49	11.97	0.65
110489.92	20947.7	12580.08	924.05	3426.18	63.44	
*41.51	0.46	*1970.97	210.5	*16.134	10.24	5392.9
7047.89	15.26	806.75		6.91	12.67	0.33
34301.58	3141.65	11531.56	1563.53	*33.371	53.35	
*41.51	0.73	*1970.97	271.86	*16.134	36.96	6838.43
7047.89	68	2288.8		5.89	7.75	0.51
59634.92	5406.35	19728.38	2248.87	709.86	33.29	
230.44	0.6	*673.809	197.43	*0.579	*1.378	4834.44
5270.01	17.05	445.66		6.88	11.26	0.48
37473.71	16067.05	24962.43	2584.08	1814.04	101.24	
297.48	0.19	*673.809	*26.852	*0.579	*1.378	6845.31
13373.82	7.32	307.43		8.74	8.21	0.24

Table4.txt

30413.09	11706.59	25177.23	1906.44	1208.28	101.64	
*10.51	0.23	*673.809	*26.852	*0.579	*1.378	6905.35
8562.63	15.12	179.6		6.63	7.8	0.26
14019.98	5709.69	16518.44	*122.771	1046.12	29.58	
39.7	0.3	*673.809	*26.852	*0.579	*1.378	5117.58
23991.45	18.47	597.29		7.38	6.96	0.27
46861.05	4826.57	309232.56	1974.7	1589.27	70.96	
193.44	0.22	*673.809	*26.852	*0.579	*1.378	5295.02
150049.23	27.28	314.58		9.22	10.9	0.33
28776.12	9371.94	13655.05	2967.14	2484.09	21.25	
354.76	0.39	*673.809	*26.852	3.48	*1.378	4591.39
11807.3	21.53	1606.85		14.52	8.62	0.29
36200.4	6052.87	64472.98	1075.56	2117.93	49.05	
185.86	0.5	*673.809	380.33	*0.579	*1.378	7650.15
9215.7	14.39	1973.25		12.2	7.8	0.87
57445.01	6339.38	10901.93	1270.91	2604.71	44.62	
*41.51	0.6	*1970.97	237.16	*16.134	12.57	6956.41
33687.14	48.66	2771.91		17.71	9.07	0.71
65265.99	12252.35	7043.64	4740.38	*33.371	46.2	
273.2	0.41	*673.809	*26.852	10.38	11.08	5916.92
2964.53	17.81	556.85		10.87	8.01	0.37
58583.33	10829	5461.15	1873.99	1716.13	40.26	
146.86	0.39	*673.809	237.87	*0.579	*1.378	10702.48
121636.02	37.53	365.77		5.91	6.07	0.5
54079.31	8182.98	8999.19	2803.3	4527.15	20.53	
*41.51	0.37	44647.45	330.75	*16.134	28.38	3757.49
4845.96	26.82	1153.23		11.78	4.81	0.24
33001.28	5881.98	11307.93	404.1	235.75	80.49	
134.74	0.9	4366.79	*26.852	9.65	11.64	11397.12
66691.96	18.2	788.51		10.56	10.16	0.48
90502.19	5338.73	109253.53	1655.42	1952.85	31.27	
*10.51	0.35	*673.809	*26.852	*0.579	*1.378	7888.69
31141.8	43.24	275.88		3.8	7.8	0.48
43228.54	6024.25	14793.9	2403.18	3289.93	61.8	
87.89	0.26	*673.809	*26.852	*0.579	*1.378	4633.68
17154.04	16.31	185.13		10.59	7.17	0.48
18152.88	6253.38	6982.91	2176.98	1603.43	89.66	
230.44	1.96	*673.809	380.33	7.41	36.33	6725.95
38084.61	17.17	658.62		27.41	12.32	0.66
126178.96	13704.08	8261.05	2060.56	2624.75	40.8	
*10.51	0.57	*673.809	183.25	*0.579	*1.378	11573.01
14832.67	38.33	316.95		12.4	8.21	0.49
46527.42	6942.48	15640.43	826.37	1862.76	48.23	
*41.51	0.68	48497.26	245.92	*16.134	25.01	10242.21
10348.4	35.39	835.53		4.85	13.79	0.37
44646.37	16814	20826.81	1175.62	*33.371	308.32	
*41.51	1.16	64060.26	164.52	*16.134	7.97	4858.9
10687.21	41.43	419.12		2.71	6.89	0.66

Table4.txt

75661.48	5752.36	195281.36	2404.03	*33.371	163.68	
158.78	0.48	*673.809	197.43	*0.579	*1.378	4744.33
25333.02	13.16	243.3		8.88	9.01	0.32
22942.84	5338.73	16630.11	904.67	978.95	56.55	
*41.51	1.19	*1970.97	347.22	*16.134	12.3	8957.32
24833.51	35.13	1752.2		7.43	6.71	0.52
67897.59	8332.81	11345.23	3257.49	*33.371	80.59	
182.05	0.92	*673.809	211.24	*0.579	13.32	7936.82
129836.1	38.06	769.76		14.58	6.52	0.62
46527.42	12939.05	15321.34	2385.53	2416.79	41.11	
*39.77	0.79	*706.944	193.8	*21.183	14.19	3244.5
1937.47	13.44	488.5		13.75	11.4	0.66
38152.23	12878.49	15699.41	2409.98	*32.555	224.77	
197.21	0.86	*673.809	211.24	3.48	12.76	7899.37
30767.59	47.37	511.48		11.92	9.01	0.39
50332.42	9517.31	81518.88	1524.56	2537.78	53.81	
*41.51	0.13	*1970.97	*27.42	*16.134	*1.329	3983.37
3930.06	13.13	157.01		*0.028	4.81	0.17
26120.63	2569.9	95354.83	3488.26	*33.371	22.96	
50.06	0.28	6196.87	237.87	12.54	11.08	5556.7
9282.69	34.93	546.63		8.88	9.21	0.34
21612.54	11033.56	11726.03	1757.3	2069.94	63.16	
354.76	1.07	6196.87	358.08	28.75	35.77	8371.02
20950.24	72.66	1322.19		17.7	20.15	0.71
76157.04	13468.52	37817.71	1184.13	1288.39	46.36	
189.66	0.19	*673.809	*26.852	*0.579	*1.378	7750.43
11225.74	7.97	370.33		6.71	9.59	0.33
15575.14	9226.65	26552.97	2019.9	1918.26	65.79	
*41.51	1.12	37400.42	263.27	*16.134	11.01	6925.57
15855.78	51.07	764.27		3.65	5.21	0.46
97559.13	9956.34	174800.24	4262.62	*33.371	145.92	
307.75	0.82	*673.809	183.25	3.48	9.39	7803.47
11284.75	22.9	482.05		16.58	7.8	0.45
24464.66	11267.5	29027.29	1024.68	1758.17	51.98	
113.97	1.49	*673.809	323.77	7.41	8.27	5091.17
7725.34	57.46	347.4		12.91	15.79	0.51
59247.63	6110.14	6726.72	1481.31	696.47	38.51	
*41.51	0.84	*1970.97	271.86	*16.134	11.79	6143.32
36705.35	29.56	457.8		10.84	9.71	0.77
102353.17	5492.9	54606.79	*40.28	*33.371	55.02	
575.51	0.61	*677.872	291.81	34.08	22.48	1184.92
94044.67	8.18	372.09		15.72	37.83	0.21
45221.98	11816.93	12101.36	792.28	1164.25	149.46	
374.89	0.97	*677.872	257.05	47.99	17.22	960.1
7580.4	11.3	507.54		41	73.58	0.23
60710.34	9016.7	61329.49	1992.25	1328.76	89.73	
41.68	0.41	*677.872	336.29	8.04	9.35	6175.56
28979.55	8.51	354.7		416.51	25.91	0.19

Table4.txt

58165.53	2220.12	145180.53	1957.05	600.15	155.08	
322.05	1.39	*677.872	363.21	35.82	16.7	1694.88
50062.65	9.36	418.9		33.19	31.75	0.43
89655.83	9284.17	15197.42	1248.63	1042.05	123.91	
1271.05	1.23	*677.872	825.46	80.52	54.54	2630.42
50871.43	15.6	757.93		28.33	42.4	0.5
47099.57	9666.67	26607.58	2257.29	901.03	48.45	
927.25	0.36	*677.872	1117.26	6.23	10.4	2121.28
44749.49	10.03	6839.92		45.07	23.41	0.3
131661.29	5979.55	27706.95	1476.01	854.03	97.47	
702.54	0.35	*677.872	557.54	6.69	10.93	3427.63
302227.36	22.17	2429.41		18.46	15.2	0.28
71637.14	2881.04	25509.72	3199.08	1215.96	102.43	
859.8	0.73	*677.872	336.29	33.64	29.6	1401.82
9450.59	23.04	664.75		28.86	29.33	0.31
102137.44	7038.09	18115.93	1403.83	1512.06	119.13	
848.47	2.12	*677.872	314.29	11.62	12.5	2282.48
35088.45	20.2	558.84		13.16	28.43	0.47
128804.26	10375.52	66008.51	2501.56	2315.92	88.87	
573.49	1.1	*677.872	529.03	718.27	106.31	5395.53
12003.67	18.62	253.47		47.35	21.81	0.76
146045.08	4627.28	30083.78	1830.04	1690.67	56.55	
625.65	1.7	*677.872	1016.74	19.6	28.81	5707.59
74514.51	17.13	1494.2		48.69	20.56	0.29
126823.42	4067.27	40494.05	1542.51	1032.65	33.83	
439.21	1.23	*677.872	182.49	75.59	27.75	4845.2
5141.25	21.48	518.02		11.1	18.48	0.66
20381.42	12163.71	24995.55	870.67	1403.96	64.13	
370.54	0.68	*677.872	460.79	11.62	14.34	2723.74
5321.32	5.97	1000.58		15.01	14.91	1
145184.98	7322.5	9208.61	1055.52	1493.26	68.65	
*12.832	0.43	*677.872	721.41	4.42	586.99	3221.86
2391.42	5.76	274.2		165.2	6.06	0.25
97994.21	11431.99	5423.32	1557.99	703.59	22.88	
54.06	0.3	*677.872	846.72	7.36	320.47	3515.89
3043.23	20.14	261.11		192.51	28.54	0.23
71560.82	3620.97	13125.52	1543.7	1164.25	13.61	
583.58	0.83	*677.872	3966.92	47.99	71.53	1677.84
907.29	13.08	330.19		188.9	12.25	0.64
120743.17	10548.18	13073.54	1952.19	1314.66	13.97	
47.94	0.57	*677.872	1790.51	16.95	46.97	3722.74
45113.94	13.04	137.58		70.83	8.3	0.44
98750.26	7455.34	11037.49	1676.2	1032.65	11.45	
159.81	0.22	4540.43	480.56	8.49	174.58	1778.28
4055.19	19.3	223.6		147.6	12.25	0.25
116153.42	11085.89	17190.36	1187.88	1460.36	160.54	
*12.832	0.5	*677.872	942.98	31.02	105.17	5804.62
6634.03	13.01	221.53		216.64	10.67	0.41

Table4.txt

125324.58	8349.15	10406.81	1534.19	1460.36	24.46	
244.47	0.46	*677.872	604.2	333.88	23.26	6531.12
8898.37	13.31	272.35		20.47	8.13	0.31
67164.85	5283.29	19314.44	1210.05	1286.46	70.53	
162.32	0.26	*677.872	*27.062	*0.661	*1.383	1903.24
5321.32	11.88	335.17		8.12	8.83	0.51
8494.63	3435.51	8320.69	1707.36	901.03	122.08	
71.77	0.1	*677.872	*27.062	*0.661	*1.383	6181.06
32742.37	13.17	168.09		11.66	13.16	0.15
27652.29	2366.52	20631.79	1686.98	656.57	29.36	
*12.832	0.19	*677.872	*27.062	*0.661	19.85	1714.08
8517.37	27.08	285.15		13.13	6.84	0.18
23692.33	8558.78	8818.72	1418.01	971.54	157.42	
109.72	0.5	4996.3	*26.852	5.09	129.43	6431.73
2344.1	53.68	340.44		14.61	11.26	0.48
45668.73	6368.05	11216.97	857.84	2172.61	30.74	
*10.51	0.39	*673.809	*26.852	6.65	15.56	13057.97
10439.47	65.18	764.11		22.51	10.71	0.99
40388.19	8240.84	*134.38	1197.09	1966.67	28.12	
*11.11	1.55	*648.383	489.82	43.63	50.81	6878.13
17264.21	18.6	913.61		11.79	15.33	0.72
68644.7	14885	39705.59	1693.48	949.53	144.41	
50.71	1.97	*648.383	445.99	*1.463	29.74	6760.47
10237.03	29.22	600.16		1.86	8.01	1.25
65389.19	4601.65	26089.22	3150.2	4867.08	30.47	
*11.11	0.41	8302.85	329.09	12.4	19.09	5801.01
5660.55	27.47	638.06		8.79	17.32	0.58
85943.37	7440.15	10237.56	1263.82	2699.27	20.51	
*10.51	0.22	*673.809	*26.852	*0.579	*1.378	3635.95
27109.85	11.67	196.05		7.54	7.8	0.29
27429.1	4372.9	26428.07	1294.21	1230.19	251.12	
*10.51	0.25	*673.809	*26.852	*0.579	*1.378	2256.43
4972.54	29.71	517.73		2.61	4.88	0.27
21947.58	4174.93	202711.77	2131.24	993.92	103.17	
*11.11	0.54	4448.53	319.59	29.53	23.75	6589.75
8991.29	16.69	585.74		5.26	18.78	0.72
70066.36	7907.38	20213.46	3071.51	2265.05	48.56	
287.13	0.51	*673.809	323.77	17.44	14.72	5926.28
2258.61	42.89	1057.35		16.44	6.07	0.46
55596.09	9837.4	40674.62	1332.2	1230.19	46.06	
50.71	1.05	4448.53	221.35	*1.463	22.98	4557.79
14867.2	12.92	483.58		5.72	8.01	0.59
84672.1	6741.09	12973.43	1812.48	806.66	40.09	
*11.11	0.55	*648.383	245.78	25.07	23.75	6424.94
2605.26	29.39	481		2.66	8.34	0.6
63093.34	10099.03	41481.91	2509.4	687.67	26.61	
*11.11	3.1	*648.383	1625.07	59.75	154.09	6634.53
5586.98	25.84	973.74		22.29	13.91	0.92

Table4.txt

135702.62	28660.6	20247.58	1966.48	1607.99	92.78	
*39.77	0.58	4519.74	218.86	*21.183	10.64	2935.8
5905.87	17.45	458.19		22.28	8.08	0.33
52736.95	7252.37	66082.73	2686.95	*32.555	24.38	
397.23	0.26	*673.809	168.62	*0.579	*1.378	8398.54
30045.07	14.78	417.29		9.97	14.34	0.48
37571.37	10682.97	9384.62	4818.63	1164.32	31.84	
*39.77	0.44	4889.12	260.3	*21.183	12.65	5719.17
12321.47	16.91	473.44		10.49	7.5	0.44
34458.25	11941.06	23484.54	1620.3	*32.555	83.88	
101.11	0.54	*673.809	*26.852	*0.579	*1.378	6543.81
116476.07	8.52	288.12		5.14	6.52	0.54
31979.94	4656.26	113595.28	2139.11	2267.93	25.82	
*39.77	0.55	*706.944	*28.096	*21.183	15.23	6927.68
2083.03	19.37	843.78		7.61	4.14	0.3
29324.15	9192.18	200229.11	1970.34	*32.555	154.88	
*39.77	0.51	*706.944	*28.096	*21.183	*1.362	3524
9370.27	15.49	798.24		8.86	5.72	0.25
34855.93	3136.07	34518.65	1235.14	*32.555	40.65	
166.61	0.57	*673.809	*26.852	*0.579	*1.378	5056.05
1791.68	44.28	589.26		8.32	9.97	0.47
41835.13	10070.42	6662.4	2851.13	1134.91	32.41	
*11.11	1.86	4448.53	445.99	20.15	26.77	5205.74
21042.99	22.87	1319.89		5.88	13.91	0.55
52195.25	13891.35	20519.79	2449.55	896.37	45.8	
324.71	0.5	*673.809	*26.852	*0.579	*1.378	6195.83
18113.85	48.55	333.44		6.32	7.39	0.38
30616.25	12116.93	14793.9	2004.3	1149.62	63.48	
*11.11	1.27	25498.96	398.93	72.99	32.66	6243.95
19163.52	24.96	1959.28		2.86	28.07	0.64
145241.7	8746.74	35840.47	716.24	824.72	30.24	
*10.51	2.53	12509.86	455.02	19.48	348.33	7280.96
70368.66	26.79	490.5		19.22	14.67	0.76
334292.69	4033.72	10625.1	*122.771	3626.17	49.35	
*39.77	1.06	*706.944	*28.096	*21.183	*1.362	4396.16
4124.45	30.15	329.65		9.19	6.32	0.51
23472.77	5417.48	13897.12	880.88	*32.555	89.08	
*11.11	0.56	*648.383	194.55	*1.463	41.2	4462.11
3889.23	32.58	438.99		1.8	*0.579	0.58
50619.15	14646.32	14429.05	4460.86	1251.54	107.05	
*11.11	1.09	*648.383	208.29	29.53	26.77	7688.44
28537.19	30.23	470.63		4	7.67	0.52
104077.49	6199	121685.68	1446.41	2070.64	39.15	
*39.77	0.52	*706.944	268.55	*21.183	*1.362	7314.44
7786.39	22.43	376.08		13.32	8.93	0.3
40043.65	4225.35	83331.4	1137.44	*32.555	26.82	
*10.51	1.08	*673.809	391.29	6.27	16.12	6114.89
33121.35	19.45	1125.13		6.55	11.97	0.52

Table4.txt

43851.69	5224.76	11334.75	2781.9	1331.84	13.89	
*10.51	0.48	*673.809	*26.852	*0.579	*1.378	6865.3
81024.65	23.31	275.88		11.52	6.96	0.38
17853.93	4174.93	25499.22	*122.771	665.2	93.11	
*10.51	0.34	4366.79	224.7	8.17	*1.378	8343.55
35409.39	18.57	314.58		11.94	7.8	0.33
50237.47	5053.97	77635.99	956.03	1610.5	40.84	
146.86	0.23	*673.809	*26.852	*0.579	8.83	8509.08
144069.02	19.28	285.69		12.76	6.96	0.26
43564.19	5652.56	20562.8	3340.15	1475.51	52.46	
*39.77	0.53	*706.944	168.58	*21.183	*1.362	4722.91
88533.6	23.93	1034.47		18.98	7.5	0.53
42052.7	8954.79	127624.89	1524.6	*32.555	12.78	
*11.11	0.51	6479.5	257.31	*1.463	22.22	7968.96
2309.19	60.32	204.42		*0.027	10.2	0.41
91195.1	6373.08	273320.27	1416.71	1575.39	54.09	
*39.77	0.36	*706.944	235.48	*21.183	*1.362	6334.26
15789.55	19.62	847.25		14.62	6.02	0.31
95654.03	3495.71	26078.97	1509.34	*32.555	55.35	
142.4	1	*648.383	194.55	*1.463	20.66	6323.2
18958.77	43.16	398.26		2.87	8.99	0.97
83503.49	4238.32	159191.71	1568.57	1427.32	105.16	
*39.77	0.4	*706.944	235.48	*21.183	*1.362	4028.08
3803.47	29.29	553.09		13.15	7.65	0.31
17126.38	8974.55	43334.84	1287.36	*32.555	52.04	
*39.77	0.46	*706.944	218.86	*21.183	*1.362	4185.39
26940	23.44	373.7		11.51	4.47	0.42
71676.32	3950.21	16168.35	1083.04	*32.555	30.04	
*10.51	0.32	*673.809	*26.852	*0.579	*1.378	7158.13
25657.79	24.04	447.82		6.32	6.52	0.5
18980.21	2382.32	106431.66	3102.35	1222.89	49.72	
*39.77	0.3	*706.944	227.18	*21.183	13.16	5787.86
13847.17	30.13	599.14		17.41	8.08	0.47
68044.25	2957.68	52297.48	2661.99	*32.555	14.08	
166.61	0.44	*673.809	288.11	*0.579	9.96	10453.67
67592.48	33.32	283.24		8.83	7.39	0.65
34276.1	4203.19	11726.03	1089.76	2322.19	34.71	
74.22	0.34	*673.809	*26.852	11.11	*1.378	10652.46
17649.02	16.83	235.61		6.27	6.52	0.38
27845.33	3808.14	22662.92	1181.25	1973.57	65.01	
130.64	1.05	*673.809	183.25	*0.579	*1.378	18532.26
88353.39	57.79	544.58		9.58	7.39	1.14
54695.5	8009.47	22139.52	2021.46	4047.82	40.99	
*39.77	0.49	*706.944	210.52	*21.183	*1.362	6935.98
11043.15	14.07	553.09		11.17	6.02	0.37
23843.16	5436.33	98375.69	2407.41	*32.555	60.53	
*11.11	0.65	8302.85	221.35	34.99	31.21	6796.6
3889.23	27.11	417.45		4.17	24.4	0.86

Table4.txt

33701.34	3895.04	62019.57	765.86	2676.7	55.52	
*41.51	4.73	*1970.97	173.9	*16.134	47.53	2111.95
38824.8	24.91	1072.51		39.66	13.24	0.44
146063.82	15971.86	95731.71	2110.56	*33.371	112.78	
39.7	0.97	*673.809	300.17	*0.579	13.32	16762.71
23898.04	35.17	268.46		14.35	7.39	0.9
24787.01	5196.28	7741.75	2199.12	2544.48	82.05	
185.86	1.42	*673.809	380.33	71.45	36.33	10948.21
264146.54	48.51	482.05		18.47	5.13	0.67
87405.41	11794.48	77518.58	1319.03	2450.46	13.12	
*39.77	0.52	*706.944	168.58	*21.183	8.66	7174.55
66986.84	46.68	378.46		13.32	6.92	0.32
55751.66	3640.57	19783.49	917.3	*32.555	43.82	
*39.77	0.34	5257.04	252.04	*21.183	12.91	5358.71
6214.79	18.88	557.15		11.12	6.32	0.25
53991.89	6385.98	9812.05	1095.21	*32.555	38.94	
*39.77	0.39	*706.944	325.93	*21.183	8.66	5849.21
25116.12	26.9	5032.66		18.44	4.78	0.52
79210.38	6061.49	104146.99	2170.92	*32.555	61.08	
*39.77	0.43	*706.944	177.01	*21.183	*1.362	7417.01
27742.62	17.63	800.01		15.53	7.5	0.36
45844.33	2341.65	38983.61	2142.03	*32.555	21.84	
*11.11	0.45	*648.383	289.73	12.4	20.66	4363.03
3578.49	16.45	277.74		4.37	10.49	0.36
71030.39	5774.14	10331.87	2872.47	1460.42	18.65	
185.86	0.95	*673.809	224.7	*0.579	23.96	5073.6
10746.24	32.43	356.62		12.26	6.07	0.6
63525.42	13880.84	58735.18	1388.02	1186.32	48.5	
*13.55	0.29	*679.575	*27.296	*0.555	*1.377	8061.81
27516.51	15.54	373.01		8.05	*0.714	0.23
29580.6	3844.35	25668.35	5268.7	*34.349	25.05	
114.31	0.31	12334	350.67	41.98	17.92	3925.93
47147.95	22.07	2242.63		7.34	11.1	0.51
86231.11	10263.62	113147.65	2867.71	268.54	138.4	
*13.55	0.96	*679.575	*27.296	*0.555	*1.377	5072.16
16491	57.41	698.92		15.88	11.33	0.62
47099.39	34783.33	11306.39	2526.03	*34.349	51.71	
114.31	0.49	*679.575	*27.296	*0.555	*1.377	11036.18
21107.24	39.06	369.36		4.77	7.14	0.32
31126.01	9839.53	21721.44	2455.56	*34.349	15.81	
*13.55	1.66	*679.575	183.58	4.85	12.94	9536.24
1290.73	40.27	1094.89		8.72	*0.714	0.61
219771.47	20611.31	48308.27	2065.94	*34.349	196.39	
*39.77	0.38	*706.944	185.41	*21.183	9.15	6390.1
3469.68	10.22	408.81		14.4	7.79	0.28
43483.53	6712.05	121317.81	1844.09	*32.555	43.57	
69.54	0.61	*673.809	183.25	*0.579	*1.378	7519.16
29380.3	22.9	297.82		11.75	7.39	0.55

Table4.txt

63144.54	6597.61	8978.82	1778.71	1904.4	37.37	
*39.77	0.44	5257.04	185.41	*21.183	12.65	6795.5
26376.2	29.07	**10790.977		17.12	7.21	0.19
67761.09	5229.41	18061.26	397.25	*32.555	17.93	
*41.51	0.5	*1970.97	*27.42	*16.134	8.72	3079.75
1463.62	15.59	470.44		4.6	7.06	0.36
40201.61	8161.48	59073.63	3741.95	*33.371	99.5	
*13.55	1.42	*679.575	*27.296	*0.555	*1.377	4519.3
11016.38	75.49	619.29		3.83	*0.714	0.42
56858.02	11892.04	131651.03	3418.28	*34.349	88.05	
*13.55	0.26	*679.575	*27.296	*0.555	*1.377	4387.64
2487.5	17.71	681.52		6.19	*0.714	0.24
54371.5	7398.13	15807.41	3829.29	*34.349	85.65	
248.45	0.66	*673.809	346.78	*0.579	12.76	5977.9
55900.01	13.39	345.08		10.79	9.4	0.57
32531.94	9488.23	172623.36	2819.78	1883.6	23.79	
*41.51	0.57	*1970.97	228.34	*16.134	8.97	6792.44
8017.82	23.88	482.98		13.39	10.17	0.62
91615.95	9828.42	122866.75	2961.91	*33.371	124.49	
199.1	0.36	10297.81	235.48	*21.183	13.16	7374.19
29833.68	17.25	2042.89		15.08	14.3	0.46
29686.41	10447.79	59053.61	1346.84	234.43	20.62	
*10.51	0.59	*673.809	*26.852	*0.579	*1.378	12110.02
15275.06	20.89	240.75		7.04	4.63	0.46
41064.18	5224.76	36807.59	1493.22	858.16	29.75	
297.48	0.91	*673.809	650.14	26.14	28.73	6277.23
8023.06	11.39	460.74		27.82	6.07	0.35
141274.57	11238.25	91141.48	993.77	1186.32	56.73	
*39.77	0.25	*706.944	*28.096	*21.183	*1.362	3800.93
1630.07	12.24	314.42		13.15	4.14	0.22
44735.62	4576.3	16112.08	1379.07	*32.555	48.27	
*10.51	2.82	6196.87	1091.06	25.48	48.23	4283.06
8313.69	24.89	745.21		7.32	7.17	0.66
52799.33	2243.9	3948.19	2023.03	3153.03	36.54	
*39.77	0.47	*706.944	202.17	*21.183	11.64	5295.9
4124.45	10.21	559.18		8.32	13.52	0.48
27581.52	14379.41	71390.22	1536.36	*32.555	42.81	
*39.77	1.01	*706.944	177.01	*21.183	*1.362	4392.73
2877.81	42.48	436.03		10.1	6.62	0.51
65869.03	6443.41	7525.53	537.21	*32.555	100.6	
139.28	0.17	*679.575	293.76	14.61	*1.377	5803.62
10775.74	21.73	230.82		12.83	*0.714	0.1
51206.54	5073.14	221335.34	5695.87	*34.349	23.64	
92.38	0.34	*679.575	*27.296	23.76	41.36	7822.28
20057.67	13.32	436.62		18.45	*0.714	0.16
32297.92	4979.18	17964.37	2900.6	*34.349	12.43	
155.31	0.84	*679.575	*27.296	*0.555	55.55	8781.54
1961.69	36.21	938.76		6.92	7.41	0.54

Table4.txt

31743.02	7705.19	13036.78	2071.3	1743.23	106.16	
54.02	0.68	*679.575	276.19	*0.555	17.36	10723.77
6960.12	114.49	2302.33		15.34	*0.714	0.28
128677.1	6380.3	17798.87	6794.86	*34.349	130.66	
178.22	0.28	*673.809	*26.852	*0.579	*1.378	5348.73
15372.3	32.6	432.63		6.99	6.74	0.33
32231.09	13350.8	26499.45	3211.59	1751.17	73.1	
*39.77	0.46	*706.944	*28.096	*21.183	*1.362	6136.62
12860.04	17.3	368.92		6.81	5.41	0.33
24802.34	3459.58	40229.62	1231.75	*32.555	60.57	
208.41	0.28	*673.809	*26.852	*0.579	*1.378	8157.92
8737.57	19.74	426.08		7.88	7.8	0.43
28363.39	8588.33	8033.28	1169.76	1461.22	66.92	
*39.77	0.55	*706.944	185.41	*21.183	9.64	3713.25
1109.73	44.83	873.1		15.48	5.72	0.35
29324.15	15478.63	37718.83	1883.14	*32.555	84.03	
182.05	0.23	*673.809	*26.852	*0.579	*1.378	7592.38
49830.1	49.99	324.05		8.66	5.37	0.25
48812.28	5909.8	7237.41	1752.72	1446.91	32.54	
*10.51	0.32	*673.809	*26.852	*0.579	*1.378	8448.19
151531.77	12.69	258.48		13.9	5.13	0.37
17067.33	6368.05	8074.78	2040.22	2477.37	25.26	
122.37	0.43	*673.809	*26.852	*0.579	13.6	6412.33
37790.2	17.42	426.08		12.91	6.52	0.29
44426.18	4174.93	19688.13	3363.92	1553.83	18.78	
*10.51	0.27	*673.809	*26.852	*0.579	*1.378	6870.3
64832.75	13.14	176.82		*0.027	7.8	0.45
23380.75	4429.52	9263.2	3605.02	781.65	14.79	
87.89	1.1	6196.87	312.05	5.09	23.96	5888.87
28927.1	10.93	900.77		14.72	6.52	0.32
61432.24	7720.57	21832.22	1764.94	2069.94	29.75	
96.75	0.34	*673.809	*26.852	*0.579	*1.378	14159.62
10315.13	18.14	356.62		6.99	4.88	0.32
41690.7	5452.78	190405.08	1780.24	688.67	26.51	
223.15	0.54	*673.809	*26.852	*0.579	*1.378	5034.15
3105.97	30.38	507.3		18.18	6.52	0.34
36102.16	6425.42	108721.88	1602.57	1468.37	17.55	
*10.51	0.49	*673.809	*26.852	*0.579	9.39	10916.53
8241.67	33.34	404.03		10.68	5.61	0.37
17793.91	4883.39	40887.85	1035.96	1814.04	36.86	
237.68	0.7	*673.809	275.88	*0.579	10.8	6296.45
60749	16.29	1700.52		6.66	7.39	0.39
43276.5	10099.56	24586.23	1560.49	1281.13	20.57	
396.53	0.7	*677.872	420.51	41.91	29.34	3283.1
61345.07	16.12	803.78		22.4	15.2	0.56
113287.65	4833.16	9208.61	1055.52	910.44	45.13	
1008.57	1.86	*677.872	450.81	7.59	23	3309.07
1203.32	20.84	795.55		24.96	23.04	0.93

Table4.txt

219428.97	10433.06	8712.18	2663.15	966.84	44.38	
*12.832	1.56	4067.23	208.27	4.42	13.29	2340.31
21352.3	18.24	404.12		12.9	17.68	0.39
180120.42	13051.3	8605.54	1605.67	1850.48	110.02	
506.08	1.06	7714.91	357.88	99.56	63	4564.48
2976.11	47.51	1163.44		13.22	19.53	0.53
152615.64	10586.56	17876.07	901.49	1408.66	44.87	
253.8	2.74	5007.58	245.15	55.35	51.83	3422.87
2055.15	17.09	294.1		12.9	9.68	0.37
209550.22	17320.51	65189.64	610.43	957.44	34.6	
306.37	1.19	6379.16	257.05	10.72	17.22	2472.34
39255.56	14.89	433.39		14.95	33.04	0.51
58827.93	5377.22	6902.68	425.76	2583.98	48.97	
688.85	0.57	*677.872	440.78	7.14	*1.383	3667.18
37919.2	19.86	3661.28		25.36	23.29	0.24
53117.4	6659.43	18578.36	1328.41	1685.97	87.53	
1687.2	1.61	*677.872	*27.062	10.72	*1.383	1491.77
30245.78	14.82	378.31		15.11	72.62	0.6
63718.35	9475.36	9102.39	2428.54	571.93	28.62	
239.79	3.36	4540.43	450.81	22.69	24.06	5052
7081.53	26.39	364.24		25.16	66.61	0.97
140431.26	9437.11	44774.49	1324.88	1634.26	57.74	
370.54	1.8	*621.156	249.29	*19	8.46	3795.46
2282.59	12.94	229.74		52.18	35.51	0.36
61545.07	7094.94	27834.62	1727.76	1773.51	106.73	
611.69	5.61	*677.872	352.52	105.53	31.46	1219.77
2546.87	20.17	441.96		16.17	7.95	0.5
93256.07	19702.81	28171.26	2165.36	642.46	42.4	
2213.65	0.89	*677.872	291.81	157.97	36.78	7407.5
7580.4	22.37	427.62		20.51	21.31	1.05
64763.77	3955.55	18184.45	1173.9	821.12	23.12	
110.58	2.27	*677.872	*27.062	6.69	12.5	2739.72
6557.43	10.86	395.12		51.94	16.87	0.52
145286.02	8349.15	14094.02	1347.23	1352.26	33.6	
*12.832	0.43	*677.872	233.06	37.13	20.9	7625.21
100895.84	48.54	233.79		14.56	9.68	0.4
78897.39	9265.05	16091.75	1173.9	2903.87	39.91	
1139.31	0.77	*677.872	182.49	14.51	15.65	5856.02
3109.27	13.84	573.73		18.95	14.34	0.55
225891.95	8520.65	26350.14	1410.92	661.27	43.2	
402.98	0.72	4540.43	389.56	13.62	18.53	6461.18
72079.58	28.48	706.13		31.26	42.89	0.57
115164.64	3658.1	15868.32	1561.56	807.02	49.67	
405.13	0.64	*677.872	*27.062	10.28	12.5	3287.82
4814.85	11.35	453.24		13.99	42.79	0.39
93009.04	3955.55	19519.79	1754.19	2330.03	21.28	
105.2	2.81	*677.872	485.46	34.95	22.48	3053.4
14828.44	20.79	447.62		55.73	21.06	0.54

Table4.txt

355673.3	11585.92	13056.22	1572.28	1338.16	52.6		
*12.832	1.64	*677.872	1008.61	188.58	31.19	1527.51	
2838.4	17.42	308.12		373.77	21.06	0.57	
134744.82	3528.2	9491.44	1981.32	435.54	37.72		
335.82	1.42	*675.007	1411.8	103.14	5289.6	1450.94	
3883.51	11.93	331.51		125.38	8.11	0.58	
129437.47	12412.11	28991.65	1813.63	1394.42	7.03		
*11.424	0.24	*675.007	259.89	5.23	31.57	1648.92	
13667.77	18.16	255.52		27.7	10.71	0.34	
86032.94	9614.49	43987.64	2353.61	2813.64	90.58		
137.88	0.58	*675.007	347.35	9.42	15.84	2128.55	
68240.48	31.17	191.62		35.44	7.96	0.63	
213519.49	8439.49	17978.8	2677.89	4303.45	101.15		
279.11	0.85	*675.007	421.8	4.78	311.14	3178.67	
3035.15	17.87	386.55		47.08	8.11	0.43	
106894.01	9415.92	23566.91	2170.7	1825.65	18.68		
*11.424	0.72	*675.007	259.89	*0.647	16.5	7120.06	
10211.18	31.13	267.78		22.08	6.52	0.78	
99282.9	6709.94	45731.62	819.53	2214.78	50.07		
*11.424	0.43	*675.007	1075.83	42.32	62.91	7258.98	
838.79	62.07	321.74		426.83	24.92	0.45	
189078.41	7416.5	28823.77	1803.51	1606.4	72.7		
556.34	0.77	7990.97	524.4	6.12	41.98	1937.37	
11712.49	10.84	1130.85		51.6	23.67	0.36	
169951	10386.8	79257	1448.54	3309.89	133.24		
52.48	0.16	*675.007	384.99	7.45	390.48	5192.72	
30023.2	11.67	276.82		59.69	6.81	0.26	
49434.03	2781.64	47571.49	1935.26	4054.67	16.52		
*11.424	1.93	6391.86	742.8	188.13	54.56	1007.76	
40957.46	32.62	198.55		26.38	4.21	0.74	
148122.28	12314.24	16336.52	1311.02	4663.37	67.72		
361.92	1.15	*675.007	914.1	92.09	38.17	3596.92	
3883.51	21.03	257.07		167.19	27.71	0.94	
107682.51	8199.44	6184.87	933.93	1478.54	69.71		
253.87	0.99	*675.007	164.51	11.81	16.95	1609	
15755.76	23.73	155.17		10.59	5	0.42	
129908.5	4789.92	14354.79	3215.91	1139.19	63.63		
204.22	0.25	5140.13	286.77	7.45	12.12	7211.51	
48232.55	11.87	263.21		59.39	40.47	0.2	
62267.01	3416.01	13852.83	1299.79	1184.57	19.76		
225.02	0.2	*675.007	232.32	4.33	*1.379	3053.47	
61388.3	7.54	158.97		11.7	14.09	0.25	
56479.07	4417.73	30671.65	2408.77	1801.41	71.1		
1506.96	0.51	*675.007	607.79	8.77	20.53	4877.02	
4798.64	10.84	429.8		21.57	27.49	0.32	
211582.2	8918.48	26195.27	*40.87	1854.71	47.42		
69.11	5.2	107482.98	1993.32	103.53	117.88	4332.52	
3580.85	32.47	495		141.17	21.82	0.93	

Table4.txt

247870.19	24426.74	72053	2430.6	3434.12	68.1	
292.87	0.65	*675.007	493.35	18.65	336.61	8165.96
32808.35	14.54	266.26		65.23	29.03	0.34
133829.12	3205.36	8130.95	477.16	3484.63	39.32	
892.31	0.22	*675.007	445.94	30.38	102.85	3424.65
50617.37	16.71	195.1		37.08	15.72	0.31
406443.4	2052.43	12931.27	2367.72	2897.6	51.66	
141.21	0.21	*675.007	277.88	5.68	14.3	5974.15
13911.28	20.41	433.52		53.83	174.33	0.31
44687.61	2482.88	17470.06	3043.65	2423.65	39.86	
279.11	0.54	*675.007	532.09	14.18	15.62	4550.45
3092.5	24.54	327.34		41.47	24.12	0.28
62175.9	5856.49	13565.38	1606.73	1917.52	100.53	
509.69	5.46	*675.007	1095.7	35.34	279.1	6030.6
4171.58	4.16	951.06		77.46	85.01	0.94
225877.64	13135.15	8130.95	2052.17	4560.12	133.03	
430.08	1.1	4710.06	313.07	22.45	20.99	3960.53
3580.85	11.94	321.74		17.2	90.2	0.66
116303.68	3394.98	164708.56	456.63	2080.99	68.22	
964.78	1.19	*675.007	1648.37	224.82	29.71	7652.48
28004.29	23.94	287.22		104.59	36.95	1.01
182581.12	5815.68	19275.7	1727.7	1723.64	44.97	
322.56	0.72	*675.007	528.25	24.13	29.47	5485.14
2674.78	9.96	198.55		143	27.71	0.5
152169.69	4624.71	15426.21	2523.16	717.08	54.05	
134.53	1.02	*675.007	313.07	16.53	15.18	4251.53
25597.28	22.79	158.97		29	7.96	0.58
123509.3	3918.68	8040.29	2002.57	2109.72	76.97	
270.77	0.56	*675.007	477.67	6.57	28.31	3889.25
5991.97	20.66	253.97		366.09	78.5	0.47
62996.77	3078.6	39186.07	1823.75	2243.36	123.76	
*11.424	0.87	*675.007	397.35	7.45	29.71	9096.77
4124.48	11.41	437.24		100.59	46.54	0.42
86098.83	27519.83	13766.64	1349.72	1199.67	128.34	
382.45	0.27	*675.007	*27.419	*0.647	8.7	4343.35
6066.02	20.78	321.74		235.29	7.68	0.25
63575.57	5406.71	11363.38	2006.38	1869.22	70.17	
356.74	0.9	*675.007	203.95	16.95	10.4	4262.3
20442.12	19.46	182.8		184.88	27.05	0.53
30888.07	2781.64	9627.2	791.31	1239.83	72.27	
356.74	0.43	*675.007	208.74	*0.647	9.12	8399.05
44870.21	10.12	396.9		30.85	56.32	0.47
17254.98	5713.59	21130.08	1350.97	1399.38	71.28	
113.91	0.35	*675.007	213.51	10.51	*1.379	1789.91
2674.78	9.15	313.26		69.82	31.21	0.28
70726.15	6507.32	20582.84	603.23	955.98	112.27	
120.89	2.4	*675.007	232.32	7.45	9.12	4776.74
8617.59	6.9	338.42		13.87	12.04	0.34

Table4.txt

77251.55	5037.14	21550.72	1231.26	1409.3	61.21		
*11.424	1	4272.22	397.35	17.8	28.31	7278	
36670.78	15.95	362.82		43.78	34.84	0.81	
174406.14	8359.52	14641.04	2043.26	2104.94	49.38		
692.79	0.93	*675.007	845.05	114.92	28.08	5682.71	
1832.47	18.76	755.23		114.17	21.48	0.39	
151269.41	4975.4	11246.51	3223.75	2579.3	37.6		
514.4	1.69	9150.09	347.35	296.14	64.89	7069.78	
28478.82	26.13	290.16		100.02	7.39	0.58	
172447.71	15524.25	9389.52	1794.66	3346.74	71.44		
73.09	1.94	*675.007	232.32	19.5	10.83	3918.25	
1489.82	9.58	131.48		21.7	7.68	0.35	
118019.85	6669.44	20877.57	1558.95	632.39	50.69		
992.57	0.58	*675.007	364.19	15.25	10.4	4580.63	
35125.5	14.19	191.62		19.74	27.49	0.34	
90150.36	1791.75	2820.95	2038.17	1012.27	26.49		
92.24	0.08	4272.22	222.96	8.77	11.25	11692.44	
9139.4	7.66	147.45		37.83	5.92	0.23	
35370.3	3793.37	21690.88	941.33	1542.59	33.71		
253.87	0.46	*675.007	184.49	18.65	14.3	1715.82	
37891.26	8.65	205.39		24.6	9.08	0.34	
71537.8	7758.32	7280.21	1755.48	1027.57	36.26		
420.18	1.12	*675.007	347.35	26.63	27.39	7772.35	
57025.24	7.13	118.95		104.02	8.81	0.88	
119898.96	9832.65	27257.59	2045.81	1269.88	84.78		
298.33	0.88	*675.007	164.51	10.51	11.69	5841.11	
18129.14	17.87	205.39		69.55	22.29	0.35	
42951.65	3120.88	2332.78	295.8	1073.36	50.49		
69.03	0.75	*679.575	163.77	*0.555	14.31	4163.46	
5385.85	35.02	1303.84		9.88	8.7	0.48	
30137.5	32417.86	14156.45	5971.73	*34.349	143.68		
215.81	1.58	*673.809	183.25	*0.579	9.96	6725.95	
24270.47	13.87	660.58		11.77	7.39	0.76	
33729.83	4401.21	9344.18	1456.04	1156.97	81.01		
69.54	0.42	*673.809	*26.852	*0.579	*1.378	6880.3	
55523.13	21.15	212.12		5.5	6.74	0.43	
10637.34	3050.4	16611.51	1900.25	948.92	18.92		
*37.47	0.33	*684.082	216.75	*2.588	*1.393	3940.3	
184832.91	14.54	278.84		5.72	9.66	*0.42	
70647.91	3059.77	28961.91	2012.81	1478.44	160.06		
123.26	0.28	*684.082	194.67	*2.588	*1.393	5873.4	
20761.76	27.57	192.23		7.91	8.07	0.52	
52635.12	3952.81	35500.56	889.51	1561.68	124.43		
*37.47	0.9	*684.082	248.91	*2.588	19.96	8767.31	
32999.53	25.03	195.11		9.04	8.61	0.47	
112659.16	3487.98	55363.8	1463.44	3462.76	60.63		
306.26	0.92	*684.082	238.31	*2.588	8.36	9798.81	
43507.43	14.87	585.12		11.31	*0.555	0.47	

Table4.txt

58203.41	4017.29	96445.89	2902.99	1789.76	31.43	*37.47	0.25	*684.082	*27.695
*2.588	*1.393	7001.2	1474.85	21.9	309.44	8.17	5.71	*0.42	
32786.1	1717.09	43161.95	1492.03	1510.51	56.33	*37.47	0.2	*684.082	*27.695
*2.588	*1.393	6217.47	8329.69	31.86	125.48	2.22	*0.555	*0.42	
21585.14	2683.25	12386.44	1903.2	4334.64	165.72	*37.47	0.69	*684.082	*27.695
*2.588	8.36	5014.81	24629.84	22.4	411.83	15.18	6.34	*0.42	
49334.08	4146.52	73325.41	1323.3	1060.22	17.52	*37.47	0.56	*684.082	*27.695
*2.588	*1.393	8842.56	4460.8	37.72	195.11	9.74	*0.555	*0.42	
38952.36	2157.41	19174.99	1430.91	1139.85	71.33	202.3	0.32	*684.082	269.8
19.07	*1.393	7978.06	6202.17	16.71	214.74	9.39	*0.555	*0.42	
50140.71	2450.1	14347.67	1873.05	1915.08	30.21	*13.55	0.54	*679.575	190.07
*0.555	9.71	4919.8	5518.58	25.3	463.79	16.5	8.7	0.23	
26751.52	12162.4	4788.01	2560.41	*34.349	54.39	*37.47	0.35	*684.082	238.31
*2.588	11.6	5178.51	126867.91	14.4	233.54	12.91	7.51	*0.42	
63029.88	966.69	141909.82	632.4	1510.51	26.33	*13.55	0.3	*679.575	*27.296
*0.555	*1.377	11177.02	9106.3	35.81	332.09	13.62	*0.714	0.15	
61407.17	5167.01	11740.75	1957.13	*34.349	39.6	*13.55	0.29	*679.575	163.77
*0.555	9.98	5676.17	6388.94	14.74	1030.46	15.2	*0.714	0.21	
44782.97	3398.77	18056.28	2993.97	*34.349	18.64	277.17	0.52	*684.082	205.78
*2.588	8.89	8279.25	4460.8	37.31	665.11	35.26	*0.555	*0.42	
131888.94	4912.19	72095.38	1426.85	2002.26	35.92	128.57	0.22	4104.49	*27.695
*2.588	11.87	7765.65	6412.19	21.91	222.89	6.77	14.94	*0.42	
49430.8	1212.8	19348.14	790.12	1133.23	115.3	255.84	0.7	*684.082	398
76.32	20.25	2792.91	20443.86	24.25	217.48	23.71	9.66	0.47	
107566.95	5954.07	59649.02	432.09	1459.15	33.21	129.98	1.73	*682.921	206.25
*1.666	*1.361	9797.01	54365.11	83.26	1868.2	17.39	6.58	0.51	
81720.87	6028.65	71571.44	975.53	*34.126	256.57	*37.47	0.28	*684.082	*27.695
*2.588	*1.393	6888.46	1712.43	15.02	152.57	8.75	*0.555	*0.42	
81707.55	1212.8	73748.12	2366.27	2187.7	41.59	*39.33	0.26	*682.921	*27.643
*1.666	10.47	9052.78	24096.1	22.17	669.76	11.8	*0.658	0.24	
55104.51	4018.54	13413.26	2389.46	*34.126	149.82	*39.33	0.32	*682.921	*27.643
*1.666	*1.361	3711.07	1626.04	42.98	563.55	8.93	*0.658	0.18	

Table4.txt

44690.39	4811.35	10470.56	2295.61	*34.126	232.94	
*37.47	0.19	*684.082	*27.695	*2.588	*1.393	13487.27
45418.61	25.46	276.42		14.86	*0.555	*0.42
27101.35	3743.84	67389.05	897.75	1587.2	74.82	
272.95	0.34	5195.35	183.4	*2.588	*1.393	2240.26
19961.76	16.05	351.69		12.47	12.99	*0.42
44107.63	8390.18	15563	2443.42	2285.89	62.58	
183.53	0.54	*684.082	*27.695	*2.588	13.25	7286.47
9895.35	16.71	318.55		13.34	6.93	*0.42
77885.11	3122.91	56782.56	2587.78	993.36	21.05	
*39.33	1.22	*682.921	*27.643	*1.666	*1.361	6365.78
25006.55	35.69	1147.42		7.09	*0.658	0.93
42993.26	4221.47	75337.69	915.92	*34.126	165.26	
*41.51	0.46	*1970.97	192.36	*16.134	9.48	3625.92
7900.08	16.56	337.82		9.44	5.4	0.33
77410.69	3535.92	187672.68	2784.36	*33.371	104.49	
*37.47	0.3	*684.082	*27.695	*2.588	*1.393	8979.83
9195.42	34.66	177.49		10.03	*0.555	*0.42
38571.26	1463.14	54858	537.98	2407.99	29.12	
*39.33	0.74	*682.921	206.25	*1.666	*1.361	5770.83
28504.78	20.26	1056.05		13.16	7.84	0.69
60716.49	9701.47	4547.56	2400.89	*34.126	86.79	
314.42	0.62	*684.082	*27.695	*2.588	*1.393	7156.47
12696.75	22.51	309.44		18.71	*0.555	*0.42
32722.35	1552.38	108007.3	1400.55	1368.79	14.47	
*39.33	0.96	*682.921	373.54	*1.666	8.74	6328.91
36805.02	28.85	621.66		20.89	*0.658	0.64
38856.25	8062.56	154052.99	1947.78	*34.126	115.39	
154.26	0.45	*684.082	216.75	*2.588	*1.393	6387.8
22439.17	29.26	855.25		14.57	*0.555	0.67
41781.35	7299.01	26161.92	2182.44	1073.53	60.63	
*39.33	0.8	*682.921	280.4	*1.666	13.39	3372.13
19010.58	16.4	500.43		16.8	6.58	0.45
70826.39	5636.19	47010.99	2894.78	*34.126	127.04	
346.47	0.89	10790.29	503.92	40.93	17.7	3638.84
16196.91	17.19	377.14		22.83	18.36	0.46
21753.91	5654.72	89445.3	1678.63	3788.64	68.79	
*39.33	0.56	*682.921	297.95	*1.666	*1.361	6068.24
6405.21	41.35	5572.35		17.74	*0.658	0.62
44251.78	14207.93	65872.37	3701.31	*34.126	116.22	
*37.47	0.34	*684.082	*27.695	*2.588	8.36	7574.4
26465.51	25.26	307.14		9.45	*0.555	*0.42
66880.84	2295.67	228792.97	1835.51	1612.67	44.17	
*39.33	0.84	*682.921	*27.643	12.94	9.31	4876.38
13001.05	19.74	1164.02		10.78	*0.658	0.53
17952.81	10708.59	88401.08	4307.99	*34.126	478.84	
*39.33	0.61	*682.921	*27.643	*1.666	13.98	7017.85
1078.06	20.53	299.38		12.41	*0.658	0.2

Table4.txt

53635.19	4176.31	24548.43	2329.64	*34.126	142.68	
141.78	0.71	8195.43	*27.643	*1.666	*1.361	5469.28
39497.57	37.74	277.5		8.13	*0.658	0.24
45376.66	5452.14	18357.91	1950.51	*34.126	127.69	
*37.47	*0.013	*684.082	*27.695	*2.588	*1.393	6482.84
13111.47	20.23	139.35		10.03	7.51	*0.42
81779.55	1271.35	11388.65	1537.2	986.64	37.31	
192.98	0.2	*684.082	*27.695	*2.588	*1.393	6641.9
3494.81	32.14	329.78		8.46	*0.555	*0.42
52018.15	1974.21	43925.89	3264.53	2101.39	39.07	
*41.51	0.9	*1970.97	245.92	*16.134	9.99	3164.6
7378.66	36.68	1153.23		7.2	5.01	0.53
86757.07	5146.48	26672.53	2758.25	*33.371	142.19	
362.17	0.28	*684.082	*27.695	*2.588	*1.393	3731.26
27471.09	14.35	452.83		12.62	*0.555	*0.42
80701.68	1403.89	29112.33	1624.24	1000.06	57.22	
381.52	0.52	*684.082	*27.695	*2.588	12.15	8529.1
3641.9	41.42	368.75		13.95	*0.555	0.43
109574.99	2855.32	71219.34	1684.93	1877.58	54.51	
*41.51	0.15	*1970.97	271.86	*16.134	8.47	4562.63
58209.37	7.27	225.38		18.25	7.41	0.15
22011.85	4625.74	165630.04	2840.7	*33.371	44.1	
*37.47	0.27	*684.082	*27.695	*2.588	*1.393	3937.38
5544.98	17.77	186.4		7.5	*0.555	*0.42
46409.88	895.23	68777.42	1405.6	1205.73	50.02	
122	0.86	8195.43	186.42	*1.666	46.29	7412.88
41487.28	25.51	1004.54		25.63	6.58	0.42
61702.68	11311.18	35100.75	1895.99	*34.126	54.06	
488.74	0.72	*684.082	*27.695	*2.588	*1.393	2714.79
72815.35	19.09	825.56		57.33	7.51	0.53
61090.08	6960.68	11907.62	971.74	1013.47	117.94	
*37.47	0.23	*684.082	*27.695	*2.588	*1.393	3269.39
22590.49	28.8	103.14		10.44	*0.555	*0.42
23194.38	1552.38	35915.21	2905.35	551.22	23.28	
*39.33	0.36	*682.921	*27.643	20.53	8.45	5654.95
22045.27	21.81	601.52		12.06	*0.658	0.2
34576.99	4606.57	17044.52	997.15	*34.126	28.82	
*37.47	0.32	*684.082	259.41	*2.588	*1.393	5616.34
40709.72	30.62	349.53		9.56	9.66	0.5
41431.36	3952.81	81032.88	2473.06	959.74	66.8	
238.39	0.73	*684.082	*27.695	*2.588	8.89	2927.37
21828.17	43.34	793.88		22.44	*0.555	0.51
83115.32	4405.96	18445.79	1984.47	1777.18	78.57	
164.19	0.31	*684.082	183.4	*2.588	8.62	9249.28
*151.463	47.99	512.07		11.66	*0.555	*0.42
65185.4	3249.51	12643.11	3719.57	2033.29	132.31	
*37.47	0.46	*684.082	*27.695	*2.588	*1.393	5221.09
46533.29	41.34	243.95		14.42	*0.555	*0.42

Table4.txt

66473	3808.04	38683.81	1865.53	1166.25	122.89		
463.54	0.41	*684.082	259.41	*2.588	13.8	4431.1	
54474.66	24.37	168.36		24.16	11.85	0.44	
117984.63	14344.49	87123.29	1394.5	685.57	55.34		
*37.47	0.19	*684.082	*27.695	*2.588	*1.393	1995.69	
9445.9	9.47	641.14		13.87	7.23	*0.42	
29201.27	7197.37	34272.66	2447.98	544.05	38.45		
*39.33	0.66	6181.59	191.44	*1.666	15.16	6917.93	
42717.72	49.93	601.52		14.92	*0.658	0.34	
45899.02	3996.03	38382.69	1339.75	*34.126	99.3		
*39.33	1	*682.921	*27.643	*1.666	*1.361	6004.76	
2481.2	43.59	650.09		7.21	*0.658	0.33	
53973.58	4743.02	5948.14	2068.82	*34.126	37.02		
65.06	1.11	*675.007	222.96	9.86	11.69	2367.83	
25815.21	8.51	308.98		22.41	33.57	0.38	
98936.11	3876.94	25594.26	2435.73	1552.42	120.47		
554.03	0.24	*675.007	562.64	*0.647	10.83	919.71	
33507.28	17.41	2666.16		16.5	28.37	0.16	
30435.41	11234.71	20442.45	2538.61	2309.92	42.9		
437.47	1.45	*675.007	286.77	8.99	14.3	6485.29	
2674.78	40.96	409.68		18.16	18.16	0.79	
97140.54	14924.07	27313.51	1652.05	2028.23	39.42		
664.35	0.52	*675.007	*27.419	*0.647	*1.379	5150.11	
43759.96	22.01	170.14		9.35	37.99	0.39	
95357.72	2802.91	11392.58	1647.01	1124.03	29.06		
873.96	2.76	*675.007	988.87	49.66	37.22	4646.67	
12337.59	20.08	1086.19		24.92	17.56	1.01	
285632.6	10070.35	75223.62	1912.42	2640.39	41.72		
412.71	2.67	*675.007	286.77	30.17	18.29	4882.61	
86041.38	12.85	170.14		10.46	29.36	0.42	
73010.66	4624.71	17583.18	952.43	1542.59	63.7		
615.47	0.6	*675.007	938.02	5.45	*1.379	2914.54	
170529.54	15.39	1062.3		19.64	20.31	0.35	
56449.14	3416.01	25803.92	1889.6	1419.21	25		
776.33	0.38	*675.007	184.49	27.47	*1.379	5152.95	
78769.16	14.91	212.13		17.84	51.67	0.23	
24713.36	1791.75	19528.97	2177.08	1557.34	53.38		
73.09	4.33	8958.96	338.85	82.57	84.95	8890.19	
1297.59	16.13	273.82		12.56	7.1	1.18	
192111.42	17163.87	31849.25	2894.13	2588.7	14.84		
576.99	0.6	*675.007	*27.419	18.01	9.12	5720.72	
171568.64	19.75	306.12		15.09	69.3	0.5	
38416.87	1922.34	16988.84	1360.96	3060.28	21.02		
970.76	0.58	*675.007	291.19	4.33	18.29	2956.57	
140867.17	9.65	266.26		15.92	32.72	0.31	
26120.36	4002.09	25943.69	1782.02	1517.98	30.07		
*11.424	2.46	5140.13	585.31	7.45	24.17	7293.86	
2798.26	13.59	621.17		23.82	139.21	0.34	

Table4.txt

154023.12	6811.12	64922	1358.46	2518.08	31.83	207.23	0.59	
*675.007	174.57	6.12	9.12	4037.45	55206.99	8.37	201.98	
7.76	45.04	0.3	42951.65	2009.12	5193.31	2098.01	1264.87	
30.87	346.32	0.71	*675.007	493.35	14.18	10.4	1026.33	
10657	16.33	296.01	14.45	33.57	0.27	120314.29	7918.88	
15269.4	2243.51	1369.59	17.26	351.54	0.36	*675.007	*27.419	
*0.647	*1.379	2823.49	26309.76	5.35	257.07	14.54	26.38	
0.26	68582.61	5570.5	20624.96	978.34	685.43	66.73	346.32	
0.86	4272.22	241.6	15.25	8.28	2776.97	45229.89	5.98	
208.77	11.51	38.51	0.45	35399.97	6709.94	55009.45	1562.72	
695.99	22.53	495.47	0.71	*675.007	477.67	13.53	11.25	
4316.29	161325.16	15.28	2075.22	20.54	11.51	0.31	123854.1	
3226.46	16421.69	1745.38	3328.32	44.2	219.13	0.26	*675.007	
259.89	3.88	11.25	4699.13	20512.54	20.29	269.3	22.89	
7.68	0.4	39006.72	3458.05	11158.78	1736.54	2729.47	116.37	
367.08	0.26	*675.007	184.49	*0.647	*1.379	5318.28	14021.12	
9.67	135.55	4.08	13.84	0.34	49670.49	926.98	38079.13	
1649.53	1179.54	62.88	325.23	0.47	*675.007	*27.419	*0.647	
*1.379	1571.44	16020.4	10.59	284.27	5.22	10.45	0.38	
28063.48	7517.13	6231.58	3975.31	1616.2	256.75	*11.424	2.5	
*675.007	347.35	41.5	19.18	5410.15	17365.47	30.42	195.1	
30.17	4.37	0.67	83149.78	3709.71	5699.58	1917.5	595.02	
48.57	*11.424	1.81	*675.007	724.88	70.21	20.99	3483.57	
7605.05	6.96	301.8	68.08	5.31	1.04	155585.28	3709.71	
20905.63	1301.04	955.98	57.19	2014.33	0.94	*675.007	914.1	
12.24	16.06	2465.33	8735.22	8.45	314.68	46.75	26.82	
0.6	71787.98	6365.27	4777.47	2431.88	343.19	38.36	447.28	
3.42	*675.007	886.61	51.28	23.26	4165.56	13845.12	23.32	
290.16	4.9	7.1	0.83	160729.21	5713.59	11392.58	1164.11	
1999.4	34.51	748.76	1.47	*675.007	982.12	26.63	106.98	
8543.52	1832.47	30.01	223.71	32.54	5.31	0.49	108185.6	
8079.27	10484.03	1577.8	1364.62	21.52	69.11	3.86	31900.6	
907.25	37.4	29.71	4208.49	55718.88	20.53	131.48	158.33	
5.62	1.08	214818.39	12764.14	65231.15	932.7	3800.13	12.68	
*11.424	2.65	*675.007	338.85	36.58	8.7	3586.58	1084.37	
10.36	247.73	75.57	7.96	0.52	161173.68	5488.64	8732.65	
1623.09	1394.42	18.28	*11.424	0.33	*675.007	194.28	*0.647	
*1.379	3068.44	128578.71	15.34	129.43	10.27	5.31	0.25	

Table4.txt

42245.57	2117.3	22951.27	1422.24	1625.99	26.94				
372.22	0.19	4272.22	313.07	6.57	23.71	2968.95			
16402.66	6.21	296.01		27.18	13.07	0.14			
39596.17	3458.05	16847.16	349.61	3590.04	47.42				
*10.951	3.28	*674.132	1230.1	638.75	111.67	1665.16			
9373.88	19.42	458.83		43.93	61.78	0.99			
141133.19	13669.11	19682.52	1498.39	1337.13	222.47				
*10.951	0.61	*674.132	289.24	6.51	9.39	4561.69			
107417.75	8.69	142.95		14.04	4.06	0.19			
52224.38	2999.04	9141.76	805.18	1308.91	35.93				
*10.951	0.9	*674.132	534.7	12.13	19.95	4232.72			
70136.31	17.39	303.84		35.1	8.64	0.73			
119064.81	8725.79	21506.43	915.26	6235.15	66.16				
130.66	0.35	*674.132	390.5	17.59	12.66	3629.84			
21818.82	14.8	167.49		56.27	6.82	0.32			
42927.17	2369.17	52342.32	1056.81	1652.98	188.41				
429.8	0.63	6414.89	779.77	119.8	48.44	3533.47			
4013.23	12.73	229.51		43.32	9.22	0.61			
130644.72	6649.42	19174.43	912.65	4065.37	127.45				
*10.951	0.3	5477.33	320.18	18.13	13.1	1907.19			
50649.3	6.24	195.08		28.68	20.86	0.21			
51520.39	6564.95	16517.06	752.09	1438.69	62.62				
*10.951	0.09	*674.132	289.24	7.65	12	4450.3			
70164.65	9.38	127.35		26.08	3.67	0.2			
33409.08	2248.17	61805.31	1556.69	2154.37	13.94				
*10.951	0.99	*674.132	360.65	8.22	8.96	2598.39			
18515.73	28.23	142.95		83.94	14.19	0.43			
200278.77	2248.17	26182.93	343.14	1094.36	232.16				
97.06	0.33	*674.132	247.06	11.02	14	4611.05			
15029.64	19.82	203.92		19.91	4.8	0.31			
101939.77	4884.93	15081.1	1283.3	2345.75	83.02				
*10.951	0.63	4044.79	370.65	17.05	10.68	2090.26			
17797.1	20.72	172.22		21.79	5.51	0.46			
43178.71	5560.59	11512.97	950.25	1822.06	127.45				
390.75	0.45	*674.132	330.37	22.95	15.12	2219.59			
134083.73	15.28	241.86		72.36	9.5	0.61			
143541.2	8517.29	41837.6	593.48	2936.34	68.66				
595.79	0.76	8713.38	477.91	36.06	16.03	1348.18			
7530.28	15.82	267.76		69.37	22.74	0.37			
76815.07	9126.89	14702.69	606.27	1957.27	245.34				
117.06	0.29	*674.132	192.48	8.78	15.8	7238.38			
21308.78	2.73	172.22		18.16	11.41	0.2			
45842.94	4445.22	28699.6	525.7	1681.16	35.85				
48.5	0.22	5947.63	284.03	14.33	16.49	5597.73			
9602.01	9.15	245.92		13.87	24.16	0.18			
39349.18	6700.16	39275.71	288.95	1681.16	81.93				
1335.73	0.91	4526.33	1004.53	41.21	44.83	2762.42			
5280.65	12.41	181.51		47.5	10.61	0.27			

Table4.txt

133945.72	7124.52	9525.44	812.82	2458.29	70.36			
874.91	0.48	5003.69	340.52	4.18	11.12	2791.92		
8718.87	33.6	265.81		55.84	35.28	0.42		
156991.06	9899.37	12198.38	1018.35	1714.98	253.64			
*10.951	0.33	*674.132	192.48	10.74	*1.37	1478.89		
10313.78	9.99	216.87		15.82	8.93	0.22		
74218.17	5328.84	24042.36	672.65	783.45	114.77			
*10.951	0.99	*674.132	268.29	12.13	10.68	1324.86		
1137.61	17.64	339.96		25.31	29.11	0.21		
64563.39	8309.32	179234.95	1303.92	437.89	120.17			
206.32	0.41	*674.132	268.29	7.36	17.4	11446.14		
2474.07	16.98	353.96		302.91	25.85	0.17		
79373.42	3108.07	156129.56	1029.06	2840.76	32.91			
278.59	0.17	8713.38	330.37	12.13	16.94	985.97		
2184.37	4	525.33		125.9	71.27	0.18		
10107.51	1537.64	361806.01	*40.515	1433.04	103.88			
*10.951	0.81	*674.132	273.55	*0.598	21.12	7365.7		
990.37	16.44	352.23		159.98	38.81	0.32		
44033.64	3295.92	118347.51	2158.89	1173.43	31.02			
525.62	0.54	*674.132	299.61	8.22	15.57	3925.49		
5677.42	5.85	239.82		63.42	78.36	0.31		
42474.29	5361.89	188158.35	*40.515	1726.25	101.39			
237.23	0.19	4044.79	268.29	*0.598	27.09	4216.59		
15546.26	8.59	195.08		82.25	33.51	0.3		
56757.66	3516.5	431872.86	390.98	1872.77	50.99			
263.52	0.9	*674.132	370.65	28.76	17.63	3205.19		
3411.71	6.36	352.23		191.65	53.1	0.34		
77805.47	2490.83	135071.6	1133.7	2345.75	78.03			
487.57	0.27	*674.132	458.74	39.67	17.86	5985.78		
1137.61	9.68	519.43		151.17	51.42	0.14		
43882.8	3738.55	111782.02	2451.07	1116.95	42.26			
343.25	0.6	*674.132	*27.362	5.93	*1.37	4068.84		
*138.366	20.96	332.87		39.24	68.87	0.28		
66297.9	8343.95	123347.67	2740.67	2413.28	82.95			
98.61	0.6	*674.132	164.17	7.65	15.8	5775.13		
*138.366	25.05	157.87		52.49	5.51	0.24		
33664.6	3611.49	158680.47	410.16	1320.2	48.75			
*10.951	0.15	*674.132	192.48	9.9	10.25	4460.1		
47744.6	6.36	206.1		27.31	14.67	0.17		
64665.29	4445.22	9256.92	407.2	1241.18	32.64			
5276.72	2.55	11407.53	636.36	1824.77	209.46	2101.45		
3567.13	34.62	311.2		18.7	28.36	0.69		
248629.18	19647.66	2007.22	730.4	1071.76	97.79			
296.27	0.6	*674.132	419.97	27.71	13.32	1678.6		
2474.07	11.56	249.95		64.16	15.63	0.3		
49108.19	7826.23	4364.67	1462.69	1049.17	85.05			
82.9	2.01	*674.132	1946.39	250.29	29.77	2854.06		
21609.51	7.27	614.84		222.63	22.22	1.44		

Table4.txt

433959.55	7107.49	11322.36	886.6	2593.31	80.46	
*10.951	0.57	4044.79	268.29	10.46	12.66	8825.93
4769.19	20.15	199.52		9.76	31.43	0.22
63443.45	2127.85	15213.49	471.02	1720.62	110.64	
51.87	0.87	*677.552	196.62	12.04	16.23	5511.89
2329.49	13.57	541.31		36.28	6.31	0.29
48438.37	15249.66	190679.51	3187.47	*32.367	190.26	
470.97	0.28	*674.132	214.6	4.77	12.44	2051.17
6289.02	9.79	387.99		17.23	35.8	0.26
60499.13	10838.38	479349.32	1608.59	1602.24	106.47	
*10.951	1.52	*674.132	419.97	20.82	13.77	951.51
1647.7	15.54	601.01		37.77	74.85	0.76
78693.34	9214.33	170863.29	640.1	2165.63	64.3	
*10.951	0.38	4044.79	236.33	8.22	*1.37	3153.66
12031.53	12.64	371.14		86.49	138.23	0.31
21553.32	4934.05	189248.29	479.42	1071.76	45.69	
311.12	0.55	*674.132	192.48	23.22	15.12	5559.67
2379.63	8.99	176.89		35.96	22.64	0.21
51922.64	2127.85	134551.9	649.83	1218.6	64.52	
*10.951	0.14	*674.132	257.72	*0.598	8.75	1681.29
64256.49	3.29	281.28		50.15	36.85	0.13
28042.95	6043.84	177396.43	224.76	1145.19	37.94	
71.68	0.37	*674.132	186.88	3.59	*1.37	1186.39
21729.23	8.09	332.87		26.2	24.06	0.23
31974.6	3850.1	**100666.874	1598.77	1410.48	55.15	
1074.44	0.71	4044.79	268.29	180.6	44.06	3748.74
1761.91	14.57	277.45		48.68	13.95	0.18
39349.18	1508.68	126351.83	692.34	1658.61	102.05	
*10.951	1.22	5003.69	458.74	9.34	22.07	2135.08
1872.26	10.51	372.84		19.33	27.21	0.47
115610.33	3264.53	117048.36	677.57	5103.16	46.32	
199.22	0.21	4286.12	289.24	10.46	9.82	1335.22
6485.9	6.08	249.95		26.88	13.2	0.15
47751.87	4737.88	436633.87	669.38	1568.4	102.53	
106.36	0.99	*677.552	225.27	*0.496	17.17	5922.55
4437.09	20.77	1319.22		9.48	108.58	0.24
82115.8	17505.37	134384.78	5132.19	*32.367	138.75	
*10.951	0.64	*674.132	257.72	5.35	*1.37	1005.74
830.19	4.17	152.97		27.87	23.25	0.21
126133.03	4106.34	96390.14	715.46	1133.9	57.83	
NA	0.19	*674.132	203.59	8.22	10.25	5118.53
20208.36	8.8	132.63		12.22	5.16	0.12
17665.67	1222.48	221931.82	1776.54	1838.96	77.29	
*10.951	0.2	*674.132	*27.362	*0.598	*1.37	5597.73
26778.09	3.57	181.51		24.08	29.11	0.15
23659.32	943.19	199279.82	1062.2	823.05	21.08	
103.26	0.95	7800.81	2169.4	9.9	28.55	1762.37
2283.12	12.58	409.45		105.28	13.08	0.29

Table4.txt

30688.03	5032.45	128310.15	560.96	4166.4	87.39	
35.53	0.93	*677.552	409.26	8	19.07	6072.84
1486.82	24.45	1021.32		35.09	87.42	0.25
28252.83	19050.3	47236.2	3221.54	*32.367	96.9	
106.35	0.26	5947.63	299.61	4.47	10.03	7645.28
28510.68	9.29	148		19.24	21.6	0.22
36159.77	1712.56	139222.37	753.77	1133.9	24.1	
205.55	0.75	*677.552	191.76	25.93	19.07	3465.23
2117.69	19.35	782.45		19.25	23.88	0.39
125933.05	13507.09	144211.6	1478.35	*32.367	95.5	
*10.36	0.98	*677.552	225.27	9.37	11.18	4886.5
*130.377	24.96	635.81		52.65	23.35	0.46
77145.52	13636.25	81653.93	3272.72	*32.367	166.06	
*10.951	0.81	*674.132	562.72	4.18	78.89	7748.13
4434.16	9.13	269.71		618.29	63.07	0.37
227364.35	4445.22	168672.17	1103.71	3863.28	45.09	
507.91	0.41	*674.132	214.6	9.9	14	3229.5
21878.44	13.97	233.66		12.66	12.95	0.22
55043.25	6043.84	8988.14	1756.47	45460.4	63.3	
550.03	3.27	*677.552	859.07	351.63	61.32	10145.3
65257.18	42.49	967.07		61.97	32.87	0.42
148042.08	24447.51	20033.2	3320.17	*32.367	79.6	
141.76	2.45	7420.62	683.35	20.38	85.71	8852.97
1211.97	8.55	807.73		29.72	35.51	0.42
62730.63	16990.07	82256.17	2457.42	*32.367	77.25	
124.46	1.25	*677.552	417.53	24.1	16.23	3498.48
1816.63	24.96	1268.31		38.13	104.09	0.25
29266.23	25345.7	95499.84	2916.11	*32.367	57.79	
*10.36	0.34	6946.9	*27.835	2.98	*1.385	2046.14
1306.9	10.84	417.1		21.76	6.31	0.17
28252.83	10888.54	85386.22	3028.91	*32.367	49.33	
*10.36	0.74	*677.552	225.27	23.48	11.86	6109.23
1486.82	46.6	642.8		70.33	40.92	0.5
88855.03	10240.99	27240.59	2779.37	*32.367	115.91	
*10.36	0.63	*677.552	537.99	13.03	20.27	4249.87
3034.27	40.41	593.08		100.84	32.62	0.3
86245.89	14798.1	4125.46	2387.09	*32.367	209	
169.25	0.36	*677.552	215.82	25.32	15.3	4588.64
21889.4	17.59	563.77		15.3	27.75	0.35
98081.99	7418.55	10149.45	2331.66	*32.367	64.58	
*10.951	0.33	*674.132	203.59	4.77	*1.37	5024.04
14005.28	4.94	162.71		7.4	27.02	0.18
27990.77	1508.68	21262.1	1416.65	1714.98	18.67	
706.65	1.04	*677.552	490.53	350.23	51.09	5793.61
60563.32	24.2	495.01		12.09	9.57	0.34
116777.02	7353.54	6527.91	1192.81	*32.367	152.69	
474.19	0.48	36813	333.16	63.53	15.3	6559.98
17802.52	39.71	266.27		13.17	9.35	0.22

Table4.txt

66286.98	3537.24	36330.57	3667.71	*32.367	99.23	
482.47	0.27	4526.33	273.55	5.35	16.03	2703.61
26425.33	11.74	203.92		18.64	9.36	0.19
44435.82	2490.83	5542.3	*40.515	1827.69	90.01	
813.95	0.88	13010.4	280.35	41.68	20.03	5706.24
37178.01	16.8	740.55		16.2	29.26	0.47
72437.66	10726.69	12203.11	3187.47	*32.367	135.06	
*10.951	0.66	4526.33	553.4	49.38	22.07	1428.99
47266.8	14.99	229.51		83.03	24.86	0.41
100340.73	6060.58	17026.52	575.99	2447.04	19.66	
139.63	0.49	4044.79	289.24	10.46	12	2880.78
20609.06	14.75	172.22		29.89	14.67	0.19
32538.91	6161.11	7485.32	1495.49	1331.48	54.42	
266.26	0.99	69901.97	2786.85	228.37	87.44	1314.52
3252.39	17.33	443.16		81.76	2.84	0.49
252627.63	7141.55	26746.26	1059.5	1878.4	52.38	
144.08	0.26	*674.132	268.29	5.93	8.54	2166
42317.21	9.59	152.97		12.8	12.7	0.16
45239.97	4591.3	163702.84	1133.7	3526.35	16.18	
*10.951	0.68	*674.132	979.02	13.78	24.92	2845.17
4191.36	16.85	195.08		197.87	21.6	0.25
99790.86	5760.04	19419.09	711.32	2390.77	39.26	
*10.951	0.22	5477.33	299.61	9.9	9.39	3548.98
76223.33	13.26	110.89		11.1	11.67	0.18
28407.84	1393.45	46836.53	512.5	1523.29	23.06	
453.02	0.25	*674.132	*27.362	5.06	9.39	5583.89
2566.62	12.19	132.63		9.47	8.64	0.18
52425.56	1566.66	9141.76	2042	2278.21	59.6	
348.56	0.58	*674.132	*27.362	*0.598	11.34	2163.18
4296.32	12.06	210.44		15.56	29.21	0.35
22583.76	7637.29	9678.77	1014.79	1658.61	55.4	
177.72	0.52	*674.132	792.99	13.23	19.95	2163.18
3252.39	10.45	199.52		97.86	4.8	0.67
125838.2	4884.93	5893.67	596.67	3672.37	67.73	
*39.33	1.33	*682.921	196.42	*1.666	12.21	6837.42
16011.77	25.41	478.83		12.47	*0.658	0.33
30240.28	4538.45	24811.78	923.04	*34.126	107.93	
289.74	0.37	*684.082	*27.695	*2.588	*1.393	7512.01
18134.61	33.48	171.43		7.21	11.61	0.61
42513.57	1702.06	285689.52	2671.06	926	34.98	
*37.47	0.45	*684.082	*27.695	*2.588	*1.393	4645.29
24389.14	19.99	132.5		10.2	11.61	0.58
36983.59	2035.12	13081.33	2856.98	1080.18	23.7	
*37.47	0.63	4104.49	*27.695	*2.588	*1.393	10103.99
68005.24	41.44	211.99		9.36	6.34	0.47
49559.79	1672.04	222959.33	1742.92	2529.4	73.76	
381.52	0.6	*684.082	*27.695	*2.588	*1.393	8121.6
7019.43	18.98	311.73		10	9.66	0.47

Table4.txt

49753.34	1883.12	8066.85	1169.78	1238.53	68.49			
*39.33	1.55	*682.921	280.4	*1.666	12.5	9232.49		
948.17	31.19	3263.98		16.06	6.58	0.86		
108343.31	7685.58	14933.77	1574.42	*34.126	217.05			
*39.33	0.34	6181.59	186.42	*1.666	9.89	7036.94		
5495.03	24.09	1870.28		20.29	12.88	0.33		
33683.82	13058.52	6004.77	2924.66	*34.126	163.27			
198.56	0.56	7469.65	165.86	*1.666	9.02	6989.25		
9517.05	18.61	789.64		7.9	6.8	0.5		
54425.4	4447.72	12657.69	1540.45	*34.126	50.88			
*39.33	0.35	5621.44	*27.643	*1.666	10.47	5315.96		
2916.86	33.47	444.26		10.55	6.58	0.2		
25945.46	4674.76	6950.68	2914.19	*34.126	89.03			
277.17	0.73	*684.082	189.06	*2.588	*1.393	2074.21		
5430.99	17.14	529.9		10.96	8.88	*0.42		
32913.6	3281.23	31879.77	1313.34	685.57	39.34			
*39.77	0.31	*706.944	*28.096	*21.183	12.65	8504.98		
59396.14	21.68	422.51		13.58	9.49	0.29		
38297.49	6004.39	13521.3	963.71	*32.555	41.25			
*39.77	0.42	*706.944	177.01	*21.183	*1.362	5429.28		
8175.91	28.79	364.11		11.17	7.79	0.36		
22505.3	4280.58	55869.87	1463.74	*32.555	54.22			
*37.47	0.36	*684.082	*27.695	*2.588	75.59	6192.31		
4838.05	43.01	259.18		11.19	6.93	*0.42		
81923.61	8682.08	14867.63	1822.68	1695.14	36.72			
*39.77	0.75	*706.944	268.55	*21.183	10.14	5841.53		
4734.97	19.43	1573.83		14.91	6.32	0.56		
31061.35	11941.06	4106.81	2932.64	*32.555	98.43			
*41.51	2.05	*1970.97	237.16	*16.134	66.57	6377.63		
19232.69	19.51	519.94		51.34	13.51	0.67		
93604.17	4799.47	7238.43	1715.83	*33.371	81.36			
463.54	0.86	*684.082	340.23	16.42	35.04	4150.88		
1931.78	20.85	338.62		25.01	12.08	*0.42		
86321.35	8630.51	139739.29	1136.87	1066.88	18.13			
*39.77	0.69	*706.944	*28.096	*21.183	10.14	4273.32		
65005.34	33.71	399.58		7.95	6.92	0.37		
59738.54	5814.44	130705.49	2501.59	*32.555	92.94			
197.65	0.69	*684.082	216.75	*2.588	8.89	4398.52		
1474.85	29.44	325.31		16.99	6.93	0.63		
56819.21	7146.6	18062.49	3864.82	1231.98	49.5			
*37.47	1.15	4762	290.32	20.8	12.15	4720.02		
41463.5	11.9	189.33		15.44	19.5	0.63		
65253.02	5208.16	4651.93	*40.56	1218.86	92.17			
*11.332	2.43	*682.162	494.65	8.86	30.49	2560.48		
24291.27	46.35	1625.85		26.95	6.77	1.05		
95755.39	21994.79	17082.25	2610.72	3961.12	125.97			
202.3	0.81	*684.082	183.4	*2.588	27.71	8856.26		
14507.57	18.12	731.63		15.15	8.61	*0.42		

Table4.txt

42099.64	2403.68	26060.96	2585.47	959.74	17.04	
*37.47	0.5	4104.49	259.41	19.94	8.62	4888.12
4198.47	16.5	311.73		19.06	23.29	0.5
51304.98	3297.09	47903.31	344.19	1303.84	99.81	
*41.51	2.17	*1970.97	201.47	*16.134	11.01	5445.63
10107.73	25.59	657.26		10.78	6.35	0.43
91396.13	7646.94	16797.16	2219.55	*33.371	72.38	
*37.47	0.45	*684.082	171.96	*2.588	11.6	2581.44
8594.74	11.67	318.55		9.27	5.71	*0.42
51726.24	1492.84	92569.41	2647.87	1231.98	44.38	
1022.35	0.27	*684.082	194.67	*2.588	*1.393	2927.37
44042.28	11.11	808.36		8.26	*0.555	0.54
33678.04	4211.25	179033.91	1724.95	664.56	19.16	
*41.51	0.27	*1970.97	*27.42	*16.134	*1.329	5226.01
65086.66	28.79	217.25		2.93	7.41	0.22
50373.51	3579.66	193235.55	2481.1	*33.371	43.25	
*41.51	1.15	*1970.97	192.36	*16.134	10.5	7858.27
20858.06	41.65	1443.2		3.71	9.39	0.64
117300.12	8846.29	101081.98	4190.41	*33.371	109.59	
*37.47	0.46	*684.082	183.4	*2.588	*1.393	4300.98
76161.68	16.72	569.85		6.6	*0.555	*0.42
48046.52	4503.58	178149.74	1330.28	1720.43	35.82	
*41.51	1.03	*1970.97	183.18	*16.134	14.14	3894.45
2604.15	31.92	603.02		14.25	7.41	0.5
79868.15	7990.06	26655.18	2441.54	*33.371	99.93	
*41.51	0.96	*1970.97	263.27	*16.134	9.23	9368.94
32931.72	19.37	1855.19		26.73	3.97	0.39
68626.25	6787.42	103932.02	2060.19	*33.371	56.9	
*41.51	0.89	*1970.97	201.47	*16.134	9.48	5455.23
14021.9	45.89	753.53		14.96	8.75	0.53
60211.85	18369.23	46530.22	3987.43	*33.371	83.43	
164.19	0.32	*684.082	194.67	*2.588	*1.393	7107.86
8059.59	19.55	165.26		3.79	10.16	*0.42
25994.7	1169.04	12312.96	2166.9	1026.85	132.09	
*41.51	0.27	*1970.97	192.36	*16.134	*1.329	5990.13
29502.9	22.88	1885.79		8.84	5.6	0.34
80077.04	6141.01	218721.76	4401.15	*33.371	78.33	
*10.36	1.05	5195.1	*27.835	*0.496	9.41	6491.41
4187.1	29.19	1163.75		4.1	4.24	0.32
72872.94	5367.55	7430.62	1498.27	*32.367	94.55	
*41.51	1.8	*1970.97	*27.42	*16.134	11.01	4700.95
10416.63	30.53	522.99		14.81	8.75	1.05
91139.93	7131.53	24270.31	2945.71	*33.371	149.43	
*41.51	0.97	*1970.97	*27.42	*16.134	10.5	2424.89
4099.46	22.98	1004.57		4.57	7.75	0.51
16888.52	4886.28	179152.9	1405.65	*33.371	168.58	
338.54	0.41	4543.89	269.8	*2.588	39.19	7725.98
38310.47	21.11	1326.01		8.11	18.36	0.43

Table4.txt

20223.86	895.23	19001.66	601.12	878.52	68.58	
*37.47	0.9	*684.082	*27.695	*2.588	*1.393	8011.38
59363.57	22.32	259.18		15.62	7.51	0.51
60124.86	2004.65	6950.58	928.12	643.49	35.43	
*37.47	0.47	*684.082	*27.695	*2.588	*1.393	2492.94
63274.17	15.47	281.25		7.47	5.71	*0.42
50981.24	5987.41	2398.57	*40.56	775.81	24.5	
*37.47	0.55	*684.082	183.4	*2.588	13.25	5054.14
52769.98	39.34	1058.5		30.98	*0.555	*0.42
62225.66	12013.05	76650.35	3494.13	1271.23	46.27	
*37.47	1.33	4543.89	290.32	*2.588	33.86	8121.6
25249.76	15.19	610.14		20.27	10.65	*0.42
207689.38	3376.52	29479.82	974.54	1106.74	41.18	
*41.51	1.8	*1970.97	263.27	*16.134	22.24	7183.81
166949.49	43.46	470.44		15.62	5.6	0.65
115825.39	10041.59	33729.73	1933.02	*33.371	114.93	
238.39	0.42	*684.082	*27.695	*2.588	*1.393	5854.75
13585.96	15.39	241.37		3.79	*0.555	*0.42
58566.92	2188.07	41801.06	2852.27	1297.32	15.48	
66.72	0.28	*677.552	*27.835	*0.496	21.95	6078.03
66236.02	22.83	350.33		2.7	3.97	0.35
24146.52	4028.33	79189.88	4272.19	487.7	65.83	
*10.36	0.27	6471.56	*27.835	4.47	8.53	4089.25
3153.14	46.21	1066.03		13.46	1.85	0.15
26446.8	3635.51	7629.82	4444.74	*32.367	33.94	
*39.77	0.14	*706.944	185.41	*21.183	10.64	2941.83
16859.74	18.16	309.27		11.37	5.41	0.46
18389.63	11900.46	65597.42	1897.82	*32.555	100.93	
*39.77	0.36	5257.04	177.01	*21.183	366.89	5711.56
24063.48	19.21	361.69		8.12	5.72	0.59
57678.79	6962.42	26508.01	2057.07	7723.6	58.7	
*39.77	0.34	20544.07	*28.096	*21.183	20.51	5757.29
3238.87	27.61	359.27		7.78	4.78	0.37
56405.17	4631.95	251439.88	904.42	*32.555	57.83	
*10.36	0.37	7735.6	*27.835	*0.496	*1.385	5675.47
1486.82	22.12	1226.94		8.5	2.81	0.27
49915.41	6377.67	6393.22	4104.45	*32.367	66.6	
*10.36	0.43	*677.552	*27.835	*0.496	*1.385	8978.61
37011.76	28.64	571.16		5.39	3.97	0.23
30390.73	13765.4	112311.22	4810.49	*32.367	37.76	
*10.36	0.33	*677.552	225.27	*0.496	*1.385	6517.76
23874.19	25.18	454.8		17.5	3.4	0.2
31792.69	9981.85	17853.6	2991.27	*32.367	47.56	
51.87	0.77	*677.552	*27.835	*0.496	24.64	8450.99
4535.04	28.9	600.3		9.11	4.51	0.25
64644.47	4420.74	14434.43	3419.09	*32.367	44.15	
*39.77	0.73	*706.944	185.41	*21.183	14.71	4722.91
7347.43	31.8	520.15		15.48	5.56	0.4

Table4.txt

31097.5	5173.11	4925.93	1328.49	*32.555	81.93			
*39.77	0.37	*706.944	*28.096	*21.183	*1.362	5650.83		
6301.77	18.82	1008.46		15.7	6.62	0.27		
32362.45	2993.28	11753.2	1126.3	*32.555	30.35			
*41.51	1.32	*1970.97	164.52	*16.134	14.14	4691.7		
9793.78	16.57	892.16		5.55	7.06	0.74		
56388.45	10212.05	7742.61	4749.02	*33.371	190.44			
*41.51	0.56	*1970.97	173.9	*16.134	14.67	3595.36		
1262.41	29.16	428.9		18.67	4.81	0.19		
23892.6	12506.77	41741.79	6151.12	*33.371	87.97			
*41.51	1.03	*1970.97	*27.42	*16.134	14.67	5706.42		
9039.6	19.84	637.46		26.95	12.39	0.5		
39352.77	4016.34	53998.29	1704.49	*33.371	16.43			
112.42	0.68	*684.082	*27.695	*2.588	*1.393	8675.21		
1931.78	17.63	197.98		23.86	*0.555	*0.42		
117942.9	3344.73	94501.21	1941.04	782.7	29.78			
*41.51	1.63	*1970.97	297.36	*16.134	14.67	2873.71		
4427.59	31.92	679.66		4.76	13.79	0.43		
82598.68	6011.53	231693.15	2431.66	*33.371	340.13			
*41.51	2.42	*1970.97	288.9	*16.134	69.34	6217.83		
21000.45	22.98	464.13		48.51	13.65	0.82		
170193.68	9998.97	20118.7	2694.11	316.02	86.2			
*41.51	0.71	*1970.97	*27.42	*16.134	*1.329	7293.13		
151276.22	47.89	316.47		8.15	4.4	0.51		
36931.5	5838.78	21215.44	4742.54	*33.371	58.87			
178.75	0.25	*684.082	*27.695	*2.588	*1.393	5579.35		
2516.55	38.25	528.13		8.93	8.07	*0.42		
47115.23	2996.74	15349.5	2146.95	1827.46	26.03			
*39.77	2.58	*706.944	243.77	*21.183	24.84	5410.67		
52399.02	37.19	2989.61		20.47	13.78	0.58		
89855.97	12266.36	7639.1	2646.24	*32.555	34.64			
51.87	0.71	4227.58	626.76	28.97	20.99	4445.77		
10111.74	12.92	354.97		79.55	13.28	0.27		
77488.85	4812.77	4961.31	5762.74	*32.367	35.73			
640.5	0.67	83217.69	333.16	130.24	21.47	6740.09		
3384.18	34.88	287.09		32.9	14.79	0.64		
82892.22	5465.39	6139.96	3633.17	*32.367	42.59			
*10.36	0.29	25206.22	191.76	8.69	12.31	6088.43		
3327.21	16.37	611.05		14.04	49.09	0.22		
62794.1	13797.68	63907.13	3445.78	*32.367	58.68			
210.57	0.59	12703.56	*27.835	*0.496	11.18	10074.03		
782.26	40.35	611.05		6.08	10.23	0.26		
117868.89	12990.32	315067.27	2479.66	*32.367	164.04			
*10.36	0.67	4873.67	*27.835	4.1	11.63	4006.86		
*130.377	50.47	820.23		17.7	29.42	0.27		
41834.64	10014.25	63843.55	2993.15	*32.367	98.75			
*10.36	0.51	8049.95	*27.835	5.19	20.27	8978.61		
2260.04	20.21	510.66		9.31	17.31	0.19		

Table4.txt

86209.9	5921.72	63240.05	2529.74	*32.367	41.53	
1075.6	1.07	4526.33	1425.64	226.28	41.26	1381.97
1761.91	8.98	277.45		37.61	41.08	0.6
115495.74	9284.35	5346.74	1237.64	907.87	56.82	
148.52	0.38	*674.132	169.9	9.9	9.82	2439.2
8036.79	11.54	116.48		14.52	3.27	0.23
30171.69	2766.81	7639.91	1029.06	1286.33	47.68	
1379.84	0.71	5947.63	534.7	102.15	29.77	1245.07
43618.3	9.38	132.63		23.74	3.67	0.36
142119.1	3611.49	6283.18	1046.94	1246.82	31.17	
106.35	0.18	*674.132	294.43	5.93	12.44	1724.45
6117.63	12.2	221.12		127.77	5.51	0.24
72614.69	7175.63	9793.71	1816.83	2036.12	43.38	
*10.951	0.26	*674.132	*27.362	*0.598	*1.37	5425.29
29345.97	8.82	87.17		8.26	3.87	0.15
38540.77	1393.45	3174.63	1070.3	743.84	10.23	
597.61	4.34	19683.38	253.14	122.98	18.59	9064.58
41573.64	60.04	495.01		50.5	7.39	0.8
155371.01	10402.92	5715.64	2232.09	*32.367	126.56	
*10.951	0.27	*674.132	192.48	3.59	*1.37	1371.56
58311.05	6.41	142.95		24.08	5.51	0.2
29654.29	2127.85	12692.7	888.34	1410.48	16.01	
434.97	0.64	5947.63	1629.4	183.88	46.89	4710.16
25408.95	9.52	360.88		247.16	6.34	0.27
242220.21	5032.45	11570.13	1259.03	2857.63	30.86	
1236.14	1.41	15300.91	177	73.47	26.61	10282.37
20573.63	33.69	690.79		36.24	4.78	0.43
192692.59	6377.67	7927.74	3282.2	*32.367	151.56	
288.12	1.05	*674.132	257.72	113.53	28.31	3985.87
3567.13	17.93	132.63		19	3.27	0.45
30481.62	3722.64	24643.25	1090.14	2081.17	34.56	
163.87	0.6	*677.552	243.93	10.72	10.29	6628.72
36745.02	21.78	510.66		189.33	14.79	0.26
112958.01	12990.32	4493	2274.46	*32.367	97.48	
210.57	0.72	5515.54	253.14	36.71	14.84	4976.46
22040.28	26.41	302.24		15.52	8.9	0.24
180820	6345.11	18844.68	2710.27	*32.367	133.78	
2412.35	1.2	8676.85	1701.13	607.13	80.09	5157.21
45277.33	19.97	899.5		345.25	33.03	0.56
143939.12	10532.44	7097.53	3637.01	*32.367	50.88	
56.91	0.2	*674.132	*27.362	5.35	*1.37	4027.31
38636.43	12.32	116.48		11.86	5.85	0.29
60296.49	1321.93	19136.78	1011.23	913.53	15.38	
*10.36	0.7	*677.552	*27.835	*0.496	11.41	4440.86
*130.377	25.89	487.09		78.72	14.39	0.26
136125.74	9528.17	195801.14	3373.4	*32.367	216.42	
*10.36	1.02	5034.51	201.46	8.69	19.07	6549.42
3211.71	38.2	663.57		38.97	27.41	0.26

Table4.txt

21670.17	9755.04	166425.51	1681.53	*32.367	114.75				
*10.36	0.35	16969.71	*27.835	*0.496	*1.385	5415.2			
899.46	31.29	1040.98		200.68	61.34	0.23			
26173.18	6247.43	115287.76	1520.01	*32.367	81.55				
*10.36	0.96	*677.552	167.01	4.47	10.29	5762.74			
2531.68	35.1	704.22		11.7	29.51	0.24			
42921.18	8912.09	173509.26	2609.66	*32.367	125.62				
*10.951	0.8	*674.132	225.51	5.93	8.54	2393.25			
990.37	15.03	162.71		118.08	6.18	0.36			
69987.08	4267.36	190619.6	250.05	2953.2	40.84				
*10.36	0.35	19983.71	206.27	2.98	*1.385	4128.1			
2788.89	23.52	914.38		2.37	42.02	0.2			
33696.77	13248.73	**101405.397	3773.46	*32.367	41.38				
*10.36	0.67	4227.58	*27.835	*0.496	8.97	14644.61			
6393.65	8.48	471.08		6.57	31.16	0.22			
30171.16	13959.09	150558.82	4770.75	*32.367	64.85				
93.75	1.04	*677.552	229.97	12.04	13.91	4856.58			
1306.9	46.76	1120.78		12.26	38.18	0.28			
66384.06	19661.45	271770.76	3660.03	*32.367	305.82				
*10.951	2.7	*674.132	739.89	53.43	15.12	3979.51			
9072.87	17.66	345.24		206.64	12.45	0.42			
170105.52	6666.33	90649.11	807.73	3520.73	26.64				
632.96	0.53	21339.63	779.77	73.94	40.24	1978.95			
5587.2	8.92	281.28		66.44	7.14	0.32			
53733.83	5527.42	98316.69	877.96	3380.3	84.81				
*10.36	0.4	4873.67	333.16	3.73	*1.385	6182.14			
135623.3	45.56	1040.98		49.61	51.41	0.24			
22552.86	22071.95	141769.48	1808.94	*32.367	43.68				
249.72	1.22	*674.132	350.61	18.13	16.49	1434.23			
1529.06	4.23	311.2		10.81	9.22	0.29			
101995.02	7929.49	130108.01	1700.55	1478.17	70.75				
608.42	0.48	*677.552	177	*0.496	*1.385	6370.46			
11174.89	32.81	949.65		77.08	70.28	0.31			
46651	25089.11	259655.7	3943.37	*32.367	128.31				
*10.36	0.47	*677.552	167.01	*0.496	9.41	3247.73			
22787.01	26	1104.48		15.78	72.73	0.23			
39366.24	11341.58	240143.37	3535.52	*32.367	63.71				
*10.36	0.53	*677.552	167.01	5.91	15.3	5258.11			
4535.04	38.09	851.12		6.64	47.55	0.23			
36196.36	13022.62	82792.45	4838.34	*32.367	71.46				
*10.36	1.82	57252.79	234.64	11.38	20.51	6926.63			
28794.37	37.71	911.41		6.11	3.54	0.77			
76017.01	13474.8	18705.49	3032.68	*32.367	90.26				
*10.36	0.53	44783.2	215.82	3.73	13.45	5056.65			
23124.26	22.55	585.82		13.91	3.4	0.25			
60899.21	6833.26	12807.29	3744.58	*32.367	39.99				
*37.47	1.15	7314.95	449.35	20.8	12.15	6454.3			
84970.2	24.13	320.81		20.47	8.61	0.81			

Table4.txt

110423.32	6054.14	16994.48	1089.8	1796.05	23.97	
*10.36	0.56	21930.57	*27.835	*0.496	*1.385	7395.43
11835.59	24.76	364.15		12.22	4.51	0.32
47586.67	7418.55	7696.11	4100.56	*32.367	124.78	
*37.47	1.67	*684.082	238.31	*2.588	11.6	11288.8
11178.15	47.94	946.85		29.24	11.14	0.61
102539.61	5323.64	11722.68	1182.41	1465.58	11.33	
*39.77	0.42	*706.944	177.01	*21.183	9.15	7111.39
106888.06	43.83	540.83		14.23	6.62	0.79
22355.83	8167.86	14385.5	2733.07	*32.555	49.42	
*10.36	0.44	26243.94	*27.835	5.19	12.54	6766.67
5055.48	64.44	563.77		3.41	5.43	0.43
34888.53	13862.25	13282.72	2717.73	*32.367	127.25	
*39.77	0.75	*706.944	*28.096	*21.183	*1.362	7918.28
7548.39	17.05	390.25		13.75	10.32	0.67
28526.31	5266.97	21485.34	1625.06	*32.555	41.5	
*39.77	0.17	*706.944	*28.096	*21.183	*1.362	6117.01
77941.49	10.39	229.82		6.76	7.5	0.24
26524.6	3351.41	167517.74	1036.78	*32.555	76.86	
*39.77	0.77	*706.944	193.8	*21.183	9.15	11268.64
6474.12	41.93	422.51		9.99	5.41	0.33
42309.11	5229.41	17049.51	2989.08	*32.555	66.29	
*37.47	0.73	*684.082	205.78	*2.588	*1.393	6138.93
14987.67	23.95	316.29		10.58	*0.555	*0.42
71476.85	5027.12	9846.35	1899.97	1218.86	13.03	
*39.77	0.57	*706.944	*28.096	*21.183	*1.362	5605.47
9977.18	35.19	238.54		13.24	5.1	0.57
25720.07	2603.99	65000.25	3217.2	*32.555	91.45	
*39.77	0.29	*706.944	*28.096	*21.183	*1.362	4772.32
42062.78	15.5	249.96		9.56	10.32	0.35
38007.02	6558.42	38834.82	2204.94	*32.555	49.79	
143.82	0.23	*706.944	177.01	*21.183	9.39	4779.4
44901.61	21.87	392.59		7.84	5.41	0.29
41576.95	3136.07	62128.08	1580	*32.555	44.7	
123.26	2.06	4324.74	216.75	*2.588	10.51	11203.71
17618.21	26.77	634.68		5.08	5.71	0.47
48657.66	4373.46	203448.56	2103.87	1638.09	28.98	
*39.77	0.94	5073.25	202.17	*21.183	29.81	2750.67
22844.66	27.22	583.28		36.34	16.09	0.36
48446.85	17656.95	147363.31	2139.52	*32.555	27.15	
*37.47	0.67	*684.082	*27.695	*2.588	*1.393	4499.35
1712.43	15.05	900.93		17.89	6.93	*0.42
33359.63	2620.91	26834.31	2191.33	885.32	16.14	
*37.47	0.58	*684.082	453.95	*2.588	15.46	6718.54
3188.93	25.26	316.29		11.95	8.61	0.69
81204.11	2745.72	105903.1	844.02	1497.69	12.77	
*37.3	0.48	*639.193	272.36	*0.68	*1.36	3378.44
10126.42	17.56	208.67		11.14	*0.751	0.28

Table4.txt

46858.57	2831.81	10974.05	*39.613	11609.29	74.07	*39.77	0.4	*706.944	177.01
*21.183	9.89	3951.86	5680.67	30.61	1973.87	18.55	4.78	0.41	37245.2
5833.41	28857.24	2821.83	*32.555	36.43	*37.3	0.34	5936.13	300.56	9.55
10.51	5043.01	50544.21	13.04	384	13.31	*0.751	0.19	180603.14	2679.11
9601.33	552.84	2573.12	72.01	66.72	0.79	7104.98	234.64	6.26	8.53
5167.28	11387.26	19.44	1648.87	7.3	5.81	0.16	83600.83	4747.45	20926
1328.22	*32.367	147.09	*10.36	0.24	*677.552	*27.835	4.47	10.29	3655.76
4916.41	54.39	690.79	8.6	3.4	0.2	27486.5	8944.53	183005.88	2208.15
*32.367	66.83	*10.36	0.46	35646.96	*27.835	5.19	*1.385	3427.28	8607.49
17.09	541.31	16.29	3.4	0.18	22387.58	4976.01	70172.35	2285.53	*32.367
43.1	*10.36	0.24	10699.64	*27.835	*0.496	9.85	5654.97	1486.82	36
1158.41	10.51	5.56	0.22	43552.68	15475.39	9987.64	1237.93	*32.367	79.83
*39.77	0.91	23608.79	*28.096	*21.183	16.27	6902.8	13234.11	20.89	601.11
7.21	4.78	0.2	31856.56	7485.12	166421.43	636.21	*32.555	90.12	249.53
0.35	*639.193	340.83	5.3	30.79	1956.47	3151.2	16.15	633.67	23.37
8.63	0.3	62764.25	7366.19	10878.88	985.27	1267.24	139.63	*10.36	0.87
*677.552	*27.835	*0.496	19.07	6793.27	1486.82	29.65	998.64	6.5	2.96
0.39	56244.8	9171.55	283580	1909.3	*32.367	64.11	66.72	0.35	7420.62
*27.835	14.33	9.85	3257.15	6555.51	16.34	510.66	3.22	5.56	0.14
26173.18	4289.98	23670.51	1975.12	*32.367	123.87	*37.3	1.07	*639.193	474.63
12.16	21.11	1244.76	44235.81	17.41	384	21.39	*0.751	0.46	212771.08
5279.84	13583.06	709.15	1968.17	114.2	*39.77	0.54	8158.53	*28.096	*21.183
16.53	11892.51	1937.47	182.36	722.58	12.53	6.62	0.45	27290.32	10829.38
224025.12	2582.18	*32.555	65.24	*39.77	0.23	*706.944	*28.096	*21.183	*1.362
4300.51	27007.29	19.75	190.21	6.93	5.72	0.31	40189.44	6808.24	58383.15
3057.93	*32.555	101.4	215.55	0.4	16060.52	*27.835	5.91	9.85	5157.21
12188.03	39.29	331.5	3.61	1.85	0.2	45777.68	2782.74	133290.1	987.26
*32.367	46.24	*39.77	0.39	*706.944	177.01	*21.183	12.4	6799.61	1630.07
46.44	664.8	19.04	3.82	0.52	57253.51	3968.5	23858.01	885.15	*32.555
127.73	*39.77	0.56	*706.944	210.52	*21.183	8.66	7494.39	208689.43	25.91
636.15	26.43	7.79	0.55						

Table4.txt

33374.1	14938.43	20943.16	3059.28	*32.555	114.58	
309.11	0.37	5204.4	427.97	*0.68	*1.36	2815.75
8921.21	16.93	553.52	11.25	*0.751	0.2	
79145.15	6133.28	26094.45	1032.53	2995.24	63.79	
*10.36	0.57	8989.45	*27.835	*0.496	8.53	5440.61
32834.71	30.42	1012.84	9.38	5.56	0.32	
43064.54	5563.21	15250.78	3028.91	*32.367	92.02	
*10.36	0.4	4551.19	*27.835	*0.496	*1.385	5562.91
5282.96	29.03	386.63	4.03	4.51	0.25	
26720.4	4812.77	32227.65	1953.17	*32.367	39.02	
*10.36	0.41	*677.552	*27.835	*0.496	8.75	6470.34
1656.02	31.83	1263.17	*0.03	4.78	0.31	
34001.23	4747.45	97572.47	4391.7	*32.367	105.65	
*39.77	0.39	*706.944	202.17	*21.183	*1.362	4104.8
10082.54	22.81	258.38	8.74	5.72	0.51	
27217.48	2709.65	6578.31	1406.81	*32.555	32.73	
*10.36	0.26	4873.67	*27.835	*0.496	*1.385	7211.35
3384.18	23.59	483.11	*0.03	3.11	0.22	
34250.54	3831.98	10633.61	2951.79	*32.367	47.59	
*39.77	0.25	*706.944	210.52	*21.183	*1.362	8390.47
28227.97	32.56	322.07	16.56	5.72	0.44	
71306.32	5795.48	38072.25	2684.32	*32.555	74.92	
171.99	0.48	*706.944	193.8	*21.183	*1.362	5073
60492.53	19.27	657.21	9.45	5.41	0.51	
46956.95	10608.3	4583.26	4450.71	*32.555	51.3	
*39.77	0.75	*706.944	*28.096	*21.183	*1.362	4754.65
5861.15	18.54	464.75	10.61	3.49	0.68	
51828.08	4817.91	40675.92	1063.17	*32.555	35.69	
*39.77	0.44	*706.944	177.01	*21.183	14.71	6207.44
10117.55	14.65	406.51	13.86	4.14	0.31	
54068.15	8698.29	280140.05	1122.96	*32.555	51.63	
*10.36	0.36	4873.67	167.01	3.73	8.53	4613.35
4727.73	32.35	391.05	*0.03	2.66	0.17	
58340.43	3078.22	210367.87	1654.28	*32.367	29.63	
*10.36	0.79	*677.552	*27.835	*0.496	14.37	7882.69
3716.14	39.57	1278.56	8.7	3.11	0.38	
67292.56	6312.55	25838.79	3295.49	*32.367	105.9	
*10.36	0.43	*677.552	215.82	*0.496	8.75	4806.77
45383.22	26.91	690.79	10.98	4.38	0.25	
50330.97	7548.54	29933.12	3673.46	*32.367	56.96	
*39.77	0.45	*706.944	*28.096	*21.183	*1.362	4579.31
59804.41	16.6	282.97	9.42	5.25	0.39	
36266.97	7601.76	21877.86	2952.77	*32.555	151.35	
*39.77	0.3	*706.944	*28.096	*21.183	*1.362	7646
75891.24	21.03	277.59	7.04	4.47	0.32	
32868.28	4557.76	25239.35	2111.97	*32.555	78.68	
*10.36	0.74	6471.56	*27.835	*0.496	*1.385	4956.44
2117.69	32.82	857.23	11.44	*0.114	0.34	

Table4.txt

60867.79	14217.3	143261.27	2522.32	*32.367	110.85	
*39.77	0.26	*706.944	*28.096	*21.183	*1.362	3391.22
8405.63	42.11	282.97		5.9	4.78	0.28
38079.62	3387.43	36565.47	2357.41	*32.555	54.1	
*37.3	0.28	*639.193	168.99	*0.68	*1.36	4225.97
21239.74	17.68	239.84		8.94	*0.751	0.22
56201.06	5128.52	10513.29	555.91	1638.58	49.43	
*37.3	0.47	*639.193	*26.646	*0.68	*1.36	3703.77
171646.44	28.09	1123.75		6.5	*0.751	0.24
137674.76	1840.92	18962.3	1728.14	2349.71	41.54	
3187.8	0.78	*701.526	389.5	161.69	28.57	4579.14
2230.49	20.29	159.96		17.48	12.28	0.34
135654.82	2927.44	9373.07	1728.04	809.47	32.93	
707.85	0.77	*701.526	838.64	88.91	30.59	1148.27
109394.34	5.94	152.74		42.67	10.59	0.66
78503.31	5579.59	24558.79	930.46	1683.04	116.56	
278.5	0.38	*701.526	247.04	9.9	9.47	4320.5
1536.03	18.75	197.48		65.7	39.16	0.26
81405	2285.05	3868.67	1445.79	784.8	28.26	
*35.8	2.42	*701.526	201.85	37.65	15.24	5867.32
3789.09	14.34	101.33		16.44	9.18	0.48
89310.46	5234.48	10625.73	337.93	1670.65	39.46	
*35.8	1.29	*701.526	247.04	26.16	20.57	3410.49
7927.53	5.55	187.57		19.89	12.93	0.4
37647.14	2717.14	7775.98	862.33	743.7	20.43	
2703.01	2.02	*701.526	470.83	550.6	85.89	9724.71
6411.97	20.14	216.68		33.82	8.08	1.6
90631	3900.85	22342.61	961.53	579.42	49.09	
553.35	1.08	*701.526	562.93	72.35	45.85	4268.78
5506.51	13.77	257.46		318.17	10.25	0.41
115385.73	3472.71	26352.47	411.05	834.14	26.32	
12827.98	0.97	6413.16	2349.16	2818.46	374.65	1634.63
1786.06	21.17	528.57		487.73	39.16	2.64
224636.7	12915.76	10139.58	476.61	480.96	49.63	
443.02	0.62	*682.162	161.46	5.36	16.8	3384.52
6461.66	14.74	554.42		11.7	33.15	0.47
31964.31	11041.69	8988.67	1545.94	1711.28	121.91	
*11.332	0.41	*682.162	172.39	4.16	*1.364	3037.38
13001.65	18.51	247.03		29.64	7.53	0.29
50182.78	5102.97	16667.68	1366.72	1426.13	132.03	
*11.332	0.6	*682.162	193.73	*0.642	*1.364	5164.97
3862.75	23.86	385.16		88.6	26	0.36
80038.54	10904.71	10384.56	1608.49	1584.96	111.41	
2784.15	0.09	*682.162	*26.909	67.26	*1.364	2892.15
*129.267	22.19	1817.91		52.8	9.39	0.09
11462.8	11745.91	1294.4	2832.13	217.02	29.43	
*11.332	0.83	*682.162	*26.909	*0.642	8.18	5739.91
47316.41	26.64	275		11.42	9.93	0.4

Table4.txt

40604.93	8866.47	5177.78	1794.08	2580.79	61.61	
454.36	2.18	*682.162	511.14	392.81	36.14	3739.27
5331.94	22.01	577.61		367.67	28.64	1.4
146181.48	5543.62	8743.07	2001.61	1110.19	50.16	
181.13	0.85	4889.12	969.15	*21.183	38.3	4403.02
12922.72	10.06	612.87		253.96	88.12	0.8
83989.12	6099.58	6843.69	1275.97	*32.555	39.11	
692.16	1.42	*682.162	486.35	327.82	24.83	4141.88
3688.37	10.9	660.96		89.53	32.99	0.65
136842.98	6658	11757.19	1906.64	810.21	57.49	
*35.8	0.86	*701.526	*26.487	5.4	9.74	2139.36
29069.89	3.11	105.64		6.44	*0.692	0.35
113674.01	4642	7864.2	882.42	1377.74	112.91	
1237.09	2.9	9313.19	1123.36	270.71	52.4	6714.91
933.19	20.62	370.05		30.52	23.38	0.77
187585.8	5626.76	21242.6	1420.02	4366.49	31.75	
173.32	1.09	*701.526	389.5	19.08	19.72	3098.19
7093.1	9.15	187.57		103.11	16.94	0.66
74445.21	2478.13	9512.69	738.9	904.06	14.15	
*11.332	1.76	*682.162	1958.03	*0.642	17.75	2537.17
77258.87	16.59	7114.38		25.96	22.27	0.43
71534.95	8335.8	18065.63	921.88	2102.32	114.18	
765.6	1.05	*682.162	161.46	*0.642	*1.364	1818.49
21095.87	25.15	432.58		11.19	40.62	0.71
66895.43	15638.87	4522.56	1339.61	2097.14	172.68	
*11.332	0.57	*682.162	283.36	*0.642	16.33	3117.77
26994.19	20.05	2890.85		14	26.27	0.33
43250.9	8394.81	22038.35	2088.43	1415.5	59.86	
478.15	0.39	*682.162	311.54	*0.642	*1.364	1948.31
9638.32	25.61	2993.79		15.9	55.38	0.29
38582.94	11941.47	15188.2	2592.63	649.18	64.55	
771.49	0.38	*682.162	*26.909	12.25	*1.364	2187.62
43146.37	6.52	504.52		13.12	37.45	0.29
28311.53	9474.83	9141.71	2165.87	1018.11	63.09	
631.11	0.86	*682.162	820.82	5.96	10.12	4213.15
41745.96	10.64	8210.46		74.24	31.62	0.55
72052.51	7902.71	152386.93	3491.7	2355.2	36.82	
*11.332	0.41	*682.162	214.45	9.15	19.17	2406.53
19093.38	16.69	387.48		11.9	16	0.32
90568.96	10650.28	74101.62	1871.07	1951.73	108.56	
392.11	0.5	*682.162	444.33	4.76	*1.364	2809.54
15169.88	22.85	334.77		109.48	37.77	0.23
30432.08	7488.63	20925.49	2660.2	1319.6	24.85	
83.35	0.6	*682.162	1240.11	8.86	10.6	3114.79
352156.03	28.7	7427.82		61.91	48.18	0.72
55880.74	13056.06	11326.7	2973.21	2463.04	144.55	
136.67	1.12	*682.162	1509.84	6.55	11.56	7311.84
136135.33	19.82	8466.81		67.9	48.33	0.48

Table4.txt

52857.34	9259.06	19385.35	2075.33	1789.91	62.1	
170.51	0.29	4873.53	919.2	*0.642	*1.364	3279.29
109905.9	14.78	6151.53		69.9	59.42	0.42
63739.15	5383.61	4163.41	1547.12	2169.59	118.57	
811.42	0.7	*682.162	339.09	7.13	*1.364	2989.87
48834.38	25.37	609.73		46.23	112.94	0.37
41850.64	12997.4	4386.31	2799.37	2200.6	55.09	
*11.332	0.59	*682.162	254.43	11.69	10.6	2560.48
5769.53	27.59	443.5		22.66	5.13	0.35
142037.31	10082.42	4809.92	2170.64	1574.41	86.48	
348	0.51	*682.162	193.73	*0.642	*1.364	4163.55
10402.94	15.17	396.69		65.97	11.24	0.3
26678.42	12078.36	18406.78	2318.78	1196.39	122.05	
197.13	0.29	*682.162	*26.909	8.86	9.4	4487.43
2787.64	23.14	354.37		25.15	29.53	0.33
42531.54	10199.95	6962.76	1555.38	1056.09	209.61	
*11.332	0.46	*682.162	418.66	13.91	8.18	2110.39
38652.12	5.9	291.15		42.58	7.68	0.33
254304.71	8001.2	23092.89	1911.38	1637.67	79.85	
*41.51	0.36	*1970.97	210.5	*16.134	15.2	7895.72
15910.44	28.37	1019.25		12.95	3.97	0.22
89499.94	7646.94	18927.98	6007.89	*33.371	108.34	
*11.11	0.64	4448.53	319.59	*1.463	21.44	7033.05
3124.4	30.45	856.55		6.49	13.91	0.6
126916.4	17718.57	42874.64	3559.01	696.93	57.22	
*10.48	0.69	*623.86	*26.389	*0.506	30.02	6231.92
71618.97	14.56	477.55		13.17	7.58	0.34
48558.49	9288.45	34454.15	1896.91	*33.693	35.86	
*41.51	2.76	*1970.97	559	*16.134	40.45	7142.29
89110.15	29.7	2623.56		20.93	5.79	1.04
216304.43	10893.19	27885.13	1902.35	*33.371	126.09	
*41.51	0.73	*1970.97	254.62	*16.134	12.05	5590.11
3144.29	23.03	1467.27		15.65	7.06	0.28
31487.52	6615.2	21621.12	3827.73	*33.371	93.96	
*41.51	0.47	*1970.97	*27.42	*16.134	*1.329	7235.8
68084.23	23.69	344.83		4.99	6.16	0.29
26919.27	5536.17	73943.71	3069.53	*33.371	55.52	
*41.51	0.44	*1970.97	164.52	*16.134	9.48	8817.91
23058.97	35.01	479.85		7.69	6.71	0.48
72100.95	11997.81	183844.16	5183.49	*33.371	205.73	
*41.51	1.8	*1970.97	*27.42	*16.134	*1.329	7350.61
1995.44	56.72	419.12		2.14	13.51	0.85
28844.68	9956.34	7626.55	5760.69	*33.371	109.06	
*41.51	0.72	*1970.97	210.5	*16.134	12.57	4622.45
34657.41	40.59	737.33		16.45	9.71	0.51
56515.06	6959.53	56788.31	3779.58	*33.371	286.57	
*41.51	0.09	*1970.97	*27.42	*16.134	72.43	5716.14
18202.8	30.5	570.87		4.32	4.81	0.17

Table4.txt

44646.37	4277.77	170978.66	2033.13	1335.61	103.4	
645.57	4.27	*706.944	419.11	180.81	45.82	7511.64
3120.64	24.66	378.46		111.97	8.36	0.82
121287.44	2957.68	29844.87	1201.29	*32.555	24.62	
587.78	1.44	*706.944	276.78	159.62	20.77	5080.25
1466.21	15.37	309.27		26.89	8.08	0.55
95058.18	2780.3	18491.99	579.89	*32.555	23.15	
1334.86	1	9587.58	1103.69	198.99	33.18	3687.4
2083.03	15.48	339.65		52.05	6.32	0.7
165232.7	3136.07	6312.79	824.6	*32.555	15.87	
445.93	2.67	*706.944	358.48	*21.183	21.58	5810.83
21346.89	29.25	244.28		21.7	8.36	0.51
107529.76	3895.39	37049.16	1751.98	*32.555	67.26	
181.13	1.18	*706.944	342.22	*21.183	29.81	4950.43
1293.56	10.85	520.15		18.44	4.78	0.53
105314.73	8737.7	16299.62	1932.17	*32.555	65.43	
453.26	1.35	*706.944	463.29	169.21	36.3	2872.73
66568.7	26.68	288.31		31.45	48.91	0.63
45289.5	2133.76	3228.27	307.48	*32.555	15.19	
*11.332	0.34	*682.162	*26.909	*0.642	*1.364	6521.59
59840.27	17.92	337.24		10.13	6.46	0.49
34893.15	7449.16	26936.78	2819.99	1468.59	30.46	
*11.332	2.95	*682.162	244.6	4.76	29.55	2010.71
20851.3	21.6	687.63		18.14	4.78	0.53
138773.92	9141.33	65067.69	2067	1595.51	37.97	
70.61	0.44	*682.162	214.45	*0.642	*1.364	5002.15
43607.72	28.59	337.24		15.5	7.08	0.49
32639.23	7607.02	11638.62	2263.77	1023.54	68.78	
*11.332	0.43	*682.162	*26.909	*0.642	*1.364	2510.98
22510.06	23.35	403.54		12.75	4.96	0.36
57411.43	6974.86	221980.56	2486.7	1700.77	132.84	
*11.332	0.29	*682.162	*26.909	*0.642	*1.364	3538.59
50738.58	14.93	165.51		67.93	5.81	0.4
35966.77	5263.43	5738.37	2081.28	777.08	30.77	
*11.332	0.32	*682.162	172.39	*0.642	*1.364	3605.32
12968.98	14.93	351.94		18.42	9.66	0.56
23026.07	6539.02	12023.47	3039.1	952.79	116.82	
*11.332	0.76	*682.162	*26.909	*0.642	*1.364	3849.35
3776.45	45.62	773.21		19.03	7.38	0.4
56351.72	9572.88	24272.32	2269.74	925.48	93.55	
*11.332	0.41	*682.162	*26.909	*0.642	*1.364	2147.54
4999.87	14.22	285.82		6.94	6.14	0.49
32386.55	6082.06	22615.03	2433.85	930.95	72.13	
*11.332	0.19	*682.162	264.16	*0.642	*1.364	3279.29
8782.54	14.93	306.88		6.87	7.68	0.29
34893.15	5902.84	13695.45	1952.91	352.96	88.08	
*11.332	0.4	*682.162	*26.909	*0.642	*1.364	3499.24
4999.87	32.55	301.68		5.52	5.48	0.38

Table4.txt

25962.34	4619.89	10429.66	2732.74	1018.11	212.33	
*11.332	1.61	5880.65	273.8	11.13	23.42	3339.37
12337.23	42.79	959.43		10.37	5.48	0.57
173912.46	23918.47	33540.65	1671.09	1362.28	121.24	
*11.332	0.87	*682.162	*26.909	*0.642	*1.364	3990.62
9269.93	36.29	1572.88		10.07	6.77	0.74
47974.21	9474.83	6096.57	1768.04	559.23	45.95	
*11.332	1.88	*682.162	*26.909	4.16	11.08	5968.85
32326.57	31.85	481.82		17.8	6.14	0.69
69945.18	14934	16209.28	1804.73	1158.73	72.53	
*11.332	0.57	*682.162	*26.909	*0.642	*1.364	3996.78
45241.44	27.57	301.68		8.57	4.78	0.19
32048.87	8394.81	148145.86	2068.19	688.27	69.67	
*11.332	0.35	48747.27	*26.909	*0.642	8.67	5473.76
10498	456.18	1646.81		6.4	21.88	1.52
36706.17	8001.2	10309.35	2170.64	693.84	45.4	
*11.332	0.79	*682.162	193.73	*0.642	*1.364	3052.25
7691.45	32.73	929.16		14.75	7.97	0.47
47618.59	6836.3	5310.51	2369.08	5184.27	51.92	
*11.332	0.39	*682.162	*26.909	*0.642	*1.364	2354.48
26527.01	16.3	434.77		12.03	7.68	0.38
26989.75	11569.88	35887.48	1647.46	777.08	28.61	
*11.332	0.94	*682.162	161.46	*0.642	9.15	4393.64
19247.48	26.61	389.79		15.63	9.93	0.37
40685.47	7843.6	8496.52	3623.29	382	16.37	
*11.332	0.43	*682.162	183.14	*0.642	*1.364	2110.39
27425.63	11.44	354.37		18.48	11.75	0.45
7141.58	4982.45	9019.31	2611.93	626.77	81.02	
416.88	0.44	*692.51	182.2	3.86	*1.373	6000.15
25648.56	25.44	399.29		20.65	23.56	0.7
35609.93	9639.64	11392.19	4914.5	*33.406	230.06	
114.61	0.25	*692.51	164.52	*0.491	*1.373	4497.41
8142.25	15.89	318.41		41.57	68.32	0.33
17419.88	9137.27	5702.81	3235.9	*33.406	38.86	
*10.766	0.26	*692.51	246.57	3.86	*1.373	9861.23
50918.69	14.2	305.27		19.17	15.45	0.3
26360.73	10171.71	6145.76	2032.69	*33.406	51.79	
*10.766	0.31	*692.51	258.22	*0.491	*1.373	6313.3
15768.8	22.8	340.07		29.64	13.32	0.36
55002.26	8103.45	5968.83	3528.23	*33.406	59.96	
139.79	0.35	4336.24	202.75	6.67	9.36	3139.5
77675.43	13.52	488.91		14.62	16.64	0.45
28194.7	16032.93	14721.73	2274.14	*33.406	39.37	
370.51	0.99	4155.06	258.22	7.36	*1.373	5333.07
3541.91	14.54	484.91		22.32	17.38	0.6
18755.14	20748.29	24864.46	2051.56	*33.406	124.67	
70.64	0.34	*692.51	*26.929	*0.491	*1.373	4630.85
3235.82	17.87	309.66		6.96	17.17	0.38

Table4.txt

14060.68	16744.26	21698.77	5135.34	*33.406	52.84	
*10.766	0.63	*692.51	*26.929	*0.491	*1.373	6350.78
2453.16	18.7	494.89		10.92	17.7	0.69
14182.91	6126.48	12096.96	2762.51	*33.406	114.2	
*10.766	0.58	*692.51	199.82	3.13	*1.373	6773.09
4477.59	13.19	598.37		13.47	21.99	0.58
26432.81	25172.34	5835.91	2340.73	*33.406	84.89	
*10.766	0.33	*692.51	350.82	3.13	*1.373	7118.68
33662.5	10.16	726.12		26.18	37.17	0.36
38343.89	17722.59	5824.83	3124.99	*33.406	78.82	
486.84	0.26	*692.51	*26.929	*0.491	*1.373	6459.56
12313.76	10.26	278.62		8.25	10.98	0.31
37623.09	9491.87	3769.93	5196.5	*33.406	37.45	
500.65	0.41	*692.51	*26.929	*0.491	*1.373	6467.96
98746.25	16.52	324.94		18.3	24.53	0.62
37929.3	7896.77	7769.13	4580.42	*33.406	79.07	
*10.766	0.41	*692.51	185.14	3.49	*1.373	6359.13
5374.72	15.56	655.33		12.04	25.67	0.6
13361.55	29481.62	5157.24	3876.93	*33.406	34.11	
306.7	0.87	*692.51	217.39	*0.491	*1.373	8022.7
11745.39	36.18	1049.35		33.64	28.85	0.51
10376.03	8575.97	8714.19	3715.34	*33.406	97.31	
44.76	0.49	*692.51	*26.929	*0.491	*1.373	4332.4
43721.84	45.7	607.93		8.19	20.99	0.42
10737.58	10112.58	15695.56	2678.98	*33.406	22.67	
84.16	0.34	*692.51	*26.929	*0.491	*1.373	7569.47
22294.84	15.13	395.12		17.53	26.43	0.51
19584.14	9403.21	6718.71	3100.58	*33.406	86.04	
*10.766	0.33	*692.51	*26.929	*0.491	*1.373	5061.92
18078.61	13.23	324.94		14.15	31.75	0.35
8921.03	2859.53	8573.34	1615.19	*33.406	28.51	
392.01	0.31	4155.06	199.82	60.29	*1.373	4894.01
54863.75	14.54	534.41		17.93	30.67	0.4
15269.28	14373.83	11947.61	1354.66	*33.406	60.19	
469.49	0.31	*692.51	226.16	69.86	*1.373	6434.39
74112.02	15.19	592.61		10.01	74.95	0.42
28983.8	9935.21	12693.67	1323.74	*33.406	69.29	
*10.766	0.67	8015.56	240.75	11.73	11.19	4701.8
54517.17	14.16	424.11		16.54	17.7	0.47
26108.34	8132.98	20286.15	2010.68	*33.406	43.99	
*10.766	0.23	*692.51	*26.929	*0.491	*1.373	6275.9
2764.78	11.14	374.15		10.39	24.53	0.36
20443.64	10733.5	3701.47	2592.48	*33.406	63.62	
265.62	0.31	*692.51	*26.929	*0.491	*1.373	5525.84
23808.14	42.01	419.99		6.26	15.34	0.44
23243.24	15795.85	17903.05	2638.9	*33.406	69.87	
63.74	0.5	4875.71	234.91	*0.491	*1.373	6543.72
50376.57	36.42	594.53		30.36	37.51	0.44

Table4.txt

40078.53	8635.05	12267.56	3771.87	*33.406	28.02	
317.76	0.52	*692.51	164.52	3.13	*1.373	8151.64
3541.91	34.04	454.72		10.76	15.99	0.35
16177.63	14966.25	5625.08	4833.2	*33.406	209.91	
103.88	0.47	6637.57	237.83	3.13	11.19	6151.85
42375.52	16.59	917.06		25.62	23.17	0.45
26918.96	34746.42	7234.08	4277.29	*33.406	60.85	
368.71	0.62	*692.51	167.47	*0.491	*1.373	6405.08
38894.11	31.36	504.83		15.67	14	0.52
35609.93	21252.82	7157.46	4323.06	*33.406	131.47	
108.19	0.84	5232.26	269.84	4.57	10.27	5325.26
2764.78	23.95	759.17		31.44	76	0.53
22877.79	12597.35	4517.86	3989.07	*33.406	79.32	
*10.766	0.76	*692.51	*26.929	5.28	*1.373	7740.37
16897.96	25.49	470.87		16.76	19.77	0.47
20592.45	12390.18	6377.52	1774.14	*33.406	131.25	
88.6	0.21	*692.51	*26.929	*0.491	*1.373	5585.33
5212.69	13.93	468.86		11.04	20.39	0.42
9660.28	11561.68	4551.65	3903.67	*33.406	39.64	
*10.766	0.43	*692.51	246.57	6.67	*1.373	11660.88
252141.5	26.03	2894.61		14.22	43.86	0.43
22199.63	2389.91	6090.5	3118.48	*33.406	17.73	
148.03	0.82	*692.51	*26.929	4.57	*1.373	6854.54
12366.37	39.99	335.76		16.63	10.98	0.47
40622.12	2654.02	9524.54	2907.63	*33.406	62.29	
*10.766	0.35	*692.51	223.24	3.13	*1.373	3468.71
146095.13	21.99	540.28		32.4	25.48	0.59
29485.53	14373.83	7921.61	3051.82	*33.406	56.4	
*10.766	0.32	5054.28	191.02	11.73	*1.373	7524.77
28730.34	57.62	357.19		8.09	11.46	0.42
9963.05	1101.4	35430.85	221.76	*33.406	11.53	
*10.766	0.62	*692.51	164.52	*0.491	*1.373	6127.15
12523.52	27.9	456.74		20.28	29.95	0.61
19490.29	12094.26	3127.41	2429.73	*33.406	41.32	
93	0.63	4155.06	301.74	3.13	*1.373	5411.46
6299.38	17.86	413.8		48.24	23.36	0.65
18451.83	11413.77	9373.55	2065.73	*33.406	33.99	
75.18	0.49	*692.51	*26.929	*0.491	*1.373	9137.98
33356.13	17.46	278.62		13.78	15.12	0.35
18603.62	5802.2	59254.67	3226.1	*33.406	105.34	
190.33	0.77	*692.51	170.42	*0.491	18.53	10089.45
19838.55	27.11	1190.45		88.92	80.24	0.67
29790.01	29511.35	40646.52	5044.71	*33.406	69.14	
339.73	0.3	*692.51	164.52	3.86	*1.373	6760.26
21124.13	14.98	582.99		12.66	26.81	0.63
7348.82	12804.54	9265.62	2946.44	*33.406	33.83	
125.19	0.66	*692.51	794.07	*0.491	11.81	9471.59
37494.34	27.33	582.99		135.05	16.96	0.48

Table4.txt

24299.08	34270.32	15050.05	3845.2	*33.406	65.96	
84.16	0.41	*692.51	176.31	*0.491	*1.373	7302.91
60023.79	31.07	327.11		15.39	17.28	0.49
36076.68	8812.29	15124.16	2053.14	*33.406	132.32	
118.85	0.58	4155.06	164.52	8.04	*1.373	5585.33
6925.59	48.03	260.56		17.81	15.34	0.43
13278.53	5124.48	10342.21	3178.76	*33.406	106.4	
204.12	0.41	*692.51	*26.929	*0.491	*1.373	4601.09
12418.86	24.39	464.83		28.87	36.05	0.41
9542.76	15469.91	5190.74	2730.36	*33.406	55.91	
72.92	0.42	*692.51	193.95	21.09	9.96	8398.16
18511.74	16.51	278.62		39.35	13.78	0.91
34462.24	4977.21	6278.26	5861.91	*33.406	10.8	
429.24	0.51	*692.51	*26.929	*0.491	*1.373	11258.52
17933.11	47.14	337.92		6.1	11.7	0.41
42950.63	4623.86	11221.07	3820.18	*33.406	30.03	
*10.766	0.61	*692.51	*26.929	*0.491	9.06	2971.84
14306.62	11.25	305.27		14.5	12.52	0.45
8799.26	5271.78	8876.56	2410.64	211.32	54.31	
*10.766	1.05	5232.26	193.95	3.86	*1.373	6653.77
21766.38	36.18	413.8		17.99	18.33	0.38
65502.69	13130.16	7540.09	2337.56	*33.406	54.01	
172.39	0.26	*692.51	176.31	5.98	*1.373	7524.77
28296.09	15.85	434.36		22.69	62.91	0.3
18774.07	10112.58	10556.87	1930.62	*33.406	31.86	
*10.766	0.77	5232.26	229.08	9.4	8.46	6251.01
29091.93	21.79	318.41		15.77	17.28	0.41
31615.7	7040.84	8399.82	1401.08	*33.406	50.77	
*10.766	0.56	*692.51	205.68	*0.491	*1.373	2975.11
34141.58	17.8	766.48		32.46	25.48	0.43
8578.12	14255.36	3449.69	4421.64	*33.406	17.55	
765.77	1.06	*692.51	234.91	*0.491	21.86	6164.21
65898.27	15.69	466.84		25.87	32.29	0.55
38235.7	14373.83	6300.32	2904.39	*33.406	14.2	
*10.766	0.39	7157.17	188.08	25.17	151.59	4833.43
2572.3	11.64	604.11		10.11	25.67	0.76
19809.02	5095.03	3495.56	3157.56	6428.38	46.98	
141.85	0.33	*692.51	*26.929	*0.491	27.31	9977.56
4506.98	32.79	853.15		18.74	14.12	0.44
36364.07	19353.78	8963.09	4209.61	552.13	148.84	
*10.766	0.53	*692.51	164.52	3.13	*1.373	6209.62
2611.39	14.56	357.19		13.35	17.49	0.52
10961.11	16536.77	4326.06	2010.68	*33.406	23.44	
176.4	0.38	*692.51	*26.929	*0.491	9.36	8963.61
17167.03	30.41	346.51		18.43	28.02	0.41
17150.06	11591.27	9610.76	4883.34	*33.406	76.08	
*10.766	0.92	*692.51	182.2	40.16	10.27	3279.46
126361.12	6.88	296.44		17.19	17.07	0.8

Table4.txt

8329.28	6863.81	7091.75	661.23	*33.406	12.64	56.73	0.47	*692.51
188.08	*0.491	*1.373	5975.68	8271.61	35.99	651.57	14.22	31.21
0.36	29986.99	16447.85	22415.81	2923.79	*33.406	75.32	88.6	0.43
*692.51	*26.929	*0.491	*1.373	6675.01	28858.88	18.06	506.81	36.54
42.38	0.51	34605.62	5389.62	10127.34	1337.65	*33.406	51.15	*10.766
0.28	*692.51	*26.929	4.57	*1.373	4985.36	4085.85	17.98	411.73
10.51	20.79	0.4	32743.1	10378.66	5413.76	5243.77	*33.406	39.53
77.44	0.38	*692.51	*26.929	5.98	*1.373	5008.29	13006.27	22.7
386.76	16.39	41.47	0.58	11315.11	12538.16	5525.04	2323.28	*33.406
122.3	176.4	0.56	5586.56	182.2	12.72	88.18	6275.9	5999.39
10.29	563.66	8.91	50.74	0.84	9870.31	8280.63	7354.38	4073.05
2414.3	48.99	70.64	0.27	*692.51	*26.929	3.86	*1.373	4266.95
27275.01	13.85	204.66	7.56	10.62	0.29	12881.8	3741.14	6399.56
4057.91	*33.406	26.56	180.39	2.32	*692.51	*26.929	3.13	20.52
9284.47	13362.52	49.11	867.43	33.83	10.98	0.58	40549.59	12893.35
27785.29	2455.2	*33.406	113.7	*10.766	0.31	*692.51	164.52	*0.491
*1.373	7201.78	7204.93	12.89	342.22	32.28	22.58	0.59	6750.39
10230.84	13820.4	5214	*33.406	128.21	172.39	0.26	*692.51	*26.929
*0.491	*1.373	5427.18	2289.44	30.47	411.73	28.13	32.29	0.36
43096.69	11443.35	6641.76	3758.56	*33.406	42.48	354.26	0.43	*692.51
*26.929	*0.491	*1.373	5458.68	1850.02	49.79	386.76	12.1	15.56
0.51	19019.7	14492.3	12491.34	4302.71	*33.406	163.78	*10.766	0.32
*692.51	176.31	*0.491	*1.373	5050.41	146506.56	10.63	411.73	13.47
17.07	0.38	8725.84	8251.1	6123.66	3561.26	*33.406	53.63	127.29
0.59	*692.51	188.08	*0.491	*1.373	8151.64	1941.96	24.73	799.19
21.61	19.26	0.51	24843.19	10940.51	4382.53	2965.87	*33.406	85.14
*10.766	0.5	*692.51	*26.929	*0.491	*1.373	4541.75	6831.19	17.23
357.19	9.85	14.56	0.56	8076.9	9403.21	4585.43	3455.69	*33.406
49.79	*10.766	0.34	*692.51	229.08	3.49	*1.373	1518.32	6249.9
11.86	204.66	40.06	43.53	0.43	30309.25	13041.36	6013.09	3856.89
*33.406	67.72	1053.74	1.21	*692.51	229.08	*0.491	*1.373	6371.65
1117.1	14.69	380.46	26.55	11.93	0.57	44524.37	7808.2	7572.83
2650.12	*33.406	74.38	94.31	2.05	*653.597	285.04	4.44	*1.363
9628.54	23889.96	24.92	538.53	13.17	29.53	0.89		

Table4.txt

32269.28	9183.01	10773.25	6669.4	*34.389	10.24	
*13.654	1.15	*653.597	229.06	5.53	*1.363	13647.46
6132.89	13.51	527.45		7.58	43	0.96
57623.27	10143.03	20577.45	2427.72	*34.389	80.49	
40.96	0.63	8942.83	266.48	5.81	*1.363	5776.71
118181.57	29.52	254.57		14.23	50	0.86
39454.74	2822.91	9645.61	3595.32	*34.389	46.6	
*13.654	0.85	*653.597	241.58	*0.601	*1.363	5589.29
35999.91	39.47	482.96		24.46	24.67	0.83
25239.49	6330.13	4717.14	3128.62	*34.389	75.72	
55.01	0.64	5661.76	229.06	4.99	*1.363	5119.25
30316.88	13.27	258.48		22.48	56.18	0.86
46195.51	14774.07	9483.99	917.23	*34.389	73.3	
96.4	0.96	*653.597	184.82	4.99	*1.363	8602.15
25143.66	33.61	436.26		5.18	23.11	1.24
30792.21	3214.43	4429.92	1479.57	*34.389	66.01	
207.65	0.9	*653.597	247.82	9.84	12.25	4469.49
5011.03	18.46	419.35		69.29	66.28	0.89
18261.45	19193.51	12792.34	2796.35	*34.389	86.97	
311.34	1.13	*653.597	235.33	7.7	11.92	7601.06
154530.79	25.15	387.26		20.52	29.9	1.19
8726.91	7108.72	8059.72	389.6	*34.389	33.14	
*13.654	1.14	*653.597	222.79	*0.601	*1.363	7352.43
91516.72	35.24	413.7		13.7	26.57	1.01
33914.46	6973.71	8385.75	2544.38	*34.389	56.01	
*13.654	1.36	*653.597	312.72	4.44	*1.363	8972.78
127246.84	33.73	324.35		8.9	46.78	0.94
29084.68	3673.31	5545.63	2846.01	*34.389	17.54	
*13.654	1.13	*653.597	281.95	*0.601	12.42	6742.17
17810.43	40.25	778.31		39.36	199.24	1.13
35973.22	4926.65	16995.85	6584.75	*34.389	24.13	
*13.654	3.97	*653.597	232.2	9.31	10.94	5375.15
86006.06	41.25	285.75		6.93	36.76	1.22
55869.94	3426.7	14433.31	351.15	*34.389	6	
70.7	1.05	*653.597	260.27	*0.601	*1.363	8972.78
136323.44	37.61	383.48		5.83	41.77	1.01
50298.89	10275	10970.91	4887	*34.389	29.45	
476.13	0.23	*656.313	*27.445	*6.138	9.43	6908.36
6250.96	14.08	331.06		8.56	36.47	*0.029
18043.84	8385.66	5800.54	3908.72	1941.5	85.37	
326.83	3.88	*656.313	183.34	*6.138	22.88	13256.38
162098.82	50.83	672.87		13.21	13.32	*0.029
31692.15	14611.79	25478.32	5672.53	2334.14	137.24	
*13.654	2.33	4584.83	321.9	8.78	14.41	10234.64
77827.3	59.53	527.45		15.68	53.46	1.38
28242.83	4719.3	4207	3365.31	*34.389	18.1	
*13.654	0.64	*653.597	*27.335	*0.601	*1.363	7380.93
110609.24	17.65	291.56		8.45	23.31	0.59

Table4.txt

36326.61	10307.97	136895.06	2283.03	*34.389	39.4	
*13.654	1.03	*653.597	178.44	*0.601	*1.363	7853.38
5282.38	27.98	471.78		11.63	55.43	1.14
24109.45	2463.99	9359.56	1342.96	*34.389	36.6	
*13.654	0.54	*653.597	235.33	*0.601	*1.363	7390.44
29073.76	33.98	293.5		24.17	77.3	0.75
29522.21	2607.93	2888.16	4920.33	*34.389	12.56	
*13.654	1.25	*653.597	254.05	*0.601	8.98	9548.03
35608.54	25.22	250.65		8.28	27.88	0.76
87258.03	8784	24961.84	2313.25	*34.389	82.11	
*13.654	0.95	*653.597	241.58	3.61	52.94	8404.45
217265.26	47.86	697.32		9.74	82.5	1.04
34839.34	16831.83	13062.2	3549.51	1060.66	43.88	
*13.654	0.55	*653.597	*27.335	*0.601	*1.363	6637.38
14676.72	20.24	289.63		9.46	35.73	0.86
64373.28	10176.03	25954.82	3696.03	*34.389	120.72	
48.07	1.38	*653.597	278.86	*0.601	8.5	7442.85
17480.23	18.83	571.65		19.23	48.43	0.77
15710.14	8149.93	9247.5	1720.16	*34.389	59.02	
*13.654	0.54	*653.597	172.04	*0.601	*1.363	2592.88
1452.43	21.71	415.59		12.68	46.62	0.74
21581.98	25816.19	9085.5	3756.29	*34.389	112.05	
43.35	2.33	*653.597	184.82	*0.601	9.96	9574.83
37887.49	78.65	717.18		13.56	41.69	2.33
52982.25	18652.47	14359.96	3811.35	*34.389	60.32	
55.01	0.84	*653.597	216.49	*0.601	*1.363	9403.93
18517.72	20.01	486.68		17.02	68.27	0.89
48990.17	5955.69	6135.56	1756.34	*34.389	14.21	
123.06	1.34	*653.597	303.51	*0.601	9.96	7276.66
41836.95	20.28	411.82		21.3	108.92	1.34
72588.76	5202.27	5261.93	4790.95	*34.389	29.17	
*13.654	1.12	*653.597	*27.335	*0.601	*1.363	6939.96
14962.61	30.23	343.51		15.5	51	0.69
41653.41	9249.41	9483.99	3703.11	*34.389	68.08	
*13.654	0.77	5234.78	216.49	8.78	*1.363	4860.18
3428.15	21.71	549.59		6.44	72.13	1.07
40538.03	2101.71	13723.79	1961.15	*34.389	72.14	
*13.654	0.82	*653.597	254.05	*0.601	*1.363	14627.66
20056.03	40.74	183.2		29.51	67.35	0.83
35548.56	2028.8	28032.79	981.43	*34.389	16.31	
385.28	0.69	*656.313	340.51	*6.138	9.12	4987.89
43168.82	57.38	425.48		11.84	29.42	0.33
35177.61	14790.72	20545.86	4290.61	1514.67	74.8	
262.08	0.41	*656.313	263.92	*6.138	18.77	7194.33
86805.19	26.87	467.21		8.81	15.77	*0.029
29592.46	11659.37	17693.23	2744.36	1521.81	83.23	
134.58	1.18	6259.77	306.87	*6.138	13.14	9176.59
199685.76	43.94	1061.44		26.04	43.71	0.57

Table4.txt

96120.47	11507.05	18454.28	3002.69	4863.77	138.5	
387.33	0.2	4733.45	311.11	*6.138	31.51	5725.06
49584.02	21.81	447.21		18.16	28.75	*0.029
21618.96	10250.79	115330.99	4136.52	5160.37	37.56	
333.18	1.52	7722.36	398.14	*6.138	20.66	7520.86
3473.83	43.29	812.14		14.05	12.3	*0.029
133358.12	14999.23	32858.98	3068.09	2572.67	160.06	
181.46	1.8	4802.84	222.79	*0.601	8.5	8129.26
2943.88	37.53	635.64		20.37	37.61	1.88
46299.17	4337.65	11044.99	3934.31	*34.389	37.78	
137.05	0.41	6753.4	406.26	356.64	18.77	36598.31
3873.96	55.08	8636.17		12.75	25.16	1.29
35208.03	7818.82	43772.63	6664.44	1698.62	94.76	
217.34	*0.01	4733.45	272.6	*6.138	10.04	7781.19
12846.42	24.61	413.76		14.89	15.29	*0.029
55638.44	9508.88	21223.29	1993.72	1747.6	228.35	
*9.827	0.37	*656.313	272.6	*6.138	16.88	5953.75
12144.67	13.62	574.71		28.74	61.47	*0.029
23953.13	13714.17	11190.93	2559.23	6058.24	67.53	
228.66	0.59	4733.45	365.39	*6.138	11.9	7817.4
12001.37	16.79	438.86		21.91	14.96	*0.029
43633.36	10343.17	10959.42	1258.88	13277.45	94.39	
75.07	0.96	*653.597	466.7	*0.601	12.25	9855.73
34080.92	45.34	1082.56		18.73	26.01	1.05
28572.77	17311.97	8034.61	4079.39	*34.389	30.08	
98.49	1.36	4802.84	436.82	4.44	9.63	10407.19
123869.87	36.87	831.94		16.42	64.13	1.03
24260.74	10966.21	6924.58	2921.54	*34.389	11.48	
101.64	0.53	*656.313	298.36	*6.138	16.88	7808.34
96161.28	70.48	482.18		10.42	15.29	*0.029
49222.39	8699.01	10111.46	3549.16	1747.6	145.29	
70.7	0.81	*653.597	213.34	*0.601	*1.363	8010.5
1944.37	13.58	232.95		10.26	11.99	0.49
41931.84	4337.65	5132.62	1036.07	*34.389	60.46	
90.09	4.37	*653.597	260.27	*0.601	9.96	12141.18
14564.07	45.55	492.25		6.58	56.48	1.5
31261.73	3953.88	12669.61	3781.14	*34.389	27.54	
133.06	1.95	*653.597	266.48	*0.601	*1.363	5296.21
7832.69	33.66	326.27		16.71	48.2	1.28
48714.48	3107.97	9110.43	1721.8	*34.389	28.34	
83.13	0.15	4733.45	201.69	*6.138	9.43	7317.14
2308.79	46.89	442.2		9.14	46.41	*0.029
23147.99	9167.06	14470.93	3317.72	2186.51	89.97	
111.95	0.38	6259.77	323.76	*6.138	21.3	10192.69
37608.47	55.7	805.69		85.3	35.71	*0.029
25230.98	10926.53	20050.44	912.54	1172.73	107.02	
158.96	0.33	*656.313	670.14	*6.138	19.4	6656.86
98961.19	35.56	538.47		30.75	41.46	*0.029

Table4.txt

54642.06	12024.21	16957.22	1749.74	814.3	28.27	
*13.654	1.06	4365.35	238.46	13.02	*1.363	11426.28
13904.07	45.29	2066.15		23.17	54.37	1.48
28389.55	8049.55	6696.16	2782.67	*34.389	33.83	
374.56	0.95	*653.597	168.83	*0.601	*1.363	8993.59
13554.85	22.43	276.04		9.14	45.02	0.78
45607.87	5476.98	17531.99	3142.48	*34.389	23.84	
92.2	1.18	*653.597	197.54	*0.601	*1.363	5168.4
5079.68	22.44	434.38		15.54	44.54	0.72
56419.95	5133.45	10278.35	1613.53	*34.389	23.39	
*13.654	1.83	*653.597	197.54	*0.601	8.98	4884.25
29693.21	24.08	5417.39		23.38	34.34	1.37
60134.43	8584.08	12792.34	1677.46	*34.389	60.98	
455.77	1.27	*653.597	165.62	*0.601	*1.363	8208.88
4390.05	38.11	670.16		16.95	46.06	1.17
71300.82	19416.04	7908.98	4814.93	*34.389	73.91	
108.83	0.92	*653.597	175.24	*0.601	*1.363	9531.96
22066.86	10.24	632		11.17	77.57	0.9
40538.03	11981.84	9185.21	3811.35	*34.389	60	
673.92	*0.01	*637.141	189.4	*2.564	14.54	9836.42
11219.47	28.32	267.79		16.46	20.61	*0.029
10084.38	1966.99	15275.68	2103.6	1973.81	62.35	
102.65	0.69	5873.54	172.04	3.88	190.15	6296.06
47668.4	17.49	727.99		10.75	78.73	1.27
43980.69	3602.96	10501.19	1721.8	5754.35	23.51	
228.66	*0.01	*656.313	306.87	*6.138	12.52	4796.53
67502.26	25.72	776.65		10.68	23.02	*0.029
59059.39	9694.85	36078.01	1721	2347.49	27.1	
795.27	0.41	*656.313	*27.445	*6.138	*1.342	5752.96
3262.54	16.65	221.04		13.82	18.81	*0.029
12988.97	3405.23	7636.26	1533.31	1007.45	107.06	
228.66	*0.01	4205.98	509.65	*6.138	12.21	5978.03
14486.59	20.12	317.45		59.98	71.17	*0.029
22564.9	4585.29	17788.74	1027.54	2367.49	63.94	
180.35	0.25	*656.313	306.87	*6.138	8.21	4748.19
17206.04	15.26	189.54		20.82	18.35	*0.029
38693.18	8448.42	22125.27	434.86	2084.97	52.14	
*13.654	0.84	*653.597	*27.335	*0.601	*1.363	6278.31
4058.9	33.83	242.8		9.21	24.28	0.86
25949.89	4372.43	7606.96	3145.95	*34.389	70.28	
366.67	0.12	*656.313	*27.445	*6.138	8.21	7614.66
2172.16	24.7	8580.24		6.44	19.04	*0.029
22921.59	4552.02	9150.88	2785.85	1607.05	41.84	
255.46	0.19	*656.313	255.19	*6.138	11.28	7740.53
10865.66	59.18	281.54		18.88	9.65	*0.029
64361.26	5573.28	17693.23	3305.86	1927.76	42.45	
*13.654	1.28	5234.78	172.04	10.91	16.24	4629.81
3069.31	38.51	211.18		17.17	32.59	1.1

Table4.txt

17530.94	3883.86	11686.1	2205.96	211.06	54.44				
163.75	1.36	6259.77	259.56	*6.138	56.9	5193.5			
18231.82	51.3	296.96		8.17	19.19	0.47			
66016.7	5898.73	17709.16	1204	1406.98	58.33				
61.81	0.84	4365.35	178.44	9.58	10.61	6429.89			
2879.92	24.96	354.96		10.05	36.76	1.06			
84797.43	11360	8310.58	2175.87	*34.389	67.42				
114.5	1	*656.313	242.01	*6.138	14.38	12823.56			
3576.49	38.53	650.04		11.55	6.07	0.63			
97150.15	5703.67	30869.19	1749.74	4994.61	37.48				
94.31	0.88	*653.597	382.69	*0.601	12.25	6251.71			
44108.7	14.79	662.9		23.52	40.87	0.97			
122519.34	2822.91	8185.21	1876.73	*34.389	22.81				
*13.654	0.34	*653.597	235.33	5.26	*1.363	10218.01			
3655.04	32.67	211.18		11.38	21.33	0.67			
109025.27	2283.3	8335.64	4935.16	*34.389	28.34				
*13.654	3.81	*653.597	172.04	*0.601	*1.363	7409.48			
31434.99	19.02	215.15		11.13	28.07	1.39			
82561.19	5614.01	10637.26	667.62	*34.389	31.66				
50.4	1.31	4365.35	297.36	4.44	*1.363	6403.03			
2104.59	49.19	281.87		23.24	121.49	0.85			
121739.02	4650.06	7732.89	3166.76	*34.389	38.12				
736.06	0.85	11483.87	315.78	10.91	156.56	8591.96			
4754.3	17.93	1315.2		13.35	84.43	2.2			
60065.6	6023.87	22309.09	1362.44	6301.66	26.09				
85.84	1.49	7736.34	487.53	8.78	16.58	16764.53			
4006.5	53.49	690.08		15.61	79.34	0.81			
146999.84	13154.89	18628.3	3100.91	*34.389	25.68				
1246.95	*0.01	4733.45	183.34	*6.138	43.81	4987.89			
25014.42	25.69	587.85		9.59	21.13	*0.029			
22467.43	5866.26	31331.84	1913.22	5053.91	83.11				
50.4	0.88	*653.597	346.31	5.53	10.61	7755.9			
5125.14	25.21	270.19		10.26	38.95	0.6			
69390.32	10637.4	21016.24	4601.68	*34.389	77.38				
117.04	2.75	*656.313	164.67	*6.138	13.14	10754.83			
14314.78	57.22	513.68		7.08	15.45	0.76			
52772.76	8322.86	12951.08	1199.3	3103.95	168.63				
*13.654	0.53	6084.24	337.17	7.16	20.63	6673.75			
74526.01	27.74	549.59		11.1	33.12	0.73			
60685.18	11752.97	17117.72	3004.17	389.32	90.24				
161.36	0.59	*656.313	183.34	*6.138	9.43	7587.81			
4249.6	50.39	356.5		10.07	16.4	*0.029			
30706.32	6480.28	51970.47	2196.05	1733.63	51.03				
34.26	0.64	6753.4	219.77	*6.138	11.9	6083.68			
34175.48	38.86	398.65		4.21	24.52	*0.029			
18994.2	5311.6	15430.39	2118.17	1844.95	140.56				
74.98	0.61	6259.77	183.34	*6.138	10.66	9947.72			
4157.7	28.29	370.02		16.69	16.56	0.3			

Table4.txt

157671.14	8542.47	33304.17	*41.29	3078.38	11.15	
527.24	0.23	*656.313	348.84	*6.138	52.31	5590.32
27875.5	20.19	224.52		10.88	12.81	*0.029
61186.81	7184.39	14086.33	3007.72	1290.68	63.67	
185.04	*0.01	6507.41	210.76	*6.138	9.74	4897.5
8691.42	12.94	331.06		12.3	24.03	*0.029
31322.91	10127.49	1763.73	4096.39	2664.5	32.54	
40.96	0.72	5234.78	184.82	8.78	*1.363	5283.79
33517.51	14.38	473.65		13.38	62.39	0.89
19701.02	2028.8	15166.33	2966.27	*34.389	21.72	
40.96	2.88	*653.597	367.56	*0.601	8.98	8561.42
8788.34	70.08	562.47		32.13	96.14	1.24
43946.02	15901.31	10921.51	2642.84	*34.389	136.01	
*13.654	1.08	4365.35	266.48	*0.601	*1.363	6637.38
16670.22	19.76	268.25		11.73	36.84	1.31
25239.49	2210.78	4691.09	2299.82	*34.389	18.02	
*9.827	0.64	5250.73	556.22	*6.138	34.73	6284.8
2172.16	63.48	906.87		15.42	23.81	*0.029
113487.39	42344.35	15758.01	3681.08	1113.07	148.72	
170.9	0.13	4205.98	192.55	*6.138	11.28	7361.22
10217.11	46.18	267.79		12.1	27.52	*0.029
77203.05	4916.72	12261.64	3936.44	2294.02	91.08	
415.94	*0.01	*656.313	246.42	*6.138	8.21	8435.17
10916.52	16.2	450.55		15.61	20.83	*0.029
13138.41	6897.18	11102.03	2974.24	2016.85	17.01	
*13.654	1	*653.597	300.44	*0.601	*1.363	8858.75
1775.47	23.26	482.96		21.19	78.11	0.92
27765.02	2715.55	9906.4	6215.57	*34.389	16.66	
*13.654	0.73	*653.597	188	*0.601	*1.363	5325.24
5458.73	18.54	215.15		9.46	46.3	0.7
26952.93	3036.86	3505.84	3156.36	*34.389	15.2	
52.71	1.35	*653.597	178.44	4.99	9.63	4956.73
6688.57	39.25	753.18		98.88	175.75	1.29
43842.02	31237.88	7606.96	4178.35	*34.389	106.27	
*13.654	0.99	*653.597	229.06	*0.601	*1.363	5927.56
12881.86	30.5	600.97		12.29	87.73	1
41583.78	12079.84	8661.04	1734.95	*34.389	38.27	
782.56	0.35	*656.313	174.05	*6.138	9.43	2524.27
30921.3	18.93	145.25		9.59	16.09	*0.029
14858.85	3712.03	13190.24	1746.55	2334.14	143.23	
538.9	1.81	4205.98	430.46	*6.138	65.48	6392.59
73975.7	20.47	597.69		29.31	23.6	*0.029
33531.23	11171.3	31071.7	1024.43	1030.22	59.62	
*9.827	*0.01	5250.73	228.71	*6.138	17.51	8862.11
2928.24	13.28	224.52		34.25	25.02	*0.029
20133.26	2678.14	12951.08	1511.13	2585.82	31.39	
264.28	*0.01	4733.45	255.19	*6.138	13.14	7754.08
2504.69	26.96	324.26		21.81	35.2	*0.029

Table4.txt

16594.13	3712.03	12848.26	1732.17	2300.72	92.8	
50.4	1.73	*653.597	291.21	*0.601	8.66	7936.67
20620.01	43.42	479.23		36.79	220.38	1.75
37876.73	3848.82	10129.65	3987.95	*34.389	30.64	
*13.654	0.65	*653.597	197.54	*0.601	*1.363	5534.39
13723.58	26.47	266.29		22.38	70.66	1.26
28352.89	3107.97	10736.17	3128.62	*34.389	25.6	
*13.654	0.6	*653.597	181.63	*0.601	*1.363	8169.03
36279.85	13.13	362.58		10.05	68.84	0.85
19383.43	3249.87	9980.85	906.01	*34.389	28.26	
262.11	1.21	*653.597	210.19	7.16	*1.363	4956.73
78924.57	20.12	289.63		10.19	61.22	0.73
18984.62	4511.38	55847.21	3253.66	*34.389	11.01	
50.4	1.34	18345.96	502.38	22.89	343.08	8745.41
206400.41	63.62	874.66		21.48	75.59	2.58
38859.4	2283.3	7101.89	2828.88	13184.62	4.85	
77.25	0.72	*653.597	*27.335	*0.601	*1.363	9192.41
10438.29	18.12	234.93		8.55	51.77	0.69
31261.73	1955.73	11735.35	2973.15	*34.389	7.46	
127.12	0.67	6259.77	340.51	*6.138	19.4	5441.19
217627.4	14.65	666.35		12.56	12.73	0.45
32735.68	8948.92	19208.79	3760.2	2159.51	60.21	
464.21	0.63	4733.45	332.16	*6.138	10.66	5078.89
3776.45	21.87	307.21		18.13	34.62	*0.029
23599.52	3336.69	6095.87	3356.72	1052.91	24.48	
424.05	0.19	6259.77	263.92	*6.138	12.52	5721.08
41450.97	7.55	308.92		28.91	17.35	*0.029
22109.29	4552.02	42755.53	850.56	1775.5	55.78	
569.8	0.12	5250.73	281.23	*6.138	14.38	4026.67
60344.06	14.16	422.13		16.72	15.69	*0.029
28846.74	7311.69	15397.54	4419.09	1246.65	111.97	
111.95	0.84	*656.313	298.36	*6.138	15.01	13103.39
2928.24	39.15	300.38		14.96	5.11	*0.029
34568.7	6480.28	22399.09	2780.87	1831.09	141.93	
226.03	0.59	3921.58	*27.335	*0.601	*1.363	5674.18
13697.69	27.3	351.15		6.93	58.27	0.82
56076.19	12112.5	9197.67	3414.3	*34.389	31.19	
168.14	1.18	4365.35	184.82	6.62	*1.363	5798.16
14108.86	11.57	7125.36		17.1	38.95	0.82
6296.3	3953.88	13282.85	2780.96	*34.389	43.51	
*13.654	0.82	*653.597	229.06	*0.601	*1.363	6528.78
29802.02	22.75	199.22		8.45	19.08	0.53
26210.65	6669.34	5866.76	2097.44	*34.389	70.56	
*13.654	1.24	*653.597	321.9	*0.601	*1.363	4442.33
23412.57	12.49	417.47		12.15	50.69	1.01
93628.97	17631.65	7076.58	3563.6	*34.389	22.89	
*13.654	1.72	*653.597	235.33	*0.601	*1.363	9542.67
15477.56	45.47	358.78		10.33	34.17	1.5

Table4.txt

51193.71	5339.73	12755.53	3628.85	*34.389	33.68	
*13.88	3.22	*611.926	680.28	15.23	46.31	5171.92
23200.15	17.23	768.68		16	27.99	1.16
140665.24	8567.4	15320.67	986.12	1791.79	62.36	
64.39	1.51	*611.926	267.46	7.26	13.94	15119.71
117806.55	55.7	442.23		16.6	*2.511	0.62
56247.06	13930.42	23303.32	3954.67	4779.82	33.03	
*41.51	0.18	*1970.97	164.52	*16.134	*1.329	8829.03
119235.66	37.49	358.71		2.36	8.75	0.21
42815.41	5968.36	20791.45	5341.22	*33.371	20.08	
*41.51	0.12	*1970.97	201.47	*16.134	*1.329	4691.7
9510.21	20.13	241.33		1.85	7.75	0.18
79312.06	3492.17	38229.33	2415.87	*33.371	51.67	
*10.36	0.27	*677.552	*27.835	5.91	*1.385	8009.91
43026.39	16.46	412.82		21.66	1.85	0.24
58774.81	4976.01	13377.65	3858.3	210.3	64.62	
*10.36	0.12	*677.552	*27.835	*0.496	*1.385	7006.94
7106.51	33.15	321.89		*0.03	3.11	0.24
46884.52	2256.59	19061.07	1657.91	*32.367	42.52	
*10.36	0.2	*677.552	*27.835	*0.496	*1.385	5963.93
18136.75	16.6	302.24		*0.03	3.69	0.22
62667.17	3570	14324.29	2820.52	*32.367	157.73	
*10.36	0.18	*677.552	234.64	*0.496	*1.385	5056.65
7106.51	22.33	386.63		15.36	2.81	0.23
99117.32	10208.6	15172.42	2620.82	*32.367	74.56	
130.3	0.2	*677.552	*27.835	*0.496	*1.385	4667.77
899.46	43.33	302.24		8.43	2.5	0.29
45661.52	3831.98	12870.75	2676.7	*32.367	161.69	
*10.36	0.29	4227.58	*27.835	*0.496	*1.385	5425.36
30919.87	32.96	471.08		*0.03	2.5	0.25
33558.47	6084.6	16750.22	4356.39	*32.367	99.38	
155.49	0.13	*692.174	*27.599	*0.553	*1.373	5976.16
7295.19	26.24	281.02		8.7	*0.712	0.21
27564.64	2826.14	17306.69	2256.95	*33.243	19.64	
59.36	0.23	*692.174	230.64	*0.553	10.92	5033.86
2475.07	23.24	415.99		13.71	9.72	0.26
60798.83	9789.1	10730.93	3493.4	*33.243	27.98	
130.43	0.14	5589.23	258.3	5.3	*1.373	5312.38
38860.48	25.14	235.87		14.78	*0.712	0.19
34729.57	6389.18	26298.32	1621.07	*33.243	41.25	
*36.49	0.19	*644.123	*27.061	*0.591	*1.31	6846.32
5970.33	16.72	224.93		5.48	8.73	*0.029
18753.88	3088.6	6419.84	1488.53	881.67	15.44	
145.13	0.14	*644.123	*27.061	4.18	*1.31	4493.86
2364.65	17.56	220.49		5.13	12.07	0.32
24814.47	1668.46	54747.6	1528.91	297.5	15.76	
118.66	0.18	*644.123	*27.061	*0.591	*1.31	4016.05
989.21	32.5	149.05		8.35	4.17	*0.029

Table4.txt

31517.58	6408.6	879.66	3109.92	1314.27	21.97	
*36.49	0.25	*644.123	*27.061	*0.591	*1.31	8018.71
*135.54	19.26	169.95		4.76	5.3	*0.029
33508.7	2396.9	11344.05	2484.23	917.03	2.38	
*36.49	0.15	8649.81	306.19	28	10.72	5063.86
9321.53	3.68	229.33		7.18	13	*0.029
6571.09	2742.41	5478.58	837.82	1011.36	15.35	
*36.49	0.23	*644.123	*27.061	*0.591	*1.31	4721.87
2129.14	20.09	176.64		9.03	4.17	*0.029
26512.01	4990.3	2642.63	1598.49	1365.44	30.84	
431.09	0.24	7207.66	221.27	4.12	81.45	10742.72
13721	31.85	771.43		13.09	12.53	0.32
45430.45	8402.91	12680.62	4122.45	2166.42	42.84	
*14.11	0.2	*692.174	*27.599	*0.553	12.96	6754.5
18978.6	27.28	547.45		6.08	*0.712	0.3
49752.89	2967.51	72982.56	4409.84	*33.243	41.41	
103.84	0.16	*692.174	258.3	3.72	*1.373	9429.09
11848.16	38.42	422.76		14.07	*0.712	0.19
82779.26	5129.23	17058.64	3987.28	*33.243	21.71	
89.78	0.16	*692.174	202.28	6.82	9.9	5789.04
54649.86	38.89	284.97		10.05	*0.712	0.32
41570.73	2543.8	10349.77	3743.25	*33.243	53.01	
*14.11	0.18	*692.174	*27.599	*0.553	*1.373	4033.99
2038.82	12.35	227.3		5.8	*0.712	0.19
50616.21	4415.82	15774.96	1099.98	*33.243	79.1	
42.33	0.11	*692.174	*27.599	*0.553	*1.373	7955.17
32663.17	24.96	209.75		4.43	*0.712	0.18
35618.16	4558.34	8996.8	2406.96	*33.243	37.72	
*14.11	0.16	11419.51	*27.599	*0.553	*1.373	4624.81
25101.73	20.74	132.17		5.4	*0.712	0.19
30328.07	2346.5	8089.26	3945.79	*33.243	57.51	
*14.11	0.14	6678.44	225.96	*0.553	*1.373	5219.15
10125.66	12.59	345.64		11.83	*0.712	0.19
56901.35	25566.49	16632.27	2210.3	*33.243	64.04	
143.12	0.09	6410.22	*27.599	*0.553	*1.373	7127.15
2864.56	19.88	1241.89		23.51	*0.712	0.17
49081.25	9760.18	23619	1858.41	*33.243	41.06	
*10.951	0.21	5003.69	257.72	*0.598	*1.37	5528.58
5092.08	5.49	102.27		7.11	1.91	0.24
43430.2	1422.17	11055.34	1050.53	1681.16	39.19	
*10.951	0.11	*674.132	*27.362	*0.598	*1.37	1153.43
990.37	14.83	74.25		8.32	1.91	0.31
25257.28	7826.23	19005.02	1394.71	681.58	41.52	
*11.332	0.17	*682.162	*26.909	*0.642	*1.364	2380.49
9249.14	22.42	205.06		8.5	2.84	0.34
68874.29	5783.23	19908.86	2520.37	1632.4	63.12	
*11.332	0.31	*682.162	*26.909	*0.642	*1.364	4846.51
73346.59	14.1	261.19		20.39	3.67	0.36

Table4.txt

27564.92	5263.43	7938.09	*41.6	593.06	8.39	
*11.332	0.53	*682.162	*26.909	*0.642	*1.364	4219.36
2218.01	18.77	504.52		9.73	6.46	0.35
18425.71	6618.35	22446.3	2217.18	1314.26	50.67	
*11.332	0.15	*682.162	161.46	*0.642	*1.364	3678.31
59321.16	15.07	217.44		10.07	8.83	0.29
24234.09	5843.05	15173.77	3210.53	2906.69	13.59	
257.67	0.16	*656.313	*27.445	*6.138	*1.342	4331.83
210876.41	13.16	238.42		8.49	8.63	*0.029
16244.15	4318.47	14035.98	1963.1	1356.29	36.48	
343.7	0.1	*656.313	*27.445	*6.138	*1.342	4181.84
6179.03	39.68	139.88		6.25	8.73	*0.029
24497.7	3982.66	12882.55	1993.72	2091.76	82.47	
*9.827	0.11	*656.313	*27.445	*6.138	*1.342	3811.42
1184.8	19.92	283.25		4.18	6.38	*0.029
19866.62	4184.46	12538.54	3180.81	462.81	55.31	
177.99	*0.01	*656.313	*27.445	*6.138	*1.342	6669.55
106105.09	23.34	327.66		7.95	9.65	*0.029
15217.35	3061.12	25567.48	1574.55	1327.19	35.19	
156.55	0.33	*656.313	*27.445	*6.138	*1.342	6891.18
3153.6	39.06	247.08		6.7	11.96	*0.029
39206.54	4351.91	15331.79	1908.4	2186.51	153.65	
161.36	0.27	*656.313	*27.445	*6.138	*1.342	8790.28
2630.07	86.25	267.79		2.68	11.61	0.37
17219.26	4684.95	13394.39	2483.57	3078.38	97.66	
529.18	0.26	*656.313	*27.445	*6.138	*1.342	8881.32
19728.37	20.32	324.26		2.12	10.56	*0.029
28940.1	6608.82	13394.39	4012.82	1726.63	6.62	
379.09	*0.01	*656.313	*27.445	*6.138	*1.342	8491.53
13436.36	32.16	317.45		22.17	10.2	0.3
10355.19	9260.4	6878.16	1400.49	1948.37	65.29	
405.77	0.24	*656.313	*27.445	*6.138	12.83	4253.03
1724.17	31.13	157.72		8.56	7.38	*0.029
32060.9	5344.38	16311.45	3332.97	1471.74	108.16	
208.2	0.26	*656.313	*27.445	*6.138	8.82	6467.65
1724.17	13.4	221.04		8.69	6.38	*0.029
37665.22	3061.12	7279.9	1901.97	2904.9	28.49	
88.49	0.19	*656.313	*27.445	*6.138	*1.342	5040.9
7532.95	21.82	228		8.27	9.65	*0.029
47389.32	6801.19	18042.89	1884.3	1128.03	86.11	
255.46	0.21	4205.98	183.34	*6.138	9.43	4931.33
89488.71	36.04	154.16		20.72	12.3	*0.029
20564.87	2111.01	9836.95	794.87	2050.95	69.49	
144.41	0.18	*656.313	*27.445	*6.138	8.82	5224.22
2567.86	22.71	193.06		6.66	8.82	*0.029
34050.35	3678.06	11173.17	1251.03	2506.77	42.49	
440.19	0.24	4205.98	164.67	*6.138	13.14	5562.73
7596.6	41.63	175.44		6.86	8.16	*0.029

Table4.txt

57725.52	6287.01	15953.84	1552.34	2807.82	345.4	
122.1	0.1	4471.09	*27.445	*6.138	*1.342	5378.86
1724.17	55.14	245.35		9.78	10.56	*0.029
19162.69	4083.69	3385.93	1625.4	4540.25	59.78	
275.24	*0.01	*656.313	*27.445	*6.138	*1.342	5464.63
6393.31	41.64	189.54		10.07	11.61	*0.029
50004.05	3847.58	11965.71	1649.27	1202.38	109.52	
203.61	0.15	*656.313	*27.445	*6.138	41.21	7592.28
2029.86	14.08	366.64		6.12	9.65	0.29
36726.31	8761.55	11226.44	3288.93	2781.85	129.89	
*9.827	*0.01	4205.98	183.34	*6.138	*1.342	6409.24
7910.06	22.33	178.98		7.24	12.04	*0.029
19263.62	6801.19	17709.16	3581.65	2781.85	84.62	
*36.49	0.15	*644.123	164.99	*0.591	*1.31	2915.7
1120.54	28.54	199.15		4.25	2.41	*0.029
68137.01	5638.03	6023.2	767.36	3674.73	36.56	
329.13	0.23	*644.123	217.42	5.83	*1.31	6133.27
16962.83	27.42	232.24		12.36	3.45	0.39
50146.57	5088.19	15408.13	2970.75	1247.36	42.51	
*36.49	0.19	*644.123	*27.061	*0.591	*1.31	3463.03
11492.22	21.01	186.45		7.8	2.94	*0.029
41476.15	7484.61	13471.56	1734.08	1448.12	33.04	
*36.49	0.21	*644.123	*27.061	*0.591	*1.31	4126.75
17140.94	16.05	249.35		3.43	6.97	0.36
25413.38	4132.6	14240.89	3119.93	2130.04	51.19	
*36.49	0.12	*644.123	*27.061	9.86	*1.31	1576.32
37985.32	8.59	164.84		7.41	14.66	0.32
10764.72	2953.88	20477.59	319.93	901.31	90.24	
*36.49	0.19	*644.123	*27.061	*0.591	*1.31	3980.97
2387.63	19.51	243.71		6.34	4.74	*0.029
33240.59	8611.55	5795.34	754.33	4977.06	53.86	
*36.49	0.12	*644.123	*27.061	*0.591	*1.31	8878.42
9848.62	14.6	230.79		14.37	11.98	*0.029
42718.62	6091.8	12744.21	434.85	2003.82	20.6	
*36.49	0.14	*644.123	*27.061	*0.591	*1.31	3891.09
63883.52	17.43	191.26		3.55	3.69	*0.029
22425.29	4794.77	8848.84	409.72	2587.88	60.19	
*36.49	0.1	4319.13	164.99	*0.591	39.5	5304.27
30710.3	6.73	196.01		6.79	8.73	*0.029
26569.75	1630.1	15174.38	1725.33	1735.72	7.03	
*36.49	0.14	5035.74	191.23	6.24	*1.31	5463.51
103229.08	6.56	192.85		4.74	5.3	*0.029
31632.44	1936.84	13825.66	1738.46	1582.04	13.3	
*36.49	0.22	*644.123	*27.061	*0.591	*1.31	4177.3
31897.5	12.51	191.26		3.19	3.69	*0.029
10400.81	5460.99	13835.78	2412.23	2130.04	29.49	
*36.49	0.21	*644.123	*27.061	*0.591	*1.31	4863.18
24063.43	24.1	223.46		13.51	4.4	0.37

Table4.txt

47592.56	4463.19	4697.88	604.94	2055.09	35.76	
*36.49	0.14	*644.123	164.99	8.27	*1.31	6719.02
67927.74	13.38	136.17		9.66	4.17	*0.029
30177.34	1841.01	17396.21	2362.93	2374.7	8.47	
*36.49	0.1	*644.123	*27.061	*0.591	*1.31	5379.68
16943	17.69	202.27		5.4	4.4	*0.029
36807.4	3358.43	11756.5	2470.03	1483.57	12.08	
*36.49	0.14	*644.123	*27.061	3.55	*1.31	2673.11
54028.47	8.62	178.29		1.95	5.94	*0.029
23632.46	3127.11	20487.91	2682.64	755.99	365.8	
*36.49	0.16	*644.123	*27.061	*0.591	*1.31	4006.02
74752.26	12.7	276.66		5.88	4.05	*0.029
16653.45	4521.63	21946.27	1554.53	1003.5	29.85	
145.13	0.15	*644.123	*27.061	*0.591	26.36	3176.35
2786.19	6.82	310.33		6.54	4.51	*0.029
35789.72	3938.58	23171.94	550.96	975.98	9.62	
*36.49	0.23	*644.123	*27.061	5.83	*1.31	5199.72
112370.79	9.4	208.43		4.59	7.37	*0.029
21956.15	2358.54	11515.01	1327.21	1988.04	12.45	
*36.49	0.11	*644.123	*27.061	4.18	13.55	4617.88
7793.41	3.34	186.45		2.64	3.45	*0.029
26916.05	2512.01	15062.64	930.61	1526.89	20.42	
*36.49	0.1	*644.123	*27.061	6.24	*1.31	3881.13
34445.77	8.48	118.69		6.13	10.03	*0.029
24291.9	2473.63	13856.02	3338.11	1617.5	4.19	
*36.49	0.12	*644.123	*27.061	*0.591	*1.31	2555.5
10509.3	19	157.92		4.37	*0.138	0.35
35866.48	8449.87	8928.75	2098.31	1475.69	61.06	
*36.49	0.13	*644.123	*27.061	6.65	32.14	3985.98
1245.4	18.76	159.66		3.91	4.85	*0.029
44785.2	2973.11	13754.81	1341.72	1400.87	15.16	
*36.49	0.12	*644.123	*27.061	3.76	*1.31	5888.11
6274.45	7.95	173.31		4.93	4.85	*0.029
22327.65	2703.99	7443.22	1218.4	1223.75	9.14	
*36.49	0.1	*644.123	*27.061	*0.591	*1.31	7494.67
4115.21	15.17	136.17		4.34	2.54	*0.029
33240.59	2665.58	8429.59	1146.57	1838.2	7.61	
*36.49	0.14	*644.123	*27.061	*0.591	*1.31	3767
14276.65	24.28	309.07		5.53	2.54	*0.029
27761.56	5186.17	10490.41	2791.68	614.72	22.06	
*36.49	0.17	*644.123	*27.061	*0.591	*1.31	6569.58
14636.22	16.45	118.69		5.06	4.4	0.3
44902.52	1630.1	7841.44	1600.64	1522.95	7.37	
*36.49	0.15	*644.123	*27.061	*0.591	*1.31	5954.68
*135.54	26.14	235.14		7.2	2.41	*0.029
29027.75	5559.31	3732.19	2105.15	1641.14	45.38	
*36.49	0.17	*644.123	*27.061	*0.591	*1.31	5662.34
1305.8	13.67	287.23		4.3	4.17	*0.029

Table4.txt

26146.14	12266.26	5607.23	3778.79	1972.27	35.72	
*36.49	0.18	*644.123	*27.061	*0.591	*1.31	5379.68
79161.47	21.04	120.69		8.42	1.69	*0.029
55283.69	2320.19	13117.81	1679.57	905.24	84.22	
*36.49	0.2	*644.123	*27.061	*0.591	*1.31	8141.69
1536.23	11.33	226.4		7.62	2.68	*0.029
50863.25	2876.95	18974.43	2254.61	1475.69	11.61	
*36.49	0.1	*644.123	*27.061	*0.591	*1.31	4205.16
1957.28	18.71	217.51		6.18	3.45	*0.029
32359.87	4970.73	11837.03	2394.6	1365.44	32.95	
*36.49	0.11	*644.123	196.47	6.65	*1.31	4380.9
2271.74	11.12	216.01		4.25	9.57	0.31
18192.53	5225.39	4165.36	1006.53	1349.69	21.52	
*36.49	0.18	*644.123	*27.061	*0.591	*1.31	6189.41
9001.73	12.45	145.42		5.48	5.73	0.3
30943.27	3977.36	28919.79	1560.95	1507.2	25.02	
*36.49	0.21	*644.123	*27.061	*0.591	*1.31	4468.13
2612.36	28.43	302.73		4.74	2.94	*0.029
37788.04	7845.62	20725.35	2524.58	1794.84	41.14	
*36.49	0.3	*644.123	*27.061	*0.591	*1.31	3090.59
*135.54	33.73	249.35		6.56	5.19	*0.029
22073.54	7544.7	3751.86	536.07	1145.06	29.22	
*36.49	0.2	*644.123	175.49	*0.591	*1.31	3565.39
26592.05	7.65	485.01		10.95	4.17	*0.029
24988.46	15129.64	6717.61	2457.03	1003.5	12.12	
*36.49	0.14	*644.123	*27.061	*0.591	*1.31	7862.9
32509.18	17.65	163.12		12.14	4.4	*0.029
29909.2	2301.01	21200.75	1843.09	1172.6	7.22	
194.44	0.19	*644.123	*27.061	*0.591	*1.31	*27.314
7943.56	6.93	*12.996		5.58	3.69	*0.029
36884.26	8268.26	4609.06	2824.59	1633.26	17.43	
*12.46	0.16	*676.132	214.42	6.49	*1.37	6050.48
8114.82	23.76	242.15		4.52	10.01	0.29
48823.62	3599.6	10502.05	768	1025.75	46.16	
97.88	0.12	*676.132	*27.292	*0.628	*1.37	7455.53
4592.5	24.97	223.38		5.06	6.69	0.22
35755.21	2838.59	28371.54	3899.12	2169.75	5.01	
186.61	0.25	4056.79	*27.292	*0.628	*1.37	2878.95
5376.38	20.47	280.43		11.8	8.5	0.29
29030.25	6166.57	6007.76	2288.03	835.15	204.89	
*12.46	0.11	*676.132	*27.292	6.9	*1.37	5411.35
5257.6	8.01	172.23		8.17	12.98	0.23
24825.57	4493.61	11903.63	2461.27	1690.47	4.33	
*36.49	0.11	*644.123	*27.061	*0.591	*1.31	7032.88
83921.82	25.94	275.33		7.1	8.45	*0.029
14543.47	2396.9	14423.34	1998.51	913.1	31.6	
*36.49	0.17	*644.123	*27.061	4.18	*1.31	3930.98
2997.03	16.23	273.99		5.83	8.45	0.36

Table4.txt

54393.77	4755.71	13683.98	2073.26	1550.53	38.7	
*36.49	0.1	*644.123	*27.061	*0.591	*1.31	3467.89
1536.23	7.51	211.47		2.18	2.13	*0.029
17020.19	8348.94	4007.77	1701.33	1007.43	21.79	
*36.49	0.22	*644.123	*27.061	4.18	*1.31	8599.67
2007.04	10.35	173.31		2.96	5.94	*0.029
27761.56	1052.68	5330.2	979.15	1255.23	13.86	
*36.49	0.22	4678.92	*27.061	*0.591	*1.31	4139.38
4435.12	21.07	370.59		5.18	7.77	0.35
51881.65	5107.78	7592.5	344.84	2082.7	20.79	
*36.49	0.17	*644.123	*27.061	7.06	*1.31	4406.51
122585.52	26.71	220.49		7.41	2.13	*0.029
19769.7	6210.49	5369.76	1978.23	367.89	11.28	
*36.49	0.16	*644.123	*27.061	*0.591	*1.31	3911.02
6951.12	15.13	208.43		3.76	2.41	*0.029
36576.86	5854.82	6280.96	3127.43	1247.36	22.16	
*36.49	0.16	*644.123	*27.061	*0.591	*1.31	3147.71
3478.69	5.05	173.31		7.62	4.4	*0.029
41166.11	3377.72	15255.67	2819.71	842.38	31.92	
*36.49	0.13	*644.123	*27.061	*0.591	*1.31	4101.53
2828.9	14.26	141.76		6.29	1.53	*0.029
48026.62	1936.84	5112.7	1679.57	1846.09	14.6	
*36.49	0.25	*644.123	*27.061	*0.591	*1.31	4695.82
*135.54	33.47	143.6		5.73	4.85	*0.029
26377.25	5657.72	44503.09	2898.07	1156.87	57.27	
*36.49	0.11	*644.123	*27.061	*0.591	*1.31	1503.7
1055.77	6.23	173.31		7.31	8.16	*0.029
34696.57	2915.41	12320.58	1012.42	1156.87	24.7	
*36.49	0.13	*644.123	*27.061	*0.591	*1.31	4740.13
849.69	7.66	217.51		4.54	2.54	*0.029
23477.05	3977.36	4579.46	3121.18	211.57	51.23	
*12.46	0.13	*676.132	*27.292	*0.628	*1.37	9217.04
1184.5	24.2	242.15		6.42	6.09	0.25
64645.41	6009.84	7978.72	5599.08	1744.73	23.32	
*12.46	0.13	*676.132	*27.292	*0.628	*1.37	5514.91
1388.01	34.35	213.68		12.14	6.19	0.18
36139.87	9084.5	19038.11	2292.94	1250.53	25.66	
*12.46	0.16	*676.132	*27.292	*0.628	51.97	5879.35
4050.14	13.81	1345.76		3.02	8.59	0.35
35216.05	2212.42	1354.48	1992.79	2183.05	40.22	
106.36	0.16	*676.132	*27.292	5.87	*1.37	3044.68
26385.76	17.43	1262.22		5.17	4.37	0.17
33799.98	3878.48	10931.39	4191.93	911.8	8.77	
106.36	0.1	*676.132	211.55	*0.628	*1.37	6292.62
4416.5	19.54	245.21		3.56	9.13	0.32
21411.43	3679.35	7591.65	2825.39	1586.05	12.61	
*12.46	0.13	*676.132	*27.292	*0.628	*1.37	4645.89
1482.38	19.52	260.19		11.51	5.15	0.19

Table4.txt

18456.19	4552.98	15246.51	2354.28	987.89	44.22	
*12.46	0.25	*676.132	*27.292	*0.628	*1.37	5556.4
953.3	21.65	242.15		9.45	5.88	0.38
24087.07	8542.41	15761.99	3565.47	825.53	32.37	
106.36	0.21	*676.132	*27.292	*0.628	*1.37	6699.24
43752.03	18.15	175.88		4.29	6.29	0.35
17768.69	5676.33	5756.3	1893.34	3151.98	13.61	
*12.46	0.12	*676.132	*27.292	8.53	*1.37	5449.29
32657.37	7.64	220.17		13.27	7.85	0.19
26045.13	3479.85	6098.87	1051.98	1213.32	20.92	
*12.46	0.4	*676.132	*27.292	*0.628	11.53	5980.55
17835.48	16.55	506.76		25.43	4.59	0.3
126900.99	7843.85	3313.64	4116.88	1481.05	14.21	
*12.46	0.17	*676.132	*27.292	*0.628	*1.37	6155.59
62725.91	15.3	305.39		6.76	6.09	0.23
31415.25	4632.09	7824.14	2640.36	1581.5	11.6	
*36.49	0.11	*644.123	*27.061	*0.591	*1.31	2065.15
8677.02	20.91	205.36		3.57	2.54	*0.029
4747.63	4404.78	2720.98	951.91	653.95	13.2	
*36.49	0.21	*644.123	*27.061	*0.591	*1.31	4486.14
46227.7	22.38	189.66		8.37	4.85	0.37
48481.06	3165.64	13228.95	553.59	1357.57	23.57	
*36.49	0.16	3956.06	*27.061	*0.591	41.89	3231.38
28370.29	9.69	176.64		3.67	3.81	0.3
26203.93	3744.89	9288.55	1784.56	1972.27	23.98	
*36.49	0.13	*644.123	*27.061	4.6	*1.31	3284.18
49531.88	16.43	159.66		4.25	5.51	*0.029
66199.42	2973.11	6956.01	1560.95	897.38	24.25	
*36.49	0.22	5741.42	*27.061	9.86	*1.31	4675
22099.45	16.05	221.98		2.25	15.07	0.32
11371.2	7164.69	19509.02	1207.22	948.47	39.99	
258.8	0.11	*644.123	*27.061	9.06	8.76	5403.98
89581.29	16.69	174.98		8.35	2.94	*0.029
35425.2	3783.6	33889.3	2387.55	1341.82	40.96	
83.8	0.08	*661.68	*27.223	*0.573	*1.345	NA
39954.92	NA	NA		5.11	10	0.41
14834.1	NA	19336.75	NA	*33.139	58.99	
76	0.1	*661.68	*27.223	*0.573	*1.345	NA
40923.03	NA	NA		16.96	10.8	0.26
22247.37	NA	21203.16	NA	*33.139	31.61	
70.09	0.07	*661.68	*27.223	*0.573	*1.345	NA
20916.17	NA	NA		58.77	9	0.29
13691.59	NA	8333.72	NA	*33.139	69.6	
131.15	0.06	*661.68	*27.223	*0.573	*1.345	NA
43168.71	NA	NA		28.08	7.44	0.36
13847.31	NA	14646.69	NA	*33.139	34.2	
83.8	0.07	*661.68	*27.223	*0.573	*1.345	NA
171654.44	NA	NA		13.7	9.17	0.27

Table4.txt

10900.31	NA	67273.13	NA	*33.139	132.45	*11.086	0.16	*661.68	*27.223
*0.573	*1.345	NA	4176.13	NA	NA	7.83	7.97	0.2	
27398.77	NA	12344.12	NA	*33.139	72.19	75.5	0.24	4040.95	*27.042
*1.87	48.5	3916.07	58784.62	10.32	503.8	13.58	9.96	0.45	
16092.58	5047.78	13466.93	1535.61	577.28	20.24	37.85	0.15	*673.492	*27.042
*1.87	*1.369	3383.99	78014.38	18	172.82	3.48	*0.745	0.3	
21219.67	4708.08	13020.96	1255.78	644.52	41.93	*12.021	0.16	5597.94	*27.042
*1.87	*1.369	3027.58	128426.22	9.68	226.32	4.16	11.03	0.33	
20471.8	3489.71	10437.51	1160.6	857.43	19.9	46.67	0.17	*673.492	*27.042
*1.87	*1.369	3617.97	76489.57	9.63	238.75	5.07	*0.745	0.27	
17004.65	4516.6	15765.02	3568.81	1139.31	97.99	*12.46	0.16	*676.132	*27.292
*0.628	*1.37	5875.86	18114.98	28	210.39	2.49	12.34	0.49	
13635.07	1579.77	18555.28	4648.24	1157.33	77.75	47.1	0.21	*676.132	*27.292
*0.628	*1.37	3371.73	137699.6	14.69	128.94	8.62	8.77	0.3	
40887.14	3938.15	10856.35	2398.51	1185.35	27.5	*12.46	0.09	*676.132	*27.292
*0.628	*1.37	6208.24	16634.09	17.21	274.73	4.06	6.29	0.17	
26475.67	3938.15	4899.45	3482.87	1110.49	40.75	*12.46	0.16	*676.132	*27.292
*0.628	*1.37	3993.91	109656.6	13.17	210.39	3.4	9.83	0.26	
21042.1	16424.66	6201.16	2371.47	1676.88	39.03	*12.46	0.09	*676.132	*27.292
*0.628	*1.37	7451.91	90006.24	10.18	137.33	4.7	7.66	0.28	
22480.79	2435.25	19227.07	3754.27	1586.05	15.8	*12.46	0.07	*676.132	*27.292
*0.628	*1.37	2940.61	120095	28.93	305.39	3.44	8.59	0.23	
19223.04	6323.17	8000.78	1823.18	1110.49	33.67	144.68	0.1	*676.132	*27.292
*0.628	*1.37	4412.85	10394.94	45.99	210.39	3.71	6.89	0.23	
16021.65	4057.39	43333.8	1911.51	1063.48	32.18	*12.46	0.08	*676.132	*27.292
4.83	*1.37	4348.9	166897.99	22.54	183.05	5.46	9.66	0.32	
13568.23	5302.79	54131.06	1138.18	1072.9	34.34	*12.46	0.12	*676.132	*27.292
*0.628	*1.37	5013.25	38887.48	8.61	235.98	7.5	6.39	0.23	
48288.51	4513.4	23774.88	2141.3	1626.97	44.41	*12.46	0.1	*676.132	*27.292
4.41	*1.37	3572.56	239398.47	10.28	200.37	10.12	9.57	0.31	
37700.77	5656.69	10867.08	1588.4	1444.38	21.76	80.57	0.09	*676.132	*27.292
*0.628	*1.37	4318.64	6590.48	30.54	377.07	2.86	7.08	0.26	

Table4.txt

40021.64	7318.65	10416.01	1980.64	2143.12	122.49	
*12.46	0.08	*676.132	*27.292	*0.628	*1.37	3807.59
134574.94	10.72	213.68		9.05	6.99	0.23
35421.53	5892.2	10792	2595.81	1490.2	46.12	
*12.46	0.09	*676.132	*27.292	*0.628	*1.37	8684.8
51454.68	10.05	260.19		9.1	7.28	0.19
25613.02	2677.52	10995.68	2378.84	728.74	17.98	
*12.46	0.1	*676.132	*27.292	*0.628	*1.37	5266.78
3296.59	26.46	266.05		3.33	6.29	0.35
18870.4	5479.84	6110.24	1631.62	1011.56	22.88	
*12.46	0.12	*676.132	*27.292	*0.628	*1.37	4497.14
84007.17	11.65	266.05		4.1	6.89	0.24
19631.8	3778.96	17022.78	547.05	820.71	11.81	
*12.46	0.43	4056.79	*27.292	8.12	*1.37	2086.87
34828.39	5.7	268.96		15.25	21.37	0.52
88047.03	2959.19	15846.11	2886.45	796.6	235.29	
212.07	0.1	*676.132	*27.292	*0.628	*1.37	2904.9
16122.94	16.75	291.66		5.27	10.69	0.22
23259.84	13429.31	29037.01	4120.76	1199.34	94.24	
71.7	0.08	*676.132	*27.292	*0.628	*1.37	4476.89
14438.95	22.33	254.25		4.1	7.66	0.23
29846.18	2798.36	3997.41	2332.18	1231.93	14.61	
114.73	0.11	*676.132	*27.292	6.08	*1.37	2178.92
50605.63	17.47	377.07		11.88	11.19	0.33
30919.71	10801.35	10308.39	1806.27	1567.83	193.49	
*12.46	0.1	*676.132	*27.292	*0.628	*1.37	4639.12
128553.09	6.69	216.94		7.52	9.66	0.26
19046.99	1743.78	26224.76	2376.39	1608.8	5.89	
59.6	0.09	*676.132	*27.292	*0.628	*1.37	2969.85
146315.39	11.01	226.57		5.65	5.88	0.21
17618.01	5381.5	35507	2097.41	1231.93	12.86	
103.55	0.14	*676.132	176.07	5.25	*1.37	3044.68
160637.63	9.7	326.7		*0.027	6.49	0.25
16021.65	12586.97	11797.07	1460.3	978.41	*0.032	
*12.46	0.07	*676.132	*27.292	14.83	*1.37	2810.92
32625.61	12.48	271.85		3.51	7.47	0.31
14296.02	5184.66	6990.11	1565.62	1380.02	14.71	
*12.46	0.1	*676.132	*27.292	*0.628	*1.37	4399.38
14002.5	14.39	183.05		5.86	4.59	0.26
18277.7	5361.83	21749.61	2981.39	1054.06	20.63	
*12.46	0.13	*676.132	197	*0.628	*1.37	3325.78
66798.76	13.9	196.97		11.25	7.28	0.22
31649.58	4275.69	17253.76	1632.82	1068.19	36.02	
*12.46	0.14	*676.132	166.86	4.83	*1.37	3240.58
200750.94	17.07	223.38		4.91	8.22	0.28
11559.51	6967.84	6956.52	486.9	1704.04	28.56	
*12.46	0.08	*676.132	*27.292	*0.628	*1.37	6966.53
17755.26	7.95	260.19		4.01	10.35	0.3

Table4.txt

10828.77	3918.26	14203.26	3905.55	1278.37	37.84	
*12.46	0.12	*676.132	*27.292	6.49	*1.37	6564.45
73552.58	12.3	266.05		3.96	7.28	0.27
11050.43	3579.65	3474.11	2450.19	757.89	18.67	
*12.46	0.09	*676.132	*27.292	5.25	*1.37	2759.17
23428.29	19.49	223.38		7.5	9.83	0.29
20985.11	5715.6	12382.42	1424.48	968.92	59.18	
37.37	0.08	*676.132	*27.292	5.25	*1.37	3675.01
37408.62	18.13	291.66		5.79	10.26	0.24
13366.84	6244.89	12233.59	2867.75	1255.17	62.09	
*12.46	0.1	4056.79	*27.292	13.67	*1.37	2765.63
57668.46	9.91	210.39		4.66	12.58	0.34
14230.51	4236.03	10222.22	1671.28	1035.19	92.06	
133.91	0.14	*676.132	*27.292	4.41	*1.37	4666.22
51186.33	16.57	235.98		7.15	8.4	0.34
14099.12	6401.42	14213.81	1245.97	1604.25	24.54	
157.96	0.06	*676.132	*27.292	*0.628	*1.37	6713.46
56221.96	13.74	260.19		7.5	8.5	0.21
22452.83	2979.27	17736.63	2573.56	1119.87	32.61	
*12.5	0.21	*696.339	*27.577	*0.61	*1.358	6035.19
1820.83	21.99	377.89		12.2	4.89	0.41
14437.83	7719.62	17880.12	2243.26	2298.9	170.22	
*12.5	0.12	*696.339	*27.577	4.79	*1.358	3598.83
847.66	9.57	123.18		7.09	6.32	0.22
24111.16	5422.28	15917.43	2388.69	1340.98	46.11	
94.52	0.06	*696.339	*27.577	*0.61	*1.358	2742.76
847.66	16.92	151.56		6.88	4.27	0.14
19216.67	4869.46	4500.04	2409.53	674.22	81.59	
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	4407.45
8996.62	10.74	395.32		7.52	10.31	0.38
18682.39	3293.97	9337.49	1060.49	2042.03	100.05	
44.86	0.21	*696.339	*27.577	*0.61	*1.358	5573.4
3858.33	18.29	288.49		5.98	6.19	0.41
26170.78	4830	7910.97	1998.19	2857.06	56.71	
58.89	0.04	*696.339	*27.577	*0.61	*1.358	3135.55
2126.38	9.17	188.63		6.41	2.54	0.16
14561.87	4199.13	6194.76	2340.94	1431.49	108.34	
62.28	0.12	*696.339	*27.577	*0.61	*1.358	1978.51
1820.83	29.35	251.8		8.47	7.91	0.3
30700.76	6193.41	5760.63	2802.35	2003.04	103.76	
44.86	0.09	*696.339	*27.577	*0.61	*1.358	6450.53
3959.89	14	247.03		13.87	6.6	0.28
10911.51	4317.35	80030.94	1597.8	1964.04	88.57	
91.41	0.15	*696.339	*27.577	*0.61	*1.358	5019.47
12754.13	39.9	265.83		7.69	7.13	0.21
45277.79	5995.56	13997.01	3140.39	1682.62	41.28	
*12.5	0.23	*696.339	*27.577	3.89	*1.358	8482.74
50701.45	37.35	214.94		9.15	8.41	0.31

Table4.txt

27604.34	4672.2	18392.81	3406.24	2127.73	45.88	
124.61	0.23	*696.339	*27.577	*0.61	*1.358	3886
969.9	54.93	207.21	46.14	4.58	0.42	
49295.43	11525.65	14586.6	4219.46	2057.62	75.95	
191.63	0.11	*696.339	*27.577	*0.61	*1.358	4432.54
47830.13	8.03	225.04	6.41	26.79	0.29	
28140	6668.59	20478.83	2461.08	1971.84	16.11	
100.68	0.12	*696.339	*27.577	*0.61	*1.358	4552.06
*141.277	8.12	275	9.84	5.33	0.32	
16223.85	3864.37	5508.15	4903.47	1807.83	92.61	
65.64	0.09	*696.339	*27.577	*0.61	*1.358	3984.52
54638.59	11.79	227.53	7.52	8.16	0.15	
25198.01	3451.23	16637.05	*40.84	766.24	58.58	
*12.5	0.11	*696.339	*27.577	*0.61	*1.358	3532.1
31568.85	14.27	185.91	10.14	8.16	0.3	
18317.62	6292.37	5920.85	2015.1	1815.64	19.12	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	6302.46
12305.8	23	180.4	6.71	6.05	0.3	
36579.68	4475.02	14717.56	2766.29	2127.73	65.76	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	5189.98
910.03	18.6	222.54	9.75	7.91	0.22	
20910.95	5797.8	5531.14	2277.41	1270.04	44.59	
*12.5	0.1	*696.339	*27.577	*0.61	*1.358	7952.6
2795.7	24.25	177.62	9.07	6.05	0.26	
37856.48	2979.63	11104.58	2949.57	1455.08	53.35	
*12.5	0.14	*696.339	*27.577	*0.61	*1.358	4789.53
6976.15	15.09	212.38	9.41	3.61	0.22	
20406.04	8037.35	8982.12	4117.48	2562.83	34.06	
*12.5	0.18	*696.339	*27.577	12.62	*1.358	5099.77
5952.17	12	292.92	11.77	9.85	0.31	
46780.2	7283.06	21387.15	1933.05	1936.72	51.34	
*12.5	0.19	*696.339	*27.577	*0.61	*1.358	4460.8
2407.47	20.82	191.34	7.27	6.6	0.27	
37146.91	4869.46	14171.75	1008.02	2388.25	77.15	
*12.5	0.26	*696.339	*27.577	*0.61	*1.358	5041.93
41533.43	15.57	275	13.74	10.66	0.2	
23108.28	6292.37	11698.06	1984.91	379.71	21.29	
*12.5	0.16	*696.339	*27.577	25.88	*1.358	3735.9
138778.81	15.18	157.52	11.38	9.38	0.34	
11864.99	5185.27	8726.21	2480.75	877.89	108.86	
*12.5	0.42	*696.339	*27.577	*0.61	*1.358	2757.4
14276.16	9.15	207.21	6.49	9.02	0.42	
18950	7223.56	6331.37	1312.53	1537.56	156.5	
*12.5	0.17	*696.339	*27.577	*0.61	8.72	4910.65
1780.47	10.35	356.05	8.29	7.26	0.5	
17054.45	4534.16	14193.59	2201.86	1651.28	35.34	
*12.5	0.28	*696.339	*27.577	10.49	*1.358	4665.78
969.9	7.71	389.55	10.87	7.13	0.33	

Table4.txt

11026.85	11665.68	4207.01	4411.33	937.55	27.87	
41.22	0.11	*696.339	*27.577	*0.61	*1.358	2518.54
969.9	10.89	212.38	13.36	4.11	0.26	
57202.7	6193.41	13297.57	1857.26	861.96	45.06	
*12.5	0.2	*696.339	*27.577	*0.61	*1.358	6349.49
*141.277	14.33	201.99	7.18	6.05	0.26	
43926.25	8713.21	8123.63	2513.97	869.93	76.82	
58.89	0.22	*696.339	*27.577	4.79	*1.358	4681.62
131189.14	12.01	151.56	15.68	9.62	0.51	
33764.7	4159.73	7417.06	2957.08	1470.8	25.6	
*12.5	0.14	*696.339	*27.577	*0.61	40.16	5045.14
4948.12	11.15	207.21	5.64	9.38	0.24	
22539.79	3293.97	7966.96	548.94	630.09	26.23	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	5316.12
42692	20.92	232.48	14.9	3.95	0.23	
15379.93	2783.32	12082.12	2111.95	818.13	110.42	
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	6396.6
53376.98	9.41	132.95	4.61	6.87	0.38	
18529.03	4987.86	36461.77	779.39	1056.59	43.17	
*12.5	0.11	*696.339	*27.577	*0.61	*1.358	6021.89
7439.51	11.81	225.04	21.78	5.48	0.29	
21283.3	7005.46	10057.15	3731.26	925.63	76.39	
*12.5	0.19	*696.339	*27.577	5.91	*1.358	2898.46
1899.97	10.55	169.14	18.25	4.58	0.19	
35357.59	4711.64	7079.05	2070.75	1226.64	39.13	
*12.5	0.13	*696.339	*27.577	*0.61	*1.358	4824.53
1137.48	22.64	194.03	5.64	5.48	0.26	
33216.08	4277.94	9957.67	830.31	2166.66	44	
115.75	0.4	*696.339	*27.577	*0.61	*1.358	7435.22
1083.39	30.34	183.16	10.78	6.32	0.39	
43638.61	6134.05	5600.07	3472.47	1266.1	152.3	
*12.5	0.18	*696.339	*27.577	*0.61	*1.358	4542.61
3154.02	13.13	225.04	6.92	7.91	0.35	
53635.03	7183.9	10289.1	3459.72	985.21	59.6	
*12.5	0.15	*696.339	*27.577	*0.61	*1.358	2728.13
4231.63	10.48	180.4	4.87	7.13	0.14	
13260.84	5778.03	7180.56	2407.08	1639.53	59.6	
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	3827.69
2978.08	20.43	232.48	6.41	5.91	0.34	
45982.83	5303.76	22977.56	3948.34	810.15	72.56	
*12.5	0.14	*696.339	*27.577	*0.61	*1.358	2623.07
3268.13	18.77	191.34	6.37	6.05	0.37	
55449.38	5284.01	28756.21	3875.79	1266.1	60.95	
124.61	0.11	*696.339	*27.577	*0.61	*1.358	3073.08
26499	14.34	217.49	10.35	4.74	0.28	
8467.91	6450.74	12235.62	2438.98	383.77	24.96	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	3486.71
11103.07	14.57	237.38	8.34	6.19	0.27	

Table4.txt

27854.43	4790.54	8948.76	4185.43	1525.78	14.34	
55.45	0.08	*696.339	*27.577	*0.61	*1.358	3141.51
4059.94	3.18	237.38	12.58	5.48	0.26	
18124.87	5936.22	6183.36	858.12	1210.85	42.52	
*12.5	0.08	*696.339	*27.577	*0.61	*1.358	2245.21
19143.44	11.18	232.48	5.64	8.65	0.26	
15258.16	5264.26	10675.14	2531.21	838.06	28.75	
*12.5	0.13	*696.339	*27.577	*0.61	*1.358	2783.78
10124.06	11.14	284.03	8.34	6.32	0.24	
12109.4	4908.93	13188.21	2704.23	670.21	29.5	
91.41	0.17	*696.339	*27.577	*0.61	*1.358	2077.37
13143.04	10.96	212.38	16.15	10.08	0.34	
23564.99	4691.92	7473.29	3340.17	1329.16	48.85	
109.78	0.07	*696.339	*27.577	*0.61	*1.358	3932.13
1899.97	13.59	212.38	5.72	5.48	0.16	
32047.66	11185.76	5829.34	2226.2	702.25	34.49	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	2833.7
19079.19	29.69	154.55	4.61	4.89	0.19	
40078.89	3077.83	4791.47	2451.26	1218.74	21.23	
115.75	0.16	*696.339	*27.577	*0.61	8.87	3399.18
15743.63	9.49	263.52	14.56	10.31	0.29	
28888.48	6292.37	6194.76	2797.37	989.18	53.06	
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	3417.27
85907.39	17.3	299.51	17.05	6.87	0.28	
34313.29	9190.84	5577.1	1964.39	1167.39	37.57	
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	4457.66
2269.54	12.68	331.48	9.5	8.65	0.31	
11595.97	5778.03	6046.51	2512.74	1281.87	18.79	
*12.5	0.19	*696.339	*27.577	*0.61	*1.358	1927.88
2269.54	32.71	232.48	11.73	8.9	0.26	
43028.15	3038.55	13406.91	1711.08	1368.54	42.35	
*12.5	0.09	*696.339	*27.577	*0.61	*1.358	3093.88
2918.04	17.4	163.38	7.61	7.39	0.22	
10957.71	4830	11763.93	2562.02	2182.23	44.12	
44.86	0.12	*696.339	*27.577	*0.61	*1.358	5481.94
5421.66	10.03	261.19	7.48	8.41	0.3	
13196.72	2312.62	10079.25	2794.88	949.47	14.13	
*38.55	0.14	*682.952	206.43	*0.576	*1.363	4353.29
17573.05	21.69	322.15	15.65	8.15	*0.03	
22672.02	12101.67	13128.4	2413.18	653.38	87.78	
*38.55	0.13	*682.952	*27.584	*0.576	*1.363	5640.83
1277.35	22.46	210.47	8.32	6.8	*0.03	
12434.32	4414.71	5442.05	4560.48	1735.21	152.94	
*38.55	0.1	*682.952	*27.584	*0.576	*1.363	4960.77
23658.81	15.72	123.02	9.6	6.34	*0.03	
19256.44	3913.89	9392.72	3716.43	792.22	73.29	
*38.55	0.14	*682.952	*27.584	16.39	*1.363	4539.6
27212.36	15.62	540.65	11.59	10.23	0.3	

Table4.txt

9634.67	18319.79	20722.31	2612.85	880.05	50.89				
*38.55	0.11	*682.952	*27.584	*0.576	*1.363	6051.18			
972.84	15.21	191.79		7.12	12.55	*0.03			
33525.99	4183.96	8255.66	3017.29	1441.68	49.12				
*38.55	0.26	*682.952	246.57	*0.576	8.37	4909.53			
124925.08	13.68	239.16		105.17	6.8	*0.03			
11728.56	5350.78	21504.44	1745.93	1547.93	56.51				
*38.55	0.11	*682.952	*27.584	*0.576	*1.363	6212.58			
54313.02	14.65	182.11		8.65	7.93	*0.03			
12943.94	5388.79	8626.42	3119.52	1678.3	45.2				
*38.55	0.08	*682.952	*27.584	*0.576	*1.363	3999.38			
47396.22	17.74	194.18		14.04	7.71	*0.03			
9906.35	5065.2	6251.14	2347.74	1224.09	75.52				
*38.55	0.19	*682.952	*27.584	*0.576	*1.363	3530.79			
61186.09	11.57	358		10.52	12.65	*0.03			
19994.65	7741.84	16534.85	2084.96	1905.51	47.33				
*38.55	0.13	*682.952	*27.584	*0.576	*1.363	7814.04			
3956.16	16.63	201.24		8.03	5.86	0.3			
15169.07	6127.54	51705.74	2390.94	1633.53	83.19				
*38.55	0.12	*682.952	*27.584	*0.576	*1.363	4604.45			
888.06	14.76	182.11		6.51	6.1	*0.03			
12720.61	6899.42	10283.9	3318.57	1170.49	81.2				
120.47	0.4	*682.952	180.96	16.39	*1.363	3281.88			
225030.98	10.71	156.66		8.5	8.79	0.44			
42131.57	5995.29	27883.7	3809.2	1531.6	77				
*38.55	0.12	*682.952	*27.584	7.45	*1.363	5955.59			
3284.63	9.63	201.24		7.05	5.36	*0.03			
15207.48	4068.34	6723.19	1653.1	716.62	45.31				
*38.55	0.16	*682.952	*27.584	*0.576	*1.363	6239.58			
8628.14	22.47	232.7		5.47	6.57	*0.03			
26409.3	7180.74	17041.71	1331.42	1252.91	117.94				
*38.55	0.11	*682.952	*27.584	4.82	*1.363	7262.76			
11448.07	10.11	145.89		6.98	6.8	*0.03			
7152.74	4644.83	14343.76	2607.87	1945.96	16.95				
*12.5	0.09	*696.339	*27.577	*0.61	*1.358	2898.46			
1083.39	13.47	237.38		8.72	10.77	0.29			
26008.97	6450.74	5300.9	2932.06	2279.46	114.13				
*12.5	0.14	*696.339	*27.577	*0.61	*1.358	3132.57			
2638.11	24.04	185.91		12.58	10.08	0.39			
39295.62	7362.41	8670.53	1774.49	1266.1	73.33				
62.28	0.24	*696.339	*27.577	*0.61	*1.358	3393.16			
52584.29	15.71	237.38		8.77	6.05	0.31			
10064.33	4731.37	7304.51	2560.79	2636.46	29.5				
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	2945.68			
12858.44	13.39	214.94		14.47	7.13	0.34			
11954.1	4948.39	5519.65	2847.18	1392.16	36.49				
*36.49	0.14	*644.123	*27.061	5.01	28.17	3240.97			
48244.27	18.56	257.69		3.91	8.16	*0.029			

Table4.txt

6005.23	3628.82	24967.29	1868.62	1546.59	72.05	
*36.49	0.57	*644.123	*27.061	*0.591	*1.31	7978.89
52845.75	23	271.31		3.34	4.4	*0.029
24930.47	3281.28	25218.65	1090.53	1168.67	41.45	
*36.49	0.12	*644.123	*27.061	3.76	*1.31	4612.7
26466.45	19.08	257.69		7	7.18	*0.029
35828.1	2588.78	21759.73	1224.51	712.81	8.76	
174.38	0.16	*644.123	*27.061	*0.591	*1.31	4076.35
26256.65	20.78	281.97		4.93	4.4	*0.029
31900.44	8127.2	13471.56	1409.5	1243.42	47.19	
*36.49	0.16	*644.123	*27.061	8.67	*1.31	6638.42
70339.02	31.54	173.31		5.38	4.85	0.39
41592.48	2128.49	12663.48	1893.11	681.41	24.79	
*36.49	0.17	*644.123	*27.061	6.24	*1.31	6088.47
58764.72	30.75	243.71		4.39	5.3	*0.029
23165.93	3957.97	49275.61	1541.71	1617.5	12.17	
*36.49	0.12	*644.123	*27.061	*0.591	*1.31	3366.12
74287.37	13.18	161.4		4.49	6.97	0.34
29334.42	2780.84	10681.05	391.46	834.53	2.18	
*36.49	0.11	*644.123	*27.061	*0.591	*1.31	6082.88
63340.29	24.15	196.01		6.54	5.3	*0.029
18933.75	1745.17	3869.94	1187.95	1448.12	16.83	
*36.49	0.12	*644.123	*27.061	*0.591	*1.31	2537.13
30343.22	18.15	156.16		3.72	7.57	*0.029
99448.14	3861.06	13512.01	2080.08	869.88	81.12	
118.66	0.14	*644.123	*27.061	*0.591	*1.31	3727.48
122859.46	25.02	205.36		8.4	3.45	*0.029
35310.12	8086.94	9528.62	1753.8	1330.01	23.8	
232.92	0.1	*644.123	*27.061	4.18	*1.31	1873.17
132863.04	5.44	166.55		9.06	2.94	*0.029
26454.26	5382.4	13208.74	2184.19	1101.8	14.14	
433.67	0.13	5035.74	*27.061	10.26	*1.31	2291.35
49434.16	7.33	166.55		4.96	1.53	*0.029
8905.05	4054.95	11826.96	1000.65	1113.6	69.88	
*36.49	0.17	*644.123	*27.061	*0.591	*1.31	5846.62
84134.87	11.28	342.31		9.19	1.84	*0.029
34159.99	2857.72	8010.81	2603.33	1361.5	24.61	
*36.49	0.13	*644.123	*27.061	*0.591	*1.31	5069.17
83975.08	12.85	192.85		5.08	3.2	*0.029
27338.97	4016.15	26205.22	1657.86	1479.63	14.14	
*12.5	0.15	*696.339	*27.577	*0.61	*1.358	2795.52
20801.6	14.82	169.14		9.07	6.6	0.26
35640.87	3726.61	9404.04	1748.15	893.81	18.86	
*12.5	0.13	*696.339	191.94	4.34	11.22	3314.98
12819.37	8.93	496.8		5.98	9.38	0.32
16601.14	13750.39	7585.67	3886.14	798.18	44.71	
*12.5	0.19	*696.339	*27.577	*0.61	*1.358	7620.72
1899.97	20.66	196.7		14.3	5.91	0.19

Table4.txt

9823.24	6648.78	5462.15	1301.93	1565.03	7.07		
*12.5	0.15	4907.79	168.42	9.19	*1.358	2605.61	
3959.89	32.06	284.03	23.45	14	0.49		
29208.8	4869.46	30290.31	1506.33	1313.4	72.67		
48.44	0.16	*696.339	*27.577	*0.61	*1.358	3345.02	
2339.12	31.34	301.69	2.43	5.91	0.39		
43728.47	4908.93	7169.29	3411.33	1376.41	32.47		
*12.5	0.25	*696.339	186.09	*0.61	*1.358	2020.81	
52660.59	9.81	318.88	15.33	9.14	0.32		
18336.87	6312.16	10884.45	2019.94	1737.42	24.71		
*12.5	0.16	*696.339	*27.577	*0.61	*1.358	4577.29	
11271.02	12.13	194.03	8.85	7.13	0.32		
17309.12	3018.91	3805.59	1809.24	1175.3	24.84		
*12.5	0.11	*696.339	*27.577	*0.61	*1.358	3090.91	
9416.49	10.82	180.4	5.72	8.65	0.25		
9382.1	3844.69	11895.63	3401.16	1557.18	10.75		
*12.5	0.09	*696.339	283.61	*0.61	*1.358	2414.52	
1899.97	17.56	660.38	24.1	8.9	0.44		
19539.28	3687.26	5691.86	2207.94	1604.25	13.99		
*12.5	0.1	*696.339	*27.577	*0.61	*1.358	3216.13	
*141.277	12.74	217.49	14.73	2.54	0.28		
59103.85	6292.37	12520.53	2235.95	1155.54	45.23		
100.68	0.19	*696.339	*27.577	*0.61	*1.358	3742.01	
1655.91	24.02	268.14	10.1	6.87	0.37		
11483.11	5303.76	7866.15	1590.66	1455.08	48.91		
*12.5	0.14	*696.339	*27.577	7.89	*1.358	1944.74	
24071.82	12.3	272.72	5.72	15.22	0.38		
6490.55	3844.69	8614.82	821.05	861.96	22.4		
41.22	0.12	*696.339	168.42	*0.61	*1.358	2582.36	
79706.22	5.57	201.99	7.52	5.48	0.26		
19140.58	4790.54	9415.12	1507.52	977.27	44.94		
*12.5	0.15	*696.339	*27.577	*0.61	*1.358	6362.94	
7156.37	11.84	247.03	14.47	5.33	0.27		
13790.78	2351.82	8112.45	4776.3	1490.44	7.82		
*12.5	0.17	*696.339	*27.577	*0.61	*1.358	2475.13	
969.9	6.59	247.03	9.8	4.89	0.28		
11049.85	4790.54	5023.55	3408.79	1447.22	38.77		
*12.5	0.09	*696.339	*27.577	*0.61	*1.358	5629.08	
*141.277	13.29	196.7	9.41	3.95	0.19		
27711.54	2979.63	8235.42	2904.57	1329.16	31.79		
*12.5	0.08	*696.339	*27.577	*0.61	*1.358	3907.52	
3037.4	12.19	169.14	6.07	6.05	0.16		
22686.74	2940.36	6898.33	2392.37	806.16	13.16		
*12.5	0.12	*696.339	*27.577	*0.61	*1.358	5261.06	
2857.26	12.47	148.53	6.15	5.48	0.17		
10016.32	1490.71	9503.81	2776.23	806.16	4.4		
*12.46	0.12	*676.132	*27.292	*0.628	*1.37	3854.09	
10047.31	24.06	235.98	6.13	5.04	0.15		

Table4.txt

32843.59	3599.6	9638.97	2472.36	1672.35	74.86	
*12.46	0.09	*676.132	*27.292	*0.628	*1.37	3427.6
3296.59	8.78	183.05		4.52	10.09	0.24
26958.26	2192.13	43633.59	2413.27	1352.37	18.37	
*12.46	0.11	*676.132	*27.292	*0.628	*1.37	3506.6
62510.51	15.28	288.88		4.24	4.25	0.15
25937.25	3958.03	12350.54	2851.54	796.6	23.32	
755.53	0.24	*666.122	*27.161	*0.536	*1.359	5617.08
3106.56	18.91	217.06		8.38	46.1	0.32
35120.9	1425.48	9712.47	2792.8	2139.28	14.5	
518.83	0.28	*666.122	*27.161	*0.536	*1.359	3903.91
3335.87	17.23	211.59		4.47	42.7	0.39
28913.67	5831.47	34848.4	2170.96	1834.04	38.9	
447.72	0.37	*666.122	*27.161	*0.536	*1.359	3381.74
10475.39	10.57	424.67		11.51	58.31	0.41
40900.92	14329.36	14245.33	2523.58	1792	34.2	
326.78	0.3	*666.122	*27.161	*0.536	*1.359	2824.29
6831.11	9.07	173.11		9.29	40.5	0.27
33875.85	9349.77	4808.53	1335.66	2402.02	72.75	
670.1	0.26	*666.122	*27.161	*0.536	*1.359	2429.91
6147.25	6.7	102.37		12.06	26.37	0.42
23614.46	1158.7	8739.94	2868.47	1776.72	20.21	
672.8	0.35	*666.122	*27.161	*0.536	9.4	1841.64
2291.22	11.93	143.39		14.45	34.03	0.35
18379.91	25733.8	14596.3	2419.97	2024.9	60.65	
359.86	0.25	*666.122	*27.161	*0.536	*1.359	2578.18
5734.16	13.28	127.31		10.75	17.94	0.32
14114.92	8585.57	7448.91	1698.46	2265	37.15	
386.55	0.22	*666.122	*27.161	15.23	45.95	2141.54
1939.26	6.73	1121.43		3.27	13.36	0.32
17699.55	8712.58	5077.33	2142.73	260.21	41.92	
604.86	0.21	*666.122	*27.161	*0.536	*1.359	1550.56
5245.63	6.75	194.75		7.6	47.16	0.3
24705.73	11225.33	23763.32	2511.1	1259.28	37.38	
401.25	1.66	*666.122	*27.161	*0.536	*1.359	5170.44
4036.6	12.79	337.33		13.43	103.41	0.47
23265.64	16340.37	15848.31	2780.06	1807.29	42.48	
350.89	0.38	*666.122	*27.161	*0.536	*1.359	4892.7
28697.41	9.11	251.89		32.64	40.16	0.33
7892.41	12303.08	13705.86	1791.35	1883.69	29.76	
258.89	0.86	*666.122	245.14	*0.536	*1.359	2486.73
8891.5	25.27	540.99		15.37	18.6	0.49
15458.79	12396.35	2766.36	885.19	1213.13	52.88	
227.08	0.3	*666.122	*27.161	*0.536	*1.359	2183.09
15109.42	9.95	248.52		10.46	20.1	0.5
17198.72	17238.54	5304.8	2335.68	2043.97	72.43	
410.03	0.58	*666.122	*27.161	*0.536	*1.359	2155.37
7870.54	14.33	293.84		10.3	30	0.5

Table4.txt

33588.22	16035.5	8996.51	2275.41	1929.51	97.96	
239.88	0.66	*666.122	*27.161	4.7	*1.359	1342.22
4231.78	17.22	200.44		16.58	16.38	0.54
33444.35	8151.19	6509.06	1934.39	2154.53	41.98	
119.3	0.43	*666.122	*27.161	*0.536	*1.359	1987.8
1939.26	34.66	200.44		8.83	18.05	0.43
38609.17	9916.96	3441.09	976.82	1616.05	87.75	
181.26	0.51	*666.122	208.26	*0.536	*1.359	2526.65
9110.86	26.25	169.02		19.38	13.24	0.57
41068.07	7413.29	11046.78	1025.85	1738.49	68.46	
177.92	0.62	*666.122	*27.161	*0.536	43.65	2618.39
8191.34	9.97	107.58		18.46	50.05	0.44
32484.34	6325.95	11211.36	2554.83	1224.67	70.97	
377.69	0.29	*666.122	223.09	*0.536	*1.359	3454.85
35912.71	15.92	222.45		37.01	42.03	0.3
24012.14	4609.77	5451.52	1166.35	1573.93	23.79	
467.81	0.24	*666.122	*27.161	*0.536	*1.359	3390.86
7111.31	8.35	217.06		4.28	18.27	0.25
24903.38	6255.12	17623.89	2448.89	1570.1	108.88	
227.08	0.48	*666.122	*27.161	*0.536	*1.359	7464.88
55811.73	14.76	368.51		17.34	28.87	0.26
23962.48	9386.28	4996.82	3461.14	2379.19	26.35	
271.43	0.13	*666.122	*27.161	*0.536	*1.359	2393.12
2431.55	16.2	173.11		16.29	21.66	0.23
37892.93	5550.33	11893.79	1556.16	1792	123.94	
377.69	0.3	*666.122	*27.161	*0.536	*1.359	3506.84
1476.26	18.98	*12.834		12.62	21.46	0.22
40709.91	1221.09	2205.55	1770.95	2040.16	17.61	
293.16	0.11	*666.122	*27.161	*0.536	28.5	4128.39
7827.16	11.75	117.66		8.73	11.89	0.21
51678.25	2116.38	11034.12	4267.46	24657.52	45.19	
191.22	0.09	*666.122	*27.161	*0.536	*1.359	2205.31
2824.25	8.76	334.42		10.75	9.71	0.14
25026.8	6716.57	4862.4	2897.36	24504.64	13.07	
59.24	0.3	*666.122	*27.161	*0.536	*1.359	1493.45
13185.84	15.9	152.17		59.16	29.34	0.31
53229.69	7198.35	16060.97	2495.52	2036.34	32.25	
174.57	0.24	*666.122	*27.161	4.7	*1.359	3577.46
19223.92	12.97	124.94		10.33	13.96	0.36
29253.01	973.11	5398.21	454.78	566.63	9.74	
86.35	0.3	*666.122	*27.161	*0.536	*1.359	2373.36
1345.1	9.71	160.71		9.45	11.01	0.18
27600.9	8060.92	8714.25	717.54	2150.72	36.31	
214.16	0.37	*666.122	*27.161	*0.536	*1.359	6045.71
23020.78	20.55	115.18		14.58	28.2	0.34
25642.64	1189.86	8379.89	1008.29	1278.51	10.75	
323.75	0.22	*666.122	*27.161	*0.536	47.64	6176.41
7429.76	13.72	1153.12		8.7	18.38	0.46

Table4.txt

34546.51	4644.36	9060.57	2342.86	1573.93	41.7		
236.69	0.14	*666.122	*27.161	*0.536	*1.359	3800.6	
6543.53	5.78	117.66		5.77	34.75	0.21	
13444.56	820.47	15109.87	3767.08	1879.87	7.1		
217.4	0.1	*666.122	*27.161	*0.536	*1.359	3454.85	
102495.08	7.59	124.94		6.42	21.35	0.23	
26844.16	1252.37	10005.58	3083.92	1661.98	24.93		
112.12	0.1	*666.122	*27.161	*0.536	*1.359	1367.65	
6592	7.15	94.28		5.81	14.55	0.18	
19930.45	1840.79	3021.14	744.92	1466.63	25.7		
181.26	0.08	*666.122	*27.161	*0.536	*1.359	1879.34	
75096.28	14.64	198.55		13.3	15.93	0.14	
55078.91	3311.26	8970.87	2461.31	2363.97	75.14		
347.89	0.36	*666.122	*27.161	*0.536	66.29	3433.49	
17802.98	14.38	781.37		8.38	22.79	0.38	
35957.91	4506.11	10577.66	1119.76	2489.5	99.58		
112.12	0.26	*666.122	*27.161	*0.536	*1.359	1367.65	
31021.53	6.82	192.83		27.02	34.75	0.23	
21659.91	8948.84	6574.66	1052.28	2649.15	48.59		
55.22	0.21	*666.122	193.3	4.11	*1.359	3966.84	
19094.74	7.36	134.32		55.64	48.61	0.28	
32580.42	1696.13	4673.62	275.88	1960.04	10.28		
174.57	0.53	*666.122	200.79	*0.536	10.84	2045.2	
59617.2	5.56	204.19		8.51	21.56	0.34	
22465.17	14782.83	15798.26	2090.51	2835.24	46.07		
541.24	0.52	*666.122	266.97	*0.536	*1.359	1411.08	
37713.52	12.79	241.7		16.45	49.49	0.29	
20135.34	17334.31	8560.04	1875.35	1792	35		
476.37	0.2	*666.122	*27.161	3.51	*1.359	1812.13	
12178.01	9.58	164.89		7.92	22.39	0.28	
18744.03	5165.54	6495.93	1197.9	1658.16	44.3		
347.89	0.12	*666.122	*27.161	*0.536	139.04	3266.71	
1053.03	10.43	200.44		11.11	35.64	0.21	
21962.47	2775.25	6587.77	832.32	827.11	19.66		
305.45	0.35	*666.122	178.21	*0.536	*1.359	1919.88	
39614.42	9.59	256.9		16.16	34.75	0.3	
37033.2	10652.53	14846.87	1664.82	1608.4	25.23		
507.56	0.14	5828.81	*27.161	13.08	*1.359	3345.32	
7696.11	14.07	104.99		9.74	47.64	0.26	
43768.32	1189.86	8199.47	477.12	441.45	30.98		
290.07	0.84	*666.122	170.61	*0.536	*1.359	3442.64	
171119.8	50.35	215.24		11.64	17.72	0.57	
68033.85	10837.05	10590.35	3317.03	1860.78	32.94		
262.03	0.25	*666.122	*27.161	*0.536	*1.359	1833.59	
59768.18	12.49	213.42		12.94	20.73	0.24	
22941	7269.94	4389.13	1603.65	1485.8	44.08		
187.91	0.17	*666.122	237.82	*0.536	*1.359	2632.79	
31389.68	5.73	181.13		9.32	36.17	0.29	

Table4.txt

29495.16	6503.28	10806.01	2344.91	216.55	36.98	
314.62	0.47	*666.122	*27.161	*0.536	*1.359	3197.52
1476.26	48.75	348.83		3.2	11.64	0.36
57917.34	4575.2	12725.53	698.55	1631.37	22.59	
479.22	3.39	*666.122	*27.161	*0.536	*1.359	4462.62
3410.05	15.46	194.75		34.43	13.84	0.41
80900	13594.87	7552.75	1669.62	1776.72	80	
122.86	0.67	*666.122	223.09	24.11	*1.359	4391.38
20529.22	8.79	99.71		7.53	34.48	0.47
45899.41	805.32	11994.73	2516.3	3555.51	35.17	
174.57	0.17	*666.122	*27.161	*0.536	12.67	2039.72
2243.18	6.36	82.91		7.73	9.44	0.2
40757.66	3683.73	5584.61	723.33	1902.78	23.19	
42.83	0.29	*666.122	*27.161	*0.536	*1.359	2384.65
16890.09	25.14	188.97		17.01	10.37	0.3
16320.85	5673.2	13278.85	1348.57	1688.77	48.53	
*39.91	0.57	7301	272.46	9.03	*1.38	5587.62
24663.78	12.72	172.16		10.53	15.25	0.58
54471.76	3301.93	6872.17	1400.76	2449.69	35.47	
*39.91	0.53	*682.77	227.88	*0.64	10.39	4513.28
6077.12	15.3	149.74		244.78	14.8	0.49
29936.89	5998.89	12346.24	1473.72	3949.24	50.97	
*39.91	0.62	*682.77	328.83	*0.64	*1.38	3536.03
18208.05	12.91	274.83		15.68	9.02	0.89
31089.02	5648.02	9143.57	2346.59	3616.82	85.89	
*39.91	0.51	*682.77	286.85	*0.64	10.39	3845.93
20197.64	18.2	315.52		19.9	30.84	0.68
20797.54	10808.2	13459.7	2813.13	2977.92	88.69	
*39.91	0.38	*682.77	163.97	*0.64	*1.38	3420.79
5506.25	15.01	206.36		6.6	*0.756	0.58
47401.37	4780.93	10095.19	3173.5	2326.68	293.3	
*39.91	0.51	*682.77	279.68	*0.64	*1.38	2847.41
12886.15	41.01	397.69		20.65	23.95	0.69
23416.16	14592.22	4346.71	4015.6	2988.79	76.78	
*39.91	1.34	*682.77	550.69	*0.64	16.58	3851.84
12010.85	27.73	409.97		14.97	9.02	1.21
58523.37	12401.64	10189.4	2331.6	3064.76	51.57	
193.28	0.35	*682.77	*27.33	*0.64	*1.38	5361.96
19880.16	28.83	303.26		16.47	27.66	0.48
46043.92	9501.72	15878.42	1476.19	2505.35	59.61	
219.02	0.79	4592.21	395.64	4.91	9.83	2629.08
17491.33	9.82	318.55		115.63	37	0.87
20582.68	12992.05	14203.62	1824.08	2038.22	56.25	
169.51	0.44	*682.77	315.02	4.48	*1.38	4448.62
134965.36	29.12	217.21		28.77	17.67	0.91
15107.43	4780.93	8757.58	4466.13	1917.95	23.87	
*39.91	0.51	*682.77	*27.33	12.89	*1.38	2156.43
2441.64	14.52	258.48		18.19	9.21	0.55

Table4.txt

39532.58	6887.32	9143.57	3825.71	2066.72	106.57	
*39.91	0.64	*682.77	163.97	*0.64	*1.38	5245.4
7822.61	18.79	202.69		8.98	10.46	0.59
35526.54	6367.18	10844.39	3258.63	3759.73	76.16	
*39.91	0.4	*682.77	434.2	*0.64	12.64	2050.15
50713.96	7.09	187.7		34.29	15.69	0.59
54236.1	6887.32	7327.53	2122.19	1609.91	103.25	
158.73	1.43	*682.77	180.56	*0.64	*1.38	4865.78
3402.9	17.41	340.92		19.16	19.82	0.62
30357.5	9107.64	10564.6	3162.08	2298.61	34.78	
*39.91	0.34	*682.77	163.97	*0.64	9.27	4467.07
9237.58	14.38	329.07		26.87	17.11	0.66
5672.87	13636.59	20944.45	3008.78	1580.48	147.67	
*39.91	0.47	*682.77	*27.33	4.04	*1.38	7976.75
29122.66	11.68	345.31		10.08	10.98	0.47
37145.75	2989.23	10032.3	2853.46	1761.89	46.37	
*39.91	2.06	*682.77	163.97	*0.64	8.71	3620.17
2441.64	14.04	358.36		14.49	16.55	0.73
35225.62	14133.05	46583.47	4013.01	1917.95	81.42	
*39.91	1.01	*682.77	321.95	*0.64	*1.38	6017.56
3840.85	16.11	297.05		24.67	14.5	0.93
64944.42	15161	16009.53	2948.11	2583	119.59	
*39.91	0.52	*682.77	196.7	*0.64	*1.38	4120.23
7420.8	17.03	290.78		9.01	16.12	0.74
26105.69	14702.35	13758.03	2925.38	2759.4	139.75	
*39.91	0.53	7301	293.96	6.6	*1.38	3701.86
7778.87	5.72	365.51		18.41	18.89	0.81
68219.42	3135.63	10782.33	1809.21	2786.83	48.5	
*39.91	0.42	*682.77	*27.33	*0.64	*1.38	7448.58
6901.71	21.65	180		12.83	9.93	0.63
45160.23	8410.43	11522.95	3771.62	2146.26	97.41	
*39.91	0.56	*682.77	*27.33	*0.64	*1.38	4790.27
40903.92	32.8	213.62		9.17	12.64	0.84
48565.06	4461.72	6220.02	1193.03	1324.28	30.31	
*39.91	0.48	*682.77	212.46	*0.64	*1.38	4069.17
37132.65	16.33	198.99		34.44	11.32	0.53
25967.04	5314.71	3850.73	1680.36	3075.59	26.48	
*39.91	0.27	*682.77	212.46	*0.64	9.27	4687.01
14165.37	11.81	265.07		16.47	8.06	0.67
45876.89	11198.33	10937.36	4364.11	1491.76	76.37	
*39.91	0.83	*682.77	163.97	*0.64	*1.38	6499.68
11013.18	17.45	379.65		8.63	16.12	0.53
50270.53	3998.42	9111.53	2781.65	2174.57	46.02	
494.54	0.66	*682.77	328.83	*0.64	25.6	4341.43
37980.93	11.94	617.93		25.83	11.49	0.73
51735.8	10771.01	9685.04	3503.49	3328.82	91.65	
*39.91	0.44	*682.77	279.68	8.23	*1.38	4192.6
25618.88	24.63	1040.85		13.1	8.83	0.41

Table4.txt

55484.86	9051.26	10626.89	1742.29	1894.94	81.3	
383.92	0.66	*682.77	180.56	4.04	10.11	6708.77
10071.9	18.55	189.6		29.29	12.48	0.49
50814.41	4099.62	49215.44	4154.38	3414.47	68.7	
347.2	0.36	*682.77	196.7	*0.64	*1.38	6197.27
10141.62	12.37	153.92		139.69	11.99	0.4
22391.61	3590.61	12754.36	3807.67	2168.91	19.27	
*39.91	0.83	8942.04	355.98	12.89	10.95	4045.2
104010.96	12.72	467.88		120.4	22.61	1.15
114784.86	4180.38	7594.56	1001.18	2682.4	26.67	
439.93	0.5	*682.77	257.86	*0.64	*1.38	4998.77
19437.12	17.29	290.78		5.4	11.32	0.46
81335.38	6483.08	8902.71	3989.71	2885.31	23.28	
*39.91	0.6	*682.77	*27.33	*0.64	*1.38	4846.87
1875.93	12.82	202.69		9.13	15.98	0.52
23676.4	5687.11	8660.55	3345.19	2304.23	49.5	
*39.91	0.92	*682.77	163.97	9.82	*1.38	5113.62
36925.26	14.2	172.16		10.68	14.5	0.69
24193.21	5960	9031.33	4077.79	1756.07	58.42	
*39.91	0.38	10496.23	196.7	11.37	*1.38	5120.03
7188.99	5.94	261.79		8.4	21.86	0.67
33405.36	8334.82	13295.17	397.31	1521.41	55.52	
*39.91	0.27	*682.77	*27.33	*0.64	*1.38	2532.02
6998.64	11.19	168.18		11.1	13.27	0.58
33073.79	7385.03	10283.44	2331.6	1848.8	86.79	
419.94	0.46	*682.77	*27.33	*0.64	48.25	5663.51
20158.17	15.54	180		11.25	12.32	0.68
38060.02	6521.68	10220.76	2369.07	1883.42	39.57	
*39.91	0.52	7720.93	315.02	4.04	*1.38	4090.17
9716.81	11.46	236.51		13.32	29.76	0.7
37739.36	7651.88	12194.51	1954.37	2516.46	20.79	
*39.91	0.21	*682.77	227.88	*0.64	*1.38	3261.01
11332.98	18.53	278.05		8.67	13.43	0.61
23503.05	13654.99	9574.05	3391.09	2236.7	45.67	
*39.91	0.47	*682.77	163.97	*0.64	*1.38	6234.8
5854.81	18.78	158.05		9.47	8.64	0.39
38797.77	3856.25	6080.86	2847.16	2405.05	28.85	
*39.91	0.56	*682.77	*27.33	*0.64	*1.38	3103.03
14451.09	13.4	220.77		9.85	14.5	0.73
19522.86	4939.7	8967.06	1853.85	1738.62	73.83	
*39.91	0.57	*682.77	382.55	*0.64	*1.38	4758.91
76663.64	16.59	160.1		15.38	13.59	0.45
42976.71	5804.21	8302.91	3430.65	2292.99	13.11	
*39.91	1.3	*682.77	*27.33	*0.64	*1.38	5078.45
78610.63	11.36	309.42		16.66	10.98	0.77
75694.14	1956.83	11813.75	1094.05	1721.14	71.29	
*39.91	0.31	*682.77	*27.33	*0.64	*1.38	4947.98
106647.08	12.72	164.16		11.06	8.64	0.49

Table4.txt

40775.58	5334.37	18532.22	3073.33	1521.41	16.05	
*39.91	0.3	*682.77	196.7	*0.64	*1.38	4460.91
61681.15	13.31	258.48		7.26	16.55	0.6
53010.14	6154.2	14203.62	2750.18	1825.67	20.19	
*39.91	0.32	*682.77	328.83	*0.64	12.07	3498.48
9498.24	13.96	366.94		26.01	17.39	0.56
87089.51	14224.92	12315.92	3346.47	2416.22	102.63	
408.75	0.42	*682.77	*27.33	*0.64	*1.38	4967.01
7734.92	34.53	409.97		5.71	15.69	0.5
40897.05	7289.54	11859.55	3762.61	2510.9	57.31	
166.83	0.46	*682.77	180.56	4.04	*1.38	4765.17
47804.05	8.53	241.66		13.32	17.67	0.53
39557.02	7193.94	13160.31	2052.53	1491.76	58.08	
*39.91	0.43	*682.77	163.97	*0.64	12.07	4476.3
1875.93	18.89	661.48		19.64	188.39	0.55
38207.82	3322.65	20492.71	3493.26	2377.1	46.2	
*39.91	0.84	*682.77	257.86	*0.64	*1.38	5326.26
8814.46	15.76	215.42		14.15	12.64	1.26
55272.84	7708.97	20506.84	3313.35	3393.08	117.7	
335.57	5.11	*682.77	180.56	*0.64	*1.38	5423.8
27582.81	17.49	315.52		19.64	11.32	0.84
44466.05	7251.31	11584.27	2153.31	2321.07	40.46	
457.54	0.8	*682.77	196.7	*0.64	*1.38	7152.06
25119.45	11.61	390.79		16.24	30.41	0.7
33099.33	7059.93	13130.31	1447.75	2988.79	22.49	
*39.91	0.54	*682.77	243	4.48	9.83	3728.22
19760.09	27.32	310.95		13.4	39.14	0.87
61824.19	9894.74	15411.03	3715.03	1802.51	34.24	
778.23	0.44	*682.77	301.03	5.77	*1.38	6142.83
9534.97	12.89	309.42		15.5	19.82	0.67
60974.78	7308.65	8188.47	3093.6	2577.46	15.14	
*39.91	0.44	*682.77	272.46	*0.64	*1.38	3553.4
33558.34	13.86	234.79		25.79	14.5	0.65
76515.94	9838.66	11061.1	3587.98	2197.19	89.27	
*39.91	0.34	*682.77	272.46	*0.64	*1.38	4928.97
25152.97	19.78	245.06		23	17.94	0.68
46020.06	6656.59	14529.02	5780	1662.72	15.51	
*39.91	0.84	*682.77	408.6	*0.64	*1.38	2863.93
28880.08	9.62	271.6		16.84	19.29	0.7
52845.03	11661.85	13668.64	2643.35	949.1	37.05	
*39.91	0.49	6438.09	328.83	5.77	*1.38	7627.97
42357.71	5.08	200.84		243.82	23.83	0.75
11529.16	3528.99	10063.76	3098.67	1946.67	12.67	
*39.91	0.3	*682.77	*27.33	*0.64	*1.38	5866.38
15009.02	9.05	265.07		4.89	9.21	0.52
52679.89	5608.91	15790.94	3609.77	2360.31	55.44	
*39.91	0.58	*682.77	272.46	*0.64	*1.38	4544.16
68242.83	9.12	241.66		46.51	15.69	0.84

Table4.txt

18237.22	3672.58	10968.32	2843.37	1011.75	34.56	
*39.91	1	*682.77	227.88	*0.64	16.58	5666.81
12829.37	12.78	246.76		9.85	17.11	0.82
26657.44	8410.43	10611.33	3393.64	1825.67	62.65	
*39.91	0.39	5538.56	180.56	7.42	*1.38	3763.43
4386.38	23.03	227.83		10.8	12.48	0.58
30723.96	2437.05	8040.84	3585.41	1779.31	40.91	
*39.91	0.96	*682.77	163.97	*0.64	*1.38	5229.27
1875.93	23.43	253.49		18.93	12.15	0.66
35300.91	8674.7	7843.14	2853.46	1998.23	52.31	
231.66	0.96	*682.77	315.02	*0.64	*1.38	5209.94
9931.18	11.36	315.52		27.72	19.29	0.68
68124.27	10286.8	9367.26	3680.34	1545.07	49.37	
*39.91	1.99	*682.77	180.56	*0.64	8.71	4909.99
32247.2	17.4	455.01		14.67	18.89	0.86
24931.56	11049.8	15323.17	3139.24	1998.23	58.84	
*39.91	0.28	5993.44	227.88	*0.64	*1.38	2800.71
7601.71	14.24	359.79		13.62	36.01	0.68
20087.41	13986.01	6770.11	2780.39	1098.64	35.97	
*39.91	0.79	*682.77	328.83	*0.64	*1.38	3778.13
8656.12	11.07	297.05		14.97	19.82	0.6
35376.16	9445.49	12980.14	2898.87	1123.3	25.47	
295.39	0.49	*682.77	243	*0.64	*1.38	4516.37
37904.28	21.21	238.23		30.85	28.67	0.48
30958.8	7136.54	8595.75	2123.43	1306.18	27.72	
*39.91	0.52	*682.77	*27.33	*0.64	*1.38	5779.62
10618.57	36.37	345.31		12.34	14.2	0.88
24563.55	11587.75	13100.3	3131.63	1998.23	27.67	
435.5	0.52	9728.52	408.6	4.04	*1.38	5126.43
14959.01	14.49	431.42		19.98	*0.756	0.37
41236.83	9088.85	17528.75	2186.93	2814.23	21.94	
524.59	1.11	*682.77	301.03	*0.64	47.68	4702.61
61711.46	18.54	1034.52		9.58	20.72	1.03
20766.91	9239.13	11215.43	2281.68	2365.91	30.92	
226.62	0.44	*682.77	*27.33	*0.64	*1.38	6934.43
3494.52	27.07	287.62		7.18	16.83	0.64
39434.77	8012.87	9937.82	2967.06	2021.1	38.49	
*39.91	0.27	*682.77	*27.33	*0.64	9.27	4878.4
46522.17	34.21	238.23		17.74	8.45	0.55
23964.11	4541.74	22041.75	3969.01	1912.2	26.38	
*39.91	0.65	*682.77	*27.33	*0.64	*1.38	4216.81
57121.57	21.85	166.18		11.21	10.64	0.37
32484.79	2372.36	6736.02	4236.32	993.01	9.29	
466.3	0.68	*682.77	*27.33	*0.64	*1.38	4932.14
8656.12	8.63	315.52		4.93	17.67	0.52
38675.02	4361.47	4737.84	2838.33	1686.12	29.7	
581.61	0.47	*682.77	212.46	4.48	*1.38	4658.96
6803.55	11.58	202.69		41.02	22.36	0.61

Table4.txt

33277.95	4099.62	7444.6	2509.17	1562.79	20.49	
*39.91	0.31	*682.77	*27.33	*0.64	*1.38	6085.16
18014.82	13.52	215.42		14.3	10.64	0.58
44753.47	4541.74	9937.82	2965.8	1715.31	25.61	
*38.55	0.16	*682.952	*27.584	*0.576	*1.363	4496.47
6704.54	15.36	196.55		12.63	11.8	*0.03
36132.48	9710.35	3820.19	4621.18	1025.68	95.96	
*38.55	2.88	*682.952	165.5	*0.576	*1.363	7970.09
20140.03	36.51	432.81		18.7	8.15	0.55
14666.91	14220.11	7473.47	2949.32	2744.89	291.25	
*38.55	0.27	*682.952	421.01	*0.576	*1.363	2916.2
18623.59	8.93	3460.57		47.06	11.02	*0.03
28009.96	6861.87	16444.35	1156.25	1865.02	87.42	
*38.55	0.27	*682.952	*27.584	*0.576	*1.363	3807.19
39656.51	16.73	172.16		7.19	5.24	*0.03
14355.23	6146.42	8218.53	1220.01	1800.16	118.3	
*38.55	0.36	*682.952	165.5	*0.576	*1.363	3807.19
35000.36	16.8	228.34		14.79	9.42	*0.03
33423.24	6466.96	11052.53	1972.71	2388.91	89.23	
*38.55	0.28	*682.952	*27.584	9.24	*1.363	3026.14
3387.88	20.75	237.02		18.62	14.73	0.39
10352.11	6278.5	5298.28	2535.8	1384.34	109.22	
*38.55	0.28	*682.952	*27.584	*0.576	*1.363	5352.35
3609.18	9.52	284.16		11.78	10.83	*0.03
46909.85	6655.16	13455.16	296.79	1531.6	105.8	
*38.55	3.31	21645	165.5	*0.576	14.11	16411.49
1130.96	55.78	560.35		77.09	38.45	0.96
146962.79	26608.72	19768.84	2528.36	3794.89	124.55	
*38.55	0.86	*682.952	*27.584	*0.576	*1.363	6499.44
25345.79	46.83	282.2		11	7.03	0.54
11284.43	8579.99	14325.64	1790.66	4164.45	85.64	
*38.55	0.38	*682.952	*27.584	*0.576	*1.363	7302.92
26019.53	21.65	239.16		9.35	7.93	0.32
33080.79	7068.28	8700.45	2901.57	3019.6	41.24	
322.3	0.73	*682.952	*27.584	*0.576	11.88	3835.03
11847.58	3.77	307.24		113.43	16.81	0.41
29416.86	7218.21	6099.51	2700.06	1974.26	222.04	
362.3	0.26	*682.952	*27.584	*0.576	*1.363	3862.92
8236.52	31.43	266.22		30.11	9	0.44
10593.81	12412.92	13799.87	4065.63	1848.81	68.18	
122.87	0.22	*682.952	*27.584	*0.576	*1.363	4683.96
38835.8	25.93	266.22		12.55	16.13	0.39
30958.31	15166.17	9668.8	4176.3	1355.63	249.93	
*38.55	0.42	*682.952	170.67	*0.576	10.25	3971.31
111847.64	13.9	376.97		26.31	7.03	*0.03
11602.35	6353.92	17304.21	2943.03	963.38	100.07	
*38.55	0.32	*682.952	*27.584	*0.576	*1.363	7254.74
3609.18	26.67	290.02		13.41	23.94	0.31

Table4.txt

28833.89	9377.44	8811.43	3563.64	825.72	100.79				
*38.55	0.77	*682.952	*27.584	*0.576	*1.363	5449.38			
5304.75	27.5	266.22		11.92	7.26	0.38			
8892.57	5483.78	*137.987	3319.85	1560.17	74.78				
*38.55	0.27	*682.952	*27.584	*0.576	*1.363	4979.1			
21364.1	23.51	228.34		16.14	9	0.42			
14237.79	4568.19	6118.48	3043.76	1621.32	140.79				
*38.55	0.47	4247.36	170.67	7.97	*1.363	6239.58			
76322.75	16.97	312.87		21.95	20.72	0.57			
33217.76	4683.13	5183.04	2351.44	2236.29	174.33				
*38.55	0.16	*682.952	*27.584	*0.576	*1.363	4232.32			
4465.34	20.66	228.34		35.64	14.29	*0.03			
11199.06	4874.36	5009.76	2257.84	1038.13	186.86				
*38.55	0.52	*682.952	*27.584	*0.576	*1.363	3943.29			
45393.66	10.45	333.11		9.6	10.63	0.5			
17391.93	11441.53	5566.39	1456.49	2465.07	55.41				
*38.55	1.05	*682.952	*27.584	*0.576	*1.363	6220.29			
49735.5	23.21	342.1		13.26	13.84	0.43			
13566.21	8710.02	10723.43	2727.52	3747.62	33.81				
*38.55	0.59	*682.952	*27.584	*0.576	*1.363	4862.05			
6197.44	15.29	286.12		13.52	8.36	*0.03			
35205.55	5938.56	14869.19	3289.34	1625.39	65.82				
*38.55	0.27	*682.952	*27.584	*0.576	9.71	8222.45			
12367.2	14.18	323.99		8.07	11.22	0.45			
11134.85	5862.89	9051.59	2371.19	1824.49	41.92				
*38.55	0.56	*682.952	211.49	6.93	*1.363	6726.52			
3569.51	8.25	325.82		19.11	16.64	0.54			
36373.01	7629.78	6364.67	2266.45	863.35	41.75				
*38.55	0.35	*682.952	165.5	*0.576	*1.363	7512.69			
10953.14	13.3	237.02		8.29	7.26	0.34			
13366.57	4931.65	5795.35	2657.67	1824.49	52.22				
*38.55	0.68	*682.952	186.08	*0.576	13.69	8401.74			
207680.85	15.64	393.8		32.43	23.79	0.32			
25078.05	12979.75	6345.76	1865.76	1490.75	36.65				
*38.55	0.76	*682.952	*27.584	11.01	*1.363	4246.52			
3529.59	18.28	370.13		3.9	9.1	0.33			
9080.68	5198.57	3443.12	1117.38	1844.76	44.53				
*38.55	0.49	*682.952	*27.584	*0.576	*1.363	3359.96			
2428.82	20.45	345.67		8.21	11.8	0.43			
15265.06	13454.47	8617.16	3725.43	1856.92	239.7				
*38.55	0.4	*682.952	*27.584	*0.576	11.06	3167.04			
21605.77	30.01	437.56		14.64	11.41	0.68			
42427.95	11845.12	7939.68	2282.44	2095.36	238.71				
*38.55	0.64	*682.952	*27.584	10.25	*1.363	2363.92			
92105.13	17.09	205.88		14.64	11.41	0.43			
5398.34	7330.56	9641.21	2239.4	2155.81	29.33				
*38.55	0.25	*682.952	*27.584	*0.576	*1.363	3194			
50047.5	11.2	223.94		10.45	11.12	0.35			

Table4.txt

10962.91	5730.35	5528.15	2930.46	804.79	52.99	
*38.55	0.19	*682.952	165.5	*0.576	*1.363	4211.04
31677.71	8.9	223.94		16.89	10.93	*0.03
32772.64	6542.27	8700.45	2206.23	788.03	71.91	
*38.55	0.16	*682.952	*27.584	*0.576	*1.363	3575.45
2574.17	14.11	320.31		12.26	11.12	0.4
14001.98	9451.46	5537.71	2522.16	1100.25	80.41	
*38.55	0.41	*682.952	*27.584	*0.576	*1.363	5921.27
36921.52	19.67	397.12		22.64	12.74	0.35
12021.06	7517.64	12710.54	3146.07	2083.26	32.93	
198.33	0.27	*682.952	*27.584	*0.576	167.13	5285.4
9338.12	26.45	309.12		15.39	8.25	0.33
27477.12	8021.67	9153.08	3773.09	1318.69	80.47	
*38.55	0.21	*682.952	*27.584	*0.576	*1.363	5505.53
15484.21	12.42	342.1		198.99	14.56	0.38
12862.89	8969.83	9549.22	725.82	1527.52	92.76	
*38.55	0.21	*682.952	*27.584	*0.576	*1.363	7258.75
4605.07	17.02	352.74		12.26	8.36	*0.03
8797.82	15129.82	6685.52	2735.01	905.08	20.37	
*38.55	0.38	*682.952	*27.584	*0.576	*1.363	3957.3
33657.82	10.52	172.16		15.5	7.26	0.33
22987.67	6899.42	6986.44	3773.09	708.2	39.3	
*38.55	0.26	*682.952	*27.584	*0.576	*1.363	4274.94
9469.75	33.06	219.5		13.3	8.04	*0.03
22619.35	6429.29	5890.53	3950.13	1384.34	45.88	
*38.55	0.27	*682.952	*27.584	*0.576	11.61	6511.14
2621.61	22.78	388.79		33.12	13.29	0.37
14899.32	8561.41	10961.16	3998.1	1408.92	79.42	
*38.55	0.27	*682.952	*27.584	*0.576	14.67	6699.01
2806.79	13.33	331.29		86.06	8.79	*0.03
13625.9	7704.49	8032.7	3778.25	1832.6	62.76	
*38.55	0.13	*682.952	*27.584	*0.576	*1.363	4150.86
13870	15.7	258.05		9.35	5.61	*0.03
10854.89	10522.15	2676.43	5284.94	838.27	42.83	
*38.55	0.59	*682.952	*27.584	*0.576	*1.363	4924.16
9314.09	22.63	544.9		12.41	10.23	0.65
14937.94	9192.26	6430.83	3181.51	1584.64	50.45	
*38.55	0.39	*682.952	*27.584	*0.576	*1.363	2480.02
22292.08	17.16	215.01		11.15	9.93	0.34
13366.57	10558.98	5719.11	2288.6	1425.3	182.33	
*38.55	0.33	9648.28	329.97	21.39	33.79	3076.34
21796.73	6	345.67		8.76	9.62	0.43
11006	4491.49	9365.09	2158.4	1539.77	58.53	
*38.55	0.28	*682.952	*27.584	*0.576	*1.363	4428.35
53915.1	31.3	264.19		13.22	5.98	*0.03
11854.25	5407.8	4486.73	2776.26	1678.3	9.92	
127.64	0.32	6292.49	201.36	59.47	13.27	5543.04
2175.03	14.74	1302.86		10.63	10.23	0.94

Table4.txt

9725.6	9599.44	4340.51	1992.2	1478.49	127.02	
*38.55	0.26	4545.02	*27.584	*0.576	*1.363	4431.93
2428.82	17.74	243.42		10.34	13.84	0.43
11623.42	3312.2	8737.45	3118.25	1219.97	77.31	
*38.55	0.28	*682.952	*27.584	*0.576	*1.363	2979.42
26965.87	17.99	156.66		10.63	7.93	0.33
14628.06	7853.83	2460.99	2340.34	758.66	59.51	
*38.55	0.32	*682.952	*27.584	*0.576	*1.363	5810.99
19409.23	18.64	278.25		11.52	7.49	*0.03
28507.9	5141.43	9272.94	3957.91	5188.18	26.03	
*38.55	0.16	*682.952	*27.584	*0.576	*1.363	5252
26330.99	7.17	312.87		4.82	1.1	*0.03
8169.53	11221.16	5680.96	3144.81	1269.37	33.16	
*38.55	0.43	*682.952	*27.584	*0.576	*1.363	7472.22
21247.07	22.07	453.21		7.34	14.56	0.35
14413.83	6993.25	10045.43	2807.54	1796.11	69.04	
360.32	0.62	*682.952	*27.584	12.49	11.75	5430.69
4376.8	18.56	400.43		18.39	15.09	*0.03
25233.99	2387.94	4525.65	1348.06	1108.52	46.44	
*38.55	0.45	*682.952	*27.584	*0.576	*1.363	3606.43
11599.99	15.31	258.05		19.07	9.52	0.4
21047.75	5407.8	8218.53	3562.36	1617.24	34.22	
*38.55	0.2	*682.952	*27.584	*0.576	*1.363	5822.38
2941.34	16.66	290.02		17.26	2.88	*0.03
16196.72	6466.96	11052.53	4050.04	804.79	38.21	
*38.55	0.48	*682.952	*27.584	*0.576	13.27	5584.36
2761.15	21.44	373.56		28.84	15	0.56
15303.4	7255.67	12037.43	3850.52	758.66	38.96	
301.97	0.25	*682.952	*27.584	*0.576	13.41	6797.4
2668.57	14.3	343.89		66.17	5.86	*0.03
12923.69	6936.96	7678.84	3700.99	1523.44	31.64	
*38.55	0.2	*682.952	*27.584	*0.576	*1.363	4676.72
18623.59	18.87	278.25		9.13	5.61	*0.03
9336.44	10042.78	3770.78	5557.67	896.74	34.1	
*38.55	0.56	*682.952	*27.584	*0.576	*1.363	5573.09
8017.76	20.58	579.71		9.75	8.79	0.58
13804.47	9414.45	5852.47	2740.01	1363.84	24.75	
*38.55	0.39	*682.952	*27.584	*0.576	*1.363	2583.93
29716.85	17.88	230.53		11.15	3.77	*0.03
6167.86	9081.08	7454.78	2202.55	859.17	115.97	
*38.55	0.32	10194.37	344.47	23.26	32.39	3452.03
20995.49	5.69	350.98		12.22	7.03	0.33
11241.78	4568.19	9291.38	2292.29	1417.12	58.85	
*10.229	0.75	*674.175	206.41	*0.603	*1.26	5904.17
1576.89	43.71	721.66		7.53	41.55	0.91
65718.38	14426.2	16274.43	3573.62	2261.85	182.28	
*10.229	0.61	*674.175	254.9	3.62	*1.26	5834.74
35312.05	50.68	532.04		165.99	49.28	0.68

Table4.txt

52076.46	9851.64	13888.41	1027.6	2007.34	169.18			
112.31	0.67	*674.175	*27.506	*0.603	*1.26	5565.77		
39698.24	20.47	546.89		5.95	13.42	0.62		
174302.47	7118.76	21948.02	1727.01	2223.26	72.96			
*10.229	0.48	5755.18	222.96	3.62	*1.26	4559.71		
5775.6	29.65	327.18		17.57	16.89	0.61		
52813.19	8451.26	7753.57	1814.58	2007.34	78.87			
47.86	0.51	*674.175	*27.506	*0.603	*1.26	7364.3		
17527.75	26.13	364.96		10.73	28.86	0.52		
36761.33	10977.79	6993.44	2421.83	2157.68	66.57			
*10.229	0.13	*674.175	*27.506	*0.603	*1.26	6142.76		
10949.08	15.74	647.66		6.51	50.43	0.32		
34566.52	19345.4	17085.6	2288.28	2169.25	48.81			
*10.229	0.25	*674.175	*27.506	*0.603	*1.26	3405.92		
6185.78	13.37	443.13		6.29	52.48	0.33		
31453.69	9713.69	21069.16	1996.21	1127.41	41.67			
*10.229	0.56	*674.175	197.97	4.59	*1.26	4288.51		
13188.84	43.93	493.89		12.76	25.57	0.61		
44855.92	13693.78	4014.23	2480.13	1818.58	159.16			
*10.229	0.84	*674.175	180.67	4.59	*1.26	2490.04		
20251.52	13.61	270.96		8.2	23.48	0.43		
36166.8	6807.84	7542.33	1098.3	1945.7	47.88			
*10.229	0.37	4806.21	254.9	11.23	*1.26	6158.77		
36338.81	14.03	310.74		12.43	21.91	0.52		
23715.24	3193.22	6516.48	875.65	1518.03	26.9			
*10.229	0.2	*674.175	*27.506	*0.603	*1.26	3076.83		
88931.75	10.66	534.53		9.1	49.14	0.36		
16206.65	9331.55	19248.53	2813.84	1251.5	35.51			
*10.229	0.39	*674.175	*27.506	*0.603	*1.26	2932.1		
1464.03	13.96	643.16		14.12	49.21	0.65		
27675.01	14011.72	10753.13	2118.07	971.57	161.18			
*10.229	0.1	*674.175	*27.506	*0.603	*1.26	3364.76		
13732.06	16.87	568.77		5.74	89.18	0.25		
14540.84	14938.08	9296.07	3626.47	869.67	24.48			
174.38	0.34	*674.175	*27.506	4.11	*1.26	6390.82		
44763.06	18.2	394.88		6.96	23.67	0.31		
40082.51	12776.24	10459.83	3585.1	1976.52	31.95			
*10.229	0.33	4304.54	*27.506	*0.603	250.23	9637.23		
5691.29	25.79	612.38		43.78	16.89	0.36		
48749.97	12210.19	11021.8	1990.1	1568.15	81.09			
*10.229	0.19	*674.175	*27.506	*0.603	*1.26	3356.54		
6003.45	26.22	504.21		2.89	63.33	0.29		
34154.97	13852.66	10031.67	3609.22	1382.96	114.58			
*10.229	0.18	*674.175	*27.506	*0.603	*1.26	3326.44		
22824.14	28.07	415.11		4.32	27.87	0.33		
36807.07	12492.88	5526.56	2278.87	2354.5	59.84			
346.55	0.23	*674.175	*27.506	*0.603	*1.26	6222.95		
12420.23	16.92	409.39		5.52	32.68	0.24		

Table4.txt

35138.05	8511.68	12680.74	2767.04	1583.57	95.82	
*10.229	0.32	*674.175	*27.506	*0.603	*1.26	3710.88
30625.11	23.14	283.39		8.53	38.27	0.49
21969.29	7222.71	12205.19	2793.14	1598.99	52.89	
*10.229	0.79	*674.175	308.03	10.76	8.3	2250.6
80490.44	28.68	551.79		14.23	41.4	0.55
8238.84	8966.21	4829.93	1777.66	1822.43	88.17	
*10.229	0.3	*674.175	180.67	*0.603	*1.26	5553.35
41988.24	31.47	488.68		10.12	27.6	0.56
20388.29	13566.83	8137.73	2740.99	948.1	62.62	
*10.229	0.17	*674.175	*27.506	*0.603	*1.26	5051.27
170381.21	22.98	509.33		6.96	60.18	0.3
26838.79	4603.52	8951.91	2971.73	908.93	33.61	
*10.229	0.32	*674.175	*27.506	*0.603	*1.26	4404.65
7750.84	21.42	374.07		8.69	15.08	0.41
17351.94	4419.24	3036.12	2609.36	2939.49	63.41	
*10.229	0.34	5288.63	231.08	10.29	*1.26	8035.49
10776.13	17.44	456.78		5.31	21.41	0.64
27535.86	2422.52	5037.5	479.71	1868.65	109.1	
*10.229	8.56	*674.175	*27.506	*0.603	*1.26	2409.81
28783.58	13.51	283.39		7.72	15.08	0.58
16808.66	1908.47	88220.62	2999.32	1371.38	286.41	
315.31	0.75	*674.175	197.97	3.62	*1.26	5102.68
16983.85	19.24	364.96		8.58	25.39	0.39
27350.19	8572.14	7205.91	1144.05	2261.85	65.44	
*10.229	0.17	*674.175	180.67	*0.603	*1.26	4248.05
84155.72	17.43	589.02		8.15	41.71	0.33
19573.81	9301.05	6516.48	2539.78	1150.71	34.21	
544.79	0.56	*674.175	*27.506	*0.603	*1.26	5036.18
37644.64	24.51	443.13		11.76	21.71	0.82
225916.71	8859.94	7243.35	2430.29	4143.21	152.64	
160.59	0.55	*674.175	206.41	*0.603	149.38	1974.67
12473.99	26.31	486.07		7.12	36.82	0.55
41392.24	8029.56	1025.65	1768.7	1606.69	40.1	
*10.229	0.2	*674.175	*27.506	*0.603	*1.26	5060.33
26523.66	10.48	252.66		26.48	18.41	0.33
30811.2	6483.66	63095.45	1407.13	814.53	88.4	
*10.229	0.43	*674.175	197.97	*0.603	8.97	6625.66
17389.55	20.94	813.74		10.92	79.45	0.51
40702.54	6029.62	8853.45	2192.48	2084.43	60.07	
*10.229	0.13	5755.18	189.39	*0.603	*1.26	5117.83
3654.73	17.16	493.89		4.16	41.86	0.4
38363.16	7089.09	14963.56	942.66	1545.02	66.23	
201.77	0.15	*674.175	*27.506	*0.603	*1.26	5528.54
116101.08	12.55	279.87		7.39	35.44	0.31
15355.43	1157.37	17689.33	2929.89	857.87	28.53	
*10.229	0.2	*674.175	*27.506	*0.603	180.87	4550.9
10248.09	26.9	559.1		11.64	111.92	0.34

Table4.txt

32003.82	10405.42	11497.78	2918.9	2250.27	50.76	
*10.229	0.46	*674.175	197.97	*0.603	11.7	4135.82
271826.22	45.43	454.07		14.37	107.28	0.71
37104.41	13677.91	7716.32	3518.66	1957.25	90.16	
*10.229	0.23	*674.175	*27.506	4.59	12.74	3905.04
17573.71	13.2	493.89		3.5	23.58	0.3
35801	7431.05	28476.57	1650.08	1444.74	134.46	
*10.229	0.38	*674.175	*27.506	*0.603	9.3	7909.29
12820.62	26.15	448.61		5.95	57.7	0.39
12148.56	2663.61	11265.94	3126.93	1026.23	18.25	
*10.229	0.3	*674.175	*27.506	*0.603	*1.26	4930.87
10805.05	14.06	422.21		15.34	29.22	0.25
17145.65	4334.44	5308.41	1384.28	1537.31	11.33	
*10.229	0.18	*674.175	*27.506	*0.603	*1.26	5923.15
2475.93	11.93	549.35		5.95	60.84	0.26
23263.4	10575.25	15832.86	3745.43	1115.75	16.81	
*10.229	0.13	*674.175	176.26	*0.603	10.32	5800.13
56952.09	21.6	412.26		17.31	14.84	0.28
45598.67	10745.37	5820.22	2488.63	1471.75	51.34	
258.32	0.27	*674.175	*27.506	*0.603	*1.26	4173.15
24695.51	24.67	586.66		7.8	22.11	0.32
31178.44	15291.09	10520.95	3564.45	1216.64	102.44	
566.89	0.19	4806.21	*27.506	*0.603	52.54	4817.22
4628.24	17.18	608.9		7.1	40.94	0.45
9503.31	14139.11	8236.67	4585.65	1937.99	51.91	
*10.229	0.38	*674.175	*27.506	*0.603	*1.26	4689.48
149622.94	11.94	493.89		12.45	53.11	0.35
18472.93	9240.08	13107.57	595.6	1131.29	19.19	
*10.229	0.4	*674.175	*27.506	*0.603	*1.26	2596.78
18975.67	20.6	423.62		8.5	33.02	0.38
35366.65	7103.92	9296.07	1533.04	1173.99	98.4	
*10.229	0.19	*674.175	231.08	*0.603	*1.26	5000
14888.21	24.5	430.64		7.66	24.63	0.26
36349.71	8240.13	5218.29	1277.64	2586.5	22.28	
*10.229	0.22	4304.54	185.05	5.56	*1.26	3260.96
13306.14	26.84	479.49		7.93	22.4	0.29
61508.02	8059.61	24342.39	1549.52	2571.02	318.1	
*10.229	0.18	5288.63	*27.506	*0.603	137.21	4044.28
3852.09	15.99	310.74		10.04	31.66	0.39
20339.17	10776.33	9332.91	3288.28	1606.69	130.21	
118.73	0.25	*674.175	*27.506	*0.603	*1.26	7367.7
21007.04	8.39	445.88		2.89	100.89	0.37
16469.34	1445.76	4358.72	2577.2	1220.51	*0.03	
NA	0.15	*674.175	*27.506	*0.603	*1.26	3613.24
17204.58	10.56	645.41		6.16	44.29	0.24
24236.42	8059.61	8162.48	2410.2	1290.2	20.06	
*10.229	0.21	4304.54	*27.506	3.62	*1.26	3299.12
5691.29	33.49	366.48		5.76	38.58	0.54

Table4.txt

27651.82	8405.97	7542.33	2506.72	790.83	109.75	
*10.229	0.19	*674.175	*27.506	*0.603	*1.26	2990.91
2437.31	21.17	394.88		7.02	50.29	0.3
17480.46	8390.88	6162.99	3353.76	1127.41	18.81	
85.09	0.14	*674.175	206.41	*0.603	*1.26	3052.62
55850.81	9.07	383.06		11.67	31.49	0.23
17813.21	5811.13	11192.71	1892.88	834.24	24.05	
505.1	0.12	7081.66	214.74	42.16	34.74	2312.04
2908.34	17.74	667.67		12.2	27.33	0.44
27489.45	5347.8	10398.7	798.32	1352.06	47.77	
32.77	0.15	*674.175	*27.506	*0.603	*1.26	3613.24
4983.99	17.91	445.88		16.48	25.2	0.26
11364.1	4490.02	5024.56	2712.83	940.28	35.74	
*10.229	0.4	*674.175	*27.506	*0.603	*1.26	4662.86
9175.83	23.03	445.88		6.27	43.61	0.42
17634.29	3940.93	21357.48	2001.3	2223.26	50.25	
*10.229	0.2	*674.175	206.41	*0.603	29.77	7023.36
11807.21	16.98	616.99		13.41	34.2	0.25
31889.25	6219.62	6491.29	2658.84	2153.83	10.81	
*10.229	0.53	4806.21	180.67	3.62	*1.26	3806.28
10337.1	23.38	290.35		9.95	27.24	0.56
21145.84	7222.71	4094.07	2327.03	1367.51	63.01	
250.99	3.94	*674.175	*27.506	*0.603	*1.26	4012.92
43544.42	12.72	426.44		11.2	26.32	0.35
21896.92	7148.44	23515.24	2763.78	822.42	260.16	
98.11	0.36	*674.175	*27.506	*0.603	*1.26	4300.09
31530.91	21.4	488.68		19.88	51.77	0.29
27675.01	10405.42	6591.99	1452.08	869.67	87.9	
*10.229	0.21	*674.175	*27.506	*0.603	*1.26	4150.17
9426.85	15.42	413.69		12.06	32	0.26
17991.56	5738.48	6137.66	2481.19	651.59	56.71	
*10.229	0.16	*674.175	*27.506	*0.603	*1.26	2412.39
3768.41	29.99	620.44		5.21	23.09	0.36
24330.96	8466.36	10643.17	2882.7	1429.3	141.49	
328.55	0.62	*674.175	285.62	*0.603	8.47	3271.85
60518.25	27.11	819.68		14.65	79.57	0.76
30420.7	18440.97	6390.45	4096.69	1104.09	89.11	
*10.229	0.11	5288.63	*27.506	*0.603	*1.26	5325.11
12965.89	22.84	1260.57		15.17	25.2	0.37
25531	4263.9	5295.54	1534.98	857.87	74.64	
147.98	0.09	*674.175	*27.506	*0.603	*1.26	1984.71
53805.17	18.76	272.76		2.14	17.33	0.26
31339.02	9362.07	9798.97	4285.71	979.39	138.33	
*10.229	0.2	*674.175	*27.506	*0.603	*1.26	3882.42
25443.57	17.05	327.18		7.02	43.84	0.27
30765.28	8662.92	4829.93	2572.92	530.4	56.83	
*10.229	0.21	*674.175	*27.506	3.86	7.97	3282.76
11375.31	9.56	219.75		6.8	18.19	0.54

Table4.txt

19722.56	2529.39	5603.32	886.18	1398.41	33.32	
*10.229	0.2	*674.175	214.74	*0.603	*1.26	6056.52
23652.61	12.07	827.56		15.14	49	0.31
26092.62	16776.79	9296.07	2733.41	1002.82	55.23	
*10.229	0.27	4806.21	171.8	*0.603	*1.26	2892.12
16738.48	9.04	320.66		2.19	40.78	0.3
33102.82	3289.25	5449.68	1697.35	822.42	97.96	
*10.229	0.21	*674.175	*27.506	*0.603	*1.26	4515.69
4354.95	11.47	305.71		4.11	19.04	0.26
8529.36	1369.93	17936.15	3867.56	1111.86	16.69	
*10.229	0.86	*674.175	*27.506	*0.603	*1.26	3978.78
12366.37	31.72	696.02		15.76	58.98	0.4
10741.87	7849.52	4894.91	1538.85	885.38	29.19	
341.76	0.2	*674.175	*27.506	4.59	*1.26	10227.74
84498.17	14.75	1115.48		5.79	47.11	0.44
17762.14	1934.53	23566.02	2882.7	798.73	38.87	
*10.229	0.24	*674.175	206.41	*0.603	*1.26	3682.93
57057.79	25.72	556.67		12.17	26.6	0.26
25531	15467.94	7517.45	3070.2	1760.8	72.23	
*10.229	0.79	5288.63	180.67	*0.603	*1.26	3851.36
9978.5	23.13	708.9		8.15	79.45	0.44
38638.01	9667.75	7790.8	2069.77	711.5	31.59	
261.98	0.27	*674.175	*27.506	*0.603	*1.26	3837.26
13136.55	23	386.03		5.55	25.39	0.42
44438.77	8405.97	5500.94	1628.51	286.95	66.34	
34.16	0.12	*674.175	*27.506	*0.603	12.74	3671.76
3042.01	19.11	742.64		4.71	47.4	0.37
30075.85	10698.94	6943.37	2732.32	1247.63	58.14	
*10.229	0.17	*674.175	*27.506	*0.603	*1.26	3326.44
19020.2	18.11	269.16		4.76	29.04	0.49
11486.48	3578.98	5590.54	3955.33	278.19	87.73	
*12.021	0.18	*673.492	*27.042	*1.87	*1.369	3671.17
19464.18	18.75	946.82		5.8	46.32	0.28
47371.5	5576.97	3357.48	3471.11	1288.54	43.59	
*12.021	0.19	4040.95	181.31	*1.87	65.39	3036.84
22906.36	18.05	594.65		6.57	50.17	0.4
28190.88	9765.67	10417.46	1110.57	1391.82	53.56	
*12.021	0.4	*673.492	*27.042	*1.87	*1.369	3172.9
20710.16	22.21	490.81		77.84	42.12	0.43
19628.35	11594.57	13137.49	4702.35	1295.01	278.59	
*12.021	0.21	*673.492	*27.042	*1.87	*1.369	2686.29
7214.43	13.04	256.83		3.48	28.64	0.33
26640.46	6756.58	2889.24	2745.6	949.67	162.76	
*12.021	0.28	*673.492	*27.042	*1.87	8.44	3934.96
65371.45	17.39	588.67		12.81	52.81	0.33
39836.6	8515.08	8504.16	2320.39	791.23	22.08	
*12.021	0.23	*673.492	*27.042	*1.87	*1.369	2827.39
62101.85	7.62	318.63		12.28	26.6	0.39

Table4.txt

26066.21	6462.33	8895.85	3804.6	651.22	61.42	
195.46	0.18	*673.492	*27.042	*1.87	*1.369	6899.3
10938.62	10.37	434.82		6.77	47.62	0.22
22847.89	11760.61	14218.8	6771.84	386.61	11.02	
*12.021	0.43	6345.45	*27.042	*1.87	9.85	3784.04
18421.24	29.85	339.7		20.24	24.97	0.42
27097.06	5280.85	9080.45	1806.57	1145.82	117.65	
*12.021	0.22	7076.83	181.31	*1.87	8.44	2226.43
3317.13	23.48	592.66		1.52	38.98	1.1
17896.53	13854.88	11354	1478.37	1067.59	149.54	
112.68	0.55	*673.492	*27.042	*1.87	*1.369	3039.93
27608.79	23.61	404.31		5.23	26.12	0.46
30047.91	16527.47	4836.02	4210.23	1015.27	128.94	
*12.021	0.2	*673.492	*27.042	*1.87	*1.369	4966.67
16722.97	9.5	350		18.04	41.88	0.33
13902.01	1878.78	7374.39	2168.05	590.76	17	
*12.021	1.1	*673.492	285.61	*1.87	*1.369	4995.66
75637.15	12.66	679.31		10.81	45.56	0.54
22201.84	3058.37	3430.28	2514	393.49	9.03	
213.28	0.42	*673.492	193.67	*1.87	*1.369	4518.08
40674.79	22.79	820.01		*0.027	95.23	0.49
54628.68	11137.79	8400.61	2687.19	617.67	49.48	
317.24	0.96	4040.95	*27.042	*1.87	9.85	4121.14
62945.44	11.06	684.9		16.84	25.46	0.79
11646.07	6357.14	6691.49	2162.72	975.94	35.63	
*12.021	0.2	*673.492	*27.042	*1.87	*1.369	3680.56
39365.97	9.86	318.63		2.81	23.11	0.36
12899.79	11573.81	5287.62	3770.81	764.67	56.31	
*12.021	0.12	*673.492	*27.042	*1.87	*1.369	3517.99
2710.36	16.46	288.52		6.69	14.15	0.17
45286.37	4729.33	6605.32	2894.21	916.78	50.17	
*12.021	0.43	7437.19	263.55	*1.87	9.85	4327.13
17116.07	5.14	574.61		8.51	52.23	0.59
36991.84	9349.2	5017.52	1906.73	1152.33	108.02	
*12.021	0.27	*673.492	*27.042	*1.87	*1.369	3530.48
8885.38	17.02	512.36		5.64	33.7	0.27
31292.28	5872.56	13292.65	2168.05	1571.62	95.69	
*14.138	0.23	*629.29	*26.683	*0.516	203.54	5239.94
60079.18	16.64	920.21		4.82	57.03	0.35
23973.73	8250.91	20048.04	4489.53	1242.12	186.5	
84.44	0.14	*629.29	*26.683	*0.516	58.34	3026.36
11440.72	15.47	1174.51		3.31	24.69	0.61
28012.27	6502.95	17938.93	2480.76	874.99	466.04	
90.99	0.22	*629.29	*26.683	*0.516	*1.328	3803.45
32865.19	16.87	543.44		8.63	22.9	0.36
9346.68	14757.28	11850.79	3978.15	1455.42	411.33	
114.29	0.28	*629.29	*26.683	*0.516	*1.328	3084.07
13929.99	16.31	467.96		7.56	69.98	0.33

Table4.txt

57909.31	10096.12	8343.14	1580.5	1346.53	140.18	
105.93	0.35	*629.29	206.96	*0.516	86.79	4717.77
8748.79	33.81	1058.4		6.58	38.06	0.26
53490.68	10564.75	7412.92	1876.73	1935.46	93.95	
NA	0.32	*629.29	166	5.31	*1.328	6491.71
143387.1	12.37	441.2		10	16.25	0.45
38470.16	9194.12	10143.79	2665.43	2442.53	52.12	
*14.138	0.2	*629.29	*26.683	*0.516	62.86	3676.24
3026.95	12.14	752.84		7.59	33.43	0.5
15972.32	12973.01	8271.92	4067.41	1794.18	133.33	
120.48	0.24	*629.29	*26.683	*0.516	*1.328	5589.45
2759.65	9.52	562.55		6.79	25.02	0.26
30640.69	5621.09	7220.88	3557.54	2274.21	19.35	
275.64	0.12	*629.29	*26.683	*0.516	*1.328	4062.52
42743.34	16.85	533.74		3.31	28.21	0.26
35593.24	7663.93	11746.81	3180.68	915.6	134.72	
555.18	0.37	*629.29	*26.683	*0.516	*1.328	5579.6
33660.02	14.28	518.99		3.48	27.45	0.7
33435.14	9795.8	12289.14	2758.76	1242.12	106.06	
240.28	0.63	*629.29	177.75	*0.516	9.63	10014.29
85891.36	38.35	407.79		5.77	77.4	0.51
18540.02	2904.99	19980.47	3865.62	3853.92	13.54	
*14.138	0.4	*629.29	*26.683	4.22	*1.328	2929.39
5919.74	23.44	460.02		4.23	24.3	0.39
33617.43	10714.56	7795.71	1674.94	1759.99	155.42	
*14.138	0.13	*629.29	*26.683	*0.516	*1.328	4858.77
15520.02	19.04	378.69		3.68	45.53	0.38
18788.47	8439.89	8863.95	1557.23	467.16	51.82	
73.28	0.09	*629.29	*26.683	10.95	18.2	3218.11
9029.73	15.52	372.71		4.64	9.76	0.27
24615.62	4245.64	16615.2	2981.77	1391.14	27.94	
*14.138	0.17	*629.29	*26.683	*0.516	*1.328	2583.35
85593.26	9.12	714.31		9.63	70.86	0.32
8913.64	14571.65	16331.81	3804.29	910.53	136.48	
*14.138	0.16	*629.29	*26.683	*0.516	*1.328	4367.93
12472.93	10.77	734.73		5.32	66.3	0.26
31478.12	18980.32	10610.23	2993.21	1361.41	120.57	
*14.138	0.18	*629.29	*26.683	*0.516	*1.328	5275.7
27661.84	20.79	473.2		1.74	21.14	0.2
35904.71	9852.13	16286.45	2023.76	2820.18	126.66	
*14.138	0.25	*629.29	*26.683	*0.516	8.41	3263.94
30810.4	17.54	387.55		7.74	21.55	0.3
28275.99	7796.63	42547.45	2522.13	1415.88	48.05	
*14.138	0.23	*629.29	*26.683	*0.516	*1.328	4015.54
46948.79	20.46	329.19		1.44	10.64	0.33
35852.81	6005.27	6082.78	2323.23	639.27	75.9	
*14.138	0.18	*629.29	247.47	*0.516	*1.328	2523.55
13380.59	25.49	488.74		32.74	24.1	0.39

Table4.txt

21603.41	12526.02	8911.16	2130.36	535.33	86.1	
*14.138	0.14	*629.29	*26.683	*0.516	*1.328	4634.74
51880.21	19.69	562.55	6.31	29.88	0.24	
20734.07	7036.92	22703.43	3520.05	1267.03	60.31	
166.13	0.25	*629.29	*26.683	*0.516	*1.328	3414.1
33985.96	17.19	533.74	3.16	48.07	0.42	
15689.79	8968.12	13804.26	1927.33	803.68	91.4	
*14.138	0.23	*629.29	*26.683	*0.516	*1.328	6075.79
1851.94	15.69	562.55	5.8	62.59	0.37	
41908.64	10770.72	7484.82	4505.53	1401.04	30.29	
*14.138	0.22	*629.29	*26.683	*0.516	*1.328	4125.25
1919.29	16.67	697.72	5.47	15.65	0.28	
39091.17	9043.48	13483.77	3440.03	2110.05	26.31	
*14.138	0.56	*629.29	*26.683	3.66	*1.328	3949.9
39043.96	10.32	435.73	14.9	21.96	0.8	
*536.361	7074.99	6835.41	1292.13	1192.24	51.72	
*14.138	0.09	*629.29	*26.683	*0.516	*1.328	2196.66
9833.27	11.38	460.02	3.71	18.03	0.35	
15859.4	7055.96	18571.25	2669.21	951.04	321.41	
296.43	1.08	*629.29	*26.683	*0.516	*1.328	4348.95
28072.29	18.06	467.96	7.5	23.24	0.53	
14980.1	7834.53	6180.36	2958.89	905.45	64.64	
101.71	0.14	*629.29	*26.683	*0.516	109.91	4386.91
6934.19	13.31	523.93	5.59	63.35	0.21	
26928.73	6903.61	10552.01	3576.96	30354.09	56.54	
*14.138	0.4	*629.29	*26.683	*0.516	*1.328	3629.82
38262.57	31.08	523.93	5.59	35.54	0.48	
16422.86	6732.03	6423.68	2640.25	1157.25	74.28	
571.88	0.12	*629.29	*26.683	*0.516	15.92	5298.47
35616.61	9.13	509.02	*0.026	46.17	0.25	
38754.83	4576.85	16354.49	1815.11	849.56	127.68	
90.99	0.1	*629.29	*26.683	*0.516	*1.328	1966.92
102819.17	7.98	348.23	1.74	31.4	0.18	
29801.6	4245.64	21781.24	1673.71	1711.08	120.01	
*14.138	0.46	*629.29	224.37	23.71	23.19	3666.95
52113.04	22.98	676.65	4.14	25.86	0.36	
120403.44	6808.31	5321.33	1688.45	925.73	28.93	
*14.138	0.2	*629.29	*26.683	*0.516	*1.328	3887.5
9132.11	12.9	653.03	2.57	30.19	0.32	
8758.08	6770.18	8248.16	2695.67	849.56	74.32	
*14.138	0.33	*629.29	*26.683	*0.516	*1.328	5992.57
8523.69	18.24	590.53	4.82	67.89	0.37	
52687.01	8099.61	9017.33	3009.75	1465.3	32.57	
*14.138	0.25	*629.29	166	*0.516	*1.328	5071.42
41446.26	20.55	430.23	13.68	17.59	0.45	
18429.45	8232.01	15173.19	2835.89	1954.9	72.74	
*14.138	0.76	*629.29	*26.683	*0.516	*1.328	2847.81
25337.51	35.44	555.43	9.13	28.33	0.58	

Table4.txt

57492.51	17648.13	8651.21	2943.65	1031.78	65.31	NA
1.06	*629.29	*26.683	*0.516	*1.328	4529.66	9059.04
14.14	687.23	5.71	57.03	0.51	33357	15313.88
66013.68	1994.07	680.58	356.73	649.63	0.17	*629.29
*26.683	*0.516	*1.328	4469.31	12696.6	22.02	354.44
3.36	22.09	0.32	25255.78	6330.89	11109.96	1262.89
1311.78	126.75	156.44	0.18	*629.29	166	*0.516
*1.328	3524.86	6593.68	20.79	413.47	9.04	43
0.26	36942.08	12376.93	35827.56	3740.47	472.43	39.01
NA	0.16	*629.29	*26.683	*0.516	*1.328	2893.11
8778.57	17.08	438.47	4.94	42.51	0.22	42347.76
9870.91	18085.78	3039.03	696.03	45.71	120.48	0.24
*629.29	*26.683	*0.516	*1.328	3484.82	127726.95	8.91
531.3	8.54	18.61	0.3	23464.26	19664.66	14307.03
3208.82	1425.77	61.53	*14.138	0.53	*629.29	171.88
5.31	*1.328	3735.13	67700.64	12.45	583.61	5.06
56.53	0.56	14150.4	8911.58	7004.29	2509.59	1465.3
21.25	*14.138	0.2	*629.29	*26.683	3.66	18.2
7115.29	71252.7	20.7	2456.94	6.04	33.38	0.24
37745.25	14979.97	8141.2	4308.88	556.2	88.56	*14.138
0.13	*629.29	*26.683	*0.516	*1.328	3568.04	88885.74
11.3	413.47	6.86	10.29	0.3	10535.14	5505.58
17554.65	2753.71	1102.14	35.86	NA	0.2	*629.29
*26.683	*0.516	*1.328	5520.56	129406.92	22.49	473.2
*0.026	30.86	0.29	17736.34	4206.58	4322.77	4804.17
*32.158	15.94	*14.138	0.28	*629.29	*26.683	*0.516
*1.328	2862.9	7034.65	26.38	295.96	8.82	10.64
0.37	25335.69	5467.05	7028.38	2274.61	1366.36	79.01
*14.138	0.36	*629.29	*26.683	*0.516	*1.328	2808.6
35392.04	11.36	338.79	3.94	62.15	0.54	10414.36
4187.05	10528.71	2778.98	910.53	224.3	*14.138	0.55
*629.29	*26.683	*0.516	*1.328	3352.72	4386.3	25.77
452.01	4.82	17	0.42	39220.52	10808.16	5048.7
2998.3	900.38	47.65	*14.138	0.25	*629.29	*26.683
3.66	*1.328	3193.7	34310.86	15.83	595.12	7.37
45.59	0.28	11522.86	9589.13	4974.1	3816.03	1162.25
29.04	*14.138	0.36	*629.29	*26.683	*0.516	*1.328
3227.27	40978.19	11.32	648.69	7.53	64.78	0.42
11582.25	11144.89	11642.76	4075.3	1097.12	31.43	194.57
0.38	*629.29	*26.683	*0.516	*1.328	5191.23	9059.04
17.47	413.47	3.88	16.55	0.48	34502.08	3084.16
4998.98	1902.64	4988.69	55.56	214.92	0.35	*629.29
*26.683	*0.516	*1.328	3035.46	8793.45	21.56	560.18
5	50.82	0.26				

Table4.txt

11105.66	8836.18	14032.92	2840.95	NA	118.29	
313.54	0.13	*629.29	*26.683	*0.516	*1.328	2010.97
24498.04	15.73	390.48		2.07	22.43	0.26
35151.78	5235.59	20757.36	3757.39	859.74	156.16	
*14.138	0.13	*629.29	*26.683	*0.516	*1.328	2896.13
21411.11	16.17	278.5		2.74	13.47	0.26
13833.74	3834.54	19045.06	2366.92	976.31	84.1	
*14.138	0.34	*629.29	*26.683	*0.516	*1.328	3978.01
2592.39	21.99	424.68		2.1	23.7	0.38
51314.21	6827.38	6094.98	3261.34	1351.49	62.99	
327.09	0.33	*629.29	*26.683	*0.516	*1.328	3549.53
4386.3	19.35	488.74		6.49	25.08	0.28
8913.64	11574.68	9851.43	4677.93	1072.02	32.15	
*14.138	0.22	*629.29	*26.683	*0.516	*1.328	4431.26
11904.91	34.05	332.41		9.63	28.46	0.26
20352.33	4964.9	7244.91	5158.71	*32.158	22.91	
909.47	0.19	*629.29	*26.683	*0.516	300.83	3429.46
1077.26	23.81	665.98		7.56	22.3	0.29
31948.5	8118.53	7783.77	2112.99	1016.67	147.48	
*14.138	0.26	*629.29	*26.683	*0.516	*1.328	3781.7
6136.73	11.75	430.23		6.83	12.74	0.25
21467.85	10695.84	5271.87	2219.83	844.47	37.79	
*14.138	0.36	*629.29	*26.683	*0.516	*1.328	3968.64
3282.12	20.24	260.39		9.69	22.9	0.28
15122.44	3341.92	5222.35	1732.68	1137.23	118.99	
507.57	0.26	*629.29	*26.683	*0.516	12.1	2899.15
53129.51	11.57	467.96		12.02	28.89	0.36
26875.77	10058.6	5568.02	2637.73	1588.45	47.95	
NA	0.25	*629.29	*26.683	*0.516	*1.328	3407.95
46331.31	16.91	435.73		37.95	22.63	0.43
17179.15	6693.88	17622.49	2693.15	*32.158	24.93	
229.48	0.58	*629.29	*26.683	*0.516	*1.328	4644.31
2814.19	48.6	604.24		8.51	42.73	0.39
19064.02	15833.05	14032.92	5330.66	824.09	52.61	
*14.138	0.25	*629.29	*26.683	6.37	*1.328	4558.29
4103.3	9.78	1094.14		5	37.55	0.35
8508.13	3302.34	7938.83	655.12	711.46	66.86	
*14.138	0.26	*629.29	*26.683	*0.516	*1.328	5711.19
6136.73	28.55	402.07		2.63	28.21	0.48
41443.63	2685.13	29969.39	6379.89	808.79	37.59	
*14.138	0.23	*629.29	*26.683	*0.516	*1.328	5035.88
24516.41	17.93	282.04		4.29	36.92	0.34
10263.05	2201.58	30342.72	2487.03	472.43	13.65	
*14.138	0.24	*629.29	*26.683	*0.516	*1.328	2793.54
10793.41	14.28	504		7.71	26.05	0.33
51624.91	4615.73	16717.17	2993.21	608.2	72.45	
*14.138	0.21	*629.29	*26.683	*0.516	*1.328	3035.46
28938.16	10.21	613.28		7.59	76.86	0.37

Table4.txt

26955.2	15202.59	7148.75	3144.89	649.61	82.11				
158.38	0.28	*629.29	*26.683	*0.516	*1.328	2917.29			
36669.34	23.32	478.41		8.69	51.7	0.55			
17207.07	6998.85	3623.04	3418.12	925.73	55.17				
*14.138	0.12	*629.29	*26.683	*0.516	*1.328	2493.69			
26718.54	15.66	796.09		12.5	24.03	0.43			
10111.35	14645.91	13116.92	2647.8	*32.158	65.94				
*14.138	0.3	*629.29	*26.683	*0.516	*1.328	2862.9			
65836.89	9.51	332.41		8.05	21.55	0.36			
13225.98	7036.92	8461.74	3496.8	608.2	23.87				
*14.138	0.26	*629.29	*26.683	6.37	*1.328	4075.05			
44842.98	25.01	309.5		2.24	12	0.38			
11165.42	4304.18	8378.74	2989.4	1237.14	60.85				
214.92	0.41	*629.29	*26.683	9.45	22.86	3592.74			
20538.34	10.92	363.64		7.28	22.03	0.59			
5619.16	1525.59	4574.35	1779.41	1237.14	24.3				
612.48	0.17	*629.29	*26.683	*0.516	*1.328	4405.91			
21128.44	23.67	329.19		5.83	23.04	0.26			
30876.38	4401.66	20262.01	1823.73	623.75	14.6				
*14.138	0.39	*629.29	*26.683	3.1	*1.328	6212.73			
72027.35	14.37	341.95		2.18	21.41	0.31			
17374.45	2242.1	14147.17	2334.46	1142.23	28.83				
*14.138	0.24	*629.29	*26.683	*0.516	*1.328	1794.26			
35022.11	15.67	452.01		3.83	107.78	0.8			
8789.23	2765.2	7938.83	3263.91	*32.158	109.81				
49.25	1.1	*658.785	368.54	14.09	10.77	6098.91			
8222.07	37.33	653.68		32.87	105.09	0.82			
191545.75	11413.72	27876.48	8189.64	2914.41	33.36				
49.25	0.21	*658.785	*26.892	4.25	16.19	5020.5			
14650.7	31.24	329.71		3.71	31.1	0.36			
34145.99	8062.16	33620.34	2595.93	2185.73	200.83				
*14.32	1.14	5769.95	2199.05	19.9	261.13	2999.44			
7070.72	30.22	1674.35		30.94	28.88	0.45			
62381.56	10447.22	5445.34	452.49	5795.05	37.1				
49.25	1.28	*658.785	386.5	10.22	54.32	6068.87			
26244.55	26.48	456.72		17.22	15.37	0.78			
79132.64	7450.28	5679.09	667.86	6064.21	46.9				
119.33	0.79	*658.785	313.09	9.07	13.6	5280.69			
89940.63	35.3	651.56		11.53	49.08	0.31			
47933.84	6586.21	18671.15	3564.15	4529.97	19.88				
61.23	0.48	*658.785	792.66	8.5	15.67	5146.02			
14241.27	24.4	597.51		19.24	48.03	0.72			
129831.73	6145.8	14633.79	2270.49	3411.1	22.9				
94.13	0.33	4670.14	430.41	11.06	42.01	7990.84			
17790.96	20.95	506.88		13.05	32.22	0.45			
63825.29	10784.75	3177.6	2414.66	2381.48	15.79				
72.62	3.09	*658.785	464.64	*0.628	30.86	5838.8			
24282.69	36.36	1819.75		7.16	50.2	1.1			

Table4.txt

161058.77	14992.2	6368.66	1746.64	6153.42	18.71	42.97	0.92	*658.785	439.03
*0.628	40.41	6402.1	54072.1	28.41	2541.64	15.59	32.44	0.6	
154906.07	13316.23	34007.97	2256.92	5266.04	54.56	72.62	1.83	*658.785	460.4
4.25	128.85	5077.07	8660.47	12.37	1040.31	14.51	27.03	0.91	
66698.53	14029.11	23335.02	3248.46	8291.15	26.49	161.59	0.58	*658.785	331.86
11.9	12.06	7059.95	1770.58	20.49	599.71	9.42	28.52	0.36	
55734.17	13095.58	8674.09	3451.22	2234.97	65.27	205.4	0.59	7337.7	202.85
9.07	11.28	5544.99	39912.86	29.35	623.67	8.87	38.69	0.9	
147693	8014.96	21294.19	3940.57	3805.72	62.71	*10.89	1.68	*678.454	*26.439
*0.651	*1.348	2192.21	3652.72	17.94	403.89	18.64	27.09	0.51	
15849.3	10560.26	7111.51	2393.73	1053.21	49.73	*10.89	0.47	*678.454	238.68
4.55	9.84	4004.67	11715.96	27.37	328.09	8.35	23.65	0.51	
49507.6	9221.6	10871.3	4079.31	585.35	46.37	57.63	0.52	*678.454	178.12
*0.651	53.24	2127.43	13134.48	23.85	952.79	27.92	8.68	0.51	
59615.8	8857.78	7817.35	2617.05	2033.13	71.72	46.43	0.81	*678.454	232.87
4.55	9.34	7232.68	43724.27	21.19	427.87	8.9	10.96	0.28	
48824.12	4618.13	208750.83	2476.87	1269.39	88.18	*10.89	0.36	*678.454	203.06
8.32	*1.348	10863.85	19190.71	19.85	301.23	7.59	9.04	0.4	
44395.78	6911.43	109824.4	5436.23	890.28	12.15	*10.89	0.9	*678.454	411.93
5.51	21.2	5478.95	5143.78	35.84	1479.58	34.42	18.93	0.56	
51758.85	20507.87	120351.77	5171.24	1117.38	47.87	124.91	0.49	5832.85	482.99
14.36	9.34	7189.69	4385.56	21.9	558.53	26	16.83	0.35	
111331.94	9439.45	11059.34	1620.6	1027.39	65.62	*10.89	4.16	*678.454	2967.99
7.08	87.09	9550.05	8060.92	21.35	26080.88	62.31	10.79	0.65	
237322.24	11745.79	482233.48	2231.97	2033.13	78.5	34.68	1.81	*678.454	11432.98
8.94	25.17	7039.83	10937.8	22.16	**9253.687	24.68	28.27	0.6	
39089.77	3925.01	39790.07	2472.5	507.7	42.52	*10.89	0.52	*678.454	261.48
*0.651	10.85	9135.69	70420.78	50.82	439.66	10.78	11.46	0.44	
64279.61	4885.24	17499.31	1865.18	599.31	34.28	*10.89	0.87	*678.454	*26.439
4.55	*1.348	5928.62	15557.83	22.21	661.31	10.28	36.55	0.48	
32041.76	10018.88	4635.78	3980.65	682.17	56.62	34.68	0.92	*678.454	283.65
*0.651	18.32	4259.78	2948.38	18.92	518.93	2.38	51.42	0.54	

Table4.txt

50231.22	15762.6	34574.23	4238.92	5308.4	7.23				
50.69	0.89	13213.84	356.88	51.29	24.08	5214.5			
19248.93	27.9	464.22		29.41	17.68	0.87			
78838.92	3260.59	7697.98	289.71	3333.73	7.51				
*13.46	0.71	*687.243	520.07	*2.09	17.84	14930.81			
18927.01	24.58	1144.23		8.33	17.68	0.76			
64459.35	10972.02	8424.95	2007.07	2442.5	18.72				
62.5	2.44	5724.33	362.95	24.2	43.05	11622.34			
4174.49	52.63	1240.08		20.38	47.86	0.83			
116584.75	20472.49	25861.06	2488.62	3757.13	67.77				
*13.46	5.62	14817.3	543.22	36.38	133.86	18598.28			
101386.05	44.19	2686.99		59.47	26.4	1.14			
336611.21	7496.55	8152.74	508.32	3448.75	14.13				
*13.46	0.29	*687.243	321.63	*2.09	8.71	8612.94			
34134.58	40.21	862.1		6.31	21.57	0.53			
97531.79	4100.98	10209.3	391.26	2591.77	13.22				
*13.46	0.83	20689.84	189.13	39.85	52.17	5780.17			
6308.98	39.3	674.84		3.97	25.51	0.52			
70448.56	8216.57	12508.49	859.25	2207.54	62.02				
91.05	0.35	*666.198	255.09	*1.988	11.9	4962.11			
37969.34	43.2	438.38		13.85	11.56	0.71			
50834.17	7087.96	10268.77	2258.05	3337.71	91.76				
67.41	2.78	*666.198	798.71	23.66	102.47	5001.18			
25577.43	24.34	800.19		21.1	15.12	1.12			
100220.96	10222	25528.52	3535.17	3351.27	64.41				
105.97	0.78	*666.198	471.38	17.24	25.63	5090.65			
159850.34	42.26	603.81		8.22	27.82	0.82			
51979.19	16951.15	12132.28	3592.3	2475.03	41.25				
50.46	1.12	*666.198	482.75	22.11	90.14	7970.52			
10385.91	20.86	1174.7		17.57	33.74	0.46			
43724.12	8009.05	8315.73	3444.33	4535.81	71.4				
*39.09	10.08	*666.198	770.4	*1.988	138.65	4731.01			
2964.65	37.47	1150.47		14.73	20.2	1.12			
127393.13	15582.08	14585.81	4427.45	7327.9	148.15				
75.49	1.43	*666.198	494.02	*1.988	42.56	6276.03			
42319.64	15.24	1059.1		17.18	41.96	0.74			
49289.04	17142	116327.6	2394.78	2198.7	97.75				
105.97	0.72	*666.198	400.7	5.54	14.22	12532.73			
32764.91	26.67	537.81		13.53	15.76	0.52			
76217.05	9439.03	6794.7	5133.83	2334.26	59.7				
130.05	1.13	8340.53	653.05	25.19	48.71	7390.32			
40496.85	34.32	1061.6		40.85	36.49	0.73			
85484.55	22939.29	13221.26	8576.92	2191.51	210.25				
*39.09	2.11	12917.59	808.07	41.97	76.45	4828.51			
46479.84	10.83	1084.08		117.94	31.5	1.01			
83016.74	15470.25	10829.79	1642.82	1611.18	128.7				
*39.09	2.93	7274.99	388.45	39.32	73.02	6108.24			
24715.68	27.28	1089.05		25.69	26.49	0.75			

Table4.txt

74679.41	21238.43	17924.22	3751.33	3507.1	66.42			
67.41	0.51	*666.198	225.02	*1.988	8.13	4212.08		
16792.13	34.12	368.63		7.75	23.69	0.44		
39828.39	6545.76	16755.14	4377.89	1533.49	86.55			
*39.09	0.94	*666.198	255.09	*1.988	36.81	6868.01		
12081.14	28.91	537.81		21.23	20.97	0.61		
50547.46	11169.02	11458.43	7614.37	2593.23	101.19			
105.97	0.5	*666.198	400.7	*1.988	14.69	7842.76		
49724.31	13.5	401.9		64.43	36.89	0.58		
39881.6	11449.04	7626.46	1871.69	3272.75	76.13			
*39.09	3.74	7816.89	424.77	23.66	46.96	7818.48		
13386.08	34.35	1026.28		16.48	23.32	0.63		
97064.64	11806.27	11067.02	5541.28	3193.81	137.05			
75.49	1.39	*666.198	269.57	4.4	31.92	10393.86		
27681.73	26.85	550.91		33.24	52.27	0.8		
65798.33	11614.41	14190.15	4090.27	2927.38	102.36			
136.23	0.46	55874.62	538.91	27.53	19.64	4806.3		
6059.81	33.56	524.16		12.72	30.82	0.56		
27894.67	7978.33	7444.75	4077.44	2826.06	131.52			
67.41	0.76	*666.198	471.38	*1.988	15.61	7384.33		
45634.44	22.05	514.55		12.56	28.51	0.47		
43230.02	7909.65	6580.66	5300.73	2133.8	53.8			
*39.09	2.97	*666.198	538.13	*1.988	16.07	6444.65		
60745.05	34.67	767.69		29.02	19.61	0.72		
38648.49	9987.87	9655.01	7114.11	2920.65	72.82			
59.59	0.71	*642.838	304.45	*1.988	16.99	8834.56		
20461.36	39.51	612.4		25.85	26.61	0.68		
93935.1	17380.68	14871.35	3549.97	3595.29	55.55			
137.83	1.4	18927.15	406.77	25.19	23.83	8162.37		
7181.6	16.92	1550.19		8.14	36.67	0.84		
39719.04	8531.95	19497.41	2735.65	6362.8	101.68			
92.22	0.71	*642.838	234.12	*0.537	11.71	7674.76		
10750.74	28.34	539.72		10.53	18.99	0.59		
42483.77	19157	10540.74	4246.62	2739.43	107.42			
116.83	3.03	13329.36	363.46	17.24	24.73	9110.63		
32623.01	21.16	551.21		9.25	19.66	0.97		
78153.79	12798.66	31620.79	2177.36	4187.62	68.82			
81.72	4.46	7274.99	516.26	14.65	47.84	5309.22		
5007.14	46.68	568.96		15.49	29.13	0.93		
67806.64	12860.17	32233.27	2858.71	4268.09	236.18			
*12.79	0.96	9135.14	263.37	23.78	14.9	5541.67		
6532.69	25.09	516.06		10.03	25.09	0.88		
25106.87	18860.02	10727.08	1021.52	3445.5	97.37			
*13.82	1.36	*642.838	324.6	*1.988	81.17	11766.64		
7971.15	30.45	775.5		16.9	41.27	0.76		
77207.42	9935.6	11536.14	4337	4738.24	48.95			
150.29	2.81	*642.838	240.25	3.61	39.47	9035.12		
20525.65	33.9	878.17		18.29	17.97	1.16		

Table4.txt

69506.52	21695.36	21418.24	3452.77	5055.11	181.74	59.59	3.67	*642.838	642.93
*1.988	66.12	6229.66	3827.24	30.03	1046.52	36.57	66.25	1	
124141.83	20348.46	9943.16	3770.45	7323.1	73.9	206.16	1.44	10285.61	209.34
11.93	80.74	8616.52	54995.91	45.01	603.81	13.53	16.92	0.92	
42915.15	11614.41	30168.88	3915.17	5499.51	32.78	122.13	1.61	148841.07	286.95
22.56	145.06	4127.42	31242.6	86.95	707.92	64.81	7.61	1.29	
209138.09	25318.22	18227.06	799.19	4508.52	50.73	76.34	2.72	14151.42	642.93
18.9	305.42	9009.99	100192.07	30.82	1644.13	25.77	29.27	1.27	
171693.59	14835.07	20906.58	3225.29	4286.99	50.2	47.75	0.44	4194	*27.635
*0.537	*1.39	3887.78	7880.37	12.07	268.54	13.25	33.25	0.47	
36638.47	5848.72	4025.5	5175.22	1577.28	100.16	1178.65	1.98	45661.62	527.24
49.63	16.53	7703.13	43447.69	34.33	429.54	9.88	45.7	1.95	
79214.68	49041.88	19382.79	2260.12	3638.58	73.33	*13.82	0.63	*642.838	193.15
*1.988	10.96	6318.16	10361.73	32.67	325.71	3.41	20.49	0.74	
35159	10643.4	9447.24	3469.66	2221.32	51.17	59.59	2.35	12521.36	255.09
*1.988	23.83	9491.8	9693.49	33.86	533.24	10.62	11.29	0.56	
131222.75	16350.89	18175.26	4409.55	1980.24	21.64	92.22	0.65	*642.838	225.02
4.37	46.08	5292.84	12293.57	21.21	568.96	15.13	42.3	0.56	
39536.5	13581.93	31006.3	3185.37	3275.55	29.69	*13.82	1.96	4849.69	692.96
*1.988	50.47	7776.03	43262.12	42.55	833.16	42.59	28.84	1.18	
64132.63	14670.14	11145.69	1630.45	3435.81	32.5	*12.79	0.96	*642.838	*27.635
*0.537	*1.39	8809.98	23288.17	42.23	510.1	4.37	23.86	0.59	
23728.11	21133.34	8108.62	4168.07	4007.13	25.35	109.39	2.69	7722.36	647.61
*6.138	30.23	4396.67	59172.7	16.11	5977.18	34.92	31.75	0.53	
29716.49	9539.9	6593.01	1711.42	1913.99	198.65	187.38	0.37	*656.313	*27.445
*6.138	*1.342	5685.3	9542.27	22.68	351.42	6.19	11.09	*0.029	
17529.63	7375.26	7714.83	5115.64	1521.81	35.31	*11.332	1.38	*682.162	273.8
31.42	10.6	2653.94	11647.33	18.18	351.94	22.29	10.72	0.95	
101276.66	11432.96	8310.97	1590.78	1126.38	72.53	*11.332	2.6	*682.162	2409.48
*0.642	30.96	1528.38	8021.53	23.05	8499.62	33.81	8.26	1.22	
235828.51	12997.4	100817.11	2371.48	4362.87	249.5	150.72	2.26	*682.162	*26.909
*0.642	8.67	4859.19	6181.04	26.66	464.97	9.01	7.38	0.57	

Table4.txt

44167.93	12176.14	24721.29	3181.07	2703.3	237.06	
143.93	1.77	10953.75	421.4	*1.75	32.08	5252.11
2949.13	48.54	615.41		50.48	28.16	0.74
88460.86	21178.4	20337.62	2567.7	*34.54	80.83	
243.95	1.25	40649.13	215.96	*1.75	40.72	15589.17
6391.8	66.76	1173.66		14.22	16.82	1.19
138409.3	20725.25	147148.97	2132.83	*34.54	221.62	
*10.934	0.62	21180.26	425.31	*1.75	13.67	10891.25
9354.03	54.45	619.77		39.44	24.76	0.76
103741.35	9997.34	8107.72	1535.62	*34.54	62.43	
*10.934	0.61	5864.77	215.96	50.3	16.65	8659.21
8942.8	16.99	278.3		18.07	10.77	0.37
65971.41	8569.6	92498.13	1412.69	230.98	66.28	
*10.934	0.46	8216.81	189.37	*1.75	10.53	22243.35
3195.46	54.64	411.91		36.37	27.51	0.61
109679.38	12234.44	7555.71	2147.91	*34.54	190.73	
*10.934	0.4	5244.07	*27.402	*1.75	10.95	6543.01
1404.24	34.33	271.4		10.32	6.28	0.33
107694.94	7581.42	225427.66	2102.7	*34.54	80.07	
*10.934	0.48	6470.61	358.02	*1.75	12.41	7084.61
5214.94	28.4	417.37		24.99	20.25	0.69
71566.32	10315.37	100926.21	2521.93	*34.54	128.09	
*10.934	2.33	*685.577	325.63	34.69	10.53	8029.12
6671.07	29.48	459.71		26.21	9.31	0.46
39237.34	9678.75	127810.81	1974.96	*34.54	204.71	
1462.07	5.02	*685.577	1140.34	129.57	18.37	4780.98
19685.75	13.85	1004.74		25.1	10.25	1.95
135486.33	13470.7	81967.49	2794.88	*34.54	288.52	
122.05	1.53	11481.27	603.22	11.98	25.82	53356.84
1661.26	144.3	755.11		37.71	33.2	0.85
224797.05	19116.73	63118.53	2812.81	*34.54	81.64	
*11.332	0.88	*682.162	339.09	*0.642	*1.364	2386.27
22920.83	22.06	366.36		27.09	18.4	0.51
29052.26	6300.79	4437.48	1354.93	61146.1	51.37	
*10.934	1.15	7645.23	341.89	36.3	22.29	14650.11
3764.15	24.38	360.71		43.87	52.64	0.5
67383.06	7171.02	17972.78	1922.5	*34.54	136.35	
*10.934	1.47	47763.23	288.51	25.56	15.8	36906.99
75266.57	99.61	1335.36		115.27	14.9	0.95
82674.39	13512.52	73535.09	1424.96	*34.54	10.16	
*10.934	0.68	*685.577	224.69	*1.75	8.27	14123.23
17158.54	74.87	348.77		21.01	14.2	0.45
84532.94	6563.52	30335.68	1983.71	*34.54	274	
60.83	1.39	5864.77	241.98	*1.75	*1.379	3711.52
119171.67	9.51	219.89		43.69	14.44	0.53
65680.51	4628.06	96665.7	1265.9	*34.54	73.61	
505.85	1.4	4605.82	292.67	*1.75	*1.379	7403.32
449756.55	25.88	271.4		22.32	193.87	0.89

Table4.txt

116819.06	8569.6	49963.73	2112.74	*34.54	69.94			
638.98	0.43	7645.23	233.36	*1.75	12.41	3514.63		
7256.31	**116.65	727.62		47.04	56.33	0.59		
106683.62	17421.7	31916.27	2667.07	*34.54	102.72			
*10.934	6.07	4927.34	*27.402	48.78	19.24	6336.29		
1780.5	33.62	383.94		10.95	*0.115	0.8		
244617.9	8783.51	38066.02	996.56	*34.54	120.43			
*10.934	0.69	*685.577	171.28	*1.75	*1.379	4800.93		
6918.7	17.44	400.85		15.1	4.99	0.41		
28427.02	11350.77	81610.33	1251.27	*34.54	84.86			
*10.934	0.9	*685.577	317.44	*1.75	8.27	3857.44		
21475.3	24.21	298.44		61.31	9.72	0.65		
38603.84	10273	34043.36	2848.7	*34.54	112.15			
76.14	0.89	*682.162	527.51	19.88	29.55	9458.44		
12738.71	42.16	677.02		87.09	28.99	0.5		
73967.55	7725.34	72500.96	1763.31	1196.39	73.19			
99.4	0.97	*685.577	250.55	33.47	14.52	9604.7		
7676.43	46.79	570.83		8.71	3.18	0.29		
79454.55	5138.39	297293.15	699.48	*34.54	71.91			
*10.934	1.09	*685.577	189.37	*1.75	9.91	4446.63		
56783.45	13.28	278.3		13.73	7.19	0.41		
68792.81	14556.09	56508.78	1795.48	*34.54	99.15			
*10.934	0.77	48517.3	401.78	*1.75	14.73	8680.83		
27504.97	58.33	632.74		251.6	10.51	0.77		
49530.98	7710.73	39289.45	2086.39	*34.54	47.41			
*10.934	0.71	*685.577	513.64	20.33	69.57	35786.03		
12490.91	52.45	1095		23.89	78.45	0.73		
48582.34	9848.73	18207.63	1353.88	*34.54	64.72			
80.56	0.59	*685.577	*27.402	*1.75	21.86	4515.93		
72005.48	41.12	219.89		10.57	4.65	0.48		
64391.06	5469.36	61965.61	2349.57	535.47	17.18			
*10.934	1.95	21634.59	284.34	*1.75	32.08	18783.17		
111429.53	41.87	597.81		15.95	7.48	0.99		
73426.55	18207.79	39008.18	2350.83	*34.54	54.5			
113.1	0.97	8216.81	740.92	28.1	26.26	5792.76		
14780.26	20.2	464.85		48.43	10.77	0.68		
45759.48	10992.13	32564.66	1412.69	*34.54	53.01			
*10.934	0.27	14540.93	*27.402	*1.75	10.33	7879.91		
4348.41	63.12	538.41		14.92	10.77	0.35		
64099.61	5359.19	111278.75	1497.46	*34.54	30.26			
*10.934	0.83	7063.57	349.97	*1.75	22.07	10486.09		
21438.1	84.8	444.1		21.9	5.32	0.69		
72351.96	8076.41	110049.23	2017.48	*34.54	48.04			
*10.934	0.26	13539.21	309.22	*1.75	16.65	3517.85		
21673.09	60.02	304.99		20.48	7.34	0.58		
39913.39	5182.6	22792.89	1390.62	*34.54	127.83			
65.87	0.88	92710.59	*27.402	*1.75	13.67	15240.93		
1780.5	64.79	881.4		10.53	8.06	0.39		

Table4.txt

32394.73	6759.16	62694.9	1543.01	*34.54	153.13		
*10.934	0.87	*685.577	284.34	23.84	11.16	28496.64	
6770.8	126.27	422.79		14.68	5.97	0.59	
81642.23	4783.76	71610.67	575.13	*34.54	116.78		
*10.934	3.2	90918.89	456.35	47.26	24.27	3082.77	
2688.78	7.38	219.89		11.72	7.78	0.76	
61053.08	5359.19	92871.04	1093.27	*34.54	160.15		
37.02	1.81	*685.577	*27.402	32.24	13.25	10587.07	
3195.46	46.68	467.4		9.41	5.65	0.39	
42192.7	5094.16	78862.03	1867.65	*34.54	146.82		
150.37	0.54	16014.51	610.58	16.72	37.07	12452.76	
14173.75	35.91	5270.96		18.46	27.14	0.46	
100767.56	16530.77	74834.98	2173.05	*34.54	77.33		
452.54	0.57	*685.577	*27.402	*1.75	*1.379	6137.3	
33310.78	14.95	223.78		2.3	4.47	0.39	
81270.7	6061.81	303759.07	2571.52	*34.54	235.56		
133.08	0.41	*685.577	284.34	*1.75	12.83	5376.57	
66095.36	17.71	679.06		30.18	9.72	0.46	
38603.84	16717.38	58266.97	2542.26	*34.54	115.24		
*10.934	0.34	*685.577	374.03	*1.75	*1.379	6774.89	
75175.83	21.95	524.17		39.62	79.03	0.44	
29994.01	2656.02	187828.79	1670.22	*34.54	147.17		
*10.934	0.86	48893.33	309.22	*1.75	11.16	7294.52	
10713.71	37.91	467.4		11.93	4.3	0.29	
93601.15	7127.74	241440.02	1194.03	*34.54	104.63		
104	0.69	16014.51	1153.7	20.33	20.54	6212.68	
6468.71	8.26	916.6		64.83	19.52	0.52	
145116.62	8954.41	140145.7	1607.16	*34.54	73.55		
*10.934	0.75	17932.12	224.69	11	24.71	25193.04	
93442.56	59.06	597.81		15.1	19.31	0.62	
103657.44	9827.49	111737.24	1245.17	*34.54	72.22		

sHER2/sEGFR2/ sErbB2 (pg/ml)	CancerSEEK Logistic Regression Score	sPECAM-1 (pg/ml)	CancerSEEK TGFa Test Result	Thrombospondin-2 (pg/ml)	TIMP-1 (pg/ml)	TIMP-2 (pg/ml)
6832.07	0.681	9368.53	*2.681	Negative	21863.74	56428.71	39498.82
5549.47	0.986	6224.55	*2.681	Positive	29669.66	73940.49	41277.09
3698.16		4046.48	179.03		6020.47		

Table4.txt

22797.28	28440.6	0.978	Positive		
	5856	6121.93	*2.681	4331.02	
20441.19	25896.73	0.693	Negative		
	5447.93	6982.32	*2.681	2311.91	
56288.51	49425.2	0.515	Negative		
	6259.35	7935.75	*2.681	9564.37	
45870.23	48382.43	0.707	Negative		
	9336.65	7965.05	26.02	12153.76	
18718.19	24998.06	0.117	Negative		
	4845.24	4512.37	*2.681	*406.606	
19099.46	27730.8	0.381	Negative		
	4232.62	4609.75	*2.681	*406.606	
18330	29151.57	0.892	Positive		
	4474.35	5445.12	*2.681	2229.02	
11941.18	23460.29	0.557	Negative		
	3477.67	4980.39	*2.681	9633.14	
22641.94	21701.45	0.698	Negative		
	4465.13	5743.23	*2.681	*406.606	
62470.75	41075.16	0.356	Negative		
	7077.06	4152.68	*2.681	2666.43	
45976.53	37632.81	0.878	Positive		
	3836.11	2682.27	*2.681	*406.606	
50429.23	38164.65	0.998	Positive		
	4585.15	5308.6	*2.681	9335.4	
70380.06	47344.38	0.117	Negative		
	4095.8	4520.46	*2.681	*406.606	
13765.62	21637.54	0.967	Positive		
	5505.01	3648.55	*2.681	3534.48	
17332.57	21829.29	0.915	Positive		
	4305.85	6838.52	*2.681	4028.31	
18682.82	24805.66	0.574	Negative		
	3962.64	4015.16	*2.681	9564.37	
19326.5	21861.25	0.934	Positive		
	6239.88	6081.92	*2.681	10922.95	
20296.31	23268.28	0.307	Negative		
	3211.9	3485.85	*2.681	*406.606	
23132.96	31845.7	0.750	Negative		
	4687.07	6458.7	*2.681	2624.55	
41369.48	38231.2	0.999	Positive		
	5280.43	4508.32	*2.681	12270.35	
36672.51	29119.22	0.981	Positive		
	4260.06	4789.87	*2.681	2063.89	
15524.68	19113.57	0.439	Negative		
	7767.91	8023.77	*2.681	16206.63	
35140.87	30285.27	0.969	Positive		
	4951.14	6769.32	*2.681	*406.606	
27145.36	22980.34	0.996	Positive		
	3185.46	3232.72	*2.681	13370.08	

Table4.txt

20750.13	26635.99	0.951	Positive		
	3674.24	3855.74	*2.681		*406.606
28075.81	29054.55	0.606	Negative		
	4758.3	3399.66	*2.681		16206.63
31100.85	32497.95	0.116	Negative		
	5353.01	5376.72	*2.681		*406.606
20016.52	25704.04	0.904	Positive		
	3176.66	2717.42	224.47		*406.606
13501.38	21925.17	0.973	Positive		
	6184.78	6522.23	*2.681		4396.09
19949.01	26378.74	0.117	Negative		
	3471.74	4585.34	*2.681		7653.96
34875.33	31064.63	0.988	Positive		
	5435.25	4467.94	*2.681		*406.606
52458.17	38164.65	0.991	Positive		
	5120.06	5479.43	*2.681		*406.606
54220.89	46070.49	0.397	Negative		
	4412.97	5962.43	*2.681		*406.606
17132.66	22564.56	0.840	Negative		
	1924.08	1420.52	17.34		6688.42
29093.45	27279.69	0.906	Positive		
	4863.9	3909.97	*2.681		4962.71
15558.96	24292.85	0.739	Negative		
	3276.62	4279.58	*2.681		8924.27
93675.88	79745.19	0.448	Negative		
	5878.46	4822.84	*2.681		*406.606
20750.13	28795.93	0.116	Negative		
	5965.24	6778.53	*2.681		*406.606
50998.21	38664.19	0.330	Negative		
	4640.7	3886.7	*2.681		15517.57
142686.13	51912.48	0.990	Positive		
	5258.37	4480.04	*2.681		*406.606
26438.57	28150.09	0.944	Positive		
	3599.62	3565.05	*2.681		*406.606
54716.49	37632.81	0.543	Negative		
	4863.9	7906.49	*2.681		13510.95
16868.16	20583.18	0.308	Negative		
	6647.78	4255.7	*2.681		*406.606
41300.46	30934.62	0.490	Negative		
	4223.48	3625.73	*2.681		*406.606
15182.2	22692.47	0.121	Negative		
	3135.61	5257.68	*2.681		6844.97
54734.6	31845.7	0.993	Positive		
	3890.27	3875.08	*2.681		6666.08
87140.85	34495.42	0.999	Positive		
	3510.34	2731.52	*2.681		*406.606
21829.76	24164.71	0.323	Negative		
	7017.31	9135.14	*2.681		*406.606

Table4.txt

15075.3	23492.3	0.680	Negative		
	4130.76	3791.3	*2.7	3558.8	
57625.12	32837.86	0.818	Negative		
	5889.09	7047.41	*2.7	*129.5	
69646.43	28875.35	0.343	Negative		
	5662.55	5030.11	35.52	*129.5	
36705.4	30318.69	0.480	Negative		
	5843.74	3929.21	*2.7	*129.5	
36588.8	27259.35	0.300	Negative		
	3226.59	3251.24	*2.7	4704.4	
65232.48	24608.24	0.125	Negative		
	6142.21	7544.99	*2.7	9811.52	
106771.02	34442.57	0.868	Positive		
	5301.27	8310.67	*2.7	20465.66	
167486.78	33103.83	0.994	Positive		
	3330.45	4773.51	*2.7	3128.9	
79659.34	36638.81	0.998	Positive		
	5578.55	5642.96	*2.7	2244.33	
49487.04	36023.47	0.640	Negative		
	6431.92	5622.96	*2.7	20489.78	
88506.88	28298.68	0.664	Negative		
	5063.37	4252.86	*2.7	*129.5	
47856.77	34106.48	0.318	Negative		
	4372.56	4071.69	*2.7	6326.58	
72633.21	28319.99	0.999	Positive		
	4678.93	4268.02	*2.7	*129.5	
54661.21	25832.27	0.117	Negative		
	2637.17	5273.52	*2.7	732.01	
88506.88	32660.88	0.974	Positive		
	4452.25	6254.04	*2.7	*129.5	
37598.75	27301.59	0.598	Negative		
	9589.39	8117.28	*2.7	*129.5	
57938.7	31407.43	0.868	Positive		
	6546.11	5855.85	*2.7	6469.71	
43498.28	33592.97	0.451	Negative		
	4493.71	6172.29	*2.7	*129.5	
73025.64	33325.92	0.983	Positive		
	4343.89	5839.72	*2.7	*129.5	
84791.49	27153.82	0.968	Positive		
	5031.27	4730.99	*2.7	*129.5	
51888.67	25499.04	0.521	Negative		
	4858.13	5045.74	*2.7	*129.5	
73538.54	29799.64	0.937	Positive		
	4723.7	4162.11	*2.7	*129.5	
49334.58	25665.53	0.338	Negative		
	4528.81	4154.56	*2.7	*129.5	
60034.86	34240.8	0.116	Negative		
	4938.25	5839.72	*2.7	683.74	

Table4.txt

81693.71	31889.66	0.956	Positive		
	4551.15	5077.04	*2.7	*129.5	
48203.95	28277.37	0.540	Negative		
	5084.34	6154.94	*2.684	6264.92	
136363.01	57377.78	0.926	Positive		
	5778.95	5027.85	*2.684	5095.23	
72112.49	59669.66	0.621	Negative		
	4853.14	5082.54	*2.684	*445.855	
73931.88	59388.49	0.999	Positive		
	6935.33	5545.11	*2.684	*445.855	
86067.68	57704.59	0.936	Positive		
	2106.35	4710.58	*2.684	*445.855	
81139.74	66179.4	0.779	Negative		
	5807.42	3096.21	*2.684	*445.855	
63180.71	52544.71	0.614	Negative		
	3263.91	1905.96	*2.684	*445.855	
59700.78	48440.06	0.985	Positive		
	1759.17	2168.53	*2.684	5631.7	
98251.75	40124.55	0.926	Positive		
	4991.64	3985.13	*2.684	*445.855	
82000.48	80450.38	0.362	Negative		
	5411.01	3971.52	*2.684	*445.855	
81441.1	57564.51	0.966	Positive		
	3778.83	4322.61	*2.684	*445.855	
93552.46	62914.06	0.852	Negative		
	8955.64	5343.78	*2.684	*445.855	
66284.65	45779.35	0.965	Positive		
	9649.19	7351.94	*2.684	6868.37	
79321.23	58312.06	0.121	Negative		
	5140.1	4032.86	*2.684	2259.98	
64350.35	53053.97	0.990	Positive		
	2829.49	3470.64	*2.684	2752.86	
90969.03	54073.83	0.397	Negative		
	8914.82	6435.85	*2.684	7984.31	
76794.75	54630.88	0.824	Negative		
	4152.81	5392.04	*2.684	4372.28	
58036.95	36633.24	0.996	Positive		
	6652.66	5388.33	*2.684	*445.855	
53084.78	33786.36	0.998	Positive		
	7854.7	4476.64	*2.684	3155.42	
80793.43	43357.07	0.606	Negative		
	5434.47	5354.91	*2.684	6423.56	
65765.79	42718.58	0.972	Positive		
	4152.81	5432.98	*2.684	*445.855	
57034.01	46924.9	0.593	Negative		
	4491.59	3301.37	*2.684	*445.855	
75200.09	56584.9	0.981	Positive		
	5940.59	4561.31	*2.684	*445.855	

Table4.txt

76805.7	59107.47	0.507	Negative		
	5177.33	3552.82	*2.684	*445.855	
55145.06	46099.91	0.328	Negative		
	7249.49	6732.74	*2.684	6772.98	
123349.14	65989.51	0.940	Positive		
	5561.47	4094.47	*2.684	*445.855	
53819.75	40033.68	0.371	Negative		
	8711.17	7774.9	*2.684	*445.855	
49080.16	45596.25	0.117	Negative		
	5993.04	5885.7	*2.684	15648.46	
210938.12	80205.49	0.997	Positive		
	6150.86	5170.41	*2.684	2721.96	
75393.67	60232.44	0.581	Negative		
	6492.72	4703.44	*2.684	*445.855	
60130.57	39261.74	0.801	Negative		
	5821.66	7591.45	*2.684	3590.78	
78892.7	56584.9	0.788	Negative		
	4747.39	3836.14	*2.684	*445.855	
48888.33	36995.34	0.449	Negative		
	4692.38	4177.02	*2.684	10649.53	
43699.45	32929.27	0.993	Positive		
	5093.63	3748.84	*2.684	*445.855	
49859.03	43357.07	0.387	Negative		
	4027.5	2844.75	*2.684	*445.855	
37123.82	38082.49	0.368	Negative		
	4614.63	3001.26	*2.684	*445.855	
40397.27	41534.26	0.997	Positive		
	2691.37	3210.18	*2.692	*404.102	
103949.9	32314.4	0.979	Positive		
	3375.1	4401.83	51.57	*404.102	
107297.72	31572.38	1.000	Positive		
	3390.67	3073.44	*2.692	*404.102	
88191.99	27763.62	0.989	Positive		
	3754.37	3016.4	73.44	*404.102	
34135.04	22851.81	0.977	Positive		
	6950	3688.73	*2.684	*445.855	
74090.65	60138.6	0.639	Negative		
	5826.41	2177.23	*2.684	*445.855	
43615.5	46283.15	0.122	Negative		
	3823.04	2171.43	*2.684	*445.855	
57503.59	55002.55	0.123	Negative		
	7111.76	6279.29	*2.684	*445.855	
87948.95	65372.89	0.877	Positive		
	8477.96	5133.74	*2.684	*445.855	
66506.63	58639.44	0.886	Positive		
	11896.89	5148.4	*2.684	7824.57	
67449.27	51573.7	0.121	Negative		
	5902.49	4448.52	*2.684	*445.855	

Table4.txt

70241.74	67939.39	0.121	Negative		
	4651.19	2665.98	*2.684	*445.855	
41459.11	35864.25	0.404	Negative		
	5149.4	3405.27	*2.684	*445.855	
60697.85	62489.71	0.332	Negative		
	3441.38	3220.81	*2.684	*445.855	
60851.55	54584.44	0.803	Negative		
	2816.88	1606.14	*2.684	*445.855	
26612.04	28427.48	0.620	Negative		
	4854.77	6754.36	*2.692	*404.102	
61463.72	41502.75	0.975	Positive		
	3468.72	4652.09	*2.692	*404.102	
31681.29	29890.83	0.993	Positive		
	5576.42	6832.34	*2.692	4584.26	
31278.71	27219.12	0.961	Positive		
	4942.49	9039.61	*2.692	*404.102	
71685.17	34343.83	0.571	Negative		
	6487.61	7272.48	*2.692	*404.102	
49446.57	25633.78	0.727	Negative		
	5426.3	4956.85	*2.692	*404.102	
39031.77	28951.08	0.938	Positive		
	4971	11411.77	*2.692	2598.33	
100677.89	52666.14	0.564	Negative		
	5421.47	9817.65	*2.692	*404.102	
43243.57	26179.01	0.681	Negative		
	3090.25	5778.54	*2.692	*404.102	
55148.74	29890.83	0.997	Positive		
	4824.01	5158.07	*2.692	*404.102	
66888.79	27813.11	0.514	Negative		
	3533.61	6155.27	23.09	12052.02	
45807.58	27021.08	0.997	Positive		
	6677.95	6648.88	*2.692	*404.102	
72192.94	51287.1	1.000	Positive		
	2846.39	6170.29	*2.692	*404.102	
110600.08	38512.16	0.972	Positive		
	4197.87	7592.86	*2.692	*404.102	
39138.24	27714.13	0.986	Positive		
	3876.97	4417.83	*2.692	*404.102	
78925.95	45916.35	0.861	Negative		
	6993.41	5342.29	*2.736	3460.43	
77503.17	44475.85	1.000	Positive		
	7212.01	4790.14	*2.736	*170.39	
36750.11	36519.82	0.955	Positive		
	3169.33	4242.81	*2.692	*404.102	
58878.61	27120.1	0.990	Positive		
	6060.8	6372.83	*2.692	7945.95	
150551.59	38711.14	1.000	Positive		
	4975.76	4698.34	*2.692	10282.1	

Table4.txt

48099.87	24840.11	0.992	Positive		
	5612.85	5825.51	*2.692	25272.12	
102897.67	26922.04	0.999	Positive		
	6935.33	5218.19	*2.684	*445.855	
76849.55	67225.11	0.984	Positive		
	5223.93	3937.55	*2.684	*445.855	
79740.72	67605.92	0.997	Positive		
	4954.64	2957.21	*2.684	*445.855	
79027.78	61830.32	0.117	Negative		
	3927.1	3721.59	*2.692	8667.06	
80544.65	25435.43	0.993	Positive		
	2781.63	2479.29	*2.692	3621.58	
28157.71	24393.3	0.997	Positive		
	2747.19	2392.4	19.98	*404.102	
35027.41	25881.65	0.940	Positive		
	3381.77	3772.22	52.68	2867.14	
166373.66	32215.45	0.997	Positive		
	2493.27	3643.53	16.15	*404.102	
33181.7	30484.3	0.999	Positive		
	3266.41	4990.19	17.44	7125.77	
76534.79	27021.08	0.999	Positive		
	3612.2	4965.18	*2.692	3378.36	
168850.33	38164.07	0.967	Positive		
	3881.52	5344.97	*2.692	2846.55	
58056.64	34046.69	0.848	Negative		
	2310.19	2966.74	*2.692	*404.102	
78322.9	31918.64	0.997	Positive		
	2665.67	4546.58	*2.692	14682.17	
205809.28	34938.3	0.993	Positive		
	2152.12	5988.05	*2.692	*404.102	
87703.88	27367.64	0.792	Negative		
	2262.17	5586.26	*2.692	5199.62	
46897.03	24144.94	0.652	Negative		
	4294.98	12623.3	*2.692	21853.23	
141816.83	34690.57	0.997	Positive		
	4142.55	7710.81	*2.692	*404.102	
69417.16	26575.35	0.308	Negative		
	2125.27	6164.28	*2.692	22645.87	
123979.69	42152.55	0.992	Positive		
	3770.23	4303.54	*2.692	9328.93	
39118.27	31077.78	0.793	Negative		
	5576.42	10199.82	*2.692	*404.102	
102023.27	34641.03	0.977	Positive		
	4781.48	6242.55	*2.692	3133.81	
91119.7	34839.2	0.583	Negative		
	4621.43	4752.95	*2.692	*404.102	
82164.25	26030.34	0.983	Positive		
	4373.88	5362.08	*2.692	*404.102	

Table4.txt

83202.49	28901.61	0.975	Positive		
	3895.19	7096.99	*2.692	*404.102	
61775.36	30830.49	0.984	Positive		
	3063.97	4525.04	*2.692	3459.57	
123163.09	33155.6	0.997	Positive		
	3596.46	4227.02	*2.692	*404.102	
116937.17	35433.91	0.972	Positive		
	3587.47	4508.9	*2.692	*404.102	
88147.47	29594.08	0.938	Positive		
	3551.55	5265.39	*2.692	*404.102	
205865.48	30088.66	1.000	Positive		
	4318.16	4221.76	*2.692	*404.102	
93261	27813.11	0.998	Positive		
	2896.2	3299.89	*2.692	*404.102	
70186.37	30533.76	1.000	Positive		
	4576.88	6330.3	64.78	2681.3	
146501.5	32264.93	1.000	Positive		
	3215.6	4306.19	109.37	*404.102	
165139.1	36078.52	0.983	Positive		
	2550.53	6080.41	*2.692	*404.102	
239878.22	40055.65	0.919	Positive		
	2870.19	4114.37	24.93	*404.102	
113206.96	27862.6	0.998	Positive		
	2738.59	4295.6	66.96	*404.102	
160534.27	38362.96	0.996	Positive		
	2567.54	6342.44	27.95	*404.102	
235646.9	34145.73	1.000	Positive		
	3306.27	5085.09	*2.692	3297	
132467.33	30088.66	0.999	Positive		
	4068.98	3236.77	58.21	*404.102	
98697.41	30088.66	0.999	Positive		
	3024.61	4525.04	34.47	*404.102	
126679.47	36376.17	1.000	Positive		
	2825.11	3770.49	*2.795	5588.16	
89036.61	33120.88	1.000	Positive		
	4546.75	6383.08	*2.795	*434.712	
63685.39	24648.53	0.999	Positive		
	3503.43	3726.96	38.86	*434.712	
99433.42	32923.46	0.982	Positive		
	3758.12	5593.59	36.34	7906.56	
89010.7	37353.84	0.993	Positive		
	2212.93	3005.47	36.84	*434.712	
154617.01	36026.64	0.918	Positive		
	3157.72	3208.52	37.34	11492.17	
99907.71	46486.08	0.990	Positive		
	3677.11	5103.9	51.67	*434.712	
84894.84	39619.29	0.993	Positive		
	2805.72	6126.97	47.54	5845.76	

Table4.txt

**4142.527	38818.39	0.999	Positive		
	3007.83	6650.38	36.34	*434.712	
118170.46	29124.36	0.984	Positive		
	3920.98	4438.98	80.21	*434.712	
102522.67	28993.96	0.998	Positive		
	6253.43	4323.12	107.45	*434.712	
179920.4	34439.28	1.000	Positive		
	2798.46	4353.51	106.34	6796.6	
143728.69	22204.14	0.992	Positive		
	3256.62	3916.69	*2.795	*434.712	
57442.23	23231.56	0.965	Positive		
	2718.74	3651.89	*2.795	16847.76	
121601.51	25811.53	0.998	Positive		
	2103.46	2983.75	53.75	*434.712	
74155.75	33581.87	1.000	Positive		
	2412.91	3378.75	*2.795	*434.712	
101393.46	29842.31	0.999	Positive		
	1914.46	3505.99	*2.795	*434.712	
63800.93	25552.8	0.934	Positive		
	5305.73	4061.64	55.83	*434.712	
44468.41	21243.34	0.953	Positive		
	2946.73	4711.15	57.4	*434.712	
198939.23	30103.67	0.998	Positive		
	5687.35	4714.27	71.65	*434.712	
91484.07	29450.55	1.000	Positive		
	3598.91	4941.05	44.46	7331.58	
86624.09	32528.9	1.000	Positive		
	3298.8	3202.98	30.34	*434.712	
106770.12	32594.63	0.988	Positive		
	3346.04	4488.06	72.72	*434.712	
94271.78	43847.97	0.369	Negative		
	3712.52	5415.44	22.5	*434.712	
106640.43	38152.08	0.836	Negative		
	4250.03	6871.66	51.15	7331.58	
70306.17	27562.13	1.000	Positive		
	3768.26	6893.23	*2.795	13058.05	
101727.48	27302.32	0.980	Positive		
	3500.92	5484.47	*2.795	3659.28	
122388.98	32594.63	0.852	Negative		
	3709.99	3975.65	*2.795	4178.19	
112770	28537.85	0.890	Positive		
	2129.01	4283.71	*2.795	*434.712	
105339.21	40488.58	0.920	Positive		
	3212.06	7586.92	*2.795	9655.25	
**4142.527	31085.23	0.998	Positive		
	3207.11	3626.01	*2.795	*434.712	
110883.77	30365.2	0.934	Positive		
	5016.72	6175.11	*2.795	*434.712	

Table4.txt

148858.21	27562.13	0.467	Negative	
3192.28	5666.77	*2.795	2286.3	
122885.16	33647.76	0.995	Positive	
4691.11	4925.18	60.54	*434.712	
154911.14	39485.71	0.962	Positive	
3995.14	8065.03	98.11	*434.712	
**4142.527	60547.3	1.000	Positive	
2781.52	4611.55	31.33	*434.712	
79616.69	46486.08	0.965	Positive	
2412.91	4442.04	74.85	*434.712	
94799.48	36756.1	0.992	Positive	
3219.48	6306.52	96.47	*434.712	
68341.61	32069.03	1.000	Positive	
7792.66	5814.18	58.44	7708.24	
147256.2	25811.53	1.000	Positive	
3872.51	6739.25	35.33	*434.712	
**4142.527	49481.36	0.999	Positive	
2565.14	5547.2	92.11	*434.712	
92452.05	51329.43	1.000	Positive	
3651.86	7323.07	43.44	*434.712	
88519.94	33581.87	0.997	Positive	
3687.22	5461.43	177.36	11993.16	
110832.49	33120.88	1.000	Positive	
2842.09	3005.47	29.35	*434.712	
84428.46	29254.81	0.967	Positive	
2353.83	4648.82	51.15	*434.712	
61225.08	26459.05	0.998	Positive	
3824.14	4292.8	*2.795	*434.712	
154911.14	51947.17	0.921	Positive	
4494.45	9027.85	106.34	25787.35	
104341.88	35232.24	1.000	Positive	
3177.47	6278.76	64.23	*434.712	
85761.06	30954.23	0.999	Positive	
4136.42	7923.31	57.92	*434.712	
97535.48	46621.79	0.983	Positive	
4198.33	6257.98	29.35	*434.712	
101971.29	47097.11	1.000	Positive	
4038.72	4792.6	91.03	10253.15	
154382.44	45401.88	1.000	Positive	
2675.4	5474.59	*2.795	*434.712	
129785.49	33977.39	0.994	Positive	
3259.1	5620.16	103.05	*434.712	
205773.08	49071.72	0.983	Positive	
3184.87	4390.07	159.05	*434.712	
98800.56	38818.39	1.000	Positive	
3999.88	7012.76	32.2	24317.51	
234457.39	47733.94	0.988	Positive	
5052.14	4748.15	85.44	*125.26	

Table4.txt

92649.9	43533.06	0.947	Positive		
	6229.77	9326.05	66.39	*125.26	
99524.99	71815.92	0.992	Positive		
	6320.02	6761.89	55.65	*125.26	
100444.72	44313.98	0.968	Positive		
	4236.99	8237.5	47.84	*125.26	
61293.07	33385.5	0.966	Positive		
	4227.22	6540.45	78.11	*125.26	
150519.92	46328.8	0.955	Positive		
	4723.62	5785.58	66.39	906.59	
88779.64	42531.09	0.998	Positive		
	5230.15	9270.38	*2.749	9793.28	
157304.19	36618.51	1.000	Positive		
	4717.07	8266.36	18.46	*125.26	
126306.22	33549.5	0.992	Positive		
	6226.43	4690.61	59.55	*125.26	
43195.57	31856.56	0.936	Positive		
	3938.32	4011.02	72.73	*125.26	
53208.88	26524.38	0.984	Positive		
	4599.18	6463.19	43.93	2347.83	
155032.98	36124.24	0.995	Positive		
	6893.74	5883.45	49.79	70277.28	
220061.94	73517.95	0.997	Positive		
	3721.74	4305.84	55.65	16796.85	
175160.85	46946.45	0.957	Positive		
	5693.57	7844.72	44.42	*125.26	
90923.17	37828.57	1.000	Positive		
	7803.4	7182.65	109.44	92343	
141665.25	50786.69	0.997	Positive		
	4658.1	9875.83	61.5	*125.26	
144554.36	54954.71	0.992	Positive		
	5979.56	7004.88	*2.749	*125.26	
100513.29	37498.29	0.991	Positive		
	4110.2	6000.63	*2.749	2424.71	
110329.99	27719.52	0.993	Positive		
	2604.57	3146.9	*2.749	*125.26	
63604.78	28045.6	1.000	Positive		
	6286.58	6382.32	*2.749	5271.36	
40247.39	35465.85	0.982	Positive		
	5889.67	8452.63	*2.749	2725.51	
65271.73	28915.52	0.935	Positive		
	4393.37	3641.15	*2.749	4314.67	
85790.26	40644.55	0.903	Positive		
	4894.26	8669.46	*2.749	*125.26	
44321.53	30711.76	0.981	Positive		
	3986.92	4316.44	*2.749	*125.26	
70139.27	42419.9	0.900	Positive		
	4103.71	5561.17	*2.749	18295.89	

Table4.txt

68822.93	47959.23	0.994	Positive		
	3489.26	2813.71	*2.684	*445.855	
82917.96	39670.33	0.982	Positive		
	3956.18	1579.27	*2.684	*445.855	
57521.03	46191.53	1.000	Positive		
	4148.33	3702.07	*2.684	2475.23	
73205.52	61077.76	1.000	Positive		
	4834.72	3437.91	*2.684	*445.855	
27671.72	31171.86	0.501	Negative		
	2393.75	219.83	*2.684	*445.855	
91984.3	40169.98	1.000	Positive		
	11635.02	4253.11	*2.684	31446.72	
111716.25	46237.34	0.997	Positive		
	4036.43	1948.19	*2.684	*445.855	
46917.78	46420.62	0.117	Negative		
	5079.7	3153.56	*2.684	*445.855	
53752.7	41716.34	0.919	Positive		
	5926.3	1142.68	*2.684	11650.76	
155288.59	50512.01	0.293	Negative		
	2365.14	2177.23	*2.684	*445.855	
102380.6	49314.05	0.968	Positive		
	5954.89	4818.05	*2.684	*445.855	
47894.68	43493.96	0.984	Positive		
	3389.28	3304.61	*2.684	*445.855	
86129.26	54909.61	0.999	Positive		
	5646.4	3695.4	*2.684	*445.855	
47468.2	40215.42	1.000	Positive		
	6937.21	7419.06	20.86	8195.49	
40342.29	34489.03	0.125	Negative		
	3567.85	3314.31	*2.684	*445.855	
42211.75	52174.61	0.117	Negative		
	4809.45	5947.89	*2.748	9620.89	
54411.19	44887.06	0.434	Negative		
	7088.41	9909.04	*2.748	7198.97	
82593.82	52297.05	0.999	Positive		
	5429.56	6361.35	*2.748	*96.428	
62792.98	49611.26	0.987	Positive		
	4772.06	7489.91	*2.748	8182.27	
48825.08	69666.15	0.370	Negative		
	7599.51	6956.06	*2.736	6441.32	
58278.75	44381.77	0.982	Positive		
	7843.43	5289.75	*2.736	5514.11	
70046.17	44758.11	0.908	Positive		
	6238.48	4011.46	*2.736	*170.39	
93057.29	66534.01	0.998	Positive		
	3236.27	4063.89	*2.748	1531.03	
70878.55	38895.83	0.314	Negative		
	5163.31	8513.53	*2.748	4421.88	

Table4.txt

82635.3	44118.53	0.972	Positive		
	11361.52	10465.44	*2.736	10865.97	
51004.71	49183.25	0.453	Negative		
	7212.01	7262.12	*2.736	5706.09	
54596	49183.25	0.985	Positive		
	5603.06	7729.55	*2.736	3814.28	
55642.4	41277.04	0.983	Positive		
	3735.65	7171.86	*2.748	6612.86	
52074.83	32117.01	0.994	Positive		
	8312.89	7883.07	*2.736	*170.39	
50876.92	54471.2	0.218	Negative		
	8237.75	4779.82	*2.736	*170.39	
56079.81	55418.11	0.950	Positive		
	9341.23	17753.74	*2.736	27297.74	
96575.04	39818.17	0.991	Positive		
	4452.6	7458.94	*2.748	4398.12	
82912.49	39361.05	0.991	Positive		
	6637.63	3201.12	*2.736	*170.39	
28287.27	40900.63	0.503	Negative		
	7562	6735.29	*2.736	*170.39	
47793.33	44758.11	0.942	Positive		
	5170.88	5708.47	*2.748	3712.73	
62184.55	45656.8	0.256	Negative		
	3966.21	5490.69	*2.748	4850.83	
35237.59	34890.1	0.123	Negative		
	4020.58	4011.8	*2.748	*96.428	
34224.23	33544.8	0.705	Negative		
	2712.23	3325.37	*2.748	*96.428	
53254.88	44161.2	0.672	Negative		
	5655.73	6853.14	*2.748	*96.428	
46395.13	43649.45	0.117	Negative		
	2529.95	2881.67	29.72	618.01	
38443.68	31277.72	0.930	Positive		
	4496.95	8165.73	*2.748	10896.99	
72750.81	47200.04	0.767	Negative		
	7799.64	8226.8	*2.736	4617.05	
70289.29	53856.2	0.995	Positive		
	4559.9	6390.84	*2.748	8182.27	
58134.12	34721.85	0.618	Negative		
	6769.67	4549.22	*2.748	*96.428	
52224.47	37248.92	0.125	Negative		
	3733.13	3986.38	18.11	*170.39	
62265.61	42735.4	0.609	Negative		
	3069.11	3843.67	*2.748	1111.96	
59125.96	38557.69	0.998	Positive		
	5193.62	6400.68	*2.748	*96.428	
61591.86	51558.85	0.125	Negative		
	5315.17	4693.03	*2.748	*96.428	

Table4.txt

54456.78	49784	0.335	Negative			
	8338.58	9614.85	*2.748	26203.44		
97570.42	37755.26	1.000	Positive			
	5536.7	8389.9	*2.748	4019.09		
58482.46	49007.19	0.116	Negative			
	8344.21	7150.49	16.75	*170.39		
102415.79	64660.82	0.984	Positive			
	5310.56	6071.31	*2.736	*170.39		
66259.06	60072.77	0.967	Positive			
	7280.87	7531.26	*2.748	1442.14		
41182.39	37839.69	0.347	Negative			
	6182.38	4056.67	*2.736	5386.08		
78432.48	59501.36	0.724	Negative			
	5910.59	6898.4	*2.748	6175.35		
93776.84	45314.54	0.593	Negative			
	5614.53	6310.4	*2.848	16078.04		
76981.43	35311.59	0.918	Positive			
	3415.49	3719.83	*2.748	1934.77		
65101.57	52993.1	0.998	Positive			
	5584.38	3215.72	*2.736	*170.39		
28702.09	43911.37	0.620	Negative			
	8993.35	6126.87	24.66	*96.428		
65780.81	37164.56	0.996	Positive			
	4386.22	6519.1	*2.748	4731.43		
123241.53	34763.91	1.000	Positive			
	4393.58	5780	*2.748	1287.4		
46799.31	48533.17	0.521	Negative			
	7393.22	6663.87	*2.736	2363.63		
54113.95	36236.72	0.896	Positive			
	2725.82	4335.71	*2.748	2665.02		
67648.9	37375.47	0.804	Negative			
	3825.43	3458.44	*2.748	1287.4		
69685.17	35479.22	0.772	Negative			
	6799.88	7150.49	*2.736	*170.39		
86042.81	58549.95	0.996	Positive			
	5022.51	5420.08	*2.749	*125.26		
66627.11	27502.16	0.939	Positive			
	4110.2	5041.65	*2.749	15463.74		
87068.7	25112.64	0.940	Positive			
	4687.58	6084.12	*2.749	*125.26		
52903.32	41753.34	0.896	Positive			
	3016.52	6309.36	*2.749	*125.26		
90321.46	27067.54	0.886	Positive			
	4308.61	8648.53	*2.749	4379.95		
99474.22	24678.34	0.924	Positive			
	4396.63	5446.01	*2.749	*125.26		
55342.75	33002.97	0.917	Positive			
	5740.06	4918.01	*2.749	*125.26		

Table4.txt

40298.07	29459.52	4025.82	0.989	7950.54	Positive	*2.749	21460.47
65146.05	26415.77	5392.04	0.960	6305.53	Positive	*2.749	15875.26
60439.06	27719.52	4589.37	0.955	6871.35	Positive	*2.749	14973.37
201433.49	32620.65	6189.69	0.997	7147	Positive	*2.749	13830.03
60497.6	23049.57	3634.69	1.000	7658.51	Positive	*2.749	*125.26
185344.35	36124.24	3048.37	1.000	5898.54	Positive	*2.749	*125.26
282904.47	36728.41	4645	0.944	5830.7	Positive	24.36	*125.26
47227.99	27936.9	4295.59	0.974	6590.79	Positive	43.93	*125.26
63563.89	33877.62	3980.44	0.913	7052.17	Positive	114.35	13227.53
193889.7	26578.69	3522.05	0.999	4500.98	Positive	41.98	*125.26
71688.59	27991.25	3899.47	0.977	4651.12	Positive	70.29	*125.26
34566.42	27828.21	6066.22	0.751	4921.64	Negative	60.53	20960.91
55823.35	29296.29	3419.26	0.939	5342.45	Positive	55.16	*125.26
48471.94	29894.91	3464.2	0.982	3026.91	Positive	*2.749	11369.02
33798.58	33494.83	6611.46	0.123	4715.77	Negative	*2.749	*125.26
33262.1	37003.24	4815.46	0.123	3675.44	Negative	*2.749	*125.26
42482.33	35191.73	4268.63	0.116	4419.91	Negative	*2.748	*96.428
64578.02	62789.75	2979.2	0.997	5732.29	Positive	*2.748	*96.428
70470.67	39107.25	6658.35	0.374	6678.04	Negative	*2.713	6585.19
88080.1	47648.14	11651.47	1.000	6570.42	Positive	*2.713	12973.51
61823.22	47985.52	9519.73	0.836	7270.63	Negative	*2.713	2104.18
55540.03	44377.13	3010.27	0.930	4212.4	Positive	*2.748	*96.428
50040.76	51472.09	3785.88	0.125	3762.42	Negative	*2.748	*96.428
33558.37	37755.26	9323.56	0.877	7412.48	Positive	*2.713	*137.094

Table4.txt

56736.07	44329.11	0.933	Positive		
	5023.51	5261.32	*2.748	4516.99	
46766.88	46084.96	0.992	Positive		
	7422.15	6035.22	*2.713	1279.27	
64947.29	43273.07	0.954	Positive		
	8122.39	7211.23	*2.713	4297.57	
55014.72	56519.03	0.993	Positive		
	6910.27	7672.84	48.15	28576.96	
138677.99	58915.27	1.000	Positive		
	4049.2	3755.92	*2.848	5666.72	
64935.85	32211.37	1.000	Positive		
	5083.88	7345.73	*2.748	2389.52	
60652.5	51602.24	0.369	Negative		
	5557.47	6279.55	*2.848	6142.63	
47288.71	29483.66	0.473	Negative		
	4925.67	4553.69	*2.748	*96.428	
57586.34	45742.4	0.622	Negative		
	5305.72	4539.69	*2.848	7728.42	
55442.36	31864.41	0.929	Positive		
	3823.82	2290.35	*2.848	*1117.956	
46990.79	41806.24	0.995	Positive		
	4768.32	5043.87	*2.748	1575.6	
67260.01	43436.37	0.235	Negative		
	9588.11	7393.75	*2.713	3346.44	
70368.35	70963.98	0.971	Positive		
	6390.61	8325.64	*2.748	2618.97	
66829.32	52036.35	0.121	Negative		
	4112.03	4571.56	16.88	*137.094	
75379.79	46781.19	1.000	Positive		
	3180.38	3379.28	23.64	7296.95	
123056.96	45656.8	0.998	Positive		
	3854.81	4826.12	*2.848	*1117.956	
57186.82	37735.41	0.125	Negative		
	7294.72	5412.72	*2.713	15167.48	
72224.53	48950.2	0.573	Negative		
	10462.12	6385.45	*2.713	*137.094	
71285.23	48371.26	1.000	Positive		
	4162.54	3153.15	*2.848	*1117.956	
61330.52	37853.18	0.916	Positive		
	4356.77	5168.48	*2.748	3221.16	
64418.57	33628.83	0.650	Negative		
	3257.27	3383.43	*2.748	7150.01	
61693.67	53603.17	0.242	Negative		
	3948.11	3441.74	*2.748	*96.428	
49354.15	37628.65	0.610	Negative		
	4787.01	6782.92	*2.748	*96.428	
31548.44	34007.06	0.122	Negative		
	5835.4	4191.09	*2.848	*1117.956	

Table4.txt

104988.72	42763.13	0.998	Positive		
	6299.08	5020.5	*2.713	2700.32	
59700.89	48998.46	0.989	Positive		
	5581.91	4043.35	*2.848	*1117.956	
25228.48	28032.17	0.863	Positive		
	7106.21	6212.93	*2.713	*137.094	
65899.85	53695	0.883	Positive		
	3955.73	4211.36	*2.848	*1117.956	
47497.17	36091.38	0.580	Negative		
	2963.31	2654.59	*2.848	*1117.956	
51003.47	29368.86	0.686	Negative		
	5299.95	5462.46	*2.748	*96.428	
26379.63	28845.21	0.850	Negative		
	4473.39	2735.08	*2.848	*1117.956	
52741.3	26586.1	0.985	Positive		
	4772.06	6000.94	*2.748	1844.56	
73657.78	49611.26	0.324	Negative		
	4031.47	5145.34	*2.748	*96.428	
66182.98	57681.17	0.304	Negative		
	7192.55	7500.24	*2.748	1664.96	
89568.46	46342.05	0.121	Negative		
	5132.07	4692.7	*2.848	8214.76	
48678.93	36482.01	0.856	Negative		
	3551.96	4361.44	*2.713	*137.094	
76220.39	59454.59	0.995	Positive		
	8394.32	4986.89	66.04	50328.89	
84994.34	40241.79	0.998	Positive		
	8909.99	4181.71	*2.748	18748.47	
86455.69	49568.08	0.965	Positive		
	3100.34	6504.27	*2.748	8281.02	
66917.44	28090.43	1.000	Positive		
	5152.22	5426.52	*2.848	*1117.956	
33276.04	28222.84	0.553	Negative		
	4107.77	2801.13	*2.848	*1117.956	
46096.3	28260.99	0.998	Positive		
	5419.21	4780.34	*2.848	10180.04	
58033.78	39546.42	0.995	Positive		
	3994.64	3484.34	*2.848	*1117.956	
38417.07	35506.36	0.842	Negative		
	9085.59	7118.81	*2.713	*137.094	
41275.46	39726.91	0.956	Positive		
	5498.39	5387.37	*2.748	6564.16	
73233.03	35984.47	0.970	Positive		
	11201.59	8185.06	*2.726	*115.47	
61797.2	46298.94	0.298	Negative		
	3696.9	3816.81	232.7	2752.64	
19076.77	30752.35	1.000	Positive		
	11087.68	12061.47	*2.726	26004.47	

Table4.txt

109401.87	56916.61	0.155	Negative			
	10280.27		8378.3	*2.726		9391.97
49838.78	48667.12	0.312	Negative			
	8326.2		8769.32	*2.726		5767.06
43789.99	40538.14	0.997	Positive			
	5362.42		3035.58	*2.848		*1117.956
38110.19	27651.12	0.640	Negative			
	5906.71		8535.09	*2.748		1777.08
49286.72	45015.27	0.498	Negative			
	3665.57		4238.43	*2.848		*1117.956
51060.98	23180.49	0.976	Positive			
	6138.75		4795.3	*2.736		*170.39
67198.74	59263.4	0.596	Negative			
	7088.66		5270.79	*2.726		*115.47
78025.81	55020.36	0.629	Negative			
	7588.68		5564.94	*2.726		*115.47
36980.96	51413.75	0.121	Negative			
	6555.98		9152.04	*2.748		9670.74
66052.28	42925.34	0.955	Positive			
	5740.04		7306.88	*2.736		3202.8
68907.31	52343.85	0.992	Positive			
	6094.56		5666.41	635.23		4421.42
19769.27	16353.29	0.992	Positive			
	3897.52		4756.31	*2.748		*96.428
51785.32	42840.21	0.578	Negative			
	4415.7		4442.13	*2.748		16369.24
100044.25	35605.51	1.000	Positive			
	3893.58		2958.9	*2.848		*1117.956
36306.21	23557.67	0.326	Negative			
	5406.65		7520.92	86.38		24668.88
154769.56	50778.7	0.911	Positive			
	5176.42		8295.34	*2.848		7159.08
100506.51	38560.8	0.960	Positive			
	4703.51		4773.31	*2.848		*1117.956
85625.53	51694.63	0.855	Negative			
	9137.6		5648.96	*2.726		*115.47
17446.71	19444.67	0.965	Positive			
	7518.01		4598.54	*2.726		*115.47
25991.63	34496.63	0.987	Positive			
	7282.64		6842.01	*2.726		*115.47
61515.64	49545.95	0.495	Negative			
	10149.01		7140.57	*2.726		9520.31
46106.93	42772.21	0.980	Positive			
	5140.59		5866.17	*2.748		6807.89
27766.36	30312.92	0.322	Negative			
	4991.33		4133.82	*2.848		*1117.956
66726.66	37617.68	0.569	Negative			
	6085.45		5899.78	*2.748		5258.11

Table4.txt

48408.21	37797.47	0.121	Negative		
	3901.34	4374.58	*2.848	4778.85	
112743.33	49843.22	0.829	Negative		
	3915.57	4124.87	*2.748	*96.428	
53470.13	46899.56	0.300	Negative		
	4854.38	4792.58	*2.748	3128.03	
59607.84	45357.31	0.117	Negative		
	3789.48	3450.09	*2.748	*96.428	
48741.49	46427.78	0.238	Negative		
	4649.03	7791.4	*2.748	1397.82	
40029.79	41819.76	0.312	Negative		
	5536.7	6371.17	209.47	1353.59	
36084.7	30690.41	0.945	Positive		
	3426.08	3635	*2.748	*96.428	
46161.84	37713.05	0.877	Positive		
	3854.24	4702.06	*2.748	*96.428	
45546.4	36237.21	0.620	Negative		
	5513.71	5914.2	*2.748	916.62	
78093.92	43862.61	0.979	Positive		
	4434.14	6102.59	*2.748	*96.428	
68897.32	39699.6	0.883	Positive		
	3464.2	8167.53	*2.749	*125.26	
82878.97	22343.54	0.953	Positive		
	3531.69	8056.77	*2.749	20560.59	
187551.75	49200.69	0.813	Negative		
	4546.85	9189.22	*2.749	*125.26	
70636.69	29786.05	0.683	Negative		
	3406.43	8320.04	*2.749	*125.26	
186334.44	27447.83	0.994	Positive		
	1969.7	5213.6	71.27	41644.82	
148609.69	23429.66	0.991	Positive		
	5889.67	5789.34	22.4	*125.26	
120270.39	36124.24	0.413	Negative		
	4713.79	5804.37	*2.749	*125.26	
38538.07	30439.4	0.690	Negative		
	5966.24	7162.84	*2.749	10149.85	
83340.18	35685.23	0.666	Negative		
	3099.36	9407.61	*2.749	10012.96	
281022.53	52208.59	1.000	Positive		
	4103.71	7238.2	*2.676	21360.63	
184926.25	61314.71	0.774	Negative		
	5154.28	7453.54	*2.749	14947.51	
104164.95	33276.19	1.000	Positive		
	4227.22	5834.47	*2.749	20485.46	
121018.5	32839.09	0.711	Negative		
	3207.9	5136.62	*2.749	24564.89	
181346.16	44202.33	0.985	Positive		
	3560.64	6934.11	*2.749	*125.26	

Table4.txt

48114.18	23864	3262.26	0.817	6879.19	Negative	*2.749	21085.89
65083.3	29622.77	4848.28	0.697	9627.74	Negative	*2.749	*125.26
70636.69	22126.25	3112.12	0.950	5483.1	Positive	*2.749	*125.26
100410.46	24841.2	4815.46	0.777	6133.58	Negative	*2.749	3195.35
165364.86	33713.54	4950.14	1.000	5921.19	Positive	*2.749	3440.48
160777.27	40866.1	3488.87	0.996	5069.85	Positive	67.62	12804.83
240645.57	37807.54	3914.76	0.980	5062.91	Positive	*2.761	2441.07
58883.03	37145.81	5542.67	0.956	6038.4	Positive	*2.761	5063.66
48265.51	26798.49	6302.99	0.878	7079.61	Positive	156.49	*452.14
78417.57	35400.74	14896.72	0.993	3964.73	Positive	*2.761	*452.14
117754.41	52727.96	6022.07	1.000	7857.64	Positive	46.29	11235.66
77104.67	23815.05	61539.85	0.999	5970.01	Positive	*2.761	86518.84
169343.47	30866.34	5148.54	1.000	5114.96	Positive	18.43	*452.14
48417.17	25815.05	4386.85	0.985	5341.76	Positive	35.1	18716.56
268815.64	33280.16	3447.95	0.993	5552.96	Positive	*2.761	*452.14
142585.61	31439.68	4653.94	0.999	4328.72	Positive	*2.761	*452.14
21785.36	24305.1	5568.35	0.900	4318.63	Positive	*2.761	4282.6
45559.34	23438.28	5023.87	0.901	4084.35	Positive	*2.761	*452.14
33776.08	26987.81	3325.29	0.855	5461.22	Negative	17.6	*452.14
97163.39	28542.88	5218.92	0.994	11787.82	Positive	**2003.144	13828.3
333714.66	38978.77	5449.61	1.000	2599.26	Positive	17.19	*452.14
104937.91	43750.43	6225.42	0.999	3891.92	Positive	*2.761	3795.95
34904.18	23928.11	4746.3	1.000	7143.54	Positive	*2.761	16205.81
55420.9	27101.43	3744.19	0.380	5076.78	Negative	20.49	*452.14

Table4.txt

51611.86	23099.32	0.989	Positive		
	**30169.62	8640.21	*2.761	86362.95	
321136.51	31439.68	1.000	Positive		
	4012.81	6364.89	*2.761	4185.17	
167102.26	31745.8	1.000	Positive		
	6412.98	6592.29	43.5	16908.03	
181080.43	33972.74	1.000	Positive		
	3621.18	5146.24	*2.761	8655.88	
108240.14	40980.38	1.000	Positive		
	3630.64	7222.74	*2.761	11235.66	
222802.48	25437.24	0.998	Positive		
	4129.95	5773.1	*2.761	2850.99	
99233.83	32704.03	0.972	Positive		
	4762.23	9279.05	17.19	*452.14	
83290.36	35903.91	0.971	Positive		
	6160.82	5602.5	*2.761	*452.14	
64969.3	47272.6	0.695	Negative		
	3388.17	4766.61	*2.761	*452.14	
348414.92	42085.16	0.988	Positive		
	4367.8	5313.73	*2.761	2585.59	
93177.98	42401.6	0.123	Negative		
	3124.33	5468.27	*2.761	5234.88	
85073.65	45746.03	0.991	Positive		
	3017.74	4338.82	*2.761	*452.14	
70724.78	31669.25	0.880	Positive		
	7515.93	7203.86	*2.761	*452.14	
73837.6	25437.24	0.989	Positive		
	5007.9	6655	*2.761	*452.14	
74130.78	31095.58	0.993	Positive		
	5318.19	8540.58	*2.761	4331.33	
184727.16	26041.85	0.996	Positive		
	3074.15	4993.69	*2.761	2754.42	
161476.25	26836.35	0.928	Positive		
	10519.51	4399.48	*2.761	7026.99	
53385.23	26836.35	0.982	Positive		
	3917.92	5278.75	*2.761	*452.14	
14644.82	22158.34	0.824	Negative		
	6691.69	4544.99	*2.761	*452.14	
38891.49	23588.97	0.932	Positive		
	5957.59	6933.54	*2.761	20654.83	
103703.48	22685.19	0.999	Positive		
	4275.77	7630.16	*2.761	*452.14	
111955.72	36718.36	0.552	Negative		
	11321.56	10294.76	*2.726	20956.16	
69689.26	48925.39	0.528	Negative		
	4290.63	4322.46	*2.748	*96.428	
67615.48	75251.64	0.448	Negative		
	3847.03	3985.81	*2.748	3104.77	

Table4.txt

56806.28	54345.27	0.117	Negative		
	5232.72	5236.1	*2.757	3783.81	
27928.1	28678.71	0.848	Negative		
	4670.45	6549.21	*2.757	*354.923	
41217.83	37349.33	0.943	Positive		
	9076.52	6632.87	*2.757	27025.29	
50656.88	29851.77	1.000	Positive		
	6230.35	6640.49	*2.757	9017.91	
41188.02	32044.38	0.615	Negative		
	4752.71	6150.1	*2.757	*354.923	
39587.38	32508.05	0.572	Negative		
	5904.1	6785.72	*2.757	3759	
22298.43	29327	0.116	Negative		
	3726.1	5372.48	*2.757	16293.88	
49728.26	32786.35	0.997	Positive		
	6432.85	10035.02	*2.757	15545.46	
32009.88	30253.08	0.122	Negative		
	4894.23	6097.89	*2.757	*354.923	
46453.98	29234.39	0.509	Negative		
	9113.86	5383.11	*2.726	*115.47	
38954.96	31848.57	0.524	Negative		
	5852.51	6732.12	*2.757	*354.923	
25277.8	26020.61	0.642	Negative		
	10345.94	7156.39	*2.726	*115.47	
38396.94	28266.32	0.125	Negative		
	10555.02	6459.84	*2.726	*115.47	
25418.79	26876.81	0.858	Negative		
	4911.96	5864.44	*2.757	*354.923	
37688.72	31611.81	0.923	Positive		
	6402.11	5293.41	*2.757	*354.923	
35563.9	39224.72	0.122	Negative		
	3239.86	4342.38	*2.757	25638.22	
52115.07	26546.71	1.000	Positive		
	4684.91	5534.98	*2.757	*104.283	
78363.27	57094.5	0.947	Positive		
	5607.6	6606.22	*2.757	5981.15	
37222.45	37536.47	0.991	Positive		
	7945.47	5606.41	*2.757	*104.283	
46554.03	39605.96	0.122	Negative		
	6017.52	4624.2	*2.757	*104.283	
42239.66	46880.96	0.637	Negative		
	4988.91	6307.44	*2.757	1938.02	
26202.06	29944.38	0.761	Negative		
	6996.08	5684.55	*2.757	14191.74	
19780.28	27566.88	0.502	Negative		
	5125.47	4616.87	*2.757	8554.04	
41606.86	25246.03	0.991	Positive		
	4490.21	3986.3	*2.757	*104.283	

Table4.txt

67607.5	55804.44	0.983	Positive		
	5354.12	4584.47	*2.736	*170.39	
29824.38	31361.14	0.999	Positive		
	4732.13	7532.1	*2.757	*354.923	
44047.83	39444.12	0.588	Negative		
	8736.62	7731.27	*2.757	3364.42	
91532.89	54717.04	0.898	Positive		
	5024.48	6360.11	*2.757	*354.923	
39040.19	33436.1	0.852	Negative		
	7777.8	4891.65	*2.757	11292.95	
78388.37	44667.33	0.933	Positive		
	6534.46	7801.38	*2.757	15835.25	
66941.07	38129.65	0.208	Negative		
	5903.32	8009.98	*2.757	17433.3	
82490.53	39035.87	0.997	Positive		
	4250.76	3297.59	63.43	6693.53	
31865.03	24780.66	0.982	Positive		
	8621.35	7741.92	*2.757	722.02	
65617.66	48945.17	0.978	Positive		
	6153.89	7992.98	*2.757	3013.3	
23791.47	27814.03	0.975	Positive		
	7476.28	7891.62	*2.757	*104.283	
75886.86	44379.43	0.932	Positive		
	6409.21	4570.36	*2.757	*104.283	
36112.14	34552.87	0.950	Positive		
	7950.89	4133.39	*2.757	*104.283	
43159.42	46655.84	0.505	Negative		
	5397.2	5250.41	*2.757	*354.923	
18561.18	27505.08	0.421	Negative		
	5334.31	5264.74	*2.757	*354.923	
26608.92	27937.58	0.813	Negative		
	6263.42	3697.16	*2.736	*170.39	
37303.4	44805.16	0.909	Positive		
	5149.28	6488.54	*2.757	*354.923	
30559.43	34644.34	0.421	Negative		
	3198.18	3892.85	*2.757	*354.923	
54050.07	34148.38	0.966	Positive		
	5715.13	4006.45	*2.736	*170.39	
30686.98	40618.29	0.644	Negative		
	5955.76	7469.11	*2.757	*354.923	
39775.84	27381.48	0.959	Positive		
	4075.14	5080.19	*2.757	3652.77	
63042.99	37202.05	0.991	Positive		
	5655.85	8201.95	*2.757	10285.21	
66663.31	43672.64	0.630	Negative		
	3723.26	3322.92	*2.757	12981	
13524.94	19194.84	0.571	Negative		
	5583.29	5317.78	*2.757	*104.283	

Table4.txt

45388.14	37581.1	1.000	Positive		
	4873.55	5358.08	*2.757	*354.923	
54209.58	39256.05	0.950	Positive		
	5119.52	7753.68	*2.757	*354.923	
41968.43	36601.59	0.837	Negative		
	4123.69	5268.32	*2.757	2439.25	
33259.65	27906.69	0.125	Negative		
	5190.98	6360.11	*2.757	8383.02	
40440.61	32724.5	0.951	Positive		
	3626.93	6142.64	*2.757	4254.56	
66605.6	30129.59	0.898	Positive		
	6791.03	6606.22	*2.757	11622.43	
38342.59	33219.46	0.568	Negative		
	6403.97	5841.77	*2.757	*104.283	
22242.9	30019.56	0.866	Positive		
	5276.15	6046	*2.757	*104.283	
*19.531	40303.44	0.950	Positive		
	4399.56	5478.84	*2.761	8655.88	
55636.3	28960.96	0.966	Positive		
	4960	5517.64	*2.761	10688.76	
41590.05	26912.07	0.847	Negative		
	4813.23	9463.94	*2.761	7248.67	
98402.59	31324.94	0.379	Negative		
	5864.17	5609.59	*2.761	*452.14	
50367.97	37068.05	0.828	Negative		
	5295.76	6784.61	*2.761	15529.28	
206018.45	29722.09	0.999	Positive		
	3763.13	4986.78	*2.761	*452.14	
120915.01	30942.74	0.955	Positive		
	4765.42	4609.57	*2.761	*452.14	
50812.1	35362.06	0.640	Negative		
	5494.52	6430.7	*2.761	2441.07	
46422.25	27859.57	0.412	Negative		
	5170.93	11155.13	*2.761	157461.07	
223753.85	27707.85	1.000	Positive		
	6685.2	7877.01	*2.761	4185.17	
61459.31	41216.76	0.342	Negative		
	4857.88	5170.6	*2.761	*452.14	
42404.64	28163.14	0.339	Negative		
	3766.29	8692.18	*2.761	9646.38	
138264.63	28656.87	0.986	Positive		
	5677.58	6544.44	*2.761	3553.11	
44261.11	28163.14	0.121	Negative		
	3024	3622.46	*2.761	3189.53	
43991.71	19939.77	0.834	Negative		
	2611.24	3655.16	*2.761	*452.14	
60909.9	20428.47	0.372	Negative		
	3061.61	5503.52	*2.761	*452.14	

Table4.txt

89296.04	26798.49	0.966	Positive		
	4209.17	4609.57	*2.761	*452.14	
31279.86	35091.47	0.974	Positive		
	7156.77	5609.59	21.31	*452.14	
24484.77	24078.88	0.351	Negative		
	5065.41	4555.18	*2.761	*452.14	
34168.71	33433.95	0.811	Negative		
	4361.45	5194.98	*2.761	*452.14	
41102.75	37418.12	0.698	Negative		
	3331.58	6610.72	*2.761	*452.14	
272147.02	37340.29	0.998	Positive		
	3741.04	3385.09	*2.761	*452.14	
128786.36	26457.87	0.999	Positive		
	5030.26	7053.33	*2.761	*452.14	
168948.83	34705.29	0.979	Positive		
	4431.32	5620.22	*2.761	*452.14	
86725.78	20578.84	0.974	Positive		
	3577.06	6758.63	27.03	*452.14	
107124.78	20842.02	0.999	Positive		
	3981.17	7714.75	*2.761	90964.46	
152021.73	32972.78	1.000	Positive		
	4950.42	4708.45	*2.761	*452.14	
49582.64	34049.78	0.980	Positive		
	4552.11	2996.81	*2.761	*452.14	
34003.15	28694.87	0.125	Negative		
	4079.28	3845.7	*2.761	*452.14	
69121.15	32320.44	0.117	Negative		
	3847.58	8337.41	*2.757	19408.04	
261866.04	34306.25	0.999	Positive		
	2523.8	3659.73	*2.757	*424.639	
52845.25	41205.64	0.291	Negative		
	5139.97	6642.27	*2.757	20530.15	
116033.39	37774.11	0.988	Positive		
	3580.19	4657.33	*2.757	*424.639	
85710.11	34027.34	0.992	Positive		
	4206.5	8364.46	*2.757	6494.01	
187892.36	41149.21	0.999	Positive		
	3850.57	4324.11	16.75	*424.639	
29910.13	26748.24	0.539	Negative		
	4664.13	3326.32	*2.757	*424.639	
33288.07	32578.58	0.591	Negative		
	2402.51	3174.4	*2.757	*424.639	
78800.85	36653.44	0.974	Positive		
	7721.97	5073.15	*2.757	2911.87	
41578.08	32022.03	0.897	Positive		
	2885.4	3227.02	*2.757	*424.639	
64281.56	33358.36	0.813	Negative		
	6078.13	5001.82	*2.757	*424.639	

Table4.txt

100338.39	33637.03	1.000	Positive		
	3799.79	6770.6	18.4	*424.639	
148054.08	39684.14	0.998	Positive		
	3859.55	3591.66	*2.757	*424.639	
60816.99	39234.14	0.548	Negative		
	3093.81	4124.96	*2.757	*424.639	
46342.56	24088.37	0.948	Positive		
	1573.35	3008.23	*2.757	*424.639	
116281.1	33358.36	0.986	Positive		
	3907.48	4650.01	*2.757	*424.639	
60189.9	37101.47	0.681	Negative		
	2676.9	3949.5	*2.757	*424.639	
41730.16	34976.07	0.667	Negative		
	5228.58	6262.65	*2.757	13694.25	
87658.09	46425.37	0.964	Positive		
	3509.5	4657.33	*2.757	*424.639	
27909.04	24864.13	0.998	Positive		
	3019.28	5137.24	*2.757	*424.639	
63166.02	29077.35	0.965	Positive		
	4103.34	5084.44	*2.757	*424.639	
59883.4	36205.73	0.932	Positive		
	3674.86	4804.56	*2.757	*424.639	
55636.33	29632.38	0.774	Negative		
	3050.77	3759.06	*2.757	*424.639	
46602.8	37549.82	0.931	Positive		
	2945.09	3598.45	*2.757	*424.639	
48309.84	28799.92	0.999	Positive		
	2187.49	3838.37	*2.757	*424.639	
68840.66	32745.62	0.998	Positive		
	5013.89	6992.11	*2.757	*424.639	
80931.32	56592.17	0.923	Positive		
	3229.37	2860.39	*2.757	*424.639	
51120.46	35646.51	0.977	Positive		
	2601.54	3296.44	*2.757	*424.639	
41199.27	30854.33	0.125	Negative		
	2862.73	4863.84	*2.757	24536.39	
219430.38	35478.84	0.998	Positive		
	3168.67	5415.41	*2.757	*424.639	
61379.2	28023.36	0.910	Positive		
	5847.2	9500.87	*2.757	98685.33	
186760.08	42505.27	1.000	Positive		
	3371.82	5212.98	*2.757	*424.639	
68371.22	34641.08	0.998	Positive		
	6610.45	7008.96	*2.783	6260.09	
89105.79	37909.81	0.986	Positive		
	3162.9	6014	*2.757	10476.46	
32573.8	20872.13	0.961	Positive		
	2945.09	5254.78	*2.757	8979.39	

Table4.txt

136089.6	35311.21	1.000	Positive		
	4602.18	5757.1	*2.757	*424.639	
80825.3	31410.2	0.927	Positive		
	2763.9	3322.99	*2.757	10453.79	
57212.81	34306.25	0.923	Positive		
	2794.89	3217.14	*2.757	*424.639	
56994.84	29632.38	0.762	Negative		
	2548.74	3289.81	*2.757	*424.639	
41935.96	33804.28	0.714	Negative		
	2257.86	3223.73	*2.757	*424.639	
46505.1	37157.49	0.998	Positive		
	3521.26	7089.06	*2.757	*424.639	
106747.4	37886.3	0.998	Positive		
	1857.58	3177.68	*2.757	*424.639	
28797.3	23811.29	0.993	Positive		
	8254.55	9542.7	*2.783	13458.99	
86402.84	45818.43	0.991	Positive		
	2037.31	3043.87	*2.757	2198.37	
54395.08	33525.55	1.000	Positive		
	2187.49	3362.93	*2.757	*424.639	
31135.65	32801.3	0.877	Positive		
	3418.57	2325.14	*2.757	*424.639	
34298.17	30798.75	0.888	Positive		
	4540.4	6416.79	85.52	25323.39	
53480.8	29576.87	1.000	Positive		
	6539.63	9888.55	*2.783	11700.98	
73883.6	33019.51	0.998	Positive		
	4807.19	4934.55	68.1	*424.639	
43028.03	35422.96	0.838	Negative		
	4518.37	5830.49	*2.783	12165.66	
108834.76	30601.26	0.999	Positive		
	6900.51	6932.06	*2.783	7562.41	
67708.34	42462.87	0.925	Positive		
	5592.35	6424.94	*2.757	*424.639	
51068.33	33414.09	1.000	Positive		
	3348.48	4723.41	*2.757	*424.639	
49530.86	30354.29	0.432	Negative		
	9908.9	11860.03	18.05	39043.28	
109233.64	25002.1	0.999	Positive		
	5653.75	7025.48	*2.783	17252.59	
231237.93	33643.13	1.000	Positive		
	7126.48	10936.28	*2.783	18840.98	
110547.43	39756.53	0.999	Positive		
	4594.65	6103.33	*2.783	2720.26	
41964.78	26941.94	0.857	Negative		
	5974.15	7907.06	*2.783	*103.34	
154275.12	48256.53	0.881	Positive		
	7449.83	9957.06	*2.783	*103.34	

Table4.txt

113328.07	33900.02	0.932	Positive		
4932.02	6443.94	*2.783	*103.34		
107512.85	32212.97	0.854	Negative		
5798.64	6085.83	*2.757	8706.79		
39348.5	38222.96	0.207	Negative		
4061.47	6713.78	18.72	*103.34		
150394.08	33459.68	1.000	Positive		
4823.72	3847.2	37.83	*103.34		
106597.95	52110.03	0.997	Positive		
3357.23	2815.78	*2.757	*424.639		
34049.67	26859.09	0.310	Negative		
4423.07	6219.81	*2.783	1698.06		
101943.65	31919.81	0.955	Positive		
3497.74	4775	17.57	*424.639		
94403.13	45570.33	0.989	Positive		
2457.51	2121.37	*2.757	*424.639		
37693.46	28189.73	0.614	Negative		
4356	7481.92	22.6	40798.25		
176049.91	33804.28	1.000	Positive		
2908.11	2527.21	*2.757	*424.639		
26426.96	25695.29	0.641	Negative		
3269.95	5647.62	16.75	*424.639		
87339.55	31132.23	1.000	Positive		
5550.63	3376.27	*2.757	*424.639		
42226.6	30798.75	0.831	Negative		
4255.21	6033.92	*2.757	*424.639		
42726.45	32188.96	0.326	Negative		
4788.49	5998.08	*2.757	*424.639		
59303.79	33525.55	0.382	Negative		
3430.28	4613.44	*2.757	17284.93		
95712.71	40359.83	0.996	Positive		
6184.19	4539.04	*2.757	*104.283		
58132.32	45403.91	0.999	Positive		
4688.06	5279.07	*2.757	*354.923		
39892.14	37786.12	0.877	Positive		
6996.08	5772.47	*2.757	*354.923		
61853.63	44277.04	0.117	Negative		
6359.1	10922.75	*2.757	3709.38		
34902.31	33714.73	0.943	Positive		
5943.6	8882.74	*2.757	13683.47		
68788.77	40637.59	0.626	Negative		
5717.17	10010.58	*2.757	3184.11		
119224.18	59825.16	0.991	Positive		
7487.01	5953.33	113.33	*104.283		
57913.72	37612.7	0.559	Negative		
7358.31	6144.07	*2.757	*104.283		
41231.36	45403.91	0.977	Positive		
5408.92	4755.09	*2.757	*104.283		

Table4.txt

25469.2	30019.56	0.116	Negative		
	4793.93	2973.07	*2.757	*354.923	
51934.14	34768.4	0.758	Negative		
	5289.53	7074.94	*2.848	*1117.956	
49732.1	30633.63	0.778	Negative		
	4791.21	5632.99	*2.848	*1117.956	
44986.59	42045.15	0.589	Negative		
	6405.18	5699.18	*2.757	*354.923	
46618.16	33033.81	0.806	Negative		
	7184.28	6160.53	*2.848	2721.84	
83393.95	39704.43	0.239	Negative		
	13227.69	6718.79	*2.736	29871.03	
106789.35	36567	0.984	Positive		
	3312.3	9831.16	*2.757	36439.24	
73802.53	28709.58	1.000	Positive		
	5136.1	3956.79	*2.848	1628.72	
35682.95	32558.68	0.908	Positive		
	4407.46	6247.37	*2.757	16872.85	
59598.71	33931.52	0.583	Negative		
	5779.78	7312.26	*2.757	*354.923	
59846.29	37006.46	0.914	Positive		
	4887.24	6141.02	*2.748	11545.26	
126320.42	57394.84	0.955	Positive		
	5964.89	3705.66	*2.757	13804.52	
55549.75	37162.28	0.998	Positive		
	3309.51	5072.26	*2.757	2289.11	
44220.77	43196.39	0.958	Positive		
	7474.47	4370.11	*2.736	966.48	
69957.95	44287.69	0.378	Negative		
	4407.46	4126.05	*2.757	*354.923	
46716.9	33962.49	0.948	Positive		
	4971.14	5336.5	315.94	2088.62	
15201.96	21974.51	0.974	Positive		
	6824.85	6303.74	*2.736	*170.39	
43081.64	42970.59	0.947	Positive		
	6300.82	9674.5	*2.736	2039.94	
52347.12	43723.21	0.997	Positive		
	3745.98	3566.08	64.74	*354.923	
36945.96	36259.29	0.986	Positive		
	4713.71	4076.78	*2.736	5225.98	
66848.94	54518.53	0.874	Positive		
	7043.37	5733.9	*2.736	*170.39	
73591.88	49041.89	0.997	Positive		
	7499.48	10762.19	*2.736	16626.62	
104794.67	57124.97	0.656	Negative		
	4491.96	4203.46	*2.757	*354.923	
28081.05	33962.49	0.395	Negative		
	7887.23	5808.56	22.95	1650.68	

Table4.txt

35549.82	41277.04	0.993	Positive		
7398.05	6283.61	*2.783	*103.34		
64847.54	50783.77	0.995	Positive		
5509.69	7520.35	*2.736	1877.87		
88389.65	66053.15	0.842	Negative		
7712.07	5044.09	*2.736	*170.39		
67283.78	53241.56	0.977	Positive		
13520.56	6477.18	*2.757	*354.923		
41742.17	31055.84	0.979	Positive		
5454.19	6847.11	*2.757	*354.923		
81371.08	47545.05	0.354	Negative		
4239.18	3780.9	*2.757	4724.32		
60438.4	44787.03	0.342	Negative		
8253.98	8331.26	*2.757	13368.66		
43867.61	36321.51	0.956	Positive		
14876.75	6258.62	*2.757	*354.923		
55867.9	30500.06	0.987	Positive		
5783.63	5368.59	*2.736	4745.32		
118386.61	54991.89	0.975	Positive		
5949.68	6732.12	*2.757	*354.923		
31802.17	27721.35	0.812	Negative		
9266.09	10665.45	*2.783	*103.34		
50792.85	43467.21	0.829	Negative		
8222.02	4433.68	*2.783	1163.62		
32598.04	31297.03	0.654	Negative		
7489.23	4896.82	*2.848	6649.45		
28456.75	31594.8	0.598	Negative		
6939.96	4812.02	31.86	*1117.956		
50071.23	36091.38	0.201	Negative		
4647.82	5024.9	*2.848	1174.65		
34953.2	24917.96	0.993	Positive		
7107.1	7386.32	*2.783	*103.34		
51628.4	51541.11	0.230	Negative		
8952.16	7827.05	*2.783	4728.71		
67563.77	44622.76	0.636	Negative		
6900.51	7130.36	*2.783	*103.34		
39310.55	40163.53	0.315	Negative		
5999.81	6508.4	*2.783	*103.34		
61639.53	53021.97	0.465	Negative		
3971.29	4326.78	*2.848	*1117.956		
36047.07	24539.71	0.469	Negative		
6280.62	4570.86	*2.848	*1117.956		
49310.65	37931.73	0.756	Negative		
10019.82	8574.15	*2.736	9595.45		
69059.62	57219.89	0.938	Positive		
9184.31	9572.42	*2.736	13085.13		
63721.64	55323.37	0.997	Positive		
4247.97	5164.05	*2.736	28584.7		

Table4.txt

130344.6	61073.8	0.958	Positive		
	4454.05	6097.89	*2.757	*354.923	
41855.19	35358.03	0.944	Positive		
	6849.81	5038.88	70.44	6249.63	
34091.62	34394.46	0.991	Positive		
	10964.2	9220.52	*2.736	47518.58	
127494.91	60310.99	0.995	Positive		
	7862.2	6227.87	*2.736	*170.39	
63216.32	52910.74	0.826	Negative		
	5021.52	5200.37	*2.757	*354.923	
21991.56	26237.29	0.117	Negative		
	7570	5089.34	*2.848	23127.15	
113283.5	43242.8	0.953	Positive		
	6269.49	5550.8	*2.783	*103.34	
69528.34	26100.3	0.993	Positive		
	6410.94	6288.94	*2.783	*103.34	
179872.1	37799.17	0.988	Positive		
	7650.64	7872.74	*2.783	2684.53	
64074.76	32982.84	0.900	Positive		
	9037.12	8218.3	*2.783	6194.33	
59967.5	43095.01	0.973	Positive		
	5148.83	6336.92	*2.783	3634.36	
96724.48	42165.65	0.982	Positive		
	5621.74	4023.29	*2.783	*103.34	
53937.88	36546.44	0.975	Positive		
	3316.45	6133.87	31.26	2741.52	
151370.48	33191.2	0.999	Positive		
	6978.89	3060.1	*2.757	*424.639	
32289.72	26526.54	0.125	Negative		
	4448.02	6584.61	*2.757	*424.639	
112638.4	28078.81	0.996	Positive		
	3272.86	4856.42	*2.757	*424.639	
53211.55	30632.06	0.543	Negative		
	3491.87	4584.25	*2.757	*424.639	
17245.27	24531.67	0.117	Negative		
	6919.87	6860.88	*2.783	5532.88	
425936.58	54432	0.987	Positive		
	3645.22	4047.48	*2.757	*424.639	
42842.3	31910.76	0.117	Negative		
	7770	10965.16	*2.757	80176.88	
110873.85	32133.31	0.997	Positive		
	5270.11	5284.91	*2.783	3703.64	
218313.77	41942.84	0.995	Positive		
	2982.14	3893.82	*2.757	*424.639	
120430.38	37157.49	0.690	Negative		
	7683.05	8322.97	*2.783	2360.66	
89652.1	44175.14	0.824	Negative		
	4938.39	5674.65	*2.783	*103.34	

Table4.txt

89364.82	29466.56	0.993	Positive		
	5884.37	6779.04	*2.783	23347.22	
226219.03	29795.94	1.000	Positive		
	2632.19	2806.25	*2.757	*424.639	
31657.19	24088.37	0.125	Negative		
	5756.21	7042.01	*2.783	600.89	
49457.43	45182.86	0.996	Positive		
	6025.48	7907.06	*2.783	*103.34	
82878.26	46305.02	0.735	Negative		
	5756.21	5997.98	*2.783	*103.34	
81001.49	44548.13	1.000	Positive		
	7320.41	6481.51	*2.783	*103.34	
51645.2	36325.59	0.970	Positive		
	3527.15	3776.26	*2.757	6264.48	
65297.82	41600.83	0.994	Positive		
	5666.55	7274.67	*2.783	5132.34	
40135.46	28076.14	0.819	Negative		
	9252.99	10315.09	*2.783	4694.92	
42768.97	31663.34	0.841	Negative		
	8952.16	9548.84	*2.783	11047.73	
70798.41	33459.68	0.984	Positive		
	3022.14	3841.83	*2.757	*424.639	
143611.96	39740.41	0.999	Positive		
	3316.45	4435.55	39.27	*424.639	
65865.27	34585.26	0.998	Positive		
	9397.07	9322.92	40.03	11172.41	
53739.23	31883.17	0.994	Positive		
	4732.45	4863.84	*2.757	*424.639	
33240.26	26415.7	0.999	Positive		
	9547.82	11400.68	*2.783	13397.64	
76934.24	35736.94	1.000	Positive		
	6823.11	7616.92	*2.783	4048.14	
91453.87	42054.24	0.946	Positive		
	7546.97	7741.63	*2.783	1995.33	
45921.21	29649.54	0.965	Positive		
	6533.19	6113.89	*2.783	3215.77	
121842.83	41386.21	1.000	Positive		
	6713.53	4128.72	*2.783	*103.34	
42655.79	31040.66	0.680	Negative		
	6479.01	9657.93	*2.757	5661.3	
76837.22	49194.9	0.985	Positive		
	9410.17	5535.37	*2.783	*103.34	
52015.71	45519.23	0.302	Negative		
	4991.87	7351.39	*2.757	*354.923	
86996.49	37006.46	0.978	Positive		
	6713.58	4053.37	*2.848	*1117.956	
77611.32	47679.25	0.121	Negative		
	8677.98	9665.66	*2.783	5566.13	

Table4.txt

88185.57	58307.64	0.688	Negative		
	3792.87	4567.39	*2.848	*1117.956	
65956.96	40773.24	0.117	Negative		
	5261.22	4766.29	*2.848	*1117.956	
40014.05	34961.32	0.771	Negative		
	4631.93	4258.77	*2.848	1679.8	
54294.24	34572.58	0.320	Negative		
	8712.03	7960.96	*2.757	*354.923	
47180.01	33281.35	0.377	Negative		
	6788.92	4903.91	*2.848	*1117.956	
65909.13	47354.14	0.836	Negative		
	7277.27	4388.27	*2.848	976.61	
63535.66	48983.68	0.571	Negative		
	4719.44	3178.05	*2.848	*1117.956	
25917.68	28833.62	0.595	Negative		
	6902.77	9002.44	*2.757	*354.923	
61544.54	44563.8	0.955	Positive		
	5671.68	4616	*2.848	*1117.956	
38749.19	34494.89	1.000	Positive		
	2958.02	4679.24	*2.757	*354.923	
46865.34	41141.37	0.239	Negative		
	4826.34	9493.94	*2.757	15835.25	
32332.39	24439.05	0.997	Positive		
	4937.74	4216.5	*2.692	*404.102	
38377.04	41802.57	0.293	Negative		
	4354.99	4036.67	*2.848	2248.5	
56871.94	43362.85	0.987	Positive		
	4954.37	5177.78	*2.692	*404.102	
22957.71	25435.43	0.385	Negative		
	6784.43	5402.1	*2.783	*103.34	
33934.98	35810.5	0.632	Negative		
	5206.27	4743.23	*2.783	*103.34	
49645.69	30271.78	0.661	Negative		
	3972.79	4099.91	*2.783	*103.34	
60907.69	43727.92	0.601	Negative		
	6732.86	6029.53	*2.783	3215.77	
77919.44	45108.15	0.213	Negative		
	4759.29	3010.98	*2.848	*1117.956	
41992.31	32790.43	1.000	Positive		
	2580.3	3757.01	*2.692	*404.102	
56037.14	30929.41	0.386	Negative		
	4632.8	4580.5	*2.783	2324.41	
67388.58	44622.76	0.997	Positive		
	4734.6	2494.96	33.47	*103.34	
36594.47	33606.44	0.336	Negative		
	4137.94	3866.46	*2.692	14428.52	
50179.81	38313.23	0.990	Positive		
	6036.83	6038.51	*2.848	8645.62	

Table4.txt

65706.24	42803.07	1.000	Positive		
	6040.96	4184.34	*2.848	1730.99	
47162.16	32829.07	0.979	Positive		
	4721.87	2807.91	*2.783	*103.34	
57693.18	40681.93	0.776	Negative		
	8631.06	5219.02	*2.848	*1117.956	
43399.6	43763.38	0.123	Negative		
	6567.42	7489.81	*2.848	3875.63	
71297.09	37617.68	0.121	Negative		
	3943.08	4742.01	*2.692	*404.102	
41577.45	37617.38	0.998	Positive		
	7048.97	5742.04	*2.783	*103.34	
59520.26	45781.02	0.511	Negative		
	9515.04	5463.5	*2.783	*103.34	
62089.69	47242.2	0.925	Positive		
	7527.54	5376.57	*2.783	*103.34	
56317.15	52299.85	0.956	Positive		
	4568.43	4629.91	*2.848	*1117.956	
39949.41	39664.92	0.117	Negative		
	6256.64	6567.65	*2.783	*103.34	
30294.24	40496.74	0.122	Negative		
	5390.81	5150.44	*2.848	*1117.956	
46586.74	40456.14	0.954	Positive		
	9048.79	11948.97	*2.848	5778.45	
112592.65	74230.07	0.175	Negative		
	4783.23	3433.27	*2.848	*1117.956	
69791.26	51323.29	0.831	Negative		
	5124.02	4539.69	*2.848	5834.37	
48227.5	29981.53	0.876	Positive		
	4404.01	3518.16	22.16	*103.34	
56361.73	37430.5	0.856	Negative		
	7158.79	5458.38	*2.783	4355.7	
71784.03	64611.98	0.609	Negative		
	6346.63	5924.54	*2.783	*103.34	
56067.94	46305.02	0.603	Negative		
	6230.93	5067.83	*2.848	2040.33	
57746.73	37696.16	0.125	Negative		
	6255.77	4629.91	*2.848	661.2	
41271.15	41130.39	0.125	Negative		
	5756.21	5478.88	*2.783	6685.94	
106986.42	61251.17	0.994	Positive		
	4386.52	2565.91	*2.848	*1117.956	
27267.21	31594.8	0.826	Negative		
	3171.53	3437.08	*2.692	*404.102	
34239.76	32710.22	0.122	Negative		
	2859.37	3336.47	*2.692	*404.102	
39438.69	33947.65	0.876	Positive		
	3157.72	4091.43	*2.795	*434.712	

Table4.txt

90474.94	24068.27	0.991	Positive		
	4374.55	6320.41	*2.795	24861.44	
78288.73	36159.18	0.976	Positive		
	3091.24	4745.55	*2.795	*434.712	
61365.88	25811.53	0.876	Positive		
	2815.41	3999.32	*2.795	*434.712	
116206.78	50712.55	0.841	Negative		
	3341.06	3698.03	*2.795	2245.35	
109578.08	33515.98	1.000	Positive		
	3890.35	8790.47	*2.795	14389.69	
**4142.527	32857.68	0.998	Positive		
	3586.33	4931.53	*2.795	*434.712	
75298.92	29059.15	0.991	Positive		
	4041.29	7198.11	27.38	17931.46	
162100.91	19774.67	0.999	Positive		
	6217.58	5767.45	*2.748	*445.15	
61484.25	34794.3	0.116	Negative		
	4737.1	2862.72	*2.748	*445.15	
44071.57	40731.15	0.356	Negative		
	6511.85	5434.04	*2.748	3255.7	
59424.33	50260.97	0.480	Negative		
	6518.71	11789.03	*2.748	30869.55	
17036.56	15026.32	0.992	Positive		
	6928.31	4985.97	*2.748	*445.15	
73261.19	49839.04	0.121	Negative		
	4907.28	4830.5	*2.748	13007.46	
195779.93	36870.8	0.997	Positive		
	6164.76	4815.55	*2.848	*1117.956	
93774.29	22577.56	0.910	Positive		
	4564.06	5646.94	*2.748	8359.12	
181136.53	41917.7	0.999	Positive		
	2873.66	2886.55	*2.795	2408.89	
80288.73	29842.31	0.392	Negative		
	3306.25	16149.58	*2.795	5607.98	
**4142.527	40421.65	0.995	Positive		
	4364.15	6171.67	90.48	17399.29	
110832.49	43241.4	0.993	Positive		
	6057.36	4848.51	*2.748	*445.15	
119641.66	49073.78	0.947	Positive		
	6210.76	6345.88	*2.748	11911.63	
98490.64	49647.5	0.986	Positive		
	5124.85	5311.82	*2.748	*445.15	
64024.49	40361.36	0.527	Negative		
	5904.35	5337.68	*2.748	7932.42	
92925.6	51608.48	0.252	Negative		
	6587.36	6187.23	*2.748	*445.15	
77331.37	38703.01	0.331	Negative		
	8492.12	5835.56	*2.748	*445.15	

Table4.txt

92284.63	38042.2	0.999	Positive		
	6402.19	6295.45	*2.748	17651.88	
66070.64	29130.04	0.992	Positive		
	5877.19	6299.32	*2.748	*445.15	
52861.96	31322.54	0.340	Negative		
	6852.38	7104.89	*2.748	*445.15	
138275.77	42960.09	0.675	Negative		
	5877.19	4744.29	*2.748	*445.15	
82159.57	30818.54	0.835	Negative		
	6108.45	4848.51	*2.748	*445.15	
77929.84	34612.73	0.779	Negative		
	6945.58	6454.92	*2.748	*445.15	
88785.36	41657.72	0.602	Negative		
	5558.93	5646.94	*2.748	6457.38	
119389.29	43969.05	0.999	Positive		
	7385.92	5934.34	*2.748	*445.15	
66719.22	35230.44	0.547	Negative		
	4960.77	5926.72	*2.748	*445.15	
74454.9	34394.97	0.123	Negative		
	9337.94	4837.7	*2.748	*445.15	
84339.04	38886.82	0.987	Positive		
	13456.09	5622.25	*2.736	4681.19	
40061.83	38311.25	0.976	Positive		
	9430.09	8823.72	*2.713	3788.53	
44225.79	39822.66	0.999	Positive		
	5646.4	4929.86	*2.684	*445.855	
60571.48	35864.25	0.561	Negative		
	16542.35	6641.92	*2.736	17352.71	
171946.12	69427.43	0.972	Positive		
	8851.84	7621.96	*2.736	*170.39	
49293.94	45699.08	0.864	Positive		
	6887.27	6065.93	*2.736	2783.61	
37239.37	40288.85	0.993	Positive		
	7862.2	6983.76	*2.736	3073.9	
45084.86	47110.97	0.967	Positive		
	9228.25	8585.79	*2.736	7047.9	
104357.39	86841.15	0.154	Negative		
	10195.93	6341.74	*2.736	3106.13	
55842.56	53714.33	0.997	Positive		
	7418.22	5712.6	*2.736	*170.39	
28164.39	43064.67	0.651	Negative		
	2780.79	4602.09	*2.848	*1117.956	
441478.79	31017.78	1.000	Positive		
	2142.45	3890.59	*2.848	2881.01	
143415.84	26358.24	0.971	Positive		
	5346.21	3328.63	*2.848	5555.15	
259815.65	33951.59	0.999	Positive		
	4041.4	3334.95	*2.848	*1117.956	

Table4.txt

167694.03	30940.92	0.987	Positive		
	5439.51	6042.31	*2.848	9511.95	
177716.64	30134.86	0.887	Positive		
	3715.65	2241.89	*2.848	*1117.956	
148819.79	25485.92	0.835	Negative		
	6773.09	6733.92	*2.748	2788.54	
73523.2	46981.59	0.328	Negative		
	4647.2	3399.39	*2.748	18737.53	
142706.42	41657.72	0.997	Positive		
	5877.19	5263.88	*2.748	*445.15	
79333.58	55188.09	0.458	Negative		
	4920.65	6357.54	*2.748	*445.15	
69265.5	41397.97	0.944	Positive		
	5269.21	4551.76	*2.748	*445.15	
80046.47	49073.78	0.458	Negative		
	6105.04	6564.52	*2.748	8958.15	
56277.55	45132.24	0.125	Negative		
	6002.91	7720.73	*2.748	*445.15	
65483.81	55384.24	0.306	Negative		
	5091.33	4658.47	*2.748	4670.5	
74353.54	55619.85	0.395	Negative		
	4169.86	5252.83	*2.748	*445.15	
48126.04	47208.97	0.343	Negative		
	6326.91	5055.07	*2.748	4263.34	
62117.26	47778.33	0.304	Negative		
	4507.6	8374.92	*2.748	14123.67	
73924.48	27983.1	0.998	Positive		
	5911.14	5000.49	*2.748	*445.15	
75258.62	58586.06	0.719	Negative		
	4853.84	5422.9	*2.748	*445.15	
98686.29	51840.26	0.672	Negative		
	5014.3	6718.11	*2.748	*445.15	
72629.23	40398.32	0.955	Positive		
	5734.78	4228.41	*2.748	*445.15	
97959.56	45998.63	0.999	Positive		
	5047.78	3382.84	*2.748	*445.15	
88582.82	51299.8	0.527	Negative		
	4627.23	5460.06	*2.748	*445.15	
62788.57	45207.46	0.810	Negative		
	7118.56	6837	*2.748	*445.15	
83320.24	41917.7	0.363	Negative		
	4113.74	4580.16	*2.748	*445.15	
67238.44	46111.85	0.541	Negative		
	8619.04	9546.9	*2.782	5997.52	
76809.87	72452.91	0.260	Negative		
	7382.92	7896.55	*2.782	2865.38	
55109.08	47813.87	0.186	Negative		
	6571.18	8355.38	*2.782	1233.01	

Table4.txt

44360.32	42867.39	0.235	Negative		
	5251.27	7226.5	*2.782	*137.6	
53239.59	46924.19	0.125	Negative		
	5191.54	7320.91	*2.782	10500.61	
89932.52	54069.72	0.117	Negative		
	9400.36	6719.99	46.72	12959.58	
99553.87	57335.19	0.175	Negative		
	9744.43	8261.72	*2.782	15067.6	
54226.33	43657.61	0.121	Negative		
	7530.26	6176.1	*2.782	*137.6	
78748.34	48767.11	0.296	Negative		
	7703.82	12037.97	*2.782	17623.48	
60285.86	46525.99	0.181	Negative		
	7960.26	9079.63	*2.782	6764.15	
61864.8	39175.48	0.435	Negative		
	9709.1	7837.19	*2.782	5933.63	
42636.15	42078.45	0.339	Negative		
	7656.06	9073.92	*2.782	7115.49	
68764.19	52884.51	0.121	Negative		
	8645.29	12595.6	*2.782	29012.26	
83273.1	53227.18	0.307	Negative		
	6407.7	6699.58	*2.782	1649.39	
61393.82	50247.77	0.315	Negative		
	6588.4	10269.57	*2.782	10788.01	
78940.67	62650.83	0.125	Negative		
	7339.61	10658.01	*2.782	816.32	
58766	55353.19	0.121	Negative		
	6450.7	4638.82	*2.782	*137.6	
56120.87	42897.76	0.326	Negative		
	6072.71	7950.65	*2.782	4911.25	
72688.41	54851.74	0.779	Negative		
	6519.54	8399.6	*2.782	1521.3	
74400.63	47875.3	0.585	Negative		
	7209.79	7352.48	*2.782	1873.5	
51467.77	36826.85	0.593	Negative		
	6985.07	8751.01	*2.782	2481.52	
61061.01	44540.57	0.125	Negative		
	6928.95	7896.55	*2.782	10756.08	
59625.85	55290.47	0.196	Negative		
	7313.64	8102.89	*2.782	13183.14	
48025.92	43961.88	0.116	Negative		
	8304.47	10997.09	*2.782	7913.93	
46644.86	51114.21	0.117	Negative		
	10378.02	15666.23	*2.782	27987.28	
51840.61	32058.81	0.239	Negative		
	7960.26	12044.46	*2.782	7083.55	
62504.87	43505.54	0.125	Negative		
	5832.67	9005.55	*2.782	6764.15	

Table4.txt

73466.84	43080.01	0.122	Negative		
	5055.09	7090.89	*2.782	10085.47	
97986.09	62715.06	0.293	Negative		
	7071.46	9119.62	*2.782	*137.6	
53711.08	45761.29	0.122	Negative		
	6094.16	4851.02	*2.782	*137.6	
56401.46	43323.13	0.494	Negative		
	4378.62	3162.61	*2.782	*137.6	
63656.15	39597.91	0.117	Negative		
	4552.82	7054.53	*2.782	7594.56	
75645.04	52791.11	0.125	Negative		
	3205.06	2918.7	*2.782	*137.6	
45046.12	36646.51	0.835	Negative		
	6898.74	6776.22	*2.782	10851.88	
54826.71	38271.21	0.116	Negative		
	7590.98	8846.82	*2.782	*137.6	
71779.99	51300.14	0.486	Negative		
	6653	8666.83	*2.782	*137.6	
52779.75	46342.34	0.603	Negative		
	7929.81	16990.15	*2.782	28083.36	
93257.19	79499.74	0.861	Negative		
	5473.32	8756.64	*2.782	2929.35	
73411.7	60315.78	0.117	Negative		
	10729.62	11709.41	*2.782	22546.58	
95396.54	65685.33	0.639	Negative		
	5926.93	6562.36	*2.782	2065.54	
29028.75	50185.96	0.298	Negative		
	5944.07	6791.58	*2.782	2673.47	
61864.8	53663.79	0.220	Negative		
	9365.13	8722.92	*2.782	5965.58	
64897.4	48767.11	0.123	Negative		
	8304.47	10353.99	*2.782	4847.34	
86168.7	41563.26	0.547	Negative		
	9810.72	9338.01	*2.782	4943.21	
53869.12	48951.88	0.121	Negative		
	5247	4869.59	*2.782	*137.6	
63506.33	42776.3	0.125	Negative		
	8138.78	9917.21	*2.782	8233.29	
37520.15	41290.72	0.345	Negative		
	6218.63	6096.78	*2.782	5678.06	
53522.01	38271.21	0.125	Negative		
	5635.78	5603.28	*2.782	*137.6	
44870.51	48151.85	0.123	Negative		
	7218.44	11760.66	*2.782	8616.51	
86587.12	48151.85	0.122	Negative		
	8365.57	11992.61	*2.782	17591.52	
90806.28	60443.25	0.125	Negative		
	4586.83	3474.32	105.15	*137.6	

Table4.txt

50393.57	40473.91	0.705	Negative		
	6184.28	8943.05	*2.782		6285.02
59459.83	41866.25	0.229	Negative		
	7196.82	9153.96	*2.782		4272.11
81495.04	45272.59	0.116	Negative		
	7538.93	8555.08	*2.782		4240.15
64639.42	55729.78	0.117	Negative		
	5781.28	5334.95	*2.782		1585.35
72994.23	51672.3	0.510	Negative		
	6317.43	10848.52	*2.782		13087.33
70800.27	40776.29	0.117	Negative		
	5824.11	5117.31	*2.782		*137.6
70526.22	57240.53	0.168	Negative		
	6399.1	10209.47	*2.782		5997.52
55068.65	41139.37	0.122	Negative		
	7010.98	8141.12	*2.782		4336.03
63740.6	55133.71	0.125	Negative		
	7595.31	9964.67	*2.782		1008.69
99081.52	63454.77	0.747	Negative		
	6519.54	8903.38	*2.782		*137.6
54979.82	39205.64	0.122	Negative		
	5029.52	4606.74	*2.782		11362.82
166991.62	51734.36	0.329	Negative		
	5319.56	5998.06	*2.782		3920.52
54979.82	45303.12	0.117	Negative		
	7352.6	10719.3	*2.782		2225.56
42889.49	37097.45	0.122	Negative		
	5725.64	7735.05	*2.782		2257.55
64145.74	48890.28	0.117	Negative		
	6012.66	7247.44	*2.782		*137.6
57075.53	44114.1	0.125	Negative		
	6132.78	10185.47	*2.782		*137.6
80933.74	49691.84	0.125	Negative		
	5396.42	7405.19	*2.782		5102.97
65378.11	45272.59	0.117	Negative		
	6523.84	7983.18	*2.782		4527.78
50423.34	33196.64	0.193	Negative		
	5481.87	5958.72	*2.782		*137.6
68529.69	46372.94	0.317	Negative		
	9034.05	15318.11	*2.71		1341.98
91999.02	63701.84	0.117	Negative		
	7118.7	9055.22	*2.71		9938.03
87167.58	73829.35	0.123	Negative		
	7184.8	8876.25	*2.71		*120.05
59946.73	55269.62	0.122	Negative		
	7392.73	8335.77	*2.71		*120.05
66478.56	60366.21	0.121	Negative		
	4713.37	5430.29	*2.71		3125.09

Table4.txt

89224.09	67191.59	0.125	Negative		
	5010.64	4203.15	*2.71	*120.05	
72708	59734.48	0.123	Negative		
	6892.33	11090.44	*2.71	9255.65	
83204.35	72227.53	0.601	Negative		
	5597.72	6993.72	*2.71	*120.05	
88945.54	72330.51	0.116	Negative		
	6290.45	7694.35	*2.71	5213.69	
104355.45	77808.18	0.179	Negative		
	6337.38	6155.76	*2.71	*120.05	
107908.11	56508.36	0.187	Negative		
	16343.71	9139.2	*2.71	*120.05	
107736	72073.16	0.245	Negative		
	4857.28	7108.98	*2.71	*120.05	
142161.54	73621.99	0.156	Negative		
	5728.52	7136.52	*2.71	624.49	
98081.57	61635.37	0.186	Negative		
	5880.43	8563.39	*2.665	*158.78	
82954.95	51315.27	0.125	Negative		
	7663.48	9255.73	*2.665	7660.14	
95401.72	47796.66	0.699	Negative		
	9672.11	6293.22	*2.71	1879.53	
118390.37	76648.76	0.597	Negative		
	4546.43	7441.62	*2.71	2159.54	
75578.3	51830.02	0.631	Negative		
	6628.69	8545.78	*2.71	*120.05	
78967.8	47481.87	0.322	Negative		
	7875.95	7790.56	*2.71	*120.05	
45558.05	53189.73	0.121	Negative		
	8780.62	5338.78	*2.71	*120.05	
78551.16	64147.31	0.845	Negative		
	6159.13	9983.12	*2.71	11295.01	
88862.24	60123.01	0.122	Negative		
	5187.44	7419.29	*2.71	1593.43	
68670.47	62174.64	0.121	Negative		
	6056.04	6592.25	*2.71	*120.05	
79528.28	69516.64	0.419	Negative		
	5504.37	9157.23	*2.71	13550.56	
75393.02	72227.53	0.125	Negative		
	5672.45	9834.22	*2.71	4274.77	
96066.54	75286.61	0.123	Negative		
	6798.11	6474.29	*2.71	*120.05	
63503.26	53377.96	0.123	Negative		
	7586.76	8481.41	*2.71	*120.05	
106638.26	65240.19	0.770	Negative		
	7653.08	7059.51	*2.71	*120.05	
68507.47	69516.64	0.116	Negative		
	5485.71	7291.32	*2.71	*120.05	

Table4.txt

98211.87	54416.27	0.122	Negative		
	6567.56	5511.97	*2.71	*120.05	
71106.6	66589.24	0.308	Negative		
	8304.63	10003.59	*2.665	12609.89	
48124.9	34102.28	0.328	Negative		
	6966.58	8618.48	*2.665	3554.76	
37079.58	26685.93	0.123	Negative		
	5734.89	7153.65	39.29	3156.51	
68135.1	48741.75	0.755	Negative		
	5176.26	6550.2	*2.665	7531.3	
34043.52	29911.37	0.630	Negative		
	4021.77	7200.33	*2.665	1676.12	
23337.65	25676.41	0.968	Positive		
	6084.15	9908.56	*2.71	*120.05	
76703.45	62076.49	0.117	Negative		
	8344.32	7236.7	451.18	11879.59	
27178.66	32474.59	1.000	Positive		
	5435.98	5781.03	*2.665	*158.78	
20283.22	25265.49	0.485	Negative		
	8295.81	9684.37	*2.665	14415.31	
48093.93	29723.38	0.192	Negative		
	5423.19	5913.15	*2.665	*158.78	
50993.3	33609.59	0.216	Negative		
	6788.7	9661.65	*2.71	11936.56	
79037.54	56365.05	0.400	Negative		
	6412.5	9283.85	*2.71	5676.91	
128489.4	89760.7	0.758	Negative		
	6827.9	8344.27	*2.665	5393.34	
55269.63	42800.38	0.123	Negative		
	4810.84	4241.63	*2.71	*120.05	
59089.51	68705.02	0.121	Negative		
	8446.63	8041.48	*2.71	6908.41	
167365.83	92063.21	0.861	Negative		
	5289.9	4610.79	*2.71	*120.05	
94561.22	74504.69	0.123	Negative		
	5261.34	6937.04	*2.665	*158.78	
21672.35	30663.97	0.122	Negative		
	4072.27	6459.53	19.1	2689.35	
51710.8	29084.66	0.538	Negative		
	6741.34	8148.8	*2.665	8495.92	
52089.13	30965.3	0.507	Negative		
	5812.67	5471.09	248.35	*120.05	
33421.05	43895.24	0.523	Negative		
	6177.88	8598.58	*2.71	*120.05	
72090.36	77491.35	0.125	Negative		
	6262.3	4976.62	*2.71	*120.05	
59540.66	43985.3	0.116	Negative		
	7847.48	7136.52	*2.71	5534.76	

Table4.txt

73690.09	63158.67	0.517	Negative		
	7373.81	12549.88	*2.71	8225.99	
88145.39	86379.62	0.377	Negative		
	8437.1	9465.92	*2.71	5070.4	
83367.66	58139.32	0.117	Negative		
	4548.88	3995.36	*2.656	*158.78	
17366	25489.6	0.122	Negative		
	6356.15	9115.17	60.45	3686.41	
115776.17	61635.37	0.184	Negative		
	3756.95	5639.98	*2.665	3089.95	
37701.23	25975.39	0.564	Negative		
	4586.93	5918.05	*2.665	*158.78	
31352.15	34747.36	0.125	Negative		
	5914.7	5350.93	*2.665	*158.78	
20627.87	27284.8	0.303	Negative		
	5410.4	5727.42	*2.665	*158.78	
38534.98	30174.67	0.122	Negative		
	6393.71	7762.22	*2.71	*120.05	
83216.89	70127.39	0.117	Negative		
	3811.55	5136.57	*2.665	*158.78	
35002.43	32361.24	0.294	Negative		
	5478.62	5264.94	*2.665	*158.78	
18282	22878.13	0.125	Negative		
	4588.15	4159.95	*2.71	*120.05	
81087.68	66689.51	0.305	Negative		
	4671.52	3540.73	*2.665	*158.78	
31328.21	30588.67	0.377	Negative		
	4908.38	6635.3	*2.71	3981.77	
78103.35	81916.42	0.404	Negative		
	4367.29	4630.34	*2.665	*158.78	
72136.31	56728.75	0.863	Negative		
	6689.85	7796.23	*2.71	*120.05	
55784.53	57082.55	0.591	Negative		
	5397.09	3049.18	*2.71	*120.05	
60644.23	88868.74	0.390	Negative		
	7667.3	5338.78	*2.71	*120.05	
81536.23	92176.15	0.411	Negative		
	5579.05	5187.12	*2.71	*120.05	
56574.59	56556.15	0.374	Negative		
	4324.16	7637.94	51.65	*120.05	
98653.76	64296	0.860	Negative		
	5611.73	8935.76	*2.71	*120.05	
63424.88	38559.56	0.603	Negative		
	5572.51	5408.44	*2.665	*158.78	
22634	25041.43	0.680	Negative		
	6187.26	6721.66	*2.71	*120.05	
47241.6	44707.15	0.553	Negative		
	7733.5	8673.7	*2.665	3554.76	

Table4.txt

74665.62	41214.88	0.327	Negative		
	5411.08	7413.71	37.5		3834.41
46990.65	45159.55	0.221	Negative		
	4249.2	5298.34	*2.665		*158.78
35815.28	27247.36	0.851	Negative		
	3417.18	3052.07	36.81		*158.78
44424.93	35241.29	0.125	Negative		
	5231.55	6364.21	*2.665		*158.78
47339.76	41871.44	0.855	Negative		
	6749.99	7325.28	*2.665		*158.78
19854.81	25938.01	0.193	Negative		
	10043.23	8951.76	*2.665		5913.99
39386.33	29798.57	0.121	Negative		
	6009.2	7436.03	*2.71		*120.05
68106.87	53754.94	0.125	Negative		
	5541.7	7224.85	*2.71		1593.43
78046.2	54889.92	0.387	Negative		
	6450.07	2675.5	*2.71		*120.05
90537.54	62027.43	0.473	Negative		
	10070.28	18449.62	*2.665		26269.35
67001.99	33193.11	0.736	Negative		
	6775.95	6803.96	*2.665		*158.78
23805.77	30400.44	0.401	Negative		
	5726.34	6834.6	*2.665		*158.78
16556.15	23623.62	0.117	Negative		
	7686.25	9594.19	*2.71		*120.05
94976.33	71662.04	0.117	Negative		
	5224.69	3926.31	*2.71		*120.05
70686.16	44752.35	0.121	Negative		
	7052.64	15272.41	*2.71		24461.77
88806.77	69923.61	0.184	Negative		
	7255.65	6624.53	*2.71		*120.05
73595.28	54463.59	0.339	Negative		
	4972.37	5255.4	*2.665		*158.78
32865.08	33723.24	0.116	Negative		
	8817.73	8159.61	*2.665		27617.18
51661.62	22282.04	0.886	Positive		
	5811.91	4249	*2.665		*158.78
14328.09	26012.77	0.338	Negative		
	5435.98	7127.75	*2.665		*158.78
27935.89	26723.34	0.121	Negative		
	8623.06	9109.17	*2.71		*120.05
105320.72	105748.64	0.388	Negative		
	7667.3	7767.89	*2.71		*120.05
74937.96	69415.01	0.121	Negative		
	6248.23	3935.79	*2.71		*120.05
100404.26	78072.57	0.156	Negative		
	6638.1	4410.82	*2.71		*120.05

Table4.txt

75501.93	43355.67	0.600	Negative		
	5929.62	5440.48	203.29	*120.05	
85027.64	46021.77	0.935	Positive		
	7364.36	7870.1	*2.71	*120.05	
75045.96	55032.23	0.117	Negative		
	8702.43	10321.12	20.27	8880.77	
21811.54	24966.76	0.511	Negative		
	7323.01	8979.74	*2.665	*158.78	
50977.09	27771.77	0.209	Negative		
	6577.11	4376.91	*2.665	*158.78	
9202.55	23996.54	0.721	Negative		
	6508.06	6702.12	45.96	*158.78	
9856.63	18596.75	0.122	Negative		
	7759.77	6580.5	*2.665	*158.78	
78010.59	37413.69	0.125	Negative		
	5136.24	5156.92	*2.71	*120.05	
64020	58476.68	0.220	Negative		
	5215.37	5707.22	26.07	*120.05	
52422.88	55745.19	0.703	Negative		
	6295.14	5146.86	*2.71	*120.05	
39442.17	45476.8	0.638	Negative		
	6694.55	10258.49	*2.71	5213.69	
71998.32	54652.96	0.827	Negative		
	6374.93	6139.96	*2.71	*120.05	
88613.07	70586.62	0.333	Negative		
	11899.13	6657.7	*2.723	13306.64	
211375.29	78772.52	0.999	Positive		
	17290.8	10257.73	*2.723	4411.95	
138413.88	99290.06	0.711	Negative		
	11165.96	7934.4	*2.736	3235.02	
57082.94	47393.44	0.117	Negative		
	9875.21	4945.36	*2.736	*170.39	
46370.67	46216.7	0.875	Positive		
	8769.32	5107.82	*2.783	*103.34	
63114.74	49047.05	0.122	Negative		
	9279.18	6627.07	*2.783	*103.34	
50221.35	64847.68	0.125	Negative		
	8854.19	5305.24	*2.783	*103.34	
46993.25	53631.1	0.116	Negative		
	8001.02	5914.07	22.5	1471.54	
45811.63	49084.73	0.610	Negative		
	8488.93	5581.69	*2.783	*103.34	
64887.38	62849.34	0.335	Negative		
	9109.05	4355.8	*2.783	*103.34	
37197.14	47542.5	0.121	Negative		
	5287.13	5670.1	*2.749	*420.896	
28853.59	43990.7	0.192	Negative		
	7905.9	6836.99	*2.749	*420.896	

Table4.txt

27490.85	31071.44	0.300	Negative		
	8796.2	5987.08	*2.749	*420.896	
38884.37	32198.76	0.116	Negative		
	5543.45	4595.34	*2.65	*485.573	
27711.55	26055.19	0.117	Negative		
	4022.56	4185.57	*2.65	*485.573	
33232.33	25681.51	0.599	Negative		
	5114.24	4271.71	*2.65	12263.87	
32032.69	33375.58	0.117	Negative		
	8992.09	7025.95	*2.65	3078.72	
34040.9	28589.53	0.116	Negative		
	6031.26	4454.44	18.24	*485.573	
28321.9	25262.71	0.660	Negative		
	4492.32	4524.71	*2.65	2463.27	
32857.37	25611.59	0.122	Negative		
	8207.27	5062.27	27.59	*420.896	
35294.99	34394.78	0.341	Negative		
	11973.8	12846.67	*2.749	*420.896	
56574.3	35873.49	0.843	Negative		
	7290.06	7407.84	*2.749	*420.896	
51749.85	42351.73	0.382	Negative		
	10398.94	8770.67	*2.749	*420.896	
33012.17	31165.35	0.558	Negative		
	6586.17	4709.27	*2.749	*420.896	
32561.62	36251.71	0.125	Negative		
	12182.72	7921.44	*2.749	*420.896	
37104.38	40147.76	0.117	Negative		
	5711.54	5789.72	*2.749	*420.896	
42084.5	51208.01	0.320	Negative		
	5108.39	4510.04	*2.749	2792.38	
41792.45	40275.13	0.116	Negative		
	5350.77	4848.58	*2.749	*420.896	
38529.77	36346.31	0.230	Negative		
	3206.22	4413.92	*2.757	*424.639	
50747.73	43865.06	0.125	Negative		
	4546.57	5577.62	*2.757	*424.639	
17791.93	37493.75	0.612	Negative		
	5077.93	4396.39	*2.748	8459.22	
62588.5	54561.53	0.677	Negative		
	6814.45	4308.7	*2.748	*445.15	
61836.26	51299.8	0.125	Negative		
	4418.02	3130.22	*2.748	*445.15	
41257	35812.79	0.319	Negative		
	9312.79	4037.91	*2.748	*445.15	
58947.44	55816.38	0.303	Negative		
	6490.8	7640.62	*2.665	*158.78	
57548.11	69972.44	0.117	Negative		
	5355.01	4212.58	*2.665	*158.78	

Table4.txt

42802.6	52430.31	0.329	Negative		
	6598.7	4943.03	*2.665	2387.34	
44571.18	52789.56	0.121	Negative		
	4553.11	3558.39	*2.665	*158.78	
54058.13	58188.79	0.125	Negative		
	3895.6	3766.88	*2.665	*158.78	
49140	56931.11	0.125	Negative		
	3962.88	3624.71	*2.665	*158.78	
52785.91	58473.52	0.122	Negative		
	8286.99	7189.95	*2.665	*158.78	
65551.33	50878.3	0.334	Negative		
	4654.6	7019.32	*2.665	2151.38	
53845.72	50243.77	0.125	Negative		
	4701.14	4422.77	*2.665	*158.78	
50420.31	53669.47	0.122	Negative		
	4460.16	5037.23	*2.665	*158.78	
79108.61	54833.2	0.121	Negative		
	5274.11	5776.15	*2.665	1982.2	
72870.49	58188.79	0.125	Negative		
	3899.8	3321.25	*2.665	*158.78	
57981.15	67693.79	0.338	Negative		
	4582.7	5514.27	*2.665	*158.78	
60633.32	62365.29	0.123	Negative		
	4021.77	4616.45	*2.665	*158.78	
15746.58	27659.36	0.316	Negative		
	5155	4695.32	*2.665	*158.78	
82679.7	57620.14	0.121	Negative		
	6564.16	4376.91	*2.665	*158.78	
42419.35	46110.08	0.633	Negative		
	5031.8	5264.94	*2.665	2252.63	
53137.21	54230.72	0.322	Negative		
	7680.98	18570.31	*2.665	*158.78	
32633	36612.03	0.297	Negative		
	3927.05	3664.05	*2.65	*485.573	
27488.58	24845.58	0.357	Negative		
	6493.62	5022.25	*2.65	8306.5	
38706.02	27777.46	0.125	Negative		
	5264.94	4104.26	*2.65	*485.573	
23087.06	29432.24	0.117	Negative		
	6769.18	9387.97	*2.65	*485.573	
54013.96	35405.87	0.117	Negative		
	3549.2	4854.45	*2.65	*485.573	
25983.51	21678.89	0.316	Negative		
	6239.17	5679.84	*2.65	*485.573	
38943.51	33325.34	0.317	Negative		
	6951.72	6292.08	*2.65	4103.65	
39517.17	35868.3	0.121	Negative		
	3362.84	3909.5	*2.65	*485.573	

Table4.txt

27446.06	26995.34	0.320	Negative	
	5817.49	5949.05	*2.65	*485.573
34029.38	28397.87	0.125	Negative	
	5707.55	5045.08	*2.65	*485.573
33486.5	28829.6	0.125	Negative	
	5747.81	4463.2	*2.65	*485.573
35802.01	26031.8	0.334	Negative	
	6231.72	3705.31	*2.65	*485.573
46904.46	38317.83	0.311	Negative	
	8729.96	8222.93	*2.65	*485.573
41047.72	29625.84	0.309	Negative	
	6205.66	5866.84	*2.65	*485.573
36885.35	30721.7	0.489	Negative	
	3230.8	3492.28	*2.65	*485.573
22731.57	29094.33	0.125	Negative	
	3767.66	4314.99	*2.65	*485.573
27394.16	22196.41	0.125	Negative	
	4660.39	3846.63	*2.65	*485.573
28958.87	24938.13	0.316	Negative	
	5452.71	5452.74	*2.65	*485.573
49064.31	24961.28	0.125	Negative	
	3386.04	4297.66	*2.65	*485.573
25682.84	21454.65	0.117	Negative	
	5942.61	4867.98	*2.65	*485.573
25433.73	29698.53	0.322	Negative	
	4780.14	5192.02	*2.65	*485.573
26232.48	25216.28	0.125	Negative	
	3865.87	2643.91	*2.65	*485.573
22343.99	25634.89	0.125	Negative	
	5333.39	5499.78	*2.65	*485.573
28629.02	29698.53	0.323	Negative	
	4249.33	3383.16	*2.65	*485.573
23074.73	22399.59	0.125	Negative	
	6433.56	3467.94	*2.65	*485.573
27864.25	26289.43	0.125	Negative	
	7215.97	5443.35	*2.65	*485.573
34868.95	28397.87	0.302	Negative	
	4558.71	5785.05	*2.65	*485.573
34868.95	29239.01	0.123	Negative	
	6735.07	7465.7	*2.65	*485.573
38320.13	30697.22	0.310	Negative	
	4727.24	4410.71	*2.65	5886.76
32740.7	28326.1	0.121	Negative	
	5423.74	5252.14	*2.65	*485.573
39685.64	34461.84	0.122	Negative	
	5510.75	4419.44	*2.65	*485.573
28225.01	25798.14	0.121	Negative	
	4632.29	4972.16	24.17	*485.573

Table4.txt

34621.96	26524.2	0.122	Negative		
	6486.11	4332.34	*2.65	7202.05	
30990.05	29916.92	0.565	Negative		
	4653.36	4155.55	*2.65	6153.76	
36816.66	29577.41	0.121	Negative		
	6456.07	4215.65	*2.65	*485.573	
23684.57	28757.52	0.320	Negative		
	9571.2	9795.52	*2.65	5185.2	
62141.3	25961.65	0.117	Negative		
	6403.57	7428.64	*2.65	*485.573	
31703.02	24984.44	0.117	Negative		
	7509.55	5886.14	*2.65	*485.573	
38587.86	27468.64	0.125	Negative		
	4506.47	4967.66	*2.7	*129.5	
29637.23	26816.75	0.121	Negative		
	4238.85	4045.38	*2.7	756.14	
42501.56	30644.27	0.121	Negative		
	2975.3	2720.32	*2.7	*129.5	
44985.54	24463.88	0.116	Negative		
	4070.41	4404.87	69.44	*129.5	
27628.05	22219.23	0.123	Negative		
	4544.71	5058.79	*2.65	*485.573	
30780.15	23741.3	0.117	Negative		
	5060.64	5978.17	*2.65	*485.573	
49854.18	30501.59	0.125	Negative		
	4249.33	4746.65	*2.65	*485.573	
35464.19	27801.25	0.117	Negative		
	4544.71	5924.83	*2.65	*485.573	
26602.74	25961.65	0.125	Negative		
	5000.01	4926.77	38.78	*485.573	
23781.08	25262.71	0.125	Negative		
	6456.07	3763.3	*2.65	6105.18	
40093.13	27872.66	0.121	Negative		
	7790.09	5660.79	*2.65	*485.573	
28152.54	27967.96	0.117	Negative		
	5322.57	5026.82	*2.65	4944.09	
26671.79	25193.07	0.355	Negative		
	3395.99	439.83	*2.65	*485.573	
31654.65	24245.99	0.121	Negative		
	3376.09	3775.77	*2.65	*485.573	
28894.61	26948.13	0.575	Negative		
	3821.79	4463.2	*2.65	11010.69	
37649.8	30355.11	0.122	Negative		
	5128.56	3215.43	*2.65	*485.573	
23814.72	24706.91	0.121	Negative		
	7359.53	7022.13	*2.7	*129.5	
32900.01	32395.9	0.320	Negative		
	4589.47	4397.24	*2.7	1693.49	

Table4.txt

35318	26564.6	0.121	Negative		
	4995.98	4313.55	*2.7	*129.5	
34193.74	39669.25	0.258	Negative		
	7564.08	5080.95	*2.7	*129.5	
36286.09	24175.71	0.532	Negative		
	5610.85	5567.06	*2.7	*129.5	
33588.35	35796.36	0.123	Negative		
	4232.49	3668.96	*2.7	2124.66	
33380.99	29132.56	0.121	Negative		
	4509.66	4196.1	*2.7	2459.64	
51557.53	33325.92	0.321	Negative		
	6282.06	4711.69	*2.7	*129.5	
57722.22	32970.77	0.309	Negative		
	4439.49	3951.65	*2.7	*129.5	
37926.05	32087.5	0.123	Negative		
	5478.5	4180.99	*2.7	1189.47	
52079.03	25187.51	0.727	Negative		
	7901.64	5646.96	*2.7	2674.85	
50967.73	38040.58	0.121	Negative		
	2641.66	4151.27	*2.65	*485.573	
29699.57	27089.83	0.123	Negative		
	5883.66	4653	*2.65	3316.3	
87946.64	40773.3	0.248	Negative		
	3044.21	2708.01	*2.65	*485.573	
28506.8	26312.88	0.121	Negative		
	4611.25	2640.15	*2.65	*485.573	
30665.27	27944.12	0.374	Negative		
	4176.93	3721.85	24.77	11035.68	
31794.57	22151.31	0.121	Negative		
	4607.74	4263.07	*2.65	*485.573	
24936.98	25751.47	0.584	Negative		
	NA	NA	*2.694	NA	
46420.32	40948.48	0.297	Negative		
	NA	NA	*2.694	NA	
43203.85	53386.89	0.117	Negative		
	NA	NA	*2.694	NA	
37636.62	56809.65	0.341	Negative		
	NA	NA	*2.694	NA	
47517.45	50526.85	0.324	Negative		
	NA	NA	*2.694	NA	
45599.22	50970.91	0.604	Negative		
	NA	NA	*2.694	NA	
56541.49	47854.59	0.116	Negative		
	5308.05	5340.98	28.72	*131.8	
44073.03	33807.09	0.117	Negative		
	4352.76	3546.11	*2.724	*131.8	
37618.49	35452.35	0.376	Negative		
	4160.25	3261.41	*2.724	*131.8	

Table4.txt

45759.95	43198.22	0.514	Negative		
	3608.61	3390.32	*2.724	*131.8	
46264.74	29075.84	0.416	Negative		
	3302.11	4340.15	*2.7	*129.5	
21431.26	24980.29	0.117	Negative		
	5365.68	4500.34	*2.7	14022.66	
45635.51	32572.49	0.116	Negative		
	4016.45	4534.81	*2.7	3988.5	
32731.5	36364.94	0.117	Negative		
	5824.31	3389.64	*2.7	*129.5	
41345.5	25270.5	0.122	Negative		
	6174.72	6745.61	*2.7	5754.06	
29727.22	26271.11	0.125	Negative		
	5288.4	4397.24	*2.7	*129.5	
25180.42	26061.93	0.242	Negative		
	4678.93	3367.73	*2.7	*129.5	
24910.24	29972.4	0.573	Negative		
	3743.95	4071.69	*2.7	*129.5	
26418.8	20236.84	0.833	Negative		
	4819.7	5014.48	*2.7	*129.5	
34742.17	35298.2	0.122	Negative		
	7004.37	4427.75	*2.7	1885.2	
40660.93	30167.07	0.117	Negative		
	5069.8	7212.28	*2.7	10886.97	
45496.52	41391.03	0.192	Negative		
	4060.88	3120.91	*2.7	*129.5	
33856.78	25519.83	0.409	Negative		
	4806.9	7855.7	*2.7	5062.26	
37758.7	29605.58	0.125	Negative		
	6330.9	6172.29	*2.7	1717.46	
15198.77	28447.91	0.121	Negative		
	5417.24	5515.25	*2.7	*129.5	
34442.52	28149.63	0.125	Negative		
	9941.87	5662.97	20.72	5205.4	
39495.3	24381.47	0.414	Negative		
	4111.7	4665.43	*2.7	11891.45	
28926.03	25915.73	0.553	Negative		
	5927.99	5747.18	*2.7	*129.5	
22172.51	31538.75	0.121	Negative		
	3339.9	4271.81	*2.7	1021.14	
38603.17	28298.68	0.117	Negative		
	4404.43	4086.73	*2.7	*129.5	
39272	33237.03	0.125	Negative		
	5986.36	5479.44	*2.7	2196.47	
35600.02	25063.13	0.576	Negative		
	6526.52	7851.36	*2.7	11221.71	
41257.42	40044.57	0.117	Negative		
	4439.49	4439.2	*2.7	*129.5	

Table4.txt

29196.14	30731.24	0.362	Negative		
	4755.69	6058.26	*2.7	*129.5	
31855.96	30253.69	0.121	Negative		
	3892.77	3850.84	*2.7	*129.5	
33743.19	24959.59	0.116	Negative		
	4509.66	4321.15	*2.7	*129.5	
41900.58	24835.46	0.125	Negative		
	5623.77	5139.75	*2.7	*129.5	
37439.5	28533.27	0.121	Negative		
	5146.89	5088.79	*2.7	*129.5	
27193.69	29476.39	0.125	Negative		
	3308.41	4147.01	*2.7	*129.5	
32650.44	27852.12	0.121	Negative		
	4079.93	5249.86	*2.7	*129.5	
33982.76	34667.15	0.123	Negative		
	3308.41	3635.71	19.11	*129.5	
30170.16	27196.02	0.331	Negative		
	6233.25	5928.54	*2.7	3988.5	
38884.41	29584.04	0.356	Negative		
	5630.23	5487.39	*2.7	5801.77	
30132.57	26943.04	0.122	Negative		
	6330.26	5308.45	*2.738	*378.8	
33908.25	26199.36	0.125	Negative		
	4370.87	3970.77	*2.738	*378.8	
21286.58	20201.15	0.125	Negative		
	3962.03	3220.5	*2.738	*378.8	
14390.11	20034.78	0.121	Negative		
	5152.88	3455.21	*2.738	*378.8	
36955.44	28910.22	0.122	Negative		
	6143.27	5560.7	*2.738	*378.8	
38549.33	41273.53	0.117	Negative		
	5634.79	4683.34	*2.738	*378.8	
22921.32	31710.49	0.123	Negative		
	4867.23	4554.37	*2.738	71023.13	
50976.82	30640.76	0.489	Negative		
	7891.5	7947.81	*2.738	*378.8	
30177.21	41348.62	0.849	Negative		
	5047.68	6413.22	*2.738	*378.8	
37615.36	30731.39	0.325	Negative		
	5900.22	5907.49	*2.738	11976.6	
49726.68	33602.32	0.122	Negative		
	6256.74	5369.2	*2.738	3589.17	
39993.91	38483.39	0.188	Negative		
	6103.26	6601.77	*2.738	*378.8	
37615.36	31208.47	0.117	Negative		
	7448.82	6900.9	*2.738	*378.8	
29722.3	36265.1	0.125	Negative		
	3430.22	277.24	*2.738	*378.8	

Table4.txt

20646.49	25158.21	0.125	Negative		
	5222	3473.66	*2.738	*378.8	
25987.6	27227.74	0.205	Negative		
	4742.82	4860.55	*2.738	10583.32	
48048.3	40376.57	0.122	Negative		
	4716.65	4702.96	*2.738	9302.7	
29690.41	30776.74	0.125	Negative		
	6457.43	5211.64	*2.738	9990.61	
19420.56	23080.71	0.125	Negative		
	5936.79	6610.38	*2.738	*378.8	
31622.63	34396.56	0.346	Negative		
	4615.35	4157.06	*2.738	5295.78	
34208.01	25244.63	0.343	Negative		
	4130.47	4531.01	*2.738	15260.16	
38488.6	29424.33	0.125	Negative		
	6836.89	6112.51	*2.738	6428.34	
29866.17	34162.35	0.117	Negative		
	5571.89	3403.63	*2.738	*378.8	
41537.38	30301.52	0.397	Negative		
	5518.97	2923.68	*2.738	2164.69	
33753.33	23570.24	0.317	Negative		
	5990.02	7706.19	*2.738	3385.53	
38610.15	26395.59	0.125	Negative		
	5963.4	6175.68	*2.738	17852.19	
40085.12	26964.32	0.593	Negative		
	4667.62	4080.82	*2.738	*378.8	
30107.26	37127.59	0.299	Negative		
	6601.59	4507.68	*2.738	*378.8	
31027.52	29963.33	0.116	Negative		
	7530.35	5832.68	*2.738	30650.82	
47818.63	31985.29	0.327	Negative		
	4244.07	1606.12	*2.738	*378.8	
29600.2	25482.6	0.121	Negative		
	6210	4403.01	*2.738	3634.56	
28217.97	33975.35	0.553	Negative		
	5093.68	2898.54	*2.738	*378.8	
30263.5	20346.88	0.570	Negative		
	5757.43	5519.81	*2.738	*378.8	
33765.22	30776.74	0.125	Negative		
	3797.22	3140.44	*2.738	*378.8	
36325.89	32214.83	0.123	Negative		
	5037.82	4523.23	*2.738	3748.22	
40043	26898.55	0.122	Negative		
	4972.16	4387.55	*2.738	*378.8	
42131.97	39561.03	0.125	Negative		
	6433.99	4287.35	*2.738	*378.8	
36370.51	42658.86	0.441	Negative		
	4795.17	4663.75	*2.738	*378.8	

Table4.txt

29563.13	23186.97	0.325	Negative		
	5757.43	4777.66	*2.738	*378.8	
25711.5	31756.24	0.125	Negative		
	5143.01	4356.67	*2.738	*378.8	
26381.74	33602.32	0.383	Negative		
	7939.34	4821.04	*2.738	*378.8	
34316.53	31962.37	0.121	Negative		
	6467.48	5626.31	*2.738	*378.8	
28679.59	29648.6	0.618	Negative		
	4919.68	4179.99	*2.738	*378.8	
23910.32	28088.03	0.304	Negative		
	4422.96	4757.98	*2.738	2208.27	
32216.32	27933.15	0.116	Negative		
	5714.32	5470.84	*2.738	*378.8	
36600.83	26635.87	0.125	Negative		
	6712.42	3955.64	*2.738	*378.8	
26184.1	36026.75	0.311	Negative		
	5638.1	4352.81	*2.738	*378.8	
20462.86	23847.75	0.117	Negative		
	5143.01	4892.22	*2.738	*378.8	
24408.87	27866.83	0.117	Negative		
	5146.3	5131.31	*2.738	*378.8	
39763.33	29401.93	0.121	Negative		
	5380.23	5264.02	*2.738	*378.8	
45339.13	31710.49	0.319	Negative		
	5916.84	4546.58	*2.738	6452.12	
31471.53	31322.36	0.122	Negative		
	4007.34	3484.74	19.78	*378.8	
45700.65	28487.27	0.125	Negative		
	5096.97	5650.96	*2.738	*378.8	
32675.28	32837	0.125	Negative		
	5179.2	4738.31	*2.738	*378.8	
24849.96	29850.82	0.123	Negative		
	6448.85	5392.04	*2.754	5251.05	
39997.27	29659.99	0.305	Negative		
	5564.81	4300.33	*2.754	*167.88	
39526.34	50424.65	0.337	Negative		
	6265.65	4419.13	*2.754	*167.88	
26216.75	29021.43	0.301	Negative		
	4796.76	6635.55	*2.754	15057.16	
77551.22	31855.51	0.366	Negative		
	4382.22	3471.78	*2.754	2757.03	
35446.16	34693.31	0.122	Negative		
	3463.7	5280.14	*2.754	7388.82	
62144.23	53421.5	0.489	Negative		
	4774.53	5429.44	*2.754	1266.55	
24452.44	21616.3	0.303	Negative		
	4442.14	4476.9	*2.754	*167.88	

Table4.txt

31110.57	26887.92	0.388	Negative		
	6304.85	6765.17	*2.754	*167.88	
64254.33	39771.45	0.403	Negative		
	5590.6	3964.66	*2.754	*167.88	
36645.71	36268.17	0.590	Negative		
	5080.28	4214.25	*2.754	6165.77	
26216.75	38435.59	0.123	Negative		
	5077.09	5280.14	*2.754	4931.7	
101272.23	63275.8	0.481	Negative		
	6465.23	5817.79	*2.754	*167.88	
42913.32	33352.78	0.191	Negative		
	4790.41	4408.31	*2.754	4907.18	
42758.34	32650.64	0.117	Negative		
	5342.85	3929.18	*2.754	*167.88	
44000.05	36441.41	0.117	Negative		
	4605.56	5340.83	*2.738	1969.49	
31088.24	32100	0.320	Negative		
	5245.05	3872.62	*2.738	*378.8	
22456.72	27008.18	0.123	Negative		
	8702.04	5807.81	*2.738	5248.98	
28483.94	36719.43	0.121	Negative		
	6934.59	4931.87	*2.738	*378.8	
31365.58	30053.41	0.307	Negative		
	5175.14	9224.83	*2.65	*485.573	
32796.21	32949.3	0.116	Negative		
	5078.49	7181.76	*2.65	*485.573	
37503.23	28709.49	0.125	Negative		
	4401.77	3363.06	*2.65	*485.573	
40291.7	31508.18	0.311	Negative		
	3954.29	3863.37	*2.65	*485.573	
30566.38	24545.36	0.125	Negative		
	3835.34	5058.79	*2.65	*485.573	
31956.74	27255.39	0.123	Negative		
	4176.93	5270.69	*2.65	*485.573	
32076.17	29263.15	0.841	Negative		
	4135.66	4129.88	*2.65	*485.573	
37439.69	28781.54	0.125	Negative		
	5387.56	5275.33	*2.65	*485.573	
31832.34	32724.34	0.125	Negative		
	4132.23	3738.41	*2.65	*485.573	
28540.97	26242.54	0.390	Negative		
	5243.36	5331.13	*2.65	*485.573	
34469.94	26406.75	0.219	Negative		
	4290.81	6591.91	*2.65	*485.573	
28109.13	22966.05	0.116	Negative		
	3669.91	3387.18	*2.65	*485.573	
37211.87	23787.08	0.299	Negative		
	6644.31	7641.43	*2.65	6421.24	

Table4.txt

29502.74	30893.22	0.123	Negative		
	3710.3	4791.47	*2.65	*485.573	
30478.14	23147.95	0.345	Negative		
	6290.15	5949.17	*2.738	*378.8	
19527.35	26177.58	0.121	Negative		
	5169.33	6158.81	*2.738	*378.8	
60018.18	33393.06	0.123	Negative		
	5294.48	5211.64	*2.738	*378.8	
48970.74	35480.58	0.125	Negative		
	5274.7	4742.24	26.33	*378.8	
38146.28	30459.7	0.553	Negative		
	7394.52	6074.7	*2.738	3070.73	
35270.52	37440.79	0.121	Negative		
	7103.35	7027.9	*2.738	*378.8	
47539.59	30640.76	0.307	Negative		
	5990.02	6879.08	*2.738	*378.8	
30032.08	32929.48	0.219	Negative		
	6840.25	4430.1	*2.738	*378.8	
34510.23	30278.95	0.122	Negative		
	4357.86	2866.26	*2.738	*378.8	
32767.77	28043.76	0.125	Negative		
	4854.12	4655.92	*2.738	2981.26	
21981.32	30912.89	0.125	Negative		
	5813.85	6277.15	*2.738	1991.11	
35494.18	33346.61	0.125	Negative		
	4348.1	3910.32	235.76	*378.8	
15782.25	22593.03	0.237	Negative		
	5057.53	5438.26	*2.738	*378.8	
32336.24	23890.5	0.117	Negative		
	7618.77	6696.68	*2.738	*378.8	
21798.91	24125.87	0.122	Negative		
	5654.66	5949.17	*2.738	*378.8	
31321.06	34466.92	0.117	Negative		
	3777.86	3140.44	*2.738	11079.31	
14359.11	21728.07	0.117	Negative		
	6016.65	5409.79	*2.738	*378.8	
19809.76	25028.69	0.125	Negative		
	5198.95	5667.42	*2.738	*378.8	
26858.74	25460.95	0.117	Negative		
	3705.99	5606.98	*2.7	*129.5	
28812.42	26501.64	0.317	Negative		
	4538.38	3070.43	*2.7	*129.5	
25244.87	21133.53	0.816	Negative		
	4461.81	5245.92	*2.7	*129.5	
27242.75	23949.81	0.117	Negative		
	6739.8	9733.94	*2.705	*129.752	
70041.55	43382.75	0.125	Negative		
	4167.94	7750.3	*2.705	2696.88	

Table4.txt

44087.6	36685.5	6228.34	0.575	9416.94	Negative *2.705	14842.63
59322.24	39404.91	4996.8	0.357	6359.54	Negative *2.705	4469.41
33955.77	28782.38	5353.63	0.117	5737.42	Negative *2.705	*129.752
47766.65	39203.85	6109.88	0.125	6866.22	Negative *2.705	*129.752
56636.82	34824.2	3809.17	0.338	4556.84	Negative *2.705	*129.752
49861.9	37641.63	4253.9	0.116	4628.1	Negative *2.705	6822.81
52837.27	33761.41	6572.91	0.818	8481.16	Negative *2.705	7206
46837.87	37601.72	6850.38	0.125	7600.14	Negative *2.705	8410.58
67152.48	39767.27	6826.89	0.325	8347.06	Negative *2.705	3522.53
58540.72	39043.13	4682.05	0.123	4585.3	Negative *2.705	3922.76
45698.18	33879.27	7059.04	0.297	7866.1	Negative *2.705	11806.33
50378.6	33761.41	4908.3	0.116	5916.9	Negative *2.705	11560.2
70514.52	44656.28	5617.67	0.355	7060.21	Negative *2.705	1469.63
57441.77	43423.72	2775.3	0.413	4478.9	Negative *2.705	1970.58
64549.6	40210.94	3361.64	0.117	6130.54	Negative *2.705	1198.1
62078.01	43710.68	5514.35	0.125	6186.45	Negative *2.705	3008.86
41134.1	33957.87	5168.28	0.308	8894.89	Negative *2.705	*129.752
56045.41	45316.55	6175.64	0.193	8942.56	Negative *2.705	5043.29
33757.26	34508.82	8363.2	0.125	7009.37	Negative *2.705	1635.01
64906.62	41994.54	4408.18	0.123	5430.64	Negative *2.705	1342.25
37049.32	41222.59	6453.25	0.117	8738.53	Negative *2.705	4043.63
36434.03	34351.28	4939.87	0.117	4366.37	Negative *2.705	1198.1
26997.65	30289.52	4457.75	0.457	5086.1	Negative *2.705	*129.752
56841.15	38722.03	3652.92	0.509	1578.35	Negative *2.705	*129.752

Table4.txt

41538.74	36208.89	0.731	Negative		
	3821.24	2957.1	*2.705		*129.752
38056.71	35693.64	0.125	Negative		
	4063.98	4692.57	*2.705		*129.752
29916.02	30599.71	0.328	Negative		
	5695.39	6186.45	*2.705		3582.29
55785.64	40049.51	0.300	Negative		
	3779.03	4757.35	24.57		*129.752
42888.75	37163.08	0.514	Negative		
	7234.95	4411.97	*2.705		*129.752
35762.76	31805.15	0.121	Negative		
	4585.24	4275.65	*2.705		7784.51
22346.09	25715.36	0.185	Negative		
	3200.07	2503.5	*2.705		*129.752
27757.91	24155.14	0.329	Negative		
	5047.5	4574.62	*2.705		*129.752
26250.35	28859.47	0.238	Negative		
	3349.84	5027.06	*2.705		*129.752
42570.63	35535.33	0.117	Negative		
	4070.08	3474.19	*2.705		1635.01
34482.91	26288.06	0.305	Negative		
	5248.03	5683.24	*2.705		*129.752
37712.93	30793.77	0.443	Negative		
	5727.83	5407.9	*2.705		7935.2
47645.17	28975.15	0.122	Negative		
	7881.2	11153.2	*2.705		29093.23
49188.27	39646.42	0.125	Negative		
	3323.32	4272.17	*2.705		*129.752
35768.46	32234.24	0.314	Negative		
	3391.17	4990.29	*2.705		*129.752
41096.33	33761.41	0.116	Negative		
	5549.83	6559.31	*2.705		3562.36
51651.09	31727.22	0.314	Negative		
	4269.29	3337.99	21.76		*129.752
39594.68	31026.82	0.600	Negative		
	6073.76	3851.68	*2.705		7612.65
65658.23	37721.49	0.550	Negative		
	5379.29	8630.42	*2.705		*129.752
39987.71	34351.28	0.117	Negative		
	6589.57	6616.89	*2.705		2716.28
30242.16	31688.26	0.296	Negative		
	306.28	2040.64	*2.705		*129.752
55568.77	44285.77	0.301	Negative		
	4278.52	3225.65	*2.705		1989.4
44408.42	37961.22	0.814	Negative		
	7729.81	6262.67	*2.705		2235.56
62809.31	39686.69	0.421	Negative		
	3620.01	4185.57	*2.705		*129.752

Table4.txt

40483.1	34390.66	0.116	Negative		
	4776.09	3578.99	*2.705	*129.752	
43941.21	33486.61	0.409	Negative		
	4924.64	3675.91	*2.8	*449.13	
46040.64	37443.35	0.295	Negative		
	9758.24	5438.02	*2.8	*449.13	
43075.52	47232.1	0.490	Negative		
	7606.39	6191.87	*2.8	8144.59	
58071.58	46794.54	0.229	Negative		
	6053.81	7160.62	*2.8	3435.05	
58738.03	55237.72	0.125	Negative		
	5623.86	3983.83	*2.8	*449.13	
37223.66	39833.43	0.125	Negative		
	5946.98	4942.58	*2.8	7156.13	
48744.38	45011.57	0.297	Negative		
	6391.77	5352.17	*2.8	55011.73	
95941.71	56460.38	0.425	Negative		
	4871.82	7299.08	*2.8	*449.13	
43948.29	38352.69	0.123	Negative		
	4957.67	5289.92	*2.8	*449.13	
53328.31	36803.03	0.617	Negative		
	5943.64	6308.94	*2.8	*449.13	
54516.13	47131.12	0.213	Negative		
	4056.47	3429.43	26.18	*449.13	
24651.93	27771.66	0.338	Negative		
	6017.07	3096.29	*2.8	*449.13	
40947.05	40640.66	0.117	Negative		
	5770.3	3814.73	23.7	*449.13	
32932.57	35115.96	0.451	Negative		
	6157.41	7060.4	*2.8	*449.13	
49026.67	44877.05	0.338	Negative		
	5890.27	7097.94	*2.8	9170.96	
52821.25	48073.88	0.246	Negative		
	5245.48	5967.34	*2.8	*449.13	
45019.15	38352.69	0.125	Negative		
	6341.5	6063.32	*2.8	11589.32	
54287.31	44574.41	0.731	Negative		
	6949.88	8137.33	*2.8	*449.13	
59798.27	49725.2	0.542	Negative		
	7240.33	8995.08	*2.8	7067.85	
55401.78	44238.16	0.123	Negative		
	5278.61	5387.26	*2.8	*449.13	
63606.67	48006.52	0.415	Negative		
	4848.72	4083.62	*2.8	2245.65	
39707.97	45415.15	0.307	Negative		
	5471.01	4135.52	*2.8	*449.13	
45748.5	44103.67	0.117	Negative		
	5278.61	3433.04	*2.8	*449.13	

Table4.txt

45412.04	42826.11	0.435	Negative	
	4838.82	3862.41	*2.8	10320
41121.46	35892.41	0.305	Negative	
	4848.72	4535.8	*2.8	*449.13
54547.77	41582.18	0.673	Negative	
	5159.38	7916.54	*2.8	*449.13
62207.46	46828.2	0.465	Negative	
	5783.62	7736.15	*2.8	7740.1
60203.83	46962.82	0.518	Negative	
	6646.88	7719.03	*2.8	*449.13
50194.09	46794.54	0.847	Negative	
	5756.98	6881.81	*2.8	*449.13
39509.28	40472.51	0.472	Negative	
	4384.48	6051.3	*2.8	*449.13
68685.23	55102	0.976	Positive	
	6936.39	7744.71	*2.8	*449.13
49189.73	44439.9	0.399	Negative	
	5963.66	6341.33	*2.8	*449.13
39021.79	42389.07	0.485	Negative	
	4391.05	4615.12	*2.8	*449.13
40255.51	39900.71	0.121	Negative	
	4739.88	4396.66	*2.8	*449.13
38305.05	38150.67	0.305	Negative	
	5106.43	4554.66	*2.8	*449.13
35887.25	39799.79	0.116	Negative	
	4138.38	4797.36	*2.8	*449.13
40923.04	43532.11	0.207	Negative	
	5893.61	4381.66	*2.8	*449.13
46207.41	36162.31	0.616	Negative	
	5643.82	6931.53	*2.8	2435.29
47192.86	41414.07	0.295	Negative	
	4089.23	5231.7	*2.8	*449.13
34378.61	33492.93	0.303	Negative	
	3997.54	5138.82	*2.8	*449.13
35908.96	39059.56	0.125	Negative	
	5520.83	5096.36	*2.8	*449.13
36741.16	31627.88	0.195	Negative	
	3879.77	4157.8	*2.8	*449.13
64483.85	37645.48	0.554	Negative	
	4934.55	4288.14	*2.8	*449.13
42688.4	38420.03	0.333	Negative	
	6980.23	5598.8	*2.8	*449.13
41217.94	39463.36	0.121	Negative	
	4710.21	5371.66	*2.8	11561.91
58532.04	53949.39	0.543	Negative	
	5803.61	8281.22	*2.8	11753.57
58781.05	44305.41	0.117	Negative	
	6217.62	10248.24	*2.8	*449.13

Table4.txt

44095.27	38420.03	0.256	Negative			
	5703.71	4747.87	*2.8	3227.92		
64889.25	45448.79	0.242	Negative			
	5218.98	5752.7	*2.8	6623.51		
60434.49	60381.88	0.125	Negative			
	4079.4	3577.75	*2.8	*449.13		
70527.65	49657.76	0.197	Negative			
	7091.61	8999.58	*2.8	*449.13		
67095.68	45314.25	0.334	Negative			
	4532.41	4804.98	*2.8	*449.13		
56863.81	39833.43	0.117	Negative			
	5850.26	7438.29	*2.8	*449.13		
57952.89	49185.76	0.117	Negative			
	5149.45	7345.4	*2.8	*449.13		
50071.03	53136.81	0.382	Negative			
	6902.68	5406.77	*2.8	*449.13		
46751.68	46693.58	0.719	Negative			
	5351.55	5061.68	*2.8	3158.13		
32717.46	35048.4	0.508	Negative			
	5690.4	3840.39	*2.8	*449.13		
61749.34	58605.51	0.666	Negative			
	5770.3	4310.55	*2.8	*449.13		
47295.23	49860.1	0.123	Negative			
	5278.61	5528.09	*2.8	*449.13		
59509.3	48612.86	0.188	Negative			
	6267.83	6268.51	*2.8	*449.13		
54992.91	54796.73	0.320	Negative			
	3784.99	2904.92	*2.8	*449.13		
34199.62	31424.02	0.122	Negative			
	6633.44	5092.51	*2.8	*449.13		
56797.55	54220.44	0.117	Negative			
	6144.04	6471.3	*2.8	*449.13		
87278.13	52392.63	0.396	Negative			
	3713.14	4404.16	*2.8	2547.09		
69693.94	53746.17	0.321	Negative			
	5444.45	6317.03	*2.8	5161.05		
53467.5	40405.25	0.125	Negative			
	6057.15	6931.53	*2.8	5717.8		
13708.42	35284.81	0.238	Negative			
	4059.75	3778.13	*2.8	*449.13		
57221.45	41884.77	0.116	Negative			
	7687.94	6993.8	*2.8	*449.13		
59282.78	46794.54	0.338	Negative			
	4440.34	4105.85	*2.8	2397.71		
50042.12	39497	0.318	Negative			
	6090.56	6683.94	29.9	*449.13		
59912.56	35959.89	0.242	Negative			
	5583.97	6828.07	*2.8	*449.13		

Table4.txt

50535.91	42691.63	0.125	Negative		
	5544.08	5776.45	*2.8	*449.13	
51471.61	43162.3	0.331	Negative		
	5613.89	6585.57	*2.8	*449.13	
18009.93	34135.84	0.125	Negative		
	4627.86	3060.74	*2.8	*449.13	
17876.89	22191.13	0.121	Negative		
	6003.72	3570.49	*2.8	*449.13	
57674.2	46458.03	0.381	Negative		
	5235.54	5469.32	*2.8	*449.13	
36268.65	36162.31	0.121	Negative		
	6109.11	6347.2	*2.754	3738.98	
35593.42	33304.26	0.301	Negative		
	4619.15	5421.96	*2.754	6016.88	
58751.77	34913.79	0.121	Negative		
	5700.36	4895.75	*2.754	*167.88	
40915.25	31207.97	0.538	Negative		
	5855.71	6169.55	*2.754	*167.88	
39396.48	40202.48	0.125	Negative		
	6154.72	6455.93	*2.754	*167.88	
58001.95	37211.03	0.117	Negative		
	3908.43	4892.08	*2.754	1221.15	
43068.88	31927.63	0.125	Negative		
	6011.51	5362.15	*2.754	*167.88	
71733.35	36367.14	0.125	Negative		
	4149.49	5508.16	*2.754	2757.03	
108126.08	51544.7	0.815	Negative		
	5281.9	5268.97	*2.754	*167.88	
80081.63	44635.16	0.121	Negative		
	6507.86	5787.43	*2.754	*167.88	
71006.81	39341.67	0.116	Negative		
	4209.15	5302.48	*2.754	*167.88	
55802.83	34033.77	0.200	Negative		
	5797.4	7548.69	*2.754	4833.66	
48704.21	44243.26	0.301	Negative		
	5464.97	6522.17	*2.754	10813.61	
61467.71	30801.63	0.117	Negative		
	5397.45	3703.12	*2.754	950.82	
46207.55	28879.88	0.480	Negative		
	4869.89	6331.7	*2.754	4150.66	
68589.9	33037.63	0.122	Negative		
	5868.68	3773.57	*2.754	*167.88	
62622.36	30944.92	0.121	Negative		
	5237.03	4139.15	*2.754	*167.88	
43033.48	34889.28	0.117	Negative		
	6102.6	5168.7	*2.754	*167.88	
68100.3	41759.43	0.125	Negative		
	5761.8	6702.24	*2.754	*167.88	

Table4.txt

39885.59	32144.18	0.192	Negative		
	5105.84	6836.15	*2.754	*167.88	
63548.29	34791.26	0.116	Negative		
	5632.54	6181.1	*2.754	2638.49	
108653.51	54006.02	0.187	Negative		
	6157.98	4567.42	*2.754	*167.88	
50183.46	30849.38	0.121	Negative		
	5022.82	5624.8	*2.754	*167.88	
72126.73	39974.13	0.123	Negative		
	5067.5	4285.97	*2.754	13029.14	
83712.49	31759.41	0.117	Negative		
	4344.41	3555.7	*2.754	*167.88	
62068.6	47861.92	0.122	Negative		
	5160.19	6413.16	*2.754	6888.13	
137372.99	42866.83	0.180	Negative		
	4733.26	6405.39	*2.754	*167.88	
85391.57	37235.92	0.335	Negative		
	4866.7	6370.46	*2.754	10097.5	
73069.53	43022.01	0.125	Negative		
	4505.29	5105.75	*2.754	1794.65	
95320.88	40075.58	0.125	Negative		
	3920.92	3629.32	*2.754	*167.88	
42248.16	32529.9	0.310	Negative		
	3808.58	4253.67	*2.754	*167.88	
104092.24	61679.41	0.187	Negative		
	5833.03	5309.93	*2.754	*167.88	
46590.68	32626.48	0.121	Negative		
	4410.59	6012.21	*2.754	5670.3	
51921.97	39467.95	0.123	Negative		
	5109.04	5302.48	*2.754	*167.88	
110729.87	46504.41	0.175	Negative		
	5716.53	6662.99	*2.754	*167.88	
68491.61	31423.52	0.122	Negative		
	4077.37	4625.51	*2.754	1085.52	
48126.22	36169.26	0.222	Negative		
	7028.68	5745.73	*2.754	5472.78	
46032.46	28903.46	0.117	Negative		
	6396.44	6211.92	*2.754	*167.88	
45782.48	30777.76	0.125	Negative		
	3603.24	3925.63	*2.754	*167.88	
47618.8	32747.3	0.125	Negative		
	6583.37	7744.25	*2.754	*167.88	
45175.03	39341.67	0.306	Negative		
	6226.47	6765.17	*2.754	*167.88	
48302.02	40711.16	0.747	Negative		
	6422.64	6655.15	*2.754	*167.88	
33083.29	23112.15	0.125	Negative		
	5115.43	5187.24	*2.754	*167.88	

Table4.txt

55557.46	48908.57	0.311	Negative		
	3895.94	3608.26	*2.754		*167.88
28916.03	21480.96	0.317	Negative		
	4259.43	2753.81	26.53		*167.88
45004.11	38561.11	0.568	Negative		
	4284.6	6204.21	*2.754		*167.88
37200.78	30944.92	0.121	Negative		
	3507.07	2569.94	513.39		2662.18
14818.49	21684.01	0.720	Negative		
	4297.18	4253.67	*2.754		*167.88
38836.35	36045.71	0.522	Negative		
	5323.59	8988.51	*2.754		*167.88
37950.84	28338.42	0.320	Negative		
	7608.03	5246.65	*2.754		8193.85
53839.23	29375.87	0.324	Negative		
	5535.8	6592.48	*2.754		4442.66
62371.84	34399.83	0.300	Negative		
	5564.81	6050.5	*2.754		*167.88
70660.07	43073.78	0.333	Negative		
	4695.2	3957.56	*2.754		*167.88
52977.06	23271.57	0.334	Negative		
	5474.63	6561.21	*2.754		*167.88
61660.04	33328.52	0.121	Negative		
	5481.06	5958.7	*2.754		*167.88
42296.81	35134.59	0.116	Negative		
	6416.09	7621.85	*2.754		*167.88
50200.18	40787.61	0.308	Negative		
	6711.64	6954.87	*2.754		*167.88
44752.7	41323.88	0.471	Negative		
	6455.4	6420.93	*2.754		*167.88
43625.1	27822.23	0.304	Negative		
	4511.61	4419.13	*2.754		*167.88
47919.36	38184.87	0.313	Negative		
	3696.47	3918.54	*2.754		*167.88
34418.77	27447.85	0.309	Negative		
	4445.29	2333	24.84		*167.88
35170.76	34009.4	0.577	Negative		
	8761.33	8251.08	*2.744		18269.3
111291.24	63076.26	0.528	Negative		
	4657.93	9226.31	*2.744		5587.21
81946.17	47000.98	0.214	Negative		
	4977.42	6591.18	*2.744		*431.385
82281.32	41854.96	0.713	Negative		
	5049.27	6101.59	*2.744		10079.01
76732.02	43769.9	0.338	Negative		
	9355.7	5245.25	*2.744		4232.96
91565.36	54042.65	0.117	Negative		
	8690.81	8896.64	*2.744		23503.31

Table4.txt

70935.25	40000.31	0.308	Negative		
	4094.93	4305.81	*2.744	12160.23	
60502.11	35508.57	0.314	Negative		
	6489.38	7607.32	*2.744	16413.81	
100570.05	41740.79	0.576	Negative		
	7603.64	8720.7	*2.744	5713.62	
70657.36	45279.82	0.566	Negative		
	4303.41	5902.44	*2.744	*431.385	
67542.72	40414.8	0.323	Negative		
	4499.71	5642.61	*2.744	6890.85	
78115.99	46686.62	0.123	Negative		
	4737.43	7417.04	*2.744	9323.67	
90516.59	41626.71	0.305	Negative		
	7722.27	11524.48	*2.744	13383.29	
102090.77	41893.03	0.178	Negative		
	9984.46	11030.63	*2.744	13277.73	
76969.85	39812.25	0.121	Negative		
	7460.52	4415.16	*2.744	17351.05	
73563.81	42656.43	0.187	Negative		
	6299.62	8238.52	*2.744	27694.61	
70733.02	42809.54	0.125	Negative		
	8770.96	10261.88	*2.744	17905.99	
70556.64	52853.18	0.353	Negative		
	4189.2	6903.41	*2.744	*431.385	
62274.2	39286.84	0.349	Negative		
	5315.38	7910.35	*2.744	*431.385	
67638.27	43577.36	0.121	Negative		
	6167.74	7721.48	*2.744	17052.59	
115290.47	43769.9	0.444	Negative		
	5947.17	10389.9	*2.744	10372.92	
96439.79	51956.96	0.123	Negative		
	6239.6	7057.36	*2.744	2245.54	
77788.35	53467.27	0.125	Negative		
	5464.01	6154.54	*2.744	*431.385	
89330.54	57541.33	0.116	Negative		
	4925.8	4670.97	*2.744	*431.385	
73233.67	43924.1	0.599	Negative		
	4328.55	3555.69	*2.744	3119	
46182.14	52322.96	0.624	Negative		
	4508.16	6746.69	*2.744	2201.27	
81251.12	46804.43	0.123	Negative		
	5781.31	8546.11	*2.744	*431.385	
83142.57	41436.74	0.123	Negative		
	5890.8	9200.12	*2.744	6701.9	
95444.24	52894.04	0.735	Negative		
	4988.9	2052.63	67.9	*431.385	
76592.56	41398.78	0.322	Negative		
	4612.62	5274.11	*2.744	*431.385	

Table4.txt

61895.7	40452.54	0.599	Negative			
	5295.04	6026.19	*2.744	2156.92		
96667.19	45786.37	0.236	Negative			
	3724.68	6086.49	*2.744	*431.385		
88872.15	54744.26	0.125	Negative			
	5155.98	5087.34	*2.744	*431.385		
68118.44	50904.5	0.125	Negative			
	5312.47	4483.89	20.6	6533.87		
114827.7	47829.19	0.155	Negative			
	6407.92	6483.04	*2.744	16052.32		
110506.58	54331.16	0.187	Negative			
	4387.34	6295.2	*2.744	*431.385		
86839.83	46647.37	0.564	Negative			
	7206.76	7332.56	*2.744	*431.385		
112389.35	49179.57	0.183	Negative			
	5578.19	5742.4	*2.744	*431.385		
97066.95	43461.95	0.175	Negative			
	6850.8	7400.92	*2.744	7520.31		
67221.43	35362.12	0.122	Negative			
	5816.77	7364.7	*2.744	4784.67		
70569.22	43461.95	0.121	Negative			
	6149.8	6754.5	*2.744	13510		
65377.25	42350.63	0.117	Negative			
	6383.82	4984.05	24.89	11066.19		
65549.75	43039.5	0.125	Negative			
	6450.13	8021.96	*2.744	13488.88		
63647.83	39887.45	0.125	Negative			
	3781.85	4494.23	*2.744	4742.32		
56362.1	33614.43	0.116	Negative			
	8029.92	9756.4	*2.744	14334.52		
105984.32	43500.41	0.154	Negative			
	3444.03	3989.08	108.72	12476.24		
51536.87	42694.69	0.344	Negative			
	5057.91	7522.09	*2.744	7184.66		
67998.01	46725.88	0.121	Negative			
	7059.03	7252.42	*2.744	5481.81		
101478.61	47671.09	0.182	Negative			
	6054.28	11007.13	*2.744	11823.37		
73762.78	35875.24	0.323	Negative			
	5286.33	8797.78	*2.744	11802.32		
78058.88	44310.26	0.117	Negative			
	5810.86	8905.25	*2.744	2377.94		
88618.86	38427.33	0.116	Negative			
	6668.09	6490.75	*2.744	*431.385		
59256.53	39586.87	0.303	Negative			
	3970.79	3876.17	24.89	*431.385		
50652.36	37646.45	0.810	Negative			
	5115.56	5328.36	*2.744	*431.385		

Table4.txt

51342.87	40830.37	0.116	Negative			
	5819.73	8571.58	*2.744	8988.11		
85140.1	48145.87	0.122	Negative			
	5089.6	4825.02	*2.744	2815.49		
61659.14	42312.45	0.332	Negative			
	4070.05	3584.81	44.16	2156.92		
48536.63	42312.45	0.116	Negative			
	4902.89	4580.63	*2.744	6932.84		
51079.53	36832.32	0.554	Negative			
	5516.65	8180.01	*2.744	*431.385		
78030.35	45396.57	0.122	Negative			
	3872	5328.36	*2.744	3549.55		
54521.16	34960.04	0.337	Negative			
	4578.69	5492.11	*2.744	*431.385		
64522.74	50139.94	0.117	Negative			
	10511.61	13075.14	*2.744	43396.61		
167205.9	50340.77	0.297	Negative			
	4505.35	7284.44	*2.744	*431.385		
64387.23	46451.27	0.237	Negative			
	4164.21	6321.92	*2.744	14249.88		
64005.09	38688.44	0.116	Negative			
	5504.94	7093.05	*2.744	7436.41		
70720.4	41626.71	0.125	Negative			
	5121.33	3843.13	*2.744	*431.385		
50930.91	42236.11	0.327	Negative			
	9997.65	15839.35	*2.744	7981.67		
97680.54	48344.12	0.226	Negative			
	3811.85	4674.46	*2.744	*431.385		
59823.81	36795.41	0.332	Negative			
	4418.19	2675.86	*2.744	*431.385		
50366.72	37017	0.125	Negative			
	5179.11	9685.04	*2.744	*431.385		
123762.98	60133.48	0.428	Negative			
	5790.17	5205.64	*2.744	*431.385		
82802.82	44426.29	0.245	Negative			
	6426	9649.44	*2.744	10456.92		
98786.98	50743.23	0.178	Negative			
	5513.72	5274.11	*2.744	7310.55		
69781.97	43692.86	0.117	Negative			
	5251.51	6738.89	*2.744	*431.385		
58634.35	44078.45	0.319	Negative			
	5049.27	5928.62	*2.744	5291.96		
86154.57	44774.9	0.125	Negative			
	3379.85	4435.75	*2.744	2553.6		
65480.68	43461.95	0.123	Negative			
	4062.58	6816.34	*2.724	3933.01		
69336.57	47933.01	0.240	Negative			
	4503.27	5369.52	76.44	*131.8		

Table4.txt

64521.68	34244.8	0.117	Negative		
	3965.06	5158.44	*2.724		9870.38
76176.84	34354.35	0.198	Negative		
	3913.1	4254.75	*2.724		*131.8
57652.5	38923.54	0.125	Negative		
	5367.87	6296.72	*2.724		1183.86
72167.99	30511.48	0.121	Negative		
	5484.38	5402.19	*2.724		8362.52
62316.27	39742.83	0.405	Negative		
	6534.34	5777.69	*2.724		*131.8
57290	34390.87	0.122	Negative		
	3382.63	5570.5	*2.724		1390.36
65291.95	42442.97	0.122	Negative		
	3547.21	3815.99	*2.724		*131.8
66972	48396.11	0.117	Negative		
	6473.19	7188.16	*2.724		14608.67
58986.98	40078.77	0.125	Negative		
	3569.82	2778.69	*2.724		*131.8
80397.48	39221.16	0.236	Negative		
	6225.94	6348.08	*2.724		*131.8
135912.88	48898.8	0.436	Negative		
	4950.45	7685.52	*2.724		2382.1
149120.26	53313.05	0.670	Negative		
	4999.98	4089.56	*2.724		*131.8
71120.75	44867.9	0.121	Negative		
	6633.01	7322.62	*2.724		*131.8
71414.62	44107.56	0.313	Negative		
	4323.36	4989.58	*2.724		3334.94
70873.36	45898.09	0.338	Negative		
	5825.36	6356.66	*2.724		5421.3
152659.24	46548.96	0.345	Negative		
	5357.9	7685.52	*2.724		*131.8
70038.59	43652.47	0.354	Negative		
	5692.58	4700.13	37.96		16954.07
71757.16	35388.8	0.240	Negative		
	3511.15	5289.24	39.36		14100.85
20842.68	26470.8	0.248	Negative		
	6010.29	7727.83	*2.543		9849.78
67272.37	36908.4	0.221	Negative		
	6272.91	7741.21	*2.543		6397.68
56201.46	42734.01	0.116	Negative		
	6336.04	6293.4	*2.543		5078.83
68578.91	33623.77	0.234	Negative		
	6318.5	4077.37	*2.543		*167
60566.62	34229.28	0.123	Negative		
	5870.51	5850.55	31.67		13050.5
58010.8	48644.6	0.331	Negative		
	6206.31	5916.91	*2.543		1505.42

Table4.txt

63270.84	34200.4	0.125	Negative		
	5237	7076.46	*2.543	*167	
45300.03	37437.68	0.125	Negative		
	5968.33	6016.77	*2.543	7707	
75769.73	43068.79	0.322	Negative		
	5365.46	7745.67	*2.543	*167	
118027.72	65078.76	0.176	Negative		
	5629.85	6632.77	*2.543	13857.17	
62469.38	38619.93	0.125	Negative		
	4628.28	4510.59	*2.543	6025.04	
68481.02	40409.21	0.125	Negative		
	4766.29	4291.15	*2.543	1197.08	
48761.71	32476.51	0.306	Negative		
	6944.84	8109.61	*2.543	10101.22	
71575.63	33106.52	0.117	Negative		
	6020.78	8584.66	*2.543	18774.75	
61487.66	33451.17	0.125	Negative		
	5671.66	6963.73	*2.543	1638.58	
59899.7	36293.04	0.121	Negative		
	4966.75	5871.27	*2.543	1438.01	
52631.91	32390.79	0.596	Negative		
	4759.38	4224.89	*2.543	835	
46019.15	38234.77	0.121	Negative		
	4628.28	5586.81	*2.543	7343.43	
49688.85	33451.17	0.322	Negative		
	4328.81	5431.48	*2.543	131014.81	
64253.94	39631.49	0.116	Negative		
	4918.32	6924.83	*2.543	3184.77	
52507.36	27910.06	0.121	Negative		
	6546.76	9191.2	*2.543	4443.23	
53758.83	30036.58	0.125	Negative		
	4291.02	5083.34	*2.543	3879.24	
43947.28	32248.01	0.125	Negative		
	5001.36	5268.98	*2.543	*167	
48720.75	28690.32	0.117	Negative		
	3531.59	4775.53	*2.543	1769.79	
43015.07	27743.34	0.125	Negative		
	6045.26	7185.33	*2.543	7629.27	
79699.04	41915.13	0.117	Negative		
	5431.49	7115.6	*2.543	7965.4	
60713.7	32305.11	0.121	Negative		
	4807.73	6761.21	*2.543	18177.03	
92867.36	55820.48	0.125	Negative		
	3889.98	5586.81	*2.543	*167	
53440.58	29193.87	0.125	Negative		
	3388.65	4310.67	*2.543	*167	
41729.87	35592.55	0.122	Negative		
	3934.45	3692.94	*2.543	*167	

Table4.txt

64130.02	39571.82	0.805	Negative		
	4061.15	5123.59	*2.543	2918.14	
51305.66	28885.96	0.125	Negative		
	5129.5	7215.89	*2.543	*167	
79848.73	34982.04	0.116	Negative		
	4174.29	3122.35	*2.543	*167	
56461.37	31507.57	0.121	Negative		
	5351.56	6125.39	*2.543	17578.18	
85787.8	39512.16	0.125	Negative		
	4098.85	6829.97	*2.543	14392.82	
119560.1	45802.46	0.710	Negative		
	3954.98	4345.84	*2.543	*167	
59395.06	36351.55	0.123	Negative		
	7745.76	6238.68	*2.543	6609.33	
51644.62	27715.57	0.587	Negative		
	7227.62	6310.26	*2.543	9344.8	
51531.36	31820.43	0.125	Negative		
	7163.93	9807.66	*2.543	12584.14	
75532.91	35127.2	0.117	Negative		
	4346	3803.87	*2.543	6820.09	
86655.02	35301.55	0.125	Negative		
	6715.67	8644.67	*2.543	9597.65	
60787.4	38323.58	0.253	Negative		
	4373.5	5862.98	*2.543	*167	
43895.78	30883.63	0.117	Negative		
	6385.17	4926.99	*2.543	1126.58	
65394.31	36322.29	0.309	Negative		
	3545.22	3317.55	*2.543	3155.33	
65555.98	40949.77	0.123	Negative		
	4266.97	4295.05	*2.543	*167	
54272.51	32076.85	0.121	Negative		
	5001.36	6050.14	*2.543	*167	
54448.06	36585.79	0.305	Negative		
	5292.53	8209.37	*2.543	7862.16	
90393.73	35971.62	0.122	Negative		
	7033.12	5204.26	*2.543	13417.67	
101520.37	37998.2	0.184	Negative		
	4421.65	5995.93	*2.543	*167	
62917.96	37880.04	0.515	Negative		
	6108.25	7303.43	*2.543	2090.51	
70207.78	54249.75	0.125	Negative		
	3266.32	4416.32	*2.543	8402.43	
56499.99	35011.07	0.122	Negative		
	3879.72	3919.1	*2.543	*167	
47461.11	27632.29	0.123	Negative		
	5501.05	6104.47	*2.543	3360.49	
60556.13	38708.94	0.125	Negative		
	6824.9	9314.25	*2.543	4831.59	

Table4.txt

79549.74	42248.26	0.121	Negative		
	4776.64	3605.28	*2.543	3678.9	
59497.63	32619.49	0.125	Negative		
	5327.25	4151.03	*2.543	5595.27	
59549	32305.11	0.116	Negative		
	5396.73	5784.36	*2.543	*167	
51314.32	24498.68	0.117	Negative		
	3535	3506.51	*2.543	*167	
49214.66	31252.03	0.125	Negative		
	4044.01	6041.79	*2.543	4331.35	
56819.82	33250.04	0.125	Negative		
	3900.24	6242.88	*2.543	8094.23	
63670.75	39661.34	0.191	Negative		
	6592.48	9725.56	*2.543	6238.34	
80663.76	34808.03	0.117	Negative		
	3524.78	4158.8	*2.543	*167	
56693.57	28104.78	0.234	Negative		
	7387.04	8984.29	*2.543	10452.16	
61253.16	41220.71	0.325	Negative		
	5035.97	4632.84	*2.543	13710.8	
63237.65	34779.04	0.803	Negative		
	4359.75	5941.84	*2.543	*167	
55780.87	33594.99	0.116	Negative		
	5542.8	7687.74	*2.543	9446.03	
74663.86	36410.08	0.125	Negative		
	6487.01	5123.59	*2.543	3447.79	
77946.77	44015.89	0.116	Negative		
	4876.84	8077.95	*2.543	13270.9	
89227.33	43434.77	0.317	Negative		
	7653.29	5767.84	*2.543	9471.32	
68947.6	43282.18	0.116	Negative		
	5139.9	5071.28	*2.543	*167	
59951.49	44169.16	0.324	Negative		
	4050.87	3317.55	*2.543	1370.01	
59816.96	40469.19	0.122	Negative		
	3449.88	3141.06	*2.543	*167	
59579.84	40979.86	0.125	Negative		
	3948.14	4318.48	*2.543	*167	
67033.91	40559.19	0.121	Negative		
	4297.89	4252.15	*2.543	*167	
63771.21	37055.26	0.123	Negative		
	7379.45	9245.94	*2.763	3884.72	
117838.24	75866.17	0.982	Positive		
	7522.16	4934.24	*2.763	*458.411	
43625.67	46574.46	0.560	Negative		
	12690.17	5359.08	43.19	16845.56	
102719.65	43100.85	0.994	Positive		
	12663.94	8360.96	*2.763	36017.95	

Table4.txt

158735.57	66317.62	0.982	Positive		
11402.59	5711.64	*2.763	3546.55		
102655.7	54948.15	0.423	Negative		
10783.2	7791.78	*2.763	3425.81		
52298.58	43848.53	0.993	Positive		
7124.39	6546.82	*2.763	3208.54		
45810.79	39642.51	1.000	Positive		
18292.01	9027.41	*2.763	14193.62		
136829.88	61947.69	0.977	Positive		
14110.61	9107.48	*2.763	9261.82		
96511.57	49554.25	1.000	Positive		
12585.3	8907.77	*2.763	44329.75		
130176.2	65057.27	0.463	Negative		
10772.91	8360.96	*2.763	3112		
93688.49	45346.3	0.605	Negative		
9334.6	3794.64	60.23	5335.58		
51202.37	57358.58	0.822	Negative		
7840.93	12007.32	*2.656	5454.63		
46989.06	39837.77	0.231	Negative		
13284.85	7506.2	*2.656	9857.64		
98102.24	76787.32	0.679	Negative		
10009.96	7762.57	*2.656	27977.9		
139580.71	36534.68	0.832	Negative		
8688.23	5769.6	*2.656	6547.37		
58818.44	55151.19	0.872	Positive		
11174.15	7820.61	*2.656	*142.74		
39209.21	39737.91	0.904	Positive		
11210.67	10898.97	*2.656	10993.75		
132733.41	51821.17	1.000	Positive		
8673.84	6298.56	22.45	5601.8		
72102.49	46159.78	0.989	Positive		
30981.02	8421.51	*2.656	16435.8		
148183.33	51970.19	1.000	Positive		
7354.21	5339.37	*2.656	5528.27		
82533.18	77145.36	0.995	Positive		
6269.76	6219.7	*2.656	4332.28		
62979.85	56245.84	0.457	Negative		
8285.67	10240.32	*2.656	*142.74		
64724.98	51970.19	0.125	Negative		
12060.37	11894.51	*2.656	16235.01		
104486.8	56693.87	0.804	Negative		
3926.45	3882.45	*2.782	*128.728		
72805.99	36214.77	0.980	Positive		
5136.61	4981.82	*2.782	5844.69		
97443.46	43503.33	0.994	Positive		
9834.63	6470.88	*2.782	11277.98		
132065.47	50216.81	0.993	Positive		
7872.55	6578.36	*2.782	21223.71		

Table4.txt

110695.5	51107.43	6012.04	0.999	5264.7	Positive	*2.782	2151.02
88586.2	47763.06	3825.99	0.911	3976.91	Positive	*2.782	6025.14
85619.07	36976.71	7633.5	1.000	8100.55	Positive	*2.759	*1116.987
59035.07	57129.3	16683.06	0.125	7635.8	Negative	*2.759	90950.02
267653.48	76660.04	11654.23	0.999	8848.09	Positive	*2.759	70423.98
108585.89	60154.26	11792.72	0.794	6736.45	Negative	*2.759	7519.85
184235.47	85539.09	31250.7	0.989	9805.27	Positive	*2.759	82632.91
292919.34	84030.45	6935.42	0.997	8490.8	Positive	*2.759	17227.03
137336.29	64755.66	14073.44	0.968	9234.17	Positive	*2.759	2059.14
97883.95	93722.51	19988.65	0.884	10154.14	Positive	*2.759	13594.5
120783.31	64321.89	9024.39	1.000	9315.88	Positive	17.18	26288.07
280016.32	65945.04	24348.92	0.999	9084.02	Positive	*2.759	11977.87
150908.39	62141.51	8708.44	0.994	5529.72	Positive	*2.759	27348.28
60844.62	68286.81	8712.75	0.117	8848.09	Negative	*2.759	5687.75
98262.17	71504.29	7059.94	0.988	9770.47	Positive	*2.759	*1116.987
94557.82	96693.57	21075.63	0.910	9253.01	Positive	17.18	17165.72
231616.4	79474.93	8064.36	0.999	11379.33	Positive	*2.759	3320.88
98191.45	73474.21	7754.58	0.978	6193.12	Positive	38.31	5746.53
79976.83	68014.71	8861.71	0.969	5667.83	Positive	*2.759	7817.09
64057.52	62859.1	16936.58	0.402	15482.2	Negative	*2.759	22686.89
91452.24	85986.95	9036.43	0.857	8573.99	Negative	*2.818	14704.14
122175.47	84979.81	9921.06	0.693	8705.52	Negative	633.22	24190.4
63136.44	59127.52	8132.48	0.987	10111.69	Positive	*2.818	13417.1
81475.11	71313.82	9772.39	0.502	8101.8	Negative	*2.818	8233.27

Table4.txt

119004.56	66380.2	0.998	Positive		
	22318.29	9473.1	*2.818		16810.12
127480.46	72379.14	1.000	Positive		
	8544.5	9137.16	22.61		7445.49
109999.93	69821.18	0.824	Negative		
	11143.21	7974.36	*2.818		8409.33
166612.52	73090.75	0.929	Positive		
	9881.52	10095.08	*2.818		21227.44
273711.63	81470.22	0.947	Positive		
	19929	9009.28	*2.818		42348.01
305270.66	80083.85	0.993	Positive		
	8503.08	9766.8	*2.818		6524.2
161026.06	78700.88	0.406	Negative		
	5763.93	8154.52	*2.818		58200.47
569512.69	55577.12	0.987	Positive		
	13116.48	9303.29	*2.818		76872.74
488282.85	65515.16	0.986	Positive		
	5795.75	3789.44	*2.818		1000.76
55464.18	50736.62	0.122	Negative		
	19001.13	11175.61	56.99		5372.83
82928.93	84030.45	0.997	Positive		
	9268.75	14252.71	*2.818		5451.65
63146.39	81026.2	0.284	Negative		
	10018.07	7466.07	*2.818		14634.33
149244.95	86771.7	0.957	Positive		
	6574.86	5670.41	*2.818		7511.66
86263.27	68667.89	0.877	Positive		
	16365.17	7127.99	*2.818		56994.31
266498.88	101574.58	0.999	Positive		
	12973.54	20178.17	*2.818		20617.11
110682.2	62919.29	0.701	Negative		
	13671.92	5331.79	*2.665		11434.47
160501.95	53949.97	0.905	Positive		
	8737.89	8795.65	*2.665		4280.53
65145.56	62365.29	0.690	Negative		
	7257.3	6513.56	*2.748		5939.83
95017.85	53663.85	0.877	Positive		
	18135.27	7392.35	*2.748		40093.01
180301	61068.51	1.000	Positive		
	8124.65	7749.69	*2.748		6791.03
90538.09	52304.5	0.224	Negative		
	11467.58	5874.98	*2.815		10400.97
104452.38	50767.63	1.000	Positive		
	5543.03	5897.2	*2.815		3799.24
214347.67	52619.83	1.000	Positive		
	2503.74	3298	*2.815		1085.39
120566.94	42593.58	1.000	Positive		
	3454.61	4864.67	*2.815		*119.88

Table4.txt

46618.62	49379.09	1.000	Positive		
	4696.29	5148.07	*2.815	2749.97	
86252.24	59523.16	0.998	Positive		
	3076.55	2704.3	*2.815	*119.88	
62201.83	53380.3	1.000	Positive		
	6401.27	4892.83	*2.815	*119.88	
93960.97	52961.71	1.000	Positive		
	3709.23	4146.58	*2.815	*119.88	
80397.85	49940.99	0.999	Positive		
	4841.3	6400.14	*2.815	*119.88	
141399.93	54181.64	1.000	Positive		
	5686.02	7594.04	*2.815	*119.88	
159645.24	68454.19	1.000	Positive		
	4903.94	3592.66	*2.748	10047.93	
100579.12	37932.2	0.836	Negative		
	3027.71	3651.43	*2.815	*119.88	
106210.73	59640.79	0.998	Positive		
	5118.72	4419.63	*2.815	3893.12	
258509.16	45520.29	1.000	Positive		
	3712.5	5676.06	*2.815	*119.88	
128320.69	55177.89	1.000	Positive		
	3725.57	3924.19	*2.815	3424.66	
122568.86	57805.48	1.000	Positive		
	5059.2	6552.76	*2.815	*119.88	
108708.09	64561.78	0.983	Positive		
	3961	6426.77	*2.815	6312.94	
132961.12	61413.17	1.000	Positive		
	2803.1	3101.24	*2.815	*119.88	
111405.73	54909.22	1.000	Positive		
	2685.96	4578.4	*2.815	*119.88	
74864.18	43030.4	0.992	Positive		
	5752.61	6113.34	*2.815	5144.78	
93127.27	53990.58	1.000	Positive		
	4930.68	3572.56	*2.748	*445.15	
103763.1	49303.1	1.000	Positive		
	1751.11	2061.7	*2.815	*119.88	
120245.16	42266.46	1.000	Positive		
	4229.64	4316.79	*2.815	*119.88	
106778.98	58975.11	0.971	Positive		
	4897.38	2685.45	*2.815	11844.9	
125850.52	44345.44	0.994	Positive		
	4482.44	4031.7	*2.815	951.77	
206008.83	50918.26	0.999	Positive		
	3464.39	3285.04	*2.815	*119.88	
66505.98	49192.1	0.999	Positive		
	4538.33	6210.99	*2.815	*119.88	
185943.89	67107.77	1.000	Positive		
	3112.38	3951.01	*2.815	*119.88	

Table4.txt

104089.92	47071.02	1.000	Positive		
	3634.11	2919.2	*2.815	*119.88	
73829.5	48036.13	1.000	Positive		
	3366.55	2941.46	*2.815	3987.09	
129377.67	45079.06	1.000	Positive		
	3732.1	3136.57	*2.815	*119.88	
117266.32	38945.68	0.871	Positive		
	4669.95	4183.9	*2.815	*119.88	
101007.89	41649.69	1.000	Positive		
	3281.8	3392.26	*2.815	*119.88	
173510.42	46183.65	1.000	Positive		
	1384.4	2610.25	*2.815	*119.88	
114792.87	46552.99	1.000	Positive		
	3197.07	2361.74	*2.815	*119.88	
47419.27	35770.3	0.999	Positive		
	4360.89	7425.41	*2.815	5596.62	
183636.9	50918.26	1.000	Positive		
	4272.28	5756.86	*2.815	*119.88	
116448.8	70842.56	0.941	Positive		
	5390.31	8538.58	*2.815	*119.88	
167799.61	50128.6	0.920	Positive		
	7951.03	12966.19	*2.815	*119.88	
123443.76	54066.98	0.990	Positive		
	2396.36	1901.41	*2.815	*119.88	
104070.89	39844.02	0.999	Positive		
	3079.81	5312.9	*2.815	6864.33	
110579.24	42921.13	1.000	Positive		
	3967.55	4045.18	*2.815	12877.1	
88464.04	47219.24	1.000	Positive		

Table5.txt

Table 5. Concordance between mutations identified in the plasma with those identified in primary tumors.

Patient ID #	Sample ID # plasma*	Mutation identified in plasma	Tumor type	AJCC Stage	Plasma volume (mL)	Plasma DNA concentration (ng/mL)	Mutant fragments/mL	Mutation identified in tumor tissue	Mutant omega score	Mutant allele frequency (%)
CRC 468	CRC 468 PLS 1	TP53 p.E286G, c.857A>G	Colorectum	III	5	12.99	15.6	Present	11.42	0.39
CRC 470	CRC 470 PLS 1	APC p.E1306*, c.3916G>T	Colorectum	II	7.5	2.79	3.1	Present	5.93	0.36
CRC 473	CRC 473 PLS 1	KRAS p.G13D, c.38G>A	Colorectum	II	7.5	6.30	71.4	Present	3.40	3.68
CRC 476	CRC 476 PLS 1	TP53 p.R249G, c.745A>G	Colorectum	II	5	8.45	188.8	Present	20.05	7.25
CRC 480	CRC 480 PLS 1	CTNNB1 p.T41A, c.121A>G	Colorectum	III	5	13.30	31.0	Present	93.61	0.76
CRC 481	CRC 481 PLS 1	PIK3CA p.H1047R, c.3140A>G	Colorectum	II	5	13.85	8.0	Present	3.18	0.19
CRC 489	CRC 489 PLS 1	KRAS p.Q61K, c.181C>A	Colorectum	II	7.5	5.77	3.0	Present	4.06	0.17
CRC 504	CRC 504 PLS 1	APC p.E1309fs, c.3927delAAAGA	Colorectum	III	7.5	14.14	72.6	Present	17.49	1.67
CRC 506	CRC 506 PLS 1	APC p.I1311fs, c.3931insA	Colorectum	III	7.5	6.87	4.0	Present	4.40	0.19
CRC 516	CRC 516 PLS 1	CTNNB1 p.T41A, c.121A>G	Colorectum	II	7.5	13.15	1.4	Present	4.69	0.03
CRC 518	CRC 518 PLS 1	TP53 p.S215fs, c.644insGTG	Colorectum	III	7.5	10.91	284.9	Present	87.57	8.48
CRC 520	CRC 520 PLS 1	KRAS p.G12V, c.35G>T	Colorectum	III	7.5	8.21	12.1	Present	4.98	0.48

Table5.txt

CRC 521	CRC 521 PLS 1	Colorectum	III	7.5	5.23	
	KRAS p.A146V, c.437C>T	3.64		0.45	7.3	
	Present					
CRC 524	CRC 524 PLS 1	Colorectum	II	7.5	7.83	
	KRAS p.G12V, c.35G>T	4.09		0.36	8.7	
	Present					
CRC 527	CRC 527 PLS 1	Colorectum	III	7.5	4.72	
	KRAS p.A146T, c.436G>A	3.10		2.30		
33.4	Present					
INDI 009	INDI 009 PLS 1	Lung	II	7.5	2.59	
	TP53 p.C176F, c.527G>T	5.51		1.06	8.5	
	Present					
INDI 014	INDI 014 PLS 1	Lung	II	7.5	1.61	
	TP53 p.E298*, c.892G>T	5.89		1.36	6.7	
	Present					
INDI 023	INDI 023 PLS 1	Lung	II	7.5	7.78	
	TP53 p.G266V, c.797G>T	7.61		0.90		
21.7	Present					
INDI 035	INDI 035 PLS 1	Colorectum	II	7.5	3.07	
	KRAS p.G12D, c.35G>A	3.13		0.57	5.4	
	Present					
INDI 070	INDI 070 PLS 1	Breast	III	7.5	16.58	
	PTEN p.C136R, c.406T>C	15.54		0.75		
38.2	Present					
INDI 074	INDI 074 PLS 1	Pancreas	II	7.5	7.45	
	KRAS p.G12V, c.35G>T	3.43		0.25	5.7	
	Present					
INDI 075	INDI 075 PLS 1	Ovary	III	7.5	2.60	
	TP53 p.Y220C, c.659A>G	7.16		8.47		
67.8	Present					
INDI 077	INDI 077 PLS 1	Liver	II	7.5	62.35	
	TP53 p.K132R, c.395A>G	98.06		4.49		
862.8	Not detected					
INDI 081	INDI 081 PLS 1	Colorectum	II	7.5	25.31	
	TP53 p.W53*, c.158G>A	30.50		0.23		
18.1	Present					
INDI 097	INDI 097 PLS 1	Colorectum	III	7.5	16.40	
	BRAF p.V600E, c.1799T>A	4.82		0.28		
14.2	Present					
INDI 108	INDI 108 PLS 1	Colorectum	II	7.5	2.95	
	TP53 p.R267W, c.799C>T	4.91		16.76		
152.3	Present					
INDI 109	INDI 109 PLS 1	Colorectum	III	7.5	21.96	
	TP53 p.R248Q, c.743G>A	3.44		4.87		
329.4	Present					
INDI 116	INDI 116 PLS 1	Stomach	I	7.5	39.39	
	TP53 p.S260Y, c.779C>A	144.55		40.92		
4,964.8	Present					

Table5.txt

INDI 119	INDI 119 PLS 1	Esophagus	I	7.5	53.59	
	TP53 p.H179R, c.536A>G	39.32		2.17		
359.0	Present					
INDI 124	INDI 124 PLS 1	Colorectum	II	7.5	20.63	
	KRAS p.G12D, c.35G>A	4.80		0.54		
34.5	Not detected					
INDI 125	INDI 125 PLS 1	Esophagus	II	7.5	23.56	
	TP53 p.L194H, c.581T>A	5.32		0.72		
52.6	Present					
INDI 126	INDI 126 PLS 1	Stomach	III	7.5	25.59	
	TP53 p.K132R, c.395A>G	7.89		0.63		
49.9	Present					
INDI 128	INDI 128 PLS 1	Colorectum	III	7.5	6.68	
	CTNNB1 p.S45F, c.134C>T	4.62		0.43	8.9	
	Present					
INDI 144	INDI 144 PLS 1	Colorectum	II	7.5	54.08	
	KRAS p.G12D, c.35G>A	4.12		0.24		
40.6	Present					
INDI 150	INDI 150 PLS 1	Colorectum	II	7.5	78.23	
	TP53 g.7578176C>T (Splice Site)	189.18		2.43		
585.4	Present					
INDI 151	INDI 151 PLS 1	Stomach	II	7.5	37.78	
	TP53 p.Y220C, c.659A>G	3.51		0.46		
53.6	Present					
INDI 156	INDI 156 PLS 1	Colorectum	III	7.5	35.66	
	TP53 p.P190fs, c.570delCCT	323.25		6.15		
675.5	Present					
INDI 171	INDI 171 PLS 1	Stomach	III	7.5	91.76	
	TP53 p.G199fs, c.597insA	3.89		0.12		
33.6	Present					
INDI 172	INDI 172 PLS 1	Stomach	II	7.5	70.98	
	TP53 p.R248Q, c.743G>A	4.20		3.23		
706.9	Present					
INDI 182	INDI 182 PLS 1	Liver	III	7.5	50.25	
	TP53 p.A159P, c.475G>C	4.64		0.11		
17.0	Present					
INDI 184	INDI 184 PLS 1	Esophagus	II	7.5	110.40	
	TP53 p.H193R, c.578A>G	3.10		0.04		
14.7	Present					
INDI 185	INDI 185 PLS 1	Stomach	II	7.5	44.97	
	TP53 p.S183fs, c.549insA	41.06		1.40		
194.4	Present					
INDI 198	INDI 198 PLS 1	Stomach	III	7.5	10.36	
	TP53 p.V274F, c.820G>T	12.36		1.67		
53.3	Present					
INDI 210	INDI 210 PLS 1	Stomach	III	7.5	6.85	
	TP53 p.C135*, c.405C>A	4.85		1.05		
22.2	Present					

Table5.txt

INDI 212	INDI 212 PLS 1	Colorectum	III	7.5	8.94	
	BRAF p.V600E, c.1799T>A	33.45		2.63		
72.4	Present					
INDI 219	INDI 219 PLS 1	Liver	III	7.5	51.72	
	KRAS p.G12C, c.34G>T	7.72		0.57		
90.9	Present					
INDI 221	INDI 221 PLS 1	Colorectum	III	7.5	4.60	
	NRAS p.G12D, c.35G>A	26.32		5.19		
73.6	Not detected					
INDI 222	INDI 222 PLS 1	Colorectum	II	7.5	29.31	
	TP53 p.G266E, c.797G>A	62.15		7.25		
654.1	Present					
INDI 224	INDI 224 PLS 1	Lung	III	7.5	48.72	
	TP53 p.H179R, c.536A>G	4.74		0.20		
30.3	Not detected					
INDI 231	INDI 231 PLS 1	Lung	III	7.5	2.04	
	KRAS p.G12D, c.35G>A	24.34		9.38		
59.0	Present					
INDI 233	INDI 233 PLS 1	Colorectum	I	7.5	6.54	
	TP53 p.G154V, c.461G>T	43.39		7.70		
155.0	Not detected					
INDI 243	INDI 243 PLS 1	Colorectum	I	7.5	6.33	
	APC p.E1309fs, c.3927delAAAGA	39.68		2.96		
57.7	Present					
INDI 244	INDI 244 PLS 1	Colorectum	III	7.5	4.06	
	KRAS p.G12C, c.34G>T	5.17		0.65	8.2	
Present						
INDI 245	INDI 245 PLS 1	Colorectum	III	7.5	4.36	
	KRAS p.Q61K, c.181C>A	7.71		1.19		
16.0	Present					
INDI 255	INDI 255 PLS 1	Colorectum	II	7.5	3.60	
	KRAS p.G13V, c.38G>T	7.72		0.57	6.4	
Present						
INDI 256	INDI 256 PLS 1	Colorectum	III	7.5	5.06	
	KRAS p.G12S, c.34G>A	9.64		3.97		
61.8	Present					
INDI 259	INDI 259 PLS 1	Colorectum	II	7.5	11.59	
	TP53 p.P151H, c.452C>A	9.52		0.92		
33.0	Not detected					
INDI 268	INDI 268 PLS 1	Colorectum	III	7.5	6.66	
	NRAS p.Q61R, c.182A>G	7.27		3.34		
68.5	Present					
INDI 284	INDI 284 PLS 1	Colorectum	II	7.5	17.11	
	APC p.E1309fs, c.3927delAAAGA	4.74		0.12	6.4	
Present						
INDI 285	INDI 285 PLS 1	Lung	II	7.5	4.88	
	TP53 p.E339*, c.1015G>T	5.83		1.29		
19.4	Present					

Table5.txt

INDI 287	INDI 287 PLS 1	Breast	III	7.5	2.11	
	TP53 p.S94*, c.281C>G	9.17		1.43	9.3	
	Present					
INDI 288	INDI 288 PLS 1	Lung	III	7.5	5.12	
	TP53 p.T125T, c.375G>T (Exon End)	16.13		8.37		
132.1	Present					
INDI 301	INDI 301 PLS 1	Breast	II	7.5	9.18	
	TP53 p.S241fs, c.723delTCC	3.25		0.06	1.8	
	Not detected					
INDI 305	INDI 305 PLS 1	Colorectum	II	7.5	20.30	
	TP53 p.S241fs, c.723delTCC	240.28		8.37		
523.1	Not detected					
INDI 306	INDI 306 PLS 1	Colorectum	III	7.5	3.55	
	APC p.E1309fs, c.3927delAAAGA	123.62		36.29		
396.8	Present					
INDI 310	INDI 310 PLS 1	Colorectum	II	7.5	13.05	
	PIK3CA p.E545A, c.1634A>C	4.41		0.70		
28.2	Present					
INDI 318	INDI 318 PLS 1	Stomach	III	7.5	5.16	
	TP53 p.K305*, c.913A>T	21.62		1.21		
19.3	Not detected					
INDI 327	INDI 327 PLS 1	Colorectum	II	7.5	2.83	
	TP53 p.I195N, c.584T>A	7.58		0.52	4.6	
	Present					
INDI 329	INDI 329 PLS 1	Colorectum	III	7.5	14.29	
	BRAF p.V600E, c.1799T>A	89.47		10.04		
442.0	Present					
INDI 331	INDI 331 PLS 1A	Lung	III	7.5	2.53	
	KRAS p.G12C, c.34G>T	56.58		10.88		
84.8	Present					
INDI 340	INDI 340 PLS 1	Colorectum	III	7.5	3.43	
	CTNNB1 p.S37F, c.110C>T	5.67		0.39	4.2	
	Present					
INDI 343	INDI 343 PLS 1	Colorectum	III	7.5	0.91	
	TP53 p.G244V, c.731G>T	3.44		0.34	1.0	
	Present					
INDI 353	INDI 353 PLS 1A	Lung	II	7.5	2.27	
	TP53 p.K132N, c.396G>T	17.68		0.24	1.6	
	Present					
INDI 365	INDI 365 PLS 1	Colorectum	II	7.5	3.06	
	APC p.E1309fs, c.3927delAAAGA	5.91		0.60	5.6	
	Present					
INDI 367	INDI 367 PLS 1	Liver	I	7.5	13.22	
	CTNNB1 p.I35S, c.104T>G	8.39		0.28		
11.6	Present					
INDI 368	INDI 368 PLS 1	Breast	II	7.5	3.09	
	TP53 p.E224*, c.670G>T	8.24		1.42		
13.5	Not detected					

Table5.txt

INDI 371	INDI 371 PLS 1A	Lung	III	7.5	1.47	
	KRAS p.G12V, c.35G>T	20.54		7.71		
34.8	Present					
INDI 377	INDI 377 PLS 1	Colorectum	II	7.5	14.70	
	BRAF p.V600E, c.1799T>A	3.35		0.05	2.2	
	Present					
INDI 380	INDI 380 PLS 1	Colorectum	II	7.5	3.57	
	TP53 p.N288fs, c.862delA	4.95		0.32	3.5	
	Present					
INDI 394	INDI 394 PLS 1A	Lung	II	7.5	6.92	
	PIK3CA p.E542K, c.1624G>A	3.31		0.10	2.1	
	Present					
INDI 395	INDI 395 PLS 1A	Lung	I	7.5	4.23	
	TP53 p.T125T, c.375G>T (Exon End)	3.12		0.27	3.5	
	Present					
INDI 397	INDI 397 PLS 1	Colorectum	III	7.5	7.43	
	PIK3CA p.H1047Q, c.3141T>G	5.54		0.33	7.6	
	Present					
INDI 439	INDI 439 PLS 1	Colorectum	III	7.5	12.99	
	BRAF p.F595L, c.1785T>G	14.83		0.91		
36.2	Present					
INDI 445	INDI 445 PLS 1	Breast	II	7.5	5.43	
	TP53 p.E171fs, c.513delGACGGAG	11.87		0.69		
11.6	Present					
INDI 447	INDI 447 PLS 1	Breast	III	7.5	26.17	
	PIK3CA p.G1049R, c.3145G>C	209.33		21.72		
1,751.3	Present					
INDI 457	INDI 457 PLS 1	Esophagus	II	7.5	35.05	
	TP53 p.E221*, c.661G>T	58.98		1.39		
150.0	Present					
INDI 459	INDI 459 PLS 1	Breast	II	7.5	41.57	
	PIK3CA p.H1047R, c.3140A>G	399.50		60.44		
7,738.7	Present					
INDI 461	INDI 461 PLS 1	Colorectum	III	7.5	8.60	
	TP53 p.V172F, c.514G>T	4.56		0.40		
10.6	Present					
INDI 462	INDI 462 PLS 1	Breast	III	7.5	82.66	
	TP53 g.7578176C>A (Splice Site)	165.23		62.32		
15,866.1	Present					
INDI 463	INDI 463 PLS 1	Colorectum	II	7.5	11.05	
	TP53 p.R273C, c.817C>T	3.59		2.43		
82.6	Present					
INDI 464	INDI 464 PLS 1	Liver	III	7.5	57.74	
	TP53 p.K132*, c.394A>T	12.33		0.32		
56.3	Present					
INDI 466	INDI 466 PLS 1	Colorectum	II	7.5	18.81	
	TP53 p.T155fs, c.463insA	5.88		0.19		
11.1	Present					

Table5.txt

INDI 470	INDI 470 PLS 1	Colorectum	III	7.5	8.40	
	TP53 p.Q100*, c.298C>T	3.75		0.28	7.3	
	Present					
INDI 494	INDI 494 PLS 1	Lung	III	7.5	4.62	
	TP53 p.G244A, c.731G>C	3.64		0.14	2.0	
	Present					
INDI 505	INDI 505 PLS 1	Lung	II	7.5	34.64	
	TP53 p.R267P, c.800G>C	4.44		0.08	8.3	
	Present					
INDI 511	INDI 511 PLS 1	Colorectum	III	7.5	4.19	
	TP53 p.S183fs, c.549insA	3.80		0.18	2.3	
	Present					
INDI 514	INDI 514 PLS 1	Stomach	I	7.5	6.42	
	CTNNB1 p.T41A, c.121A>G	5.54		0.04	0.8	
	Not detected					
INDI 515	INDI 515 PLS 1	Colorectum	III	7.5	15.27	
	TP53 p.K132N, c.396G>T	4.98		0.04	2.0	
	Not detected					
INDI 518	INDI 518 PLS 1	Colorectum	III	7.5	9.71	
	TP53 p.N131fs, c.392delCAA	6.18		0.18	5.2	
	Present					
INDI 525	INDI 525 PLS 1	Colorectum	I	7.5	31.87	
	TP53 p.C277F, c.830G>T	3.01		0.03	3.1	
	Not detected					
INDI 539	INDI 539 PLS 1	Colorectum	II	7.5	8.83	
	PTEN p.D92A, c.275A>C	8.98		0.49		
13.4	Present					
INDI 544	INDI 544 PLS 1	Colorectum	III	7.5	2.48	
	TP53 p.G334R, c.1000G>C	185.06		52.81		
403.4	Present					
INDI 555	INDI 555 PLS 1	Colorectum	II	7.5	1.44	
	APC p.E1309fs, c.3927delAAAGA	8.85		0.78	3.5	
	Present					
INDI 558	INDI 558 PLS 1	Colorectum	I	7.5	8.45	
	TP53 p.H368Y, c.1102C>T	3.95		0.11	2.8	
	Not detected					
INDI 567	INDI 567 PLS 1	Colorectum	II	7.5	3.64	
	PIK3CA p.E545K, c.1633G>A	5.37		0.89		
10.0	Present					
INDI 581	INDI 581 PLS 1	Colorectum	II	7.5	6.91	
	TP53 g.7579311C>A (Splice Site)	4.23		1.40		
29.8	Present					
INDI 585	INDI 585 PLS 1	Esophagus	III	7.5	14.36	
	PIK3CA p.E545K, c.1633G>A	5.64		0.25		
10.9	Not detected					
INDI 601	INDI 601 PLS 1	Breast	III	7.5	15.18	
	TP53 p.R213*, c.637C>T	5.23		9.25		
432.4	Present					

Table5.txt

INDI 602	INDI 602 PLS 1	Colorectum	II	7.5	3.35	
	TP53 p.E204*, c.610G>T	3.05		0.33	3.4	
	Present					
INDI 614	INDI 614 PLS 1	Colorectum	II	7.5	21.63	
	NRAS p.G12D, c.35G>A	3.65		0.12	7.8	
	Present					
INDI 623	INDI 623 PLS 1	Breast	III	7.5	6.71	
	TP53 p.R273P, c.818G>C	17.70		2.09		
43.1	Present					
INDI 625	INDI 625 PLS 1	Colorectum	II	7.5	2.73	
	KRAS p.G12S, c.34G>A	3.06		0.38	3.2	
	Present					
INDI 626	INDI 626 PLS 1	Colorectum	II	7.5	11.58	
	KRAS p.G12D, c.35G>A	4.47		0.43		
15.4	Present					
INDI 636	INDI 636 PLS 1	Liver	III	7.5	27.51	
	CTNNB1 p.T41A, c.121A>G	310.96		4.60		
390.0	Present					
INDI 639	INDI 639 PLS 1	Liver	II	7.5	18.63	
	TP53 p.R158L, c.473G>T	4.31		0.18		
10.2	Present					
INDI 645	INDI 645 PLS 1	Liver	III	7.5	27.37	
	TP53 p.R249S, c.747G>T	16.21		8.37		
706.0	Present					
INDI 648	INDI 648 PLS 1	Colorectum	III	7.5	1.21	
	KRAS p.G12V, c.35G>T	28.57		24.26		
90.6	Present					
INDI 663	INDI 663 PLS 1	Esophagus	II	7.5	29.39	
	TP53 p.Q331*, c.991C>T	100.09		1.39		
125.9	Present					
INDI 665	INDI 665 PLS 1	Esophagus	III	7.5	14.81	
	FGFR2 p.P253R, c.758C>G	51.21		0.35		
16.1	Present					
INDI 670	INDI 670 PLS 1	Colorectum	III	7.5	2.88	
	TP53 p.G117fs, c.350insGGAC	83.06		14.28		
126.9	Present					
INDI 678	INDI 678 PLS 1	Colorectum	III	7.5	2.03	
	TP53 p.E224fs, c.670insG	13.00		1.10	6.9	
	Present					
INDI 687	INDI 687 PLS 1	Lung	III	7.5	11.57	
	KRAS p.G12V, c.35G>T	56.40		5.16		
183.9	Present					
INDI 693	INDI 693 PLS 1	Lung	III	7.5	8.08	
	TP53 p.H193Y, c.577C>T	92.56		22.33		
555.6	Present					
INDI 696	INDI 696 PLS 1	Lung	II	7.5	1.71	
	HRAS p.G13V, c.38G>T	3.20		0.33	1.7	
	Present					

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INDI 701	INDI 701 PLS 1	Colorectum	II	7.5	1.54	
	BRAF p.V600E, c.1799T>A	3.67		0.17	0.8	
	Present					
INDI 702	INDI 702 PLS 1	Lung	II	7.5	22.55	
	TP53 p.E298*, c.892G>T	4.22		0.14	9.6	
	Present					
INDI 708	INDI 708 PLS 1	Colorectum	III	7.5	7.20	
	BRAF p.L597R, c.1790T>G	6.15		0.34	7.4	
	Not detected					
INDI 710	INDI 710 PLS 1	Colorectum	III	7.5	4.72	
	PIK3CA p.Q546R, c.1637A>G	3.28		0.16	2.4	
	Present					
INDI 711	INDI 711 PLS 1	Breast	III	7.5	2.28	
	PIK3CA p.E545K, c.1633G>A	4.38		0.42	2.9	
	Present					
INDI 723	INDI 723 PLS 1	Ovary	III	7.5	2.80	
	TP53 p.S215I, c.644G>T	3.13		0.69	6.0	
	Present					
INDI 751	INDI 751 PLS 1	Colorectum	III	2	1.70	
	TP53 p.E336*, c.1006G>T	3.10		0.88	4.6	
	Not detected					
INDI 753	INDI 753 PLS 1	Esophagus	III	7.5	8.37	
	TP53 p.Y220C, c.659A>G	4.61		3.46		
89.1	Present					
INDI 764	INDI 764 PLS 1	Colorectum	II	7.5	1.44	
	TP53 p.E51fs, c.151delG	8.55		1.78	7.9	
	Present					
INDI 769	INDI 769 PLS 1	Colorectum	II	7.5	1.51	
	TP53 p.I251V, c.751A>G	50.33		50.29		
234.0	Present					
INDI 770	INDI 770 PLS 1	Colorectum	II	7.5	5.95	
	APC p.E1306*, c.3916G>T	4.97		0.16	3.0	
	Present					
INDI 771	INDI 771 PLS 1	Liver	II	7.5	23.39	
	CTNNB1 p.S45A, c.133T>G	3.36		0.02	1.7	
	Present					
INDI 777	INDI 777 PLS 1	Colorectum	II	7.5	23.48	
	TP53 p.D42fs, c.124insGA	3.27		0.02	1.3	
	Not detected					
INDI 778	INDI 778 PLS 1	Liver	II	7.5	16.38	
	CTNNB1 p.I35S, c.104T>G	4.39		0.08	4.2	
	Present					
INDI 779	INDI 779 PLS 1	Colorectum	II	7.5	1.88	
	TP53 p.E11Q, c.31G>C	99.20		50.22		
291.5	Present					
INDI 782	INDI 782 PLS 1	Colorectum	III	7.5	15.27	
	BRAF p.V600E, c.1799T>A	36.75		2.88		
135.7	Present					

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INDI 786	INDI 786 PLS 1	Liver	I	7.5	3.23				
	TP53 p.C135F, c.404G>T	7.05	1.16						
11.6	Present								
INDI 798	INDI 798 PLS 1	Ovary	II	7.5	22.29				
	TP53 p.Y163C, c.488A>G	52.92	7.31						
502.2	Present								
INDI 800	INDI 800 PLS 1	Liver	II	7.5	3.60				
	CTNNB1 p.T41A, c.121A>G	5.78	0.13	1.4					
	Present								
INDI 802	INDI 802 PLS 1	Pancreas	II	7.5	15.09				
	CDKN2A p.E88*, c.262G>T	3.80	0.09	4.0					
	Present								
INDI 812	INDI 812 PLS 1	Ovary	II	7.5	3.11				
	CTNNB1 p.T41A, c.121A>G	77.58	3.18						
30.5	Present								
INDI 818	INDI 818 PLS 1	Ovary	III	7.5	6.53				
	TP53 p.G154fs, c.460delG	41.01	2.83						
56.9	Present								
INDI 819	INDI 819 PLS 1	Breast	III	7.5	1.52				
	AKT1 p.E17K, c.49G>A	8.34	6.06						
28.4	Present								
INDI 838	INDI 838 PLS 1	Colorectum	III	7.5	4.20				
	APC p.E1306*, c.3916G>T	3.44	0.11	1.5					
	Present								
INDI 850	INDI 850 PLS 1	Esophagus	II	7.5	8.01				
	TP53 p.H193P, c.578A>C	124.89	21.37						
527.0	Present								
INDI 859	INDI 859 PLS 1	Esophagus	II	7.5	15.56				
	TP53 p.Y234N, c.700T>A	7.28	0.59						
28.3	Present								
INDI 872	INDI 872 PLS 1	Breast	III	7.5	5.17				
	PIK3CA p.H1047L, c.3140A>T	13.66	0.89						
14.2	Present								
INDI 884	INDI 884 PLS 1	Breast	II	7.5	17.62				
	TP53 p.Y220C, c.659A>G	12.84	11.77						
638.8	Present								
INDI 905	INDI 905 PLS 1	Esophagus	II	7.5	19.99				
	TP53 p.K132R, c.395A>G	8.45	0.61						
37.4	Not detected								
INDI 928	INDI 928 PLS 1	Stomach	II	7.5	6.23				
	TP53 p.F338fs, c.1014delC	4.08	0.16	3.0					
	Present								
INDI 932	INDI 932 PLS 1	Ovary	III	7.5	5.40				
	TP53 p.L252fs, c.754delTCC	69.94	10.81						
179.8	Present								

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

Table6.txt

Table 6. Cancer type localization results for the 617 cancer patients identified by CancerSEEK.

Patient ID #	Sample ID #	Tumor type	Upper GI RF Probability	Breast RF Probability	Most likely Colorectum RF prediction	Lung RF Probability	Ovary RF Probability	Pancreas RF Probability	Second most likely prediction
CRC 456	CRC 456 PLS 1	Colorectum	0.08	0.534	0.088	0.048	0.074	0.088	Liver
CRC 457	CRC 457 PLS 1	Colorectum	0.136	0.574	0.032	0.084	0.062	0.016	Breast
CRC 463	CRC 463 PLS 1	Colorectum	0.29	0.382	0.008	0.122	0.124	0.016	Breast
CRC 467	CRC 467 PLS 1	Colorectum	0.098	0.586	0.032	0.1	0.016	0.054	Upper GI
CRC 468	CRC 468 PLS 1	Colorectum	0.102	0.448	0.09	0.194	0.058	0.028	Lung
CRC 470	CRC 470 PLS 1	Colorectum	0.424	0.338	0.02	0.068	0.074	0.03	Breast Colorectum
CRC 471	CRC 471 PLS 1	Colorectum	0.264	0.34	0.03	0.186	0.076	0.048	Breast
CRC 473	CRC 473 PLS 1	Colorectum	0.056	0.526	0.102	0.094	0.016	0.026	Upper GI
CRC 476	CRC 476 PLS 1	Colorectum	0.046	0.646	0.03	0.134	0.044	0.034	Lung
CRC 477	CRC 477 PLS 1	Colorectum	0.106	0.424	0.058	0.186	0.118	0.03	Lung
CRC 479	CRC 479 PLS 1	Colorectum	0.092	0.46	0.092	0.154	0.01	0.066	Lung
CRC 480	CRC 480 PLS 1	Colorectum	0.052	0.66	0.066	0.104	0.018	0.01	Lung
CRC 481	CRC 481 PLS 1	Colorectum	0.138	0.506	0.052	0.078	0.056	0.074	Breast
CRC 484	CRC 484 PLS 1	Colorectum	0.09	0.59	0.028	0.134	0.014	0.064	Lung
CRC 486	CRC 486 PLS 1	Colorectum	0.282	0.396	0.024	0.13	0.094	0.01	Breast
CRC 488	CRC 488 PLS 1	Colorectum	0.042	0.624	0.032	0.164	0.058	0.022	Lung
CRC 489	CRC 489 PLS 1	Colorectum	0.18	0.45	0.028	0.096	0.078	0.102	Breast
CRC 492	CRC 492 PLS 1	Colorectum	0.07	0.26	0.04	0.292	0.198	0.028	Lung

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Colorectum									
CRC 497	CRC 497 PLS 1	Colorectum	0.032	0.45	0.172	0.042	0.036	0.118	0.15
Colorectum	Liver								
CRC 498	CRC 498 PLS 1	Colorectum	0.084	0.432	0.02	0.164	0.052	0.114	0.134
Colorectum	Lung								
CRC 503	CRC 503 PLS 1	Colorectum	0.044	0.404	0.042	0.3	0.03	0.042	0.138
Colorectum	Lung								
CRC 504	CRC 504 PLS 1	Colorectum	0.038	0.568	0.052	0.04	0.094	0.052	0.156
Colorectum	Upper GI								
CRC 512	CRC 512 PLS 1	Colorectum	0.28	0.372	0.062	0.184	0.044	0.022	0.036
Colorectum	Breast								
CRC 513	CRC 513 PLS 1	Colorectum	0.052	0.326	0.16	0.092	0.016	0.18	0.174
Colorectum	Pancreas								
CRC 514	CRC 514 PLS 1	Colorectum	0.048	0.402	0.094	0.282	0.024	0.064	0.086
Colorectum	Lung								
CRC 518	CRC 518 PLS 1	Colorectum	0.092	0.47	0.068	0.108	0.08	0.024	0.158
Colorectum	Upper GI								
CRC 520	CRC 520 PLS 1	Colorectum	0.144	0.278	0.032	0.314	0.158	0.014	0.06
Lung									
Colorectum									
CRC 522	CRC 522 PLS 1	Colorectum	0.088	0.54	0.018	0.188	0.02	0.042	0.104
Colorectum	Lung								
CRC 524	CRC 524 PLS 1	Colorectum	0.054	0.484	0.08	0.15	0.014	0.028	0.19
Colorectum	Upper GI								
CRC 525	CRC 525 PLS 1	Colorectum	0.086	0.338	0.068	0.316	0.036	0.032	0.124
Colorectum	Lung								
CRC 527	CRC 527 PLS 1	Colorectum	0.14	0.318	0.044	0.224	0.018	0.098	0.158
Colorectum	Lung								
CRC 530	CRC 530 PLS 1	Colorectum	0.038	0.354	0.016	0.47	0.012	0.038	0.072
Lung									
Colorectum									
INDI 001	INDI 001 PLS 1	Lung	0.088	0.378	0.018	0.16	0.256	0.066	0.034
Colorectum	Ovary								
INDI 003	INDI 003 PLS 1	Lung	0.028	0.218	0.07	0.242	0.238	0.142	0.062
Lung	Ovary								
INDI 004	INDI 004 PLS 1	Lung	0.036	0.328	0.054	0.192	0.046	0.306	0.038
Colorectum	Pancreas								
INDI 009	INDI 009 PLS 1	Lung	0.066	0.204	0.03	0.566	0.046	0.016	0.072
Lung									
Colorectum									
INDI 010	INDI 010 PLS 1	Lung	0.022	0.352	0.03	0.182	0.088	0.106	0.22
Colorectum	Upper GI								
INDI 012	INDI 012 PLS 1	Lung	0.006	0.166	0.026	0.676	0.058	0.018	0.05
Lung									
Colorectum									
INDI 014	INDI 014 PLS 1	Lung	0.092	0.484	0.06	0.24	0.022	0.066	0.036
Colorectum	Lung								
INDI 016	INDI 016 PLS 1	Lung	0.074	0.25	0.006				

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	0.418	0.142	0.094	0.016	Lung				
Colorectum									
	INDI 022	INDI 022 PLS 1		Lung	0.166	0.254	0.028		
	0.438	0.094	0.008	0.012	Lung				
Colorectum									
	INDI 023	INDI 023 PLS 1		Lung	0.076	0.3	0.014		
	0.47	0.02	0.038	0.082	Lung				
Colorectum									
	INDI 025	INDI 025 PLS 1		Lung	0.092	0.326	0.024		
	0.308	0.212	0.032	0.006	Colorectum		Lung		
	INDI 027	INDI 027 PLS 1		Colorectum	0.056	0.476	0.036		
	0.21	0.168	0.018	0.036	Colorectum		Lung		
	INDI 030	INDI 030 PLS 1		Colorectum	0.132	0.424	0.026		
	0.048	0.11	0.226	0.034	Colorectum		Pancreas		
	INDI 034	INDI 034 PLS 1		Colorectum	0.044	0.43	0.052		
	0.116	0.144	0.182	0.032	Colorectum		Pancreas		
	INDI 039	INDI 039 PLS 1		Colorectum	0.136	0.496	0.056		
	0.094	0.11	0.044	0.064	Colorectum		Breast		
	INDI 043	INDI 043 PLS 1		Colorectum	0.08	0.578	0.04		
	0.116	0.086	0.02	0.08	Colorectum		Lung		
	INDI 044	INDI 044 PLS 1		Colorectum	0.29	0.318	0.054		
	0.034	0.068	0.002	0.234	Colorectum		Breast		
	INDI 045	INDI 045 PLS 1		Colorectum	0.09	0.532	0.082		
	0.028	0.01	0.008	0.25	Colorectum		Upper GI		
	INDI 046	INDI 046 PLS 1		Colorectum	0.03	0.336	0.072		
	0.048	0.004	0.014	0.496	Upper GI				
Colorectum									
	INDI 047	INDI 047 PLS 1		Colorectum	0.052	0.438	0.04		
	0.076	0.006	0.01	0.378	Colorectum		Upper GI		
	INDI 051	INDI 051 PLS 1		Breast	0.046	0.322	0.036		
	0.104	0.412	0.06	0.02	Ovary				
Colorectum									
	INDI 052	INDI 052 PLS 1		Breast	0.082	0.416	0.032		
	0.262	0.136	0.06	0.012	Colorectum		Lung		
	INDI 059	INDI 059 PLS 1		Breast	0.466	0.17	0.058		
	0.152	0.07	0.054	0.03	Breast				
Colorectum									
	INDI 060	INDI 060 PLS 1		Breast	0.528	0.262	0.02		
	0.088	0.016	0.016	0.07	Breast				
Colorectum									
	INDI 061	INDI 061 PLS 1		Breast	0.596	0.268	0.016		
	0.046	0.014	0.01	0.05	Breast				
Colorectum									
	INDI 064	INDI 064 PLS 1		Breast	0.564	0.256	0.054		
	0.046	0.034	0.008	0.038	Breast				
Colorectum									
	INDI 067	INDI 067 PLS 1		Breast	0.568	0.212	0.03		
	0.066	0.02	0.01	0.094	Breast				

Table6.txt

Colorectum								
INDI 069	INDI 069 PLS 1		Breast	0.43		0.356		0.068
0.064	0.006	0.016	0.06	Breast				
Colorectum								
INDI 070	INDI 070 PLS 1		Breast	0.33		0.198		0.164
0.116	0.076	0.04	0.076	Breast				
Colorectum								
INDI 071	INDI 071 PLS 1		Breast	0.376		0.418		0.04
0.038	0.028	0.02	0.08	Colorectum			Breast	
INDI 072	INDI 072 PLS 1		Breast	0.508		0.26		0.016
0.146	0.024	0.01	0.036	Breast				
Colorectum								
INDI 074	INDI 074 PLS 1		Pancreas	0.038		0.3		0.042
0.132	0.052	0.306	0.13	Pancreas				
Colorectum								
INDI 075	INDI 075 PLS 1		Ovary	0.214		0.298		0.012
0.166	0.222	0.066	0.022	Colorectum			Ovary	
INDI 076	INDI 076 PLS 1		Esophagus	0.074		0.344		0.152
0.052	0.002	0.02	0.356	Upper GI				
Colorectum								
INDI 077	INDI 077 PLS 1		Liver	0.054		0.194		0.33
0.056	0.028	0.054	0.284	Liver			Upper GI	
INDI 078	INDI 078 PLS 1		Liver	0.058		0.428		0.168
0.064	0.002	0.014	0.266	Colorectum			Upper GI	
INDI 079	INDI 079 PLS 1		Liver	0.012		0.272		0.262
0.014	0.01	0.02	0.41	Upper GI				
Colorectum								
INDI 080	INDI 080 PLS 1		Liver	0.062		0.416		0.064
0.252	0.046	0.118	0.042	Colorectum			Lung	
INDI 081	INDI 081 PLS 1		Colorectum	0.02		0.32		0.092
0.404	0.038	0.066	0.06	Lung				
Colorectum								
INDI 083	INDI 083 PLS 1		Stomach	0.01		0.268		0.112
0.022	0	0.006	0.582	Upper GI				
Colorectum								
INDI 084	INDI 084 PLS 1		Stomach	0.072		0.342		0.268
0.06	0.044	0.008	0.206	Colorectum			Liver	
INDI 085	INDI 085 PLS 1		Stomach	0.036		0.49		0.036
0.178	0.022	0.036	0.202	Colorectum			Upper GI	
INDI 086	INDI 086 PLS 1		Stomach	0.036		0.352		0.038
0.016	0	0.054	0.504	Upper GI				
Colorectum								
INDI 087	INDI 087 PLS 1		Stomach	0.308		0.334		0.034
0.114	0.038	0.02	0.152	Colorectum			Breast	
INDI 089	INDI 089 PLS 1		Colorectum	0.102		0.606		0.11
0.034	0.024	0.012	0.112	Colorectum			Upper GI	
INDI 090	INDI 090 PLS 1		Colorectum	0.072		0.446		0.08
0.064	0.01	0.062	0.266	Colorectum			Upper GI	

Table6.txt

INDI 093	INDI 093 PLS 1	Colorectum	0.044	0.446	0.054	0.118	0.038	0.048
0.252	Colorectum	Upper GI	INDI 094	INDI 094 PLS 1	Colorectum	0.016	0.566	0.05
0.02	0.02	0.046	0.282	Colorectum	Upper GI	INDI 097	INDI 097 PLS 1	Colorectum
0.104	0.404	0.096	0.102	0.042	0.178	0.074	Colorectum	Pancreas
INDI 100	INDI 100 PLS 1	Colorectum	0.116	0.57	0.086	0.044	0.024	0.062
0.098	Colorectum	Breast	INDI 102	INDI 102 PLS 1	Colorectum	0.062	0.458	0.072
0.132	0.018	0.052	0.206	Colorectum	Upper GI	INDI 104	INDI 104 PLS 1	Stomach
0.024	0.326	0.422	0.088	0.01	0.026	0.104	Liver	Colorectum
INDI 107	INDI 107 PLS 1	Colorectum	0.02	0.584	0.068	0.058	0.008	0.01
0.252	Colorectum	Upper GI	INDI 108	INDI 108 PLS 1	Colorectum	0.226	0.536	0.04
0.068	0.038	0.008	0.084	Colorectum	Breast	INDI 109	INDI 109 PLS 1	Colorectum
0.104	0.29	0.27	0.028	0.026	0.012	0.27	Colorectum	Liver
INDI 110	INDI 110 PLS 1	Stomach	0.016	0.574	0.046	0.056	0.006	0.008
0.294	Colorectum	Upper GI	INDI 111	INDI 111 PLS 1	Stomach	0.046	0.402	0.12
0.094	0.01	0	0.328	Colorectum	Upper GI	INDI 112	INDI 112 PLS 1	Esophagus
0.038	0.266	0.116	0.054	0.036	0.022	0.468	Upper GI	Colorectum
INDI 113	INDI 113 PLS 1	Colorectum	0.022	0.442	0.056	0.058	0.022	0.048
0.352	Colorectum	Upper GI	INDI 116	INDI 116 PLS 1	Stomach	0.026	0.326	0.096
0.142	0.018	0.018	0.374	Upper GI	Colorectum	INDI 119	INDI 119 PLS 1	Esophagus
0.076	0.196	0.09	0.05	0.23	0.03	0.328	Upper GI	Ovary
INDI 120	INDI 120 PLS 1	Stomach	0.09	0.346	0.04	0.014	0.02	0.012
0.478	Upper GI	Colorectum	INDI 121	INDI 121 PLS 1	Stomach	0.042	0.512	0.058
0.106	0.008	0.01	0.264	Colorectum	Upper GI	INDI 122	INDI 122 PLS 1	Colorectum
0.126	0.228	0.374	0.034	0.042	0.01	0.186	Liver	Colorectum
INDI 123	INDI 123 PLS 1	Colorectum	0.106	0.54	0.056	0.018	0.026	0.036
0.218	Colorectum	Upper GI	INDI 124	INDI 124 PLS 1	Colorectum	0.014	0.31	0.042
0.01	0.002	0.012	0.61	Upper GI	Colorectum	INDI 125	INDI 125 PLS 1	Esophagus
0.018	0.3	0.086	0.018	0.006	0.012	0.56	Upper GI	

Table6.txt

Colorectum						
INDI 126	INDI 126 PLS 1	Stomach	0.01	0.256	0.062	0.018
0.006	0.004	0.644	Upper GI			
Colorectum						
INDI 127	INDI 127 PLS 1	Colorectum	0.01	0.34	0.04	0.018
0.002	0.002	0.588	Upper GI			
Colorectum						
INDI 128	INDI 128 PLS 1	Colorectum	0.134	0.424	0.102	0.084
0.058	0.084	0.114	Colorectum		Breast	
INDI 129	INDI 129 PLS 1	Liver	0.144	0.296	0.346	0.02
0.014	0.026	0.154	Liver			
Colorectum						
INDI 130	INDI 130 PLS 1	Stomach	0.012	0.298	0.07	0.03
0.01	0.01	0.57	Upper GI			
Colorectum						
INDI 131	INDI 131 PLS 1	Stomach	0.024	0.286	0.104	0.03
0.018	0.016	0.522	Upper GI			
Colorectum						
INDI 132	INDI 132 PLS 1	Esophagus	0.014	0.4	0.032	0.03
0.004	0.004	0.516	Upper GI			
Colorectum						
INDI 133	INDI 133 PLS 1	Stomach	0.01	0.152	0.128	0.014
0.004	0.016	0.676	Upper GI			
Colorectum						
INDI 134	INDI 134 PLS 1	Stomach	0.016	0.31	0.032	0.004
0.002	0.008	0.628	Upper GI			
Colorectum						
INDI 135	INDI 135 PLS 1	Stomach	0.018	0.252	0.114	0.034
0.024	0.02	0.538	Upper GI			
Colorectum						
INDI 136	INDI 136 PLS 1	Colorectum	0.08	0.424	0.06	0.018
0.012	0.006	0.4	Colorectum		Upper GI	
INDI 137	INDI 137 PLS 1	Stomach	0.012	0.272	0.206	0.052
0.004	0.016	0.438	Upper GI			
Colorectum						
INDI 139	INDI 139 PLS 1	Stomach	0.098	0.384	0.066	0.036
0.034	0.038	0.344	Colorectum		Upper GI	
INDI 140	INDI 140 PLS 1	Stomach	0.014	0.298	0.102	0.008
0.004	0.004	0.57	Upper GI			
Colorectum						
INDI 141	INDI 141 PLS 1	Stomach	0.02	0.386	0.076	0.034
0.008	0.014	0.462	Upper GI			
Colorectum						
INDI 143	INDI 143 PLS 1	Colorectum	0.006	0.232	0.272	0.046
0.01	0.004	0.43	Upper GI		Liver	
INDI 144	INDI 144 PLS 1	Colorectum	0.05	0.384	0.064	0.046
0.028	0.008	0.42	Upper GI			
Colorectum						

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INDI 145	INDI 145 PLS 1	Colorectum	0.064	0.466	0.128	0.07	0.028	0.036
0.208	Colorectum	Upper GI	INDI 146	INDI 146 PLS 1	Colorectum	0.084	0.472	0.102
0.114	0.016	0.016	0.196	Colorectum	Upper GI	INDI 147	INDI 147 PLS 1	Stomach
0.264	0.42	0.064	0.024	0.016	0.038	0.174	Colorectum	Breast
INDI 148	INDI 148 PLS 1	Colorectum	0.016	0.296	0.106	0.01	0	0.032
0.54	Upper GI	Colorectum	INDI 150	INDI 150 PLS 1	Colorectum	0.11	0.274	0.074
0.014	0.03	0.02	0.478	Upper GI	Colorectum	INDI 151	INDI 151 PLS 1	Stomach
0.084	0.438	0.13	0.018	0.006	0.016	0.308	Colorectum	Upper GI
INDI 152	INDI 152 PLS 1	Colorectum	0.048	0.412	0.16	0.032	0.024	0.012
0.312	Colorectum	Upper GI	INDI 156	INDI 156 PLS 1	Colorectum	0.03	0.288	0.144
0.018	0.008	0.03	0.482	Upper GI	Colorectum	INDI 158	INDI 158 PLS 1	Colorectum
0.084	0.568	0.094	0.044	0.042	0.02	0.148	Colorectum	Upper GI
INDI 160	INDI 160 PLS 1	Colorectum	0.012	0.702	0.022	0.05	0.002	0.014
0.198	Colorectum	Upper GI	INDI 161	INDI 161 PLS 1	Stomach	0.03	0.616	0.038
0.05	0.006	0.006	0.254	Colorectum	Upper GI	INDI 162	INDI 162 PLS 1	Stomach
0.08	0.482	0.146	0.062	0.018	0.03	0.182	Colorectum	Upper GI
INDI 163	INDI 163 PLS 1	Colorectum	0.054	0.43	0.118	0.162	0.038	0.022
0.176	Colorectum	Upper GI	INDI 165	INDI 165 PLS 1	Colorectum	0.018	0.592	0.034
0.092	0.012	0.018	0.234	Colorectum	Upper GI	INDI 167	INDI 167 PLS 1	Stomach
0.022	0.38	0.062	0.008	0.016	0.004	0.508	Upper GI	Colorectum
INDI 168	INDI 168 PLS 1	Stomach	0.008	0.33	0.086	0.006	0.02	0.146
0.404	Upper GI	Colorectum	INDI 169	INDI 169 PLS 1	Colorectum	0.202	0.468	0.042
0.018	0.034	0.008	0.228	Colorectum	Upper GI	INDI 170	INDI 170 PLS 1	Colorectum
0.068	0.422	0.05	0.01	0.006	0.006	0.438	Upper GI	Colorectum
INDI 171	INDI 171 PLS 1	Stomach	0.02	0.346	0.166	0.012	0.014	0.052
0.39	Upper GI	Colorectum	INDI 172	INDI 172 PLS 1	Stomach	0.138	0.282	0.156
0.008	0.03	0.136	0.25	Colorectum	Upper GI	INDI 173	INDI 173 PLS 1	Stomach
0.012	0.376	0.064						

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0.008	0.014	0.006	0.52	Upper GI					
Colorectum									
INDI 175	INDI 175 PLS 1		Colorectum	0.012	0.374	0.072			
0.014	0.026	0.046	0.456	Upper GI					
Colorectum									
INDI 176	INDI 176 PLS 1		Stomach	0.018	0.344	0.056			
0.02	0.012	0.016	0.534	Upper GI					
Colorectum									
INDI 177	INDI 177 PLS 1		Liver	0.024	0.212	0.554			
0.01	0.006	0.016	0.178	Liver					
Colorectum									
INDI 178	INDI 178 PLS 1		Colorectum	0.028	0.408	0.088			
0.022	0.008	0.036	0.41	Upper GI					
Colorectum									
INDI 179	INDI 179 PLS 1		Colorectum	0.03	0.33	0.144			
0.024	0.002	0.018	0.452	Upper GI					
Colorectum									
INDI 180	INDI 180 PLS 1		Colorectum	0.062	0.462	0.108			
0.082	0.086	0.018	0.182	Colorectum		Upper GI			
INDI 182	INDI 182 PLS 1		Liver	0.01	0.206	0.332			
0.012	0.004	0.008	0.428	Upper GI		Liver			
INDI 183	INDI 183 PLS 1		Stomach	0.08	0.508	0.052			
0.034	0.022	0.016	0.288	Colorectum		Upper GI			
INDI 184	INDI 184 PLS 1		Esophagus	0.014	0.24	0.048			
0.012	0.022	0.008	0.656	Upper GI					
Colorectum									
INDI 185	INDI 185 PLS 1		Stomach	0.028	0.362	0.054			
0.036	0.076	0.03	0.414	Upper GI					
Colorectum									
INDI 186	INDI 186 PLS 1		Stomach	0.008	0.284	0.202			
0	0.006	0.02	0.48	Upper GI					
Colorectum									
INDI 187	INDI 187 PLS 1		Stomach	0.12	0.566	0.042			
0.038	0.044	0.002	0.188	Colorectum		Upper GI			
INDI 188	INDI 188 PLS 1		Stomach	0.056	0.368	0.09			
0.02	0.048	0.02	0.398	Upper GI					
Colorectum									
INDI 189	INDI 189 PLS 1		Esophagus	0.038	0.448	0.09			
0.02	0.04	0.004	0.36	Colorectum		Upper GI			
INDI 190	INDI 190 PLS 1		Liver	0.016	0.368	0.108			
0.016	0.008	0.018	0.466	Upper GI					
Colorectum									
INDI 191	INDI 191 PLS 1		Colorectum	0.078	0.494	0.09			
0.014	0.016	0.012	0.296	Colorectum		Upper GI			
INDI 192	INDI 192 PLS 1		Colorectum	0.028	0.366	0.126			
0.028	0.026	0.176	0.25	Colorectum		Upper GI			
INDI 194	INDI 194 PLS 1		Colorectum	0.172	0.412	0.084			
0.048	0.062	0.046	0.176	Colorectum		Upper GI			

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INDI 195	INDI 195 PLS 1	Colorectum	0.208	0.458	0.05	0.018
0.008	0.012	0.246	Colorectum		Upper GI	
INDI 196	INDI 196 PLS 1	Colorectum	0.006	0.268	0.112	0.006
0	0	0.608	Upper GI			
Colorectum						
INDI 197	INDI 197 PLS 1	Colorectum	0.072	0.402	0.128	0.022
0.028	0.038	0.31	Colorectum		Upper GI	
INDI 198	INDI 198 PLS 1	Stomach	0.026	0.174	0.55	0.014
0.01	0.028	0.198	Liver		Upper GI	
INDI 199	INDI 199 PLS 1	Stomach	0.014	0.422	0.082	0.008
0.002	0.016	0.456	Upper GI			
Colorectum						
INDI 200	INDI 200 PLS 1	Breast	0.32	0.384	0.076	0.01
0.018	0.028	0.164	Colorectum		Breast	
INDI 202	INDI 202 PLS 1	Colorectum	0.042	0.482	0.056	0.052
0.002	0.018	0.348	Colorectum		Upper GI	
INDI 203	INDI 203 PLS 1	Stomach	0.032	0.428	0.068	0.028
0.01	0.09	0.344	Colorectum		Upper GI	
INDI 205	INDI 205 PLS 1	Liver	0.026	0.28	0.242	0.034
0.02	0.236	0.162	Colorectum		Liver	
INDI 206	INDI 206 PLS 1	Stomach	0.018	0.316	0.224	0.014
0.01	0.016	0.402	Upper GI			
Colorectum						
INDI 207	INDI 207 PLS 1	Colorectum	0.158	0.622	0.02	0.034
0.032	0.016	0.118	Colorectum		Breast	
INDI 208	INDI 208 PLS 1	Liver	0.036	0.11	0.634	0.014
0.014	0.082	0.11	Liver			
Colorectum						
INDI 209	INDI 209 PLS 1	Colorectum	0.112	0.332	0.248	0.024
0.042	0.06	0.182	Colorectum		Liver	
INDI 210	INDI 210 PLS 1	Stomach	0.076	0.446	0.078	0.13
0.016	0.044	0.21	Colorectum		Upper GI	
INDI 211	INDI 211 PLS 1	Colorectum	0.01	0.476	0.074	0.036
0.022	0.008	0.374	Colorectum		Upper GI	
INDI 212	INDI 212 PLS 1	Colorectum	0.066	0.61	0.08	0.054
0.042	0.004	0.144	Colorectum		Upper GI	
INDI 213	INDI 213 PLS 1	Colorectum	0.234	0.538	0.038	0.064
0.024	0.022	0.08	Colorectum		Breast	
INDI 214	INDI 214 PLS 1	Stomach	0.06	0.6	0.08	0.084
0.006	0.044	0.126	Colorectum		Upper GI	
INDI 215	INDI 215 PLS 1	Liver	0.292	0.26	0.132	0.126
0.102	0.024	0.064	Breast			
Colorectum						
INDI 216	INDI 216 PLS 1	Colorectum	0.098	0.662	0.034	0.092
0.006	0.036	0.072	Colorectum		Breast	
INDI 218	INDI 218 PLS 1	Colorectum	0.054	0.564	0.06	0.15
0.034	0.028	0.11	Colorectum		Lung	
INDI 219	INDI 219 PLS 1	Liver	0.036	0.492	0.124	

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	0.162	0.008	0.026	0.152	Colorectum		Lung	
	INDI 220	INDI 220 PLS 1		Lung	0.12	0.206	0.004	
	0.378	0.246	0.014	0.032	Lung		Ovary	
	INDI 221	INDI 221 PLS 1		Colorectum	0.034	0.17	0.032	
	0.606	0.098	0.01	0.05	Lung			
Colorectum								
	INDI 222	INDI 222 PLS 1		Colorectum	0.038	0.434	0.026	
	0.204	0.134	0.084	0.08	Colorectum		Lung	
	INDI 224	INDI 224 PLS 1		Lung	0.04	0.316	0.076	
	0.224	0.116	0.018	0.21	Colorectum		Lung	
	INDI 225	INDI 225 PLS 1		Colorectum	0.052	0.252	0.056	
	0.044	0.028	0.478	0.09	Pancreas			
Colorectum								
	INDI 227	INDI 227 PLS 1		Lung	0.032	0.446	0.018	
	0.35	0.03	0.018	0.106	Colorectum		Lung	
	INDI 229	INDI 229 PLS 1		Colorectum	0.04	0.388	0.056	
	0.188	0.054	0.05	0.224	Colorectum		Upper GI	
	INDI 230	INDI 230 PLS 1		Colorectum	0.11	0.238	0.032	
	0.47	0.026	0.052	0.072	Lung			
Colorectum								
	INDI 231	INDI 231 PLS 1		Lung	0.07	0.246	0.036	
	0.372	0.234	0.016	0.026	Lung			
Colorectum								
	INDI 233	INDI 233 PLS 1		Colorectum	0.082	0.302	0.022	
	0.276	0.174	0.06	0.084	Colorectum		Lung	
	INDI 238	INDI 238 PLS 1		Liver	0.172	0.146	0.148	
	0.074	0.068	0.312	0.08	Pancreas		Breast	
	INDI 239	INDI 239 PLS 1		Lung	0.092	0.356	0.156	
	0.146	0.036	0.136	0.078	Colorectum		Liver	
	INDI 243	INDI 243 PLS 1		Colorectum	0.06	0.648	0.022	
	0.088	0.048	0.108	0.026	Colorectum		Pancreas	
	INDI 244	INDI 244 PLS 1		Colorectum	0.02	0.69	0.036	
	0.082	0.032	0.112	0.028	Colorectum		Pancreas	
	INDI 245	INDI 245 PLS 1		Colorectum	0.084	0.468	0.016	
	0.11	0.126	0.176	0.02	Colorectum		Pancreas	
	INDI 247	INDI 247 PLS 1		Lung	0.244	0.358	0.06	
	0.156	0.06	0.076	0.046	Colorectum		Breast	
	INDI 250	INDI 250 PLS 1		Colorectum	0.036	0.53	0.024	
	0.244	0.02	0.084	0.062	Colorectum		Lung	
	INDI 251	INDI 251 PLS 1		Colorectum	0.032	0.78	0.02	
	0.072	0.006	0.056	0.034	Colorectum		Lung	
	INDI 252	INDI 252 PLS 1		Lung	0.348	0.188	0.07	
	0.178	0.082	0.048	0.086	Breast			
Colorectum								
	INDI 255	INDI 255 PLS 1		Colorectum	0.292	0.324	0.018	
	0.128	0.168	0.062	0.008	Colorectum		Breast	
	INDI 256	INDI 256 PLS 1		Colorectum	0.178	0.394	0.062	
	0.09	0.098	0.15	0.028	Colorectum		Breast	

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INDI 257	INDI 257 PLS 1	Lung	0.078	0.412	0.082	0.134	0.024	0.148
0.122	Colorectum	Pancreas						
INDI 259	INDI 259 PLS 1	Colorectum	0.048	0.536	0.038	0.186	0.026	0.084
0.082	Colorectum	Lung						
INDI 266	INDI 266 PLS 1	Lung	0.072	0.154	0.028	0.622	0.024	0.016
0.084	Lung	Colorectum						
INDI 268	INDI 268 PLS 1	Colorectum	0.13	0.556	0.012	0.12	0.03	0.13
0.022	Colorectum	Breast						
INDI 273	INDI 273 PLS 1	Lung	0.302	0.212	0.038	0.23	0.07	0.054
0.094	Breast	Lung						
INDI 276	INDI 276 PLS 1	Liver	0.044	0.13	0.474	0.064	0.016	0.184
0.088	Liver	Pancreas						
INDI 278	INDI 278 PLS 1	Ovary	0.142	0.19	0.01	0.034	0.464	0.148
0.012	Ovary	Colorectum						
INDI 279	INDI 279 PLS 1	Colorectum	0.164	0.426	0.006	0.156	0.146	0.086
0.016	Colorectum	Breast						
INDI 284	INDI 284 PLS 1	Colorectum	0.088	0.5	0.054	0.214	0.04	0.05
0.054	Colorectum	Lung						
INDI 285	INDI 285 PLS 1	Lung	0.234	0.2	0.038	0.288	0.174	0.042
0.024	Lung	Breast						
INDI 287	INDI 287 PLS 1	Breast	0.348	0.286	0.034	0.166	0.044	0.084
0.038	Breast	Colorectum						
INDI 288	INDI 288 PLS 1	Lung	0.15	0.2	0.092	0.046	0.286	0.146
0.08	Ovary	Colorectum						
INDI 290	INDI 290 PLS 1	Colorectum	0.07	0.564	0.018	0.11	0.036	0.148
0.054	Colorectum	Pancreas						
INDI 293	INDI 293 PLS 1	Colorectum	0.166	0.48	0.018	0.19	0.042	0.086
0.018	Colorectum	Lung						
INDI 295	INDI 295 PLS 1	Colorectum	0.22	0.592	0.048	0.044	0.028	0.012
0.056	Colorectum	Breast						
INDI 296	INDI 296 PLS 1	Colorectum	0.078	0.702	0.09	0.056	0.012	0.01
0.052	Colorectum	Liver						
INDI 297	INDI 297 PLS 1	Breast	0.322	0.358	0.022	0.14	0.102	0.006
0.05	Colorectum	Breast						
INDI 298	INDI 298 PLS 1	Colorectum	0.168	0.714	0.02	0.03	0.016	0.006
0.046	Colorectum	Breast						
INDI 299	INDI 299 PLS 1	Colorectum	0.034	0.57	0.088	0.02	0.016	0.054
0.218	Colorectum	Upper GI						
INDI 300	INDI 300 PLS 1	Breast	0.644	0.238	0.02	0.048	0.012	0.008
0.03	Breast	Colorectum						
INDI 301	INDI 301 PLS 1	Breast	0.55	0.188	0.03	0.108	0.042	0.014
0.068	Breast	Colorectum						

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INDI 302	INDI 302 PLS 1	Colorectum	0.058	0.588	0.174	0.042	0.002	0.012
0.124	Colorectum	Liver						
INDI 303	INDI 303 PLS 1	Colorectum	0.152	0.472	0.094	0.144	0.004	0.05
0.084	Colorectum	Breast						
INDI 304	INDI 304 PLS 1	Colorectum	0.024	0.286	0.246	0.026	0	0.016
0.402	Upper GI	Colorectum						
INDI 305	INDI 305 PLS 1	Colorectum	0.106	0.406	0.158	0.058	0.016	0.054
0.202	Colorectum	Upper GI						
INDI 306	INDI 306 PLS 1	Colorectum	0.038	0.552	0.084	0.09	0.038	0.036
0.162	Colorectum	Upper GI						
INDI 307	INDI 307 PLS 1	Colorectum	0.066	0.438	0.104	0.054	0.014	0.034
0.29	Colorectum	Upper GI						
INDI 308	INDI 308 PLS 1	Liver	0.04	0.238	0.358	0.042	0.008	0.016
0.298	Liver	Upper GI						
INDI 309	INDI 309 PLS 1	Colorectum	0.064	0.474	0.078	0.018	0.002	0.018
0.346	Colorectum	Upper GI						
INDI 310	INDI 310 PLS 1	Colorectum	0.01	0.222	0.172	0.024	0.004	0.002
0.566	Upper GI	Colorectum						
INDI 311	INDI 311 PLS 1	Colorectum	0.144	0.426	0.034	0.016	0.006	0.014
0.36	Colorectum	Upper GI						
INDI 313	INDI 313 PLS 1	Esophagus	0.042	0.298	0.218	0.048	0.008	0.038
0.348	Upper GI	Colorectum						
INDI 314	INDI 314 PLS 1	Colorectum	0.204	0.464	0.056	0.034	0.018	0.004
0.22	Colorectum	Upper GI						
INDI 318	INDI 318 PLS 1	Stomach	0.048	0.318	0.082	0.206	0.082	0.156
0.108	Colorectum	Lung						
INDI 320	INDI 320 PLS 1	Colorectum	0.036	0.45	0.086	0.056	0.014	0.228
0.13	Colorectum	Pancreas						
INDI 322	INDI 322 PLS 1	Colorectum	0.054	0.482	0.044	0.102	0.016	0.23
0.072	Colorectum	Pancreas						
INDI 324	INDI 324 PLS 1	Lung	0.218	0.226	0.01	0.406	0.062	0.03
0.048	Lung	Colorectum						
INDI 325	INDI 325 PLS 1	Colorectum	0.21	0.47	0.04	0.084	0.03	0.138
0.028	Colorectum	Breast						
INDI 326	INDI 326 PLS 1	Lung	0.04	0.278	0.048	0.422	0.022	0.072
0.118	Lung	Colorectum						
INDI 327	INDI 327 PLS 1	Colorectum	0.214	0.494	0.034	0.138	0.056	0.042
0.022	Colorectum	Breast						
INDI 328	INDI 328 PLS 1	Colorectum	0.114	0.48	0.026	0.094	0.124	0.104
0.058	Colorectum	Ovary						
INDI 329	INDI 329 PLS 1	Colorectum	0.082	0.254	0.124	0.018	0.026	0.404
0.092	Pancreas	Colorectum						

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INDI 331	INDI 331 PLS 1A	Lung	0.122	0.372	0.006	0.336	0.088	0.032
0.044	Colorectum	Lung	INDI 335	INDI 335 PLS 1A	Lung	0.18	0.47	0.004
0.146	0.112	0.064	0.024	Colorectum	Breast	INDI 336	INDI 336 PLS 1A	Lung
0.028	0.232	0.026	0.56	0.024	0.024	0.106	Lung	Colorectum
INDI 338	INDI 338 PLS 1	Colorectum	0.096	0.31	0.036	0.052	0.096	0.39
0.02	Pancreas	Colorectum	INDI 340	INDI 340 PLS 1	Colorectum	0.028	0.45	0.084
0.092	0.074	0.164	0.108	Colorectum	Pancreas	INDI 341	INDI 341 PLS 1	Liver
0.126	0.202	0.13	0.056	0.068	0.266	0.152	Pancreas	Colorectum
INDI 344	INDI 344 PLS 1	Colorectum	0.078	0.204	0.052	0.064	0.026	0.532
0.044	Pancreas	Colorectum	INDI 346	INDI 346 PLS 1A	Lung	0.034	0.162	0.018
0.7	0.03	0.024	0.032	Lung	Colorectum	INDI 353	INDI 353 PLS 1A	Lung
0.102	0.312	0.012	0.328	0.176	0.044	0.026	Lung	Colorectum
INDI 354	INDI 354 PLS 1	Colorectum	0.142	0.448	0.052	0.15	0.104	0.062
0.042	Colorectum	Lung	INDI 355	INDI 355 PLS 1A	Lung	0.074	0.412	0.016
0.37	0.014	0.056	0.058	Colorectum	Lung	INDI 356	INDI 356 PLS 1	Colorectum
0.222	0.386	0.056	0.12	0.084	0.096	0.036	Colorectum	Breast
INDI 360	INDI 360 PLS 1A	Lung	0.23	0.23	0.004	0.392	0.06	0.016
0.068	Lung	Breast	INDI 365	INDI 365 PLS 1	Colorectum	0.088	0.438	0.08
0.126	0.08	0.114	0.074	Colorectum	Lung	INDI 366	INDI 366 PLS 1	Pancreas
0.052	0.282	0.054	0.06	0.078	0.448	0.026	Pancreas	Colorectum
INDI 367	INDI 367 PLS 1	Liver	0.112	0.24	0.106	0.122	0.038	0.32
0.062	Pancreas	Colorectum	INDI 368	INDI 368 PLS 1	Breast	0.044	0.376	0.09
0.138	0.018	0.2	0.134	Colorectum	Pancreas	INDI 371	INDI 371 PLS 1A	Lung
0.046	0.364	0.022	0.254	0.106	0.084	0.124	Colorectum	Lung
INDI 372	INDI 372 PLS 1A	Lung	0.104	0.37	0.026	0.356	0.064	0.05
0.03	Colorectum	Lung	INDI 374	INDI 374 PLS 1	Colorectum	0.062	0.542	0.044
0.078	0.016	0.164	0.094	Colorectum	Pancreas			

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INDI 375	INDI 375 PLS 1	Liver	0.106	0.212	0.136	0.212	0.178	0.05
0.106	Colorectum	Lung	INDI 377	INDI 377 PLS 1	Colorectum	0.168	0.37	0.034
0.166	0.114	0.068	0.08	Colorectum	Breast	INDI 380	INDI 380 PLS 1	Colorectum
0.062	0.618	0.036	0.088	0.016	0.124	0.056	Colorectum	Pancreas
INDI 383	INDI 383 PLS 1A	Lung	0.054	0.422	0.018	0.314	0.046	0.046
0.1	Colorectum	Lung	INDI 387	INDI 387 PLS 1	Liver	0.124	0.302	0.066
0.246	0.02	0.116	0.126	Colorectum	Lung	INDI 388	INDI 388 PLS 1	Pancreas
0.044	0.502	0.052	0.168	0.064	0.138	0.032	Colorectum	Lung
INDI 389	INDI 389 PLS 1A	Lung	0.262	0.222	0.046	0.146	0.136	0.136
0.052	Breast	Colorectum	INDI 391	INDI 391 PLS 1	Liver	0.114	0.456	0.152
0.1	0.04	0.02	0.118	Colorectum	Liver	INDI 393	INDI 393 PLS 1	Liver
0.034	0.174	0.498	0.058	0.018	0.106	0.112	Liver	Colorectum
INDI 394	INDI 394 PLS 1A	Lung	0.042	0.386	0.056	0.284	0.032	0.09
0.11	Colorectum	Lung	INDI 396	INDI 396 PLS 1	Colorectum	0.118	0.328	0.038
0.28	0.012	0.1	0.124	Colorectum	Lung	INDI 397	INDI 397 PLS 1	Colorectum
0.062	0.53	0.046	0.152	0.02	0.078	0.112	Colorectum	Lung
INDI 400	INDI 400 PLS 1	Colorectum	0.114	0.446	0.024	0.098	0.048	0.256
0.014	Colorectum	Pancreas	INDI 412	INDI 412 PLS 1	Breast	0.328	0.248	0.084
0.12	0.038	0.09	0.092	Breast	Colorectum	INDI 413	INDI 413 PLS 1	Lung
0.206	0.162	0.01	0.234	0.342	0.016	0.03	Ovary	Lung
INDI 415	INDI 415 PLS 1	Lung	0.02	0.136	0.314	0.318	0.056	0.028
0.128	Lung	Liver	INDI 417	INDI 417 PLS 1	Lung	0.068	0.422	0.056
0.344	0.016	0.03	0.064	Colorectum	Lung	INDI 418	INDI 418 PLS 1	Colorectum
0.09	0.662	0.032	0.054	0.014	0.022	0.126	Colorectum	Upper GI
INDI 422	INDI 422 PLS 1	Colorectum	0.038	0.636	0.042	0.054	0.026	0.032
0.172	Colorectum	Upper GI	INDI 423	INDI 423 PLS 1	Colorectum	0.04	0.514	0.08
0.066	0.01	0.016	0.274	Colorectum	Upper GI	INDI 427	INDI 427 PLS 1	Colorectum
0.06	0.526	0.086	0.046	0.058	0.094	0.13	Colorectum	Upper GI
INDI 429	INDI 429 PLS 1	Colorectum	0.062	0.606	0.084	0.054	0.044	0.028
0.122	Colorectum	Upper GI	INDI 433	INDI 433 PLS 1	Colorectum	0.096	0.356	0.122

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0.142	0.118	0.094	0.072	Colorectum		Lung		
INDI 437	INDI 437 PLS 1	Colorectum	0.09	0.566	0.042	0.07	0.014	0.08
0.138	Colorectum		Upper GI					
INDI 439	INDI 439 PLS 1	Colorectum	0.05	0.454	0.124	0.02	0.014	0.072
0.266	Colorectum		Upper GI					
INDI 440	INDI 440 PLS 1	Esophagus	0.012	0.294	0.152	0.012	0.008	0.02
0.502	Upper GI							
Colorectum								
INDI 441	INDI 441 PLS 1	Esophagus	0.016	0.208	0.124	0.006	0	0.002
0.644	Upper GI							
Colorectum								
INDI 442	INDI 442 PLS 1	Breast	0.452	0.294	0.026	0.098	0.042	0.016
0.072	Breast							
Colorectum								
INDI 443	INDI 443 PLS 1	Breast	0.438	0.256	0.036	0.14	0.026	0.028
0.076	Breast							
Colorectum								
INDI 444	INDI 444 PLS 1	Colorectum	0.096	0.304	0.176	0.054	0.008	0.106
0.256	Colorectum		Upper GI					
INDI 445	INDI 445 PLS 1	Breast	0.25	0.198	0.054	0.104	0.116	0.246
0.032	Breast		Pancreas					
INDI 446	INDI 446 PLS 1	Esophagus	0.054	0.366	0.184	0.04	0.02	0.062
0.274	Colorectum		Upper GI					
INDI 447	INDI 447 PLS 1	Breast	0.394	0.098	0.122	0.054	0.126	0.146
0.06	Breast		Pancreas					
INDI 449	INDI 449 PLS 1	Breast	0.576	0.256	0.026	0.042	0.008	0.006
0.086	Breast							
Colorectum								
INDI 450	INDI 450 PLS 1	Esophagus	0.042	0.338	0.238	0.02	0.002	0.026
0.334	Colorectum		Upper GI					
INDI 452	INDI 452 PLS 1	Colorectum	0.008	0.3	0.18	0.014	0.004	0.02
0.474	Upper GI							
Colorectum								
INDI 453	INDI 453 PLS 1	Breast	0.338	0.342	0.048	0.156	0.04	0.022
0.054	Colorectum		Breast					
INDI 454	INDI 454 PLS 1	Breast	0.612	0.254	0.018	0.062	0.01	0.026
0.018	Breast							
Colorectum								
INDI 456	INDI 456 PLS 1	Colorectum	0.188	0.464	0.056	0.026	0.036	0.066
0.164	Colorectum		Breast					
INDI 457	INDI 457 PLS 1	Esophagus	0.02	0.274	0.248	0.016	0.024	0.184
0.234	Colorectum		Liver					
INDI 458	INDI 458 PLS 1	Breast	0.23	0.272	0.11	0.038	0.06	0.162
0.128	Colorectum		Breast					
INDI 459	INDI 459 PLS 1	Breast	0.302	0.252	0.13	0.094	0.046	0.032
0.144	Breast							
Colorectum								
INDI 461	INDI 461 PLS 1	Colorectum	0.06	0.558	0.084			

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	0.076	0.002	0.014	0.206	Colorectum			Upper GI
	INDI 462	INDI 462 PLS 1		Breast	0.316	0.136		0.102
	0.03	0.084	0.246	0.086	Breast			Pancreas
	INDI 463	INDI 463 PLS 1		Colorectum	0.104	0.64		0.056
	0.048	0.046	0.022	0.084	Colorectum			Breast
	INDI 464	INDI 464 PLS 1		Liver	0.126	0.188		0.204
	0.038	0.118	0.066	0.26	Upper GI			Liver
	INDI 465	INDI 465 PLS 1		Esophagus	0.016	0.294		0.162
	0.014	0.02	0.018	0.476	Upper GI			
Colorectum								
	INDI 466	INDI 466 PLS 1		Colorectum	0.272	0.428		0.086
	0.058	0.038	0.024	0.094	Colorectum			Breast
	INDI 467	INDI 467 PLS 1		Colorectum	0.238	0.488		0.088
	0.026	0.018	0.03	0.112	Colorectum			Breast
	INDI 468	INDI 468 PLS 1		Colorectum	0.158	0.57		0.048
	0.036	0.054	0.032	0.102	Colorectum			Breast
	INDI 470	INDI 470 PLS 1		Colorectum	0.254	0.454		0.066
	0.076	0.038	0.018	0.094	Colorectum			Breast
	INDI 472	INDI 472 PLS 1		Colorectum	0.21	0.48		0.038
	0.106	0.078	0.014	0.074	Colorectum			Breast
	INDI 473	INDI 473 PLS 1		Breast	0.288	0.372		0.056
	0.104	0.082	0.038	0.06	Colorectum			Breast
	INDI 474	INDI 474 PLS 1		Breast	0.346	0.356		0.072
	0.032	0.036	0.084	0.074	Colorectum			Breast
	INDI 475	INDI 475 PLS 1		Liver	0.042	0.472		0.108
	0.02	0.01	0.042	0.306	Colorectum			Upper GI
	INDI 476	INDI 476 PLS 1		Esophagus	0.048	0.338		0.204
	0.038	0.012	0.028	0.332	Colorectum			Upper GI
	INDI 477	INDI 477 PLS 1		Colorectum	0.054	0.386		0.062
	0.118	0.012	0.01	0.358	Colorectum			Upper GI
	INDI 478	INDI 478 PLS 1		Breast	0.498	0.214		0.042
	0.072	0.014	0.124	0.036	Breast			
Colorectum								
	INDI 480	INDI 480 PLS 1		Breast	0.48	0.304		0.024
	0.086	0.014	0.02	0.072	Breast			
Colorectum								
	INDI 482	INDI 482 PLS 1		Liver	0.184	0.24		0.39
	0.028	0.016	0.016	0.126	Liver			
Colorectum								
	INDI 489	INDI 489 PLS 1		Breast	0.36	0.2		0.012
	0.312	0.06	0.018	0.038	Breast			Lung
	INDI 490	INDI 490 PLS 1		Breast	0.288	0.162		0.11
	0.122	0.162	0.12	0.036	Breast			
Colorectum								
	INDI 494	INDI 494 PLS 1		Lung	0.13	0.238		0.104
	0.326	0.03	0.036	0.136	Lung			
Colorectum								
	INDI 503	INDI 503 PLS 1		Lung	0.056	0.21		0.064

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0.444	0.006	0.008	0.212	Lung		Upper GI
INDI 505	INDI 505 PLS 1		Lung	0.046	0.332	0.178
0.19	0.016	0.01	0.228	Colorectum		Upper GI
INDI 506	INDI 506 PLS 1		Colorectum	0.072	0.404	0.026
0.236	0.178	0.068	0.016	Colorectum		Lung
INDI 507	INDI 507 PLS 1		Lung	0.112	0.16	0.118
0.39	0.006	0.044	0.17	Lung		Upper GI
INDI 514	INDI 514 PLS 1		Stomach	0.076	0.224	0.062
0.52	0.016	0.02	0.082	Lung		
Colorectum						
INDI 515	INDI 515 PLS 1		Colorectum	0.054	0.452	0.044
0.322	0.024	0.08	0.024	Colorectum		Lung
INDI 516	INDI 516 PLS 1		Pancreas	0.058	0.36	0.024
0.3	0.066	0.15	0.042	Colorectum		Lung
INDI 518	INDI 518 PLS 1		Colorectum	0.072	0.492	0.07
0.194	0.016	0.136	0.02	Colorectum		Lung
INDI 521	INDI 521 PLS 1		Colorectum	0.092	0.492	0.036
0.204	0.066	0.088	0.022	Colorectum		Lung
INDI 523	INDI 523 PLS 1		Colorectum	0.056	0.354	0.032
0.138	0.04	0.34	0.04	Colorectum		Pancreas
INDI 524	INDI 524 PLS 1		Lung	0.076	0.446	0.08
0.108	0.02	0.07	0.2	Colorectum		Upper GI
INDI 525	INDI 525 PLS 1		Colorectum	0.066	0.472	0.06
0.244	0.022	0.122	0.014	Colorectum		Lung
INDI 526	INDI 526 PLS 1		Esophagus	0.102	0.176	0.018
0.504	0.024	0.078	0.098	Lung		
Colorectum						
INDI 527	INDI 527 PLS 1		Colorectum	0.12	0.448	0.012
0.24	0.106	0.062	0.012	Colorectum		Lung
INDI 528	INDI 528 PLS 1		Colorectum	0.062	0.582	0.026
0.156	0.03	0.05	0.094	Colorectum		Lung
INDI 533	INDI 533 PLS 1		Pancreas	0.058	0.396	0.02
0.118	0.072	0.288	0.048	Colorectum		Pancreas
INDI 535	INDI 535 PLS 1		Lung	0.02	0.332	0.022
0.43	0.012	0.008	0.176	Lung		
Colorectum						
INDI 538	INDI 538 PLS 1		Lung	0.116	0.206	0.008
0.484	0.012	0.032	0.142	Lung		
Colorectum						
INDI 539	INDI 539 PLS 1		Colorectum	0.108	0.47	0.028
0.164	0.096	0.08	0.054	Colorectum		Lung
INDI 544	INDI 544 PLS 1		Colorectum	0.048	0.4	0.008
0.434	0.02	0.022	0.068	Lung		
Colorectum						
INDI 545	INDI 545 PLS 1		Lung	0.396	0.126	0.008
0.388	0.048	0.01	0.024	Breast		Lung
INDI 548	INDI 548 PLS 1		Breast	0.37	0.214	0.028
0.222	0.072	0.02	0.074	Breast		Lung

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INDI 549	INDI 549 PLS 1	Lung	0.332	0.366	0.022	0.122	0.092	0.01
0.056	Colorectum	Breast	INDI 551	INDI 551 PLS 1	Colorectum	0.048	0.54	0.022
0.248	0.048	0.062	0.032	Colorectum	Lung	INDI 555	INDI 555 PLS 1	Colorectum
0.022	0.598	0.028	0.232	0.022	0.024	0.074	Colorectum	Lung
INDI 558	INDI 558 PLS 1	Colorectum	0.106	0.526	0.106	0.122	0.008	0.042
0.09	Colorectum	Lung	INDI 562	INDI 562 PLS 1	Colorectum	0.118	0.508	0.182
0.034	0.008	0.036	0.114	Colorectum	Liver	INDI 564	INDI 564 PLS 1	Colorectum
0.06	0.626	0.046	0.074	0.01	0.01	0.174	Colorectum	Upper GI
INDI 567	INDI 567 PLS 1	Colorectum	0.078	0.398	0.156	0.05	0.004	0.064
0.25	Colorectum	Upper GI	INDI 570	INDI 570 PLS 1	Colorectum	0.042	0.46	0.122
0.04	0.008	0.072	0.256	Colorectum	Upper GI	INDI 574	INDI 574 PLS 1	Colorectum
0.248	0.4	0.032	0.186	0.064	0.01	0.06	Colorectum	Breast
INDI 575	INDI 575 PLS 1	Breast	0.526	0.202	0.044	0.138	0.014	0.02
0.056	Breast	Colorectum	INDI 581	INDI 581 PLS 1	Colorectum	0.114	0.324	0.106
0.054	0.062	0.036	0.304	Colorectum	Upper GI	INDI 582	INDI 582 PLS 1	Colorectum
0.028	0.478	0.1	0.008	0.008	0.01	0.368	Colorectum	Upper GI
INDI 583	INDI 583 PLS 1	Colorectum	0.156	0.55	0.036	0.03	0.052	0.02
0.156	Colorectum	Breast	INDI 584	INDI 584 PLS 1	Colorectum	0.034	0.412	0.09
0.056	0.014	0.024	0.37	Colorectum	Upper GI	INDI 585	INDI 585 PLS 1	Esophagus
0.022	0.322	0.068	0.028	0.01	0.024	0.526	Upper GI	Colorectum
INDI 586	INDI 586 PLS 1	Liver	0.088	0.264	0.258	0.064	0.066	0.082
0.178	Colorectum	Liver	INDI 587	INDI 587 PLS 1	Colorectum	0.044	0.412	0.076
0.088	0.008	0.036	0.336	Colorectum	Upper GI	INDI 591	INDI 591 PLS 1	Colorectum
0.012	0.504	0.138	0.004	0.01	0.03	0.302	Colorectum	Upper GI
INDI 593	INDI 593 PLS 1	Breast	0.196	0.332	0.248	0.026	0.004	0.064
0.13	Colorectum	Liver	INDI 594	INDI 594 PLS 1	Colorectum	0.43	0.312	0.018
0.098	0.03	0.006	0.106	Breast	Colorectum	INDI 595	INDI 595 PLS 1	Esophagus
0.032	0.234	0.154	0.014	0.014	0.022	0.53	Upper GI	Colorectum
INDI 598	INDI 598 PLS 1	Colorectum	0.088	0.534	0.102	0.078	0.006	0.024
0.168	Colorectum	Upper GI						

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INDI 599	INDI 599 PLS 1	Colorectum	0.642	0.178	0.012	0.074
0.02	0.032	0.042	Breast	Colorectum		
INDI 601	INDI 601 PLS 1	Breast	0.32	0.282	0.106	0.08
0.046	0.052	0.114	Breast	Colorectum		
INDI 602	INDI 602 PLS 1	Colorectum	0.118	0.516	0.148	0.036
0.044	0.018	0.12	Colorectum	Liver		
INDI 604	INDI 604 PLS 1	Breast	0.272	0.526	0.028	0.048
0.032	0.018	0.076	Colorectum	Breast		
INDI 605	INDI 605 PLS 1	Colorectum	0.098	0.502	0.08	0.012
0.026	0.01	0.272	Colorectum	Upper GI		
INDI 608	INDI 608 PLS 1	Colorectum	0.126	0.624	0.034	0.08
0.098	0.012	0.026	Colorectum	Breast		
INDI 609	INDI 609 PLS 1	Colorectum	0.092	0.464	0.128	0.102
0.024	0.024	0.166	Colorectum	Upper GI		
INDI 610	INDI 610 PLS 1	Colorectum	0.252	0.524	0.056	0.05
0.048	0.012	0.058	Colorectum	Breast		
INDI 611	INDI 611 PLS 1	Colorectum	0.038	0.606	0.076	0.068
0.004	0.018	0.19	Colorectum	Upper GI		
INDI 613	INDI 613 PLS 1	Breast	0.444	0.388	0.026	0.052
0.03	0.002	0.058	Breast	Colorectum		
INDI 614	INDI 614 PLS 1	Colorectum	0.202	0.538	0.084	0.054
0.018	0.006	0.098	Colorectum	Breast		
INDI 615	INDI 615 PLS 1	Colorectum	0.07	0.562	0.058	0.04
0.008	0.006	0.256	Colorectum	Upper GI		
INDI 617	INDI 617 PLS 1	Colorectum	0.054	0.51	0.08	0.132
0.038	0.062	0.124	Colorectum	Lung		
INDI 618	INDI 618 PLS 1	Colorectum	0.058	0.47	0.04	0.114
0.024	0.054	0.24	Colorectum	Upper GI		
INDI 620	INDI 620 PLS 1	Colorectum	0.03	0.44	0.102	0.034
0.006	0.022	0.366	Colorectum	Upper GI		
INDI 621	INDI 621 PLS 1	Colorectum	0.062	0.55	0.072	0.062
0.002	0.022	0.23	Colorectum	Upper GI		
INDI 622	INDI 622 PLS 1	Liver	0.022	0.19	0.528	0.012
0.01	0.032	0.206	Liver	Upper GI		
INDI 623	INDI 623 PLS 1	Breast	0.2	0.33	0.028	0.114
0.25	0.022	0.056	Colorectum	Ovary		
INDI 624	INDI 624 PLS 1	Colorectum	0.098	0.67	0.02	0.094
0.05	0.026	0.042	Colorectum	Breast		
INDI 625	INDI 625 PLS 1	Colorectum	0.32	0.474	0.04	0.102
0.012	0.012	0.04	Colorectum	Breast		
INDI 626	INDI 626 PLS 1	Colorectum	0.072	0.406	0.118	0.044
0.026	0.14	0.194	Colorectum	Upper GI		
INDI 627	INDI 627 PLS 1	Breast	0.39	0.392	0.05	0.062
0.06	0.01	0.036	Colorectum	Breast		
INDI 628	INDI 628 PLS 1	Colorectum	0.184	0.548	0.054	

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0.104	0.01	0	0.1	Colorectum		Breast		
INDI 631	INDI 631 PLS 1		Colorectum	0.128	0.612	0.04		
0.064	0.026	0.006	0.124	Colorectum		Breast		
INDI 632	INDI 632 PLS 1		Colorectum	0.152	0.382	0.16		
0.052	0.034	0.104	0.116	Colorectum		Liver		
INDI 633	INDI 633 PLS 1		Colorectum	0.262	0.486	0.036		
0.094	0.018	0.012	0.092	Colorectum		Breast		
INDI 635	INDI 635 PLS 1		Colorectum	0.032	0.684	0.034		
0.058	0.03	0.122	0.04	Colorectum		Pancreas		
INDI 636	INDI 636 PLS 1		Liver	0.072	0.486	0.068		
0.162	0.024	0.018	0.17	Colorectum		Upper GI		
INDI 637	INDI 637 PLS 1		Breast	0.404	0.214	0.038		
0.192	0.042	0.002	0.108	Breast				
Colorectum								
INDI 638	INDI 638 PLS 1		Breast	0.412	0.232	0.022		
0.236	0.042	0.006	0.05	Breast		Lung		
INDI 639	INDI 639 PLS 1		Liver	0.08	0.172	0.422		
0.044	0.014	0.06	0.208	Liver		Upper GI		
INDI 640	INDI 640 PLS 1		Colorectum	0.024	0.738	0.038		
0.034	0.022	0.054	0.09	Colorectum		Upper GI		
INDI 643	INDI 643 PLS 1		Colorectum	0.032	0.748	0.026		
0.05	0.07	0.008	0.066	Colorectum		Ovary		
INDI 644	INDI 644 PLS 1		Colorectum	0.022	0.678	0.032		
0.11	0.024	0.078	0.056	Colorectum		Lung		
INDI 645	INDI 645 PLS 1		Liver	0.052	0.206	0.428		
0.03	0.008	0.046	0.23	Liver		Upper GI		
INDI 647	INDI 647 PLS 1		Colorectum	0.094	0.404	0.074		
0.016	0.024	0.286	0.102	Colorectum		Pancreas		
INDI 648	INDI 648 PLS 1		Colorectum	0.058	0.408	0.064		
0.06	0.072	0.12	0.218	Colorectum		Upper GI		
INDI 649	INDI 649 PLS 1		Colorectum	0.02	0.65	0.048		
0.068	0.032	0.102	0.08	Colorectum		Pancreas		
INDI 651	INDI 651 PLS 1		Colorectum	0.016	0.678	0.02		
0.056	0.054	0.082	0.094	Colorectum		Upper GI		
INDI 654	INDI 654 PLS 1		Colorectum	0.024	0.618	0.05		
0.012	0.026	0.108	0.162	Colorectum		Upper GI		
INDI 657	INDI 657 PLS 1		Colorectum	0.08	0.424	0.048		
0.06	0.118	0.078	0.192	Colorectum		Upper GI		
INDI 658	INDI 658 PLS 1		Colorectum	0.1	0.38	0.036		
0.074	0.296	0.048	0.066	Colorectum		Ovary		
INDI 660	INDI 660 PLS 1		Colorectum	0.052	0.71	0.008		
0.048	0.096	0.008	0.078	Colorectum		Ovary		
INDI 661	INDI 661 PLS 1		Liver	0.166	0.414	0.086		
0.026	0.052	0.028	0.228	Colorectum		Upper GI		
INDI 663	INDI 663 PLS 1		Esophagus	0.014	0.226	0.378		
0.014	0.004	0.016	0.348	Liver		Upper GI		
INDI 665	INDI 665 PLS 1		Esophagus	0.054	0.432	0.106		
0.018	0.006	0.04	0.344	Colorectum		Upper GI		

Table6.txt

INDI 669	INDI 669 PLS 1	Liver	0.01	0.132	0.522	0.048	0.008	0.016
0.264	Liver	Upper GI	INDI 670	INDI 670 PLS 1	Colorectum	0.042	0.39	0.034
0.222	0.032	0.206	0.074	Colorectum	Lung	INDI 671	INDI 671 PLS 1	Lung
0.312	0.11	0.024	0.432	0.052	0.014	0.056	Lung	Breast
INDI 673	INDI 673 PLS 1	Breast	0.382	0.134	0.06	0.222	0.074	0.048
0.08	Breast	Lung	INDI 675	INDI 675 PLS 1	Colorectum	0.03	0.43	0.036
0.128	0.132	0.182	0.062	Colorectum	Pancreas	INDI 678	INDI 678 PLS 1	Colorectum
0.046	0.572	0.018	0.246	0.014	0.062	0.042	Colorectum	Lung
INDI 686	INDI 686 PLS 1	Pancreas	0.116	0.222	0.076	0.062	0.036	0.416
0.072	Pancreas	Colorectum	INDI 687	INDI 687 PLS 1	Lung	0.044	0.342	0.172
0.146	0.048	0.05	0.198	Colorectum	Upper GI	INDI 688	INDI 688 PLS 1	Colorectum
0.272	0.19	0.006	0.378	0.1	0.044	0.01	Lung	Breast
INDI 691	INDI 691 PLS 1	Lung	0.442	0.33	0.048	0.038	0.04	0.044
0.058	Breast	Colorectum	INDI 692	INDI 692 PLS 1	Colorectum	0.104	0.306	0.08
0.068	0.074	0.306	0.062	Colorectum	Colorectum	INDI 693	INDI 693 PLS 1	Lung
0.088	0.292	0.15	0.202	0.038	0.04	0.19	Colorectum	Lung
INDI 694	INDI 694 PLS 1	Lung	0.222	0.504	0.056	0.098	0.048	0.024
0.048	Colorectum	Breast	INDI 696	INDI 696 PLS 1	Lung	0.112	0.294	0.108
0.268	0.02	0.05	0.148	Colorectum	Lung	INDI 697	INDI 697 PLS 1	Breast
0.232	0.224	0.026	0.346	0.074	0.044	0.054	Lung	Breast
INDI 698	INDI 698 PLS 1	Ovary	0.242	0.13	0.01	0.258	0.262	0.078
0.02	Ovary	Lung	INDI 699	INDI 699 PLS 1	Pancreas	0.142	0.52	0.006
0.138	0.05	0.13	0.014	Colorectum	Breast	INDI 700	INDI 700 PLS 1	Lung
0.08	0.178	0.026	0.5	0.016	0.05	0.15	Lung	Colorectum
INDI 701	INDI 701 PLS 1	Colorectum	0.058	0.448	0.016	0.32	0.08	0.06
0.018	Colorectum	Lung	INDI 702	INDI 702 PLS 1	Lung	0.046	0.506	0.026
0.226	0.064	0.084	0.048	Colorectum	Lung	INDI 706	INDI 706 PLS 1	Lung
0.326	0.286	0.002	0.086	0.076	0.21	0.014	Breast	Colorectum
INDI 708	INDI 708 PLS 1	Colorectum	0.018	0.722	0.026			

Table6.txt

0.134	0.006	0.072	0.022	Colorectum			Lung
INDI 710	INDI 710 PLS 1		Colorectum	0.144	0.462		0.02
0.128	0.1	0.136	0.01	Colorectum			Breast
INDI 711	INDI 711 PLS 1		Breast	0.394	0.274		0.022
0.11	0.064	0.102	0.034	Breast			
Colorectum							
INDI 714	INDI 714 PLS 1		Breast	0.272	0.336		0.044
0.164	0.038	0.1	0.046	Colorectum			Breast
INDI 715	INDI 715 PLS 1		Breast	0.536	0.156		0.032
0.062	0.056	0.124	0.034	Breast			
Colorectum							
INDI 716	INDI 716 PLS 1		Colorectum	0.044	0.47		0.07
0.078	0.054	0.194	0.09	Colorectum			Pancreas
INDI 723	INDI 723 PLS 1		Ovary	0.082	0.206		0.018
0.202	0.408	0.04	0.044	Ovary			
Colorectum							
INDI 734	INDI 734 PLS 1		Pancreas	0.09	0.24		0.012
0.076	0.142	0.426	0.014	Pancreas			
Colorectum							
INDI 735	INDI 735 PLS 1		Pancreas	0.056	0.394		0.06
0.156	0.03	0.258	0.046	Colorectum			Pancreas
INDI 736	INDI 736 PLS 1		Lung	0.048	0.43		0.076
0.238	0.05	0.076	0.082	Colorectum			Lung
INDI 737	INDI 737 PLS 1		Stomach	0.038	0.248		0.068
0.42	0.042	0.032	0.152	Lung			
Colorectum							
INDI 740	INDI 740 PLS 1		Pancreas	0.126	0.324		0.02
0.156	0.28	0.08	0.014	Colorectum			Ovary
INDI 741	INDI 741 PLS 1		Pancreas	0.036	0.068		0.038
0.004	0.03	0.818	0.006	Pancreas			
Colorectum							
INDI 745	INDI 745 PLS 1		Pancreas	0.046	0.186		0.038
0.036	0.014	0.654	0.026	Pancreas			
Colorectum							
INDI 746	INDI 746 PLS 1		Colorectum	0.052	0.582		0.052
0.048	0.01	0.078	0.178	Colorectum			Upper GI
INDI 747	INDI 747 PLS 1		Colorectum	0.046	0.636		0.034
0.042	0.062	0.036	0.144	Colorectum			Upper GI
INDI 749	INDI 749 PLS 1		Colorectum	0.118	0.594		0.006
0.108	0.084	0.058	0.032	Colorectum			Breast
INDI 750	INDI 750 PLS 1		Colorectum	0.036	0.618		0.024
0.092	0.04	0.126	0.064	Colorectum			Pancreas
INDI 751	INDI 751 PLS 1		Colorectum	0.012	0.764		0.006
0.106	0.04	0.038	0.034	Colorectum			Lung
INDI 752	INDI 752 PLS 1		Colorectum	0.036	0.654		0.02
0.13	0.044	0.038	0.078	Colorectum			Lung
INDI 753	INDI 753 PLS 1		Esophagus	0.004	0.414		0.044
0.002	0	0.008	0.528	Upper GI			

Table6.txt

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Colorectum
   INDI 755     INDI 755 PLS 1      Esophagus       0.044        0.486        0.118
    0.032     0.004        0.02         0.296         Colorectum           Upper GI
   INDI 758     INDI 758 PLS 1      Colorectum      0.038        0.614        0.046
    0.054     0.068       0.112         0.068         Colorectum           Pancreas
   INDI 760     INDI 760 PLS 1        Liver         0.044        0.142        0.566
    0.018       0         0.032         0.198           Liver              Upper GI
   INDI 761     INDI 761 PLS 1      Colorectum      0.062        0.606        0.048
    0.054      0.07         0.06          0.1         Colorectum           Upper GI
   INDI 764     INDI 764 PLS 1      Colorectum      0.024         0.61        0.044
    0.096      0.04         0.05         0.136         Colorectum           Upper GI
   INDI 765     INDI 765 PLS 1      Colorectum      0.018        0.352        0.288
    0.022     0.018       0.126         0.176         Colorectum            Liver
   INDI 767     INDI 767 PLS 1      Colorectum      0.048        0.624        0.028
    0.106     0.016       0.108         0.07          Colorectum           Pancreas
   INDI 769     INDI 769 PLS 1      Colorectum      0.036        0.616        0.052
    0.124      0.06         0.03         0.082         Colorectum             Lung
   INDI 770     INDI 770 PLS 1      Colorectum      0.09         0.746          0
    0.064      0.05        0.042         0.008         Colorectum            Breast
   INDI 771     INDI 771 PLS 1        Liver         0.02          0.31         0.3
     0.17     0.016       0.026         0.158         Colorectum            Liver
   INDI 774     INDI 774 PLS 1      Colorectum      0.056        0.684        0.014
    0.066     0.068        0.08         0.032         Colorectum           Pancreas
   INDI 775     INDI 775 PLS 1        Liver         0.022         0.24         0.41
    0.038     0.016        0.01         0.264           Liver              Upper GI
   INDI 776     INDI 776 PLS 1      Esophagus       0.046        0.424        0.084
    0.092     0.014       0.034         0.306         Colorectum           Upper GI
   INDI 777     INDI 777 PLS 1      Colorectum      0.226         0.45        0.004
    0.132     0.086       0.072         0.03          Colorectum            Breast
   INDI 778     INDI 778 PLS 1        Liver         0.026        0.252        0.328
    0.152      0.02        0.012         0.21            Liver
Colorectum
   INDI 779     INDI 779 PLS 1      Colorectum      0.168         0.54         0.01
     0.14     0.064       0.048         0.03          Colorectum            Breast
   INDI 780     INDI 780 PLS 1      Colorectum      0.184        0.432        0.004
    0.208      0.1         0.058         0.014         Colorectum             Lung
   INDI 781     INDI 781 PLS 1      Colorectum      0.036        0.728        0.008
     0.12     0.022       0.054         0.032         Colorectum            Lung
   INDI 782     INDI 782 PLS 1      Colorectum      0.088        0.504         0.02
    0.044     0.208       0.118         0.018         Colorectum           Ovary
   INDI 784     INDI 784 PLS 1       Stomach        0.098        0.266        0.278
    0.124     0.022        0.09         0.122           Liver
Colorectum
   INDI 786     INDI 786 PLS 1        Liver         0.028        0.268        0.216
    0.186     0.026       0.082         0.194         Colorectum           Liver
   INDI 797     INDI 797 PLS 1       Stomach        0.064        0.268        0.066
    0.402     0.022        0.07         0.108            Lung
Colorectum
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Table6.txt

INDI 798	INDI 798 PLS 1	Ovary	0.15	0.332	0.024	0.226	0.14	0.064
0.064	Colorectum	Lung						
INDI 800	INDI 800 PLS 1	Liver	0.074	0.15	0.376	0.162	0.008	0.032
0.198	Liver	Upper GI						
INDI 802	INDI 802 PLS 1	Pancreas	0.09	0.32	0.016	0.292	0.084	0.156
0.042	Colorectum	Lung						
INDI 812	INDI 812 PLS 1	Ovary	0.106	0.308	0.024	0.228	0.202	0.104
0.028	Colorectum	Lung						
INDI 815	INDI 815 PLS 1	Colorectum	0.06	0.596	0.014	0.184	0.08	0.032
0.034	Colorectum	Lung						
INDI 817	INDI 817 PLS 1	Liver	0.096	0.31	0.202	0.11	0.01	0.026
0.246	Colorectum	Upper GI						
INDI 818	INDI 818 PLS 1	Ovary	0.048	0.186	0.006	0.07	0.61	0.072
0.008	Ovary							
Colorectum								
INDI 819	INDI 819 PLS 1	Breast	0.304	0.282	0.004	0.284	0.07	0.026
0.03	Breast	Lung						
INDI 824	INDI 824 PLS 1	Esophagus	0.104	0.244	0.104	0.308	0.012	0.14
0.088	Lung							
Colorectum								
INDI 826	INDI 826 PLS 1	Colorectum	0.056	0.446	0.018	0.43	0.004	0.02
0.026	Colorectum	Lung						
INDI 827	INDI 827 PLS 1	Colorectum	0.132	0.438	0.008	0.194	0.126	0.082
0.02	Colorectum	Lung						
INDI 830	INDI 830 PLS 0	Breast	0.2	0.302	0.008	0.342	0.102	0.036
0.01	Lung							
Colorectum								
INDI 833	INDI 833 PLS 1	Breast	0.098	0.478	0.012	0.258	0.068	0.052
0.034	Colorectum	Lung						
INDI 841	INDI 841 PLS 1	Colorectum	0.07	0.58	0.026	0.172	0.086	0.062
0.004	Colorectum	Lung						
INDI 844	INDI 844 PLS 1	Stomach	0.31	0.232	0.024	0.254	0.08	0.026
0.074	Breast	Lung						
INDI 846	INDI 846 PLS 1	Colorectum	0.028	0.416	0.034	0.06	0.008	0.006
0.448	Upper GI							
Colorectum								
INDI 847	INDI 847 PLS 1	Liver	0.09	0.226	0.464	0.012	0.012	0.022
0.174	Liver							
Colorectum								
INDI 848	INDI 848 PLS 1	Colorectum	0.106	0.516	0.026	0.062	0.01	0.048
0.232	Colorectum	Upper GI						
INDI 850	INDI 850 PLS 1	Esophagus	0.07	0.398	0.098	0.11	0.048	0.038
0.238	Colorectum	Upper GI						
INDI 853	INDI 853 PLS 1	Esophagus	0.026	0.282	0.238	0.024	0.01	0.032
0.388	Upper GI							
Colorectum								
INDI 854	INDI 854 PLS 1	Colorectum	0.006	0.294	0.108	0.002	0.002	0.002
0.586	Upper GI							

Table6.txt

Colorectum								
INDI 855	INDI 855 PLS 1		Colorectum	0.002	0.274	0.334	0.012	0.008
0.018	0.352	Upper GI	Liver	INDI 859	INDI 859 PLS 1		Esophagus	0.088
0.508	0.066	0.146	0.042	0.046	0.104	Colorectum	Lung	INDI 861
INDI 861 PLS 1		Liver	0.014	0.378	0.224	0.006	0.006	0.032
0.34	Colorectum	Upper GI	INDI 862	INDI 862 PLS 1		Pancreas	0.036	0.466
0.106	0.05	0.028	0.068	0.246	Colorectum	Upper GI	INDI 864	INDI 864 PLS 1
Liver	0.014	0.234	0.408	0.018	0.01	0.014	0.302	Liver
Upper GI	INDI 867	INDI 867 PLS 1		Esophagus	0.016	0.274	0.11	0.012
0.006	0.03	0.552	Upper GI	Colorectum				
INDI 868	INDI 868 PLS 1		Liver	0.012	0.146	0.526	0.028	0.01
0.022	0.256	Liver	Upper GI	INDI 870	INDI 870 PLS 1		Breast	0.316
0.28	0.07	0.102	0.084	0.082	0.066	Breast	Colorectum	
INDI 872	INDI 872 PLS 1		Breast	0.192	0.418	0.092	0.124	0.084
0.066	0.024	Colorectum	Breast	INDI 877	INDI 877 PLS 1		Breast	0.416
0.308	0.042	0.07	0.024	0.088	0.052	Breast	Colorectum	
INDI 878	INDI 878 PLS 1		Breast	0.394	0.306	0.092	0.07	0.042
0.07	0.026	Breast	Colorectum	INDI 884	INDI 884 PLS 1		Breast	0.172
0.352	0.06	0.088	0.23	0.038	0.06	Colorectum	Ovary	INDI 887
INDI 887 PLS 1		Breast	0.372	0.214	0.042	0.062	0.022	0.194
0.094	Breast	Colorectum	INDI 888	INDI 888 PLS 1		Pancreas	0.054	0.256
0.006	0.112	0.024	0.53	0.018	Pancreas	Colorectum	INDI 889	INDI 889 PLS 1
Colorectum	0.124	0.578	0.02	0.1	0.036	0.13	0.012	Colorectum
Pancreas	INDI 893	INDI 893 PLS 1		Pancreas	0.032	0.292	0.054	0.022
0.042	0.522	0.036	Pancreas	Colorectum				
INDI 896	INDI 896 PLS 1		Lung	0.044	0.498	0.062	0.186	0.046
0.118	0.046	Colorectum	Lung	INDI 897	INDI 897 PLS 1		Breast	0.258
0.368	0.01	0.224	0.068	0.06	0.012	Colorectum	Breast	INDI 898
INDI 898 PLS 1		Breast	0.12	0.512	0.002	0.152	0.042	0.166
0.006	Colorectum	Pancreas	INDI 902	INDI 902 PLS 1		Breast	0.206	0.262
0.016	0.106	0.154	0.248	0.008	Colorectum	Pancreas		

Table6.txt

INDI 905	INDI 905 PLS 1	Esophagus	0.008	0.36	0.074	0.054	0.032	0.034
0.438	Upper GI	Colorectum						
INDI 907	INDI 907 PLS 1	Esophagus	0.018	0.382	0.04	0.154	0.018	0.014
0.374	Colorectum	Upper GI						
INDI 908	INDI 908 PLS 1	Esophagus	0.004	0.238	0.09	0.038	0.018	0.034
0.578	Upper GI	Colorectum						
INDI 909	INDI 909 PLS 1	Esophagus	0.108	0.47	0.018	0.128	0.128	0.044
0.104	Colorectum	Lung						
INDI 911	INDI 911 PLS 1	Esophagus	0.022	0.562	0.08	0.104	0.018	0.09
0.124	Colorectum	Upper GI						
INDI 917	INDI 917 PLS 1	Liver	0.056	0.328	0.228	0.188	0.034	0.046
0.12	Colorectum	Liver						
INDI 920	INDI 920 PLS 1	Ovary	0.27	0.148	0.01	0.29	0.18	0.046
0.056	Lung	Breast						
INDI 928	INDI 928 PLS 1	Stomach	0.038	0.334	0.39	0.102	0.016	0.036
0.084	Liver	Colorectum						
INDI 931	INDI 931 PLS 1	Ovary	0.172	0.142	0.012	0.326	0.308	0.02
0.02	Lung	Ovary						
INDI 932	INDI 932 PLS 1	Ovary	0.104	0.272	0.034	0.196	0.274	0.09
0.03	Ovary	Colorectum						
LCR 812	LCR 812 PLS1	Pancreas	0.138	0.124	0.102	0.016	0.028	0.548
0.044	Pancreas	Breast						
PANC 669	PANC 669 PLS 1	Pancreas	0.048	0.208	0.04	0.026	0.022	0.606
0.05	Pancreas	Colorectum						
PANC 671	PANC 671 PLS 1	Pancreas	0.078	0.186	0.07	0.018	0.01	0.554
0.084	Pancreas	Colorectum						
PANC 672	PANC 672 PLS 1	Pancreas	0.052	0.08	0.072	0.024	0.004	0.732
0.036	Pancreas	Colorectum						
PANC 674	PANC 674 PLS 1	Pancreas	0.11	0.148	0.048	0.042	0.008	0.596
0.048	Pancreas	Colorectum						
PANC 675	PANC 675 PLS 1	Pancreas	0.344	0.198	0.06	0.064	0.054	0.188
0.092	Breast	Colorectum						
PANC 676	PANC 676 PLS 1	Pancreas	0.028	0.098	0.012	0.016	0.006	0.836
0.004	Pancreas	Colorectum						
PANC 677	PANC 677 PLS 1	Pancreas	0.05	0.066	0.02	0.016	0.008	0.82
0.02	Pancreas	Colorectum						
PANC 760	PANC 760 PLS 1	Pancreas	0.112	0.324	0.074			

Table6.txt

0.192	0.046	0.118	0.134	Colorectum		Lung
PANC 761	PANC 761 PLS 1		Pancreas	0.104	0.224	0.016
0.168	0.034	0.356	0.098	Pancreas		
Colorectum						
PANC 762	PANC 762 PLS 1		Pancreas	0.106	0.22	0.038
0.036	0.042	0.534	0.024	Pancreas		
Colorectum						
PANC 764	PANC 764 PLS 1		Pancreas	0.08	0.228	0.096
0.092	0.03	0.388	0.086	Pancreas		
Colorectum						
PANC 765	PANC 765 PLS 1		Pancreas	0.104	0.118	0.052
0.018	0.024	0.652	0.032	Pancreas		
Colorectum						
PANC 766	PANC 766 PLS 1		Pancreas	0.056	0.37	0.088
0.06	0.044	0.29	0.092	Colorectum		Pancreas
PANCA 1001	PANCA 1001 PLS 1		Pancreas	0.058	0.318	0.104
0.094	0.034	0.236	0.156	Colorectum		Pancreas
PANCA 1004	PANCA 1004 PLS 1		Pancreas	0.07	0.2	0.072
0.116	0.034	0.412	0.096	Pancreas		
Colorectum						
PANCA 1005	PANCA 1005 PLS 1		Pancreas	0.024	0.182	0.042
0.056	0.04	0.606	0.05	Pancreas		
Colorectum						
PANCA 1006	PANCA 1006 PLS 1		Pancreas	0.084	0.098	0.108
0.018	0.04	0.62	0.032	Pancreas		Liver
PANCA 1008	PANCA 1008 PLS 1		Pancreas	0.104	0.3	0.118
0.222	0.026	0.164	0.066	Colorectum		Lung
PANCA 1009	PANCA 1009 PLS 1		Pancreas	0.084	0.326	0.074
0.102	0.076	0.248	0.09	Colorectum		Pancreas
PANCA 1011	PANCA 1011 PLS 1		Pancreas	0.018	0.028	0.014
0	0	0.93	0.01	Pancreas		
Colorectum						
PANCA 1013	PANCA 1013 PLS 1		Pancreas	0.028	0.076	0.036
0.014	0.02	0.8	0.026	Pancreas		
Colorectum						
PANCA 1014	PANCA 1014 PLS 1		Pancreas	0.034	0.3	0.118
0.014	0.034	0.446	0.054	Pancreas		
Colorectum						
PANCA 1015	PANCA 1015 PLS 1		Pancreas	0.044	0.192	0.084
0.02	0.016	0.6	0.044	Pancreas		
Colorectum						
PANCA 1016	PANCA 1016 PLS 1		Pancreas	0.128	0.174	0.068
0.084	0.044	0.448	0.054	Pancreas		
Colorectum						
PANCA 1018	PANCA 1018 PLS 1		Pancreas	0.042	0.05	0.012
0.008	0.06	0.818	0.01	Pancreas		Ovary
PANCA 1020	PANCA 1020 PLS 1		Pancreas	0.092	0.204	0.184
0.022	0.03	0.384	0.084	Pancreas		

Table6.txt

```
Colorectum
  PANCA 1022   PANCA 1022 PLS 1      Pancreas      0.036        0.078        0.014
    0.004     0.008        0.85        0.01          Pancreas
Colorectum
  PANCA 1025   PANCA 1025 PLS 1      Pancreas      0.058         0.08        0.038
    0.042     0.078       0.694        0.01          Pancreas
Colorectum
  PANCA 1028   PANCA 1028 PLS 1      Pancreas      0.09          0.18        0.062
    0.042      0.05       0.514       0.062          Pancreas
Colorectum
  PANCA 1030   PANCA 1030 PLS 1      Pancreas      0.008        0.052        0.036
     0.01     0.012       0.862        0.02          Pancreas
Colorectum
  PANCA 1031   PANCA 1031 PLS 1      Pancreas      0.064        0.068        0.014
    0.018     0.022       0.808        0.006         Pancreas
Colorectum
  PANCA 1034   PANCA 1034 PLS 1      Pancreas      0.112        0.216         0.1
    0.084     0.058       0.398        0.032         Pancreas
Colorectum
  PANCA 1040   PANCA 1040 PLS 1      Pancreas      0.068        0.176        0.188
    0.048     0.026       0.434        0.06          Pancreas             Liver
  PANCA 1043   PANCA 1043 PLS 1      Pancreas      0.01         0.072        0.022
    0.002      0.01       0.872       0.012          Pancreas
Colorectum
  PANCA 1044   PANCA 1044 PLS 1      Pancreas      0.024         0.06        0.006
    0.006     0.018        0.88        0.006         Pancreas
Colorectum
  PANCA 1048   PANCA 1048 PLS 1      Pancreas      0.008        0.026        0.002
    0.008     0.022       0.934          0          Pancreas
Colorectum
  PANCA 1050   PANCA 1050 PLS 1      Pancreas      0.064        0.082        0.032
    0.024     0.024       0.754        0.02          Pancreas
Colorectum
  PANCA 1051   PANCA 1051 PLS 1      Pancreas      0.006         0.05        0.006
       0      0.006       0.902        0.03          Pancreas
Colorectum
  PANCA 1053   PANCA 1053 PLS 1      Pancreas      0.066         0.25         0.08
    0.052     0.046       0.398        0.108         Pancreas
Colorectum
  PANCA 1054   PANCA 1054 PLS 1      Pancreas      0.03         0.036        0.024
       0      0.008        0.9         0.002         Pancreas
Colorectum
  PANCA 1056   PANCA 1056 PLS 1      Pancreas      0.092        0.186        0.082
    0.032      0.03         0.5       0.078         Pancreas
Colorectum
  PANCA 1058   PANCA 1058 PLS 1      Pancreas      0.046        0.108        0.014
    0.012     0.022       0.786        0.012         Pancreas
Colorectum
```

Table6.txt

PANCA 1059	PANCA 1059 PLS 1	Pancreas	0.046	0.166	0.054	0.062	0.024	0.596
0.052	Pancreas	Colorectum						
PANCA 1061	PANCA 1061 PLS 1	Pancreas	0.022	0.064	0.04	0.006	0.016	0.838
0.014	Pancreas	Colorectum						
PANCA 1149	PANCA 1149 PLS 1	Pancreas	0.142	0.178	0.042	0.016	0.038	0.568
0.016	Pancreas	Colorectum						
PANCA 1153	PANCA 1153 PLS 1	Pancreas	0.088	0.288	0.05	0.086	0.018	0.336
0.134	Pancreas	Colorectum						
PANCA 1155	PANCA 1155 PLS 1	Pancreas	0.122	0.304	0.094	0.022	0.064	0.348
0.046	Pancreas	Colorectum						
PAP 938	PAP 938 PLS 1	Ovary	0.122	0.144	0.052	0.02	0.438	0.186
0.038	Ovary	Pancreas						
PAP 939	PAP 939 PLS 1	Ovary	0.034	0.09	0.032	0.078	0.702	0.038
0.026	Ovary	Colorectum						
PAP 940	PAP 940 PLS 1	Ovary	0.026	0.046	0.008	0.024	0.85	0.024
0.022	Ovary	Colorectum						
PAP 941	PAP 941 PLS 1	Ovary	0.112	0.234	0.016	0.172	0.402	0.016
0.048	Ovary	Colorectum						
PAP 944	PAP 944 PLS 1	Ovary	0.03	0.13	0.104	0.078	0.5	0.09
0.068	Ovary	Colorectum						
PAP 945	PAP 945 PLS 1	Ovary	0.042	0.076	0.01	0.056	0.796	0.006
0.014	Ovary	Colorectum						
PAP 946	PAP 946 PLS 1	Ovary	0.06	0.098	0.01	0.04	0.626	0.154
0.012	Ovary	Pancreas						
PAP 947	PAP 947 PLS 1	Ovary	0.048	0.334	0.02	0.142	0.356	0.054
0.046	Ovary	Colorectum						
PAP 949	PAP 949 PLS 1	Ovary	0.074	0.374	0.112	0.084	0.174	0.074
0.108	Colorectum	Ovary						
PAP 950	PAP 950 PLS 1	Ovary	0.026	0.104	0.032	0.028	0.71	0.076
0.024	Ovary	Colorectum						
PAP 953	PAP 953 PLS 1	Ovary	0.04	0.37	0.03	0.038	0.42	0.06
0.042	Ovary	Colorectum						
PAP 954	PAP 954 PLS 1	Ovary	0.02	0.096	0.024	0.066	0.746	0.022
0.026	Ovary	Colorectum						

Table6.txt

PAP 955	PAP 955 PLS 1	Ovary	0.032	0.08	0.002	0.07	0.798	0.012
0.006	Ovary	Colorectum						
PAP 956	PAP 956 PLS 1	Ovary	0.078	0.146	0.042	0.09	0.59	0.028
0.026	Ovary	Colorectum						
PAP 957	PAP 957 PLS 1	Ovary	0.12	0.256	0.022	0.108	0.41	0.04
0.044	Ovary	Colorectum						
PAP 959	PAP 959 PLS 1	Ovary	0.05	0.172	0.026	0.068	0.604	0.05
0.03	Ovary	Colorectum						
PAP 961	PAP 961 PLS 1	Ovary	0.05	0.17	0.024	0.086	0.568	0.058
0.044	Ovary	Colorectum						
PAP 962	PAP 962 PLS 1	Ovary	0.046	0.21	0.136	0.25	0.238	0.026
0.094	Lung	Ovary						
PAP 974	PAP 974 PLS 1	Ovary	0.102	0.274	0.014	0.084	0.462	0.042
0.022	Ovary	Colorectum						
PAPA 1330	PAPA 1330 PLS 1	Ovary	0.116	0.184	0.076	0.062	0.472	0.016
0.074	Ovary	Colorectum						
PAPA 1331	PAPA 1331 PLS 1	Ovary	0.022	0.092	0.01	0.058	0.79	0.012
0.016	Ovary	Colorectum						
PAPA 1332	PAPA 1332 PLS 1	Ovary	0.114	0.378	0.014	0.16	0.268	0.026
0.04	Colorectum	Ovary						
PAPA 1333	PAPA 1333 PLS 1	Ovary	0.038	0.074	0.06	0.04	0.698	0.056
0.034	Ovary	Colorectum						
PAPA 1334	PAPA 1334 PLS 1	Ovary	0.024	0.14	0.016	0.068	0.656	0.048
0.048	Ovary	Colorectum						
PAPA 1335	PAPA 1335 PLS 1	Ovary	0.086	0.286	0.058	0.248	0.208	0.01
0.104	Colorectum	Lung						
PAPA 1336	PAPA 1336 PLS 1	Ovary	0.054	0.3	0.024	0.092	0.416	0.066
0.048	Ovary	Colorectum						
PAPA 1339	PAPA 1339 PLS 1	Ovary	0.032	0.076	0.04	0.016	0.74	0.05
0.046	Ovary	Colorectum						
PAPA 1342	PAPA 1342 PLS 1	Ovary	0.028	0.064	0.012	0.108	0.724	0.048
0.016	Ovary	Lung						
PAPA 1343	PAPA 1343 PLS 1	Ovary	0.012	0.054	0.004	0.03	0.878	0.002
0.02	Ovary	Colorectum						
PAPA 1344	PAPA 1344 PLS 1	Ovary	0.12	0.18	0.014			

Table6.txt

	0.072	0.56	0.016	0.038	Ovary				
Colorectum									
	PAPA 1345	PAPA 1345	PLS 1	Ovary	0.046	0.134	0.022		
	0.062	0.706	0.01	0.02	Ovary				
Colorectum									
	PAPA 1346	PAPA 1346	PLS 1	Ovary	0.034	0.042	0.004		
	0.064	0.824	0.02	0.012	Ovary		Lung		
	PAPA 1347	PAPA 1347	PLS 1	Ovary	0.044	0.19	0.044		
	0.058	0.576	0.034	0.054	Ovary				
Colorectum									
	PAPA 1348	PAPA 1348	PLS 1	Ovary	0.066	0.138	0.014		
	0.096	0.624	0.038	0.024	Ovary				
Colorectum									
	PAPA 1349	PAPA 1349	PLS 1	Ovary	0.042	0.052	0.016		
	0.054	0.752	0.056	0.028	Ovary		Pancreas		
	PAPA 1350	PAPA 1350	PLS 1	Ovary	0.174	0.246	0.026		
	0.208	0.276	0.042	0.028	Ovary				
Colorectum									
	PAPA 1353	PAPA 1353	PLS 1	Ovary	0.14	0.234	0.01		
	0.162	0.312	0.116	0.026	Ovary				
Colorectum									
	PAPA 1354	PAPA 1354	PLS 1	Ovary	0.186	0.342	0.036		
	0.154	0.2	0.058	0.024	Colorectum		Ovary		
	PAPA 1355	PAPA 1355	PLS 1	Ovary	0.084	0.278	0.032		
	0.174	0.36	0.026	0.046	Ovary				
Colorectum									
	PAPA 1356	PAPA 1356	PLS 1	Ovary	0.05	0.112	0.066		
	0.028	0.64	0.04	0.064	Ovary				
Colorectum									
	PAPA 1357	PAPA 1357	PLS 1	Ovary	0.034	0.058	0.022		
	0.04	0.8	0.02	0.026	Ovary				
Colorectum									

Table7.txt

Table 7. General demographics and histopathology of patients with pancreatic cancer

Pancreatic cancer with undetectable KRAS (N=155)	Pancreatic cancer with detectable HGF p-value (N=23)	Pancreatic cancer with undetectable CA19-9 HGF (n = 221) (N=109)	Pancreatic cancer with detectable KRAS (N=198)	Pancreatic cancer with undetectable CA19-9 (N=66) (N=112)
Variable N (%)	N (%)	N(%) N (%)	N (%)	N (%)
Age, mean 1 SD 67.3 1 10.3	0.473	66.9 1 10.5 65.9 1 10.24	66.8 1 10.6	66.2 1 10.8 67.9 1 10.6
0.136	68.1 1 9.4			
Gender	0.07			
0.721				
?Male 91 (75.2)	10 (8.3)	121 (54.8) 61 (50.4)	111 (91.7)	30 (24.8) 60 (49.6)
?Female 64 (64.0)	13 (13.0)	100 (45.2) 48 (48.0)	87 (87.0)	36 (36.0) 52 (52.0)
Race	0.889			
0.598				
?White 133 (70.7)	16 (8.5)	188 (85.1) 95 (50.5)	172 (91.5)	55 (29.3) 93 (49.5)
?African-American 3 (75.0)	□	4 (1.8) 2 (50.0)	4 (100.0)	1 (25.0) 2 (50.0)
?Hispanic 1 (100.0)	1 (100.0)	1 (0.5) 1 (100.0)	□	□ □
?Asian 7 (58.3)	3 (25.0)	12 (5.4) 7 (58.3)	9 (75.0)	5 (41.7) 5 (41.7)
?Other or unknown 3 (60.0)	3 (18.7)	16 (7.2) 4 (25.0)	13 (81.3)	2 (40.0) 12 (75.0)

Page 1

Table7.txt

Classic symptoms of PDAC
0.194
0.69
?Absent 45 (20.4) 49 (27.8)
127 (72.2) 21 (46.7) 24 (53.3)
1 (2.2) 44 (97.8)
?Present 176 (79.6) 17 (37.8)
28 (62.2) 88 (50.0) 88 (50.0)
22 (12.5) 154 (87.5)
Abdominal pain
0.361
0.207
?Absent 127 (57.5) 41 (32.3)
86 (67.7) 58 (45.7) 69 (54.3)
12 (9.5) 115 (90.5)
?Present 94 (42.5) 25 (26.6)
69 (73.4) 51 (54.3) 43 (45.7)
11 (11.7) 83 (88.3)
Jaundice
0.528
0.841
?Absent 110 (49.8) 35 (31.8)
75 (68.2) 55 (50.0) 55 (50.0)
10 (9.1) 100 (90.9)
?Present 111 (50.2) 31 (27.9)
80 (72.1) 54 (48.7) 57 (51.3)
13 (11.7) 98 (88.3)
Tumor size (cm), median (IQR) 3.0 (2.4–3.8) 3.5 (3.0–4.5)
2.7 (2.2–3.5) 0.002 3.4 (2.5–4.5) 2.8 (2.1–3.5)
<0.001 2.7 (2.0–4.0) 3.0 (2.4–3.8)
Tumor size
0.004
0.028
??1.00 cm 2 (0.9) –
2 (100.0) – 2 (100.0)
– 2 (100.0)
?1.01–1.50 cm 22 (10.0) 5 (22.7)
17 (77.3) 6 (27.3) 16 (72.7)
5 (22.7) 17 (77.3)
?1.51–2.00 cm 12 (5.4) 2 (16.7)
10 (83.3) 4 (33.3) 8 (66.7)
1 (8.3) 11 (91.7)
?2.01–2.50 cm 47 (21.3) 4 (8.5)
43 (91.5) 20 (42.5) 27 (57.5)
4 (8.5) 43 (91.5)
?2.51–3.00 cm 38 (17.2) 12 (31.6)
26 (68.4) 17 (44.7) 21 (55.3)
4 (10.5) 34 (89.5)

Table7.txt

?3.01–3.50 cm		36 (16.3)	15 (41.7)
21 (58.3)		21 (58.3)	15 (41.7)
	2 (5.6)	34 (94.4)	
?3.51–4.00 cm		22 (10.0)	10 (45.5)
12 (54.6)		13 (59.1)	9 (40.9)
	2 (9.1)	20 (90.9)	
?>4.00 cm		42 (19.0)	18 (42.9)
24 (57.1)		28 (66.7)	14 (33.3)
	5 (11.9)	37 (88.1)	
AJCC T stage			
	0.003		
0.001			
?T1		22 (10.0)	5 (22.7)
17 (77.3)		4 (18.2)	18 (81.8)
	3 (13.6)	19 (86.4)	
?T2		46 (20.8)	5 (10.9)
41 (89.1)		18 (39.1)	28 (60.9)
	4 (8.7)	42 (91.3)	
?T3		153 (69.2)	56 (36.6)
97 (63.4)		87 (56.9)	66 (43.1)
	16 (10.5)	137 (89.5)	
AJCC N stage			
	0.004		
0.009			
?N0		51 (23.1)	7 (13.7)
44 (86.3)		17 (33.3)	34 (66.7)
	6 (11.8)	45 (88.2)	
?N1		170 (76.9)	59 (34.7)
111 (65.3)		92 (54.1)	78 (45.9)
	17 (10.0)	153 (90.0)	
AJCC M stage			
?M0		221 (100.0)	66 (29.9)
155 (70.2)		109 (49.3)	112 (50.7)
	23 (10.4)	198 (89.6)	
?M1			
AJCC stage			
	0.013		
0.035			
?IA		12 (5.4)	3 (25.0)
9 (75.0)		2 (16.7)	10 (83.3)
	3 (25.0)	9 (75.0)	
?IB		17 (7.7)	
17 (100.0)		7 (41.2)	10 (58.8)
	1 (5.9)	16 (94.1)	
?IIA		22 (10.0)	4 (18.2)

Table7.txt

18 (81.8) 8 (36.4) 14 (63.6)
2 (9.1) 20 (90.9)
?IIB 170 (76.9) 59 (34.7)
111 (65.3) 92 (54.1) 78 (45.9)
17 (10.0) 153 (90.0)
Grade of tumor differentiation
0.118
0.666
?Well/moderately differentiated 141 (63.8) 37 (26.2)
104 (79.8) 68 (48.2) 73 (51.8)
14 (9.9) 127 (90.1)
?Poorly differentiated 80 (36.2) 29 (36.3)
51 (63.7) 41 (51.3) 39 (48.7)
9 (11.3) 71 (88.7)
Perineural invasion
0.086
0.044
?Absent 26 (11.8) 4 (15.4)
22 (84.6) 8 (30.8) 18 (69.3)
3 (11.5) 23 (88.5)
?Present 195 (88.2) 62 (31.8)
133 (68.2) 101 (51.8) 94 (48.2)
20 (10.3) 175 (89.7)
Lymphovascular invasion
0.078
<0.001
?Absent 76 (34.4) 17 (22.4)
59 (77.6) 25 (32.9) 51 (67.1)
8 (10.5) 68 (89.5)
?Present 145 (65.6) 49 (33.8)
96 (66.2) 84 (57.9) 61 (42.1)
15 (10.3) 130 (89.7)
Number of harvested nodes, median (19 (15–27) 20 (17–28)
19 (14–27) 0.047 19 (16–26) 20 (14–29)
0.973 20 (17–28) 19 (15–27)
Number of harvested nodes
0.355
0.544
??20 nodes 111 (50.2) 30 (27.0)
81 (73.0) 57 (51.3) 54 (48.7)
9 (8.1) 102 (91.9)
?>20 nodes 110 (49.8) 36 (32.7)
74 (67.3) 52 (47.3) 58 (52.7)
14 (12.7) 96 (87.3)
Number of positive nodes, median (I2 (1–5) 4.0 (2.0–7.0) 1
(0.0–4.0) <0.001 3 (1–6) 2 (0–4) 0.038
2 (0–5) 2 (1–5)
Positive nodes

Table7.txt

0.004
0.009
?Absent 51 (23.1) 7 (13.7)
44 (86.3)
6 (11.8) 45 (88.2)
?Present 170 (76.9)

17 (10.0) 153 (90.0)

Pancreatic cancer Pancreatic cancer
Pancreatic cancer Pancreatic cancer Pancreatic cancer
Pancreatic cancer
with detectable with undetectable with
detectable with undetectable with detectable with
undetectable
CEA CEA OPN
OPN combination assay combination
assay
p-value (N=14) (N=207) p-value (N=15)
(N=206) p-value (N=141) (N=80)
p-value
N (%) N (%) N (%)
N (%) N (%) N (%)
0.579 68.6 1 12.0 66.8 1 10.4 0.539 70.3 1
11.4 66.7 1 10.4 0.204 66.5 1 10.1 67.7 1 11.09
0.43
0.251 0.139
0.515
0.238
5 (4.1) 116 (95.9) 7 (5.8)
114 (94.2) 73 (60.3) 48 (39.7)
9 (9.0) 91 (91.0) 8 (8.0)
92 (92.0) 68 (68.0) 32 (32.0)
0.011 0.083
0.44
0.24
12 (6.4) 176 (93.6) 13 (6.9)
175 (93.1) 119 (63.3) 69 (36.7)
 4 (100.0) 4 (100.0) 2 (50.0)
 2 (50.0)
 1 (100.0) 1 (100.0)
 1 (100.0)
 12 (100.0) 12 (100.0) 11 (91.7) 1 (8.3)
2 (12.5) 14 (87.5) 8 (50.0) 2 (12.5)
14 (87.5) 8 (50.0)

Table7.txt

0.044

0.354

2 (4.4)
164 (93.2)
12 (6.8)
42 (93.3)

0.588

0.771

9 (7.1)
118 (92.9)
5 (5.3)
88 (93.6)

0.524

0.741

6 (5.5)
103 (93.6)
8 (7.2)
103 (92.8)

0.619 4.0 (2.7□5.0)
(2.4□3.0) 3.0 (2.4□3.8)
(2.1□3.4) 0.002

0.648

0.013

□
2 (100.0)
2 (9.1)
19 (86.4)
□
12 (100.0)
1 (2.1)
42 (89.4)
2 (5.3)
34 (89.5)
1 (2.8)
36 (100.0)
2 (9.1)
22 (100.0)
6 (14.3)
39 (92.9)

0.822

0.002

1 (4.6)
19 (86.4)

0.971

43 (95.6)
114 (64.8)
164 (93.2)
27 (60.0)

0.837

118 (92.9)
80 (62.9)
89 (94.7)
61 (64.9)

0.803

104 (94.5)
69 (62.7)
103 (92.8)
72 (64.9)

3.0 (2.4□3.7) 0.343 2.5
0.312 3.2 (2.5□4.0) 2.5

0.266

2 (100.0)
□
20 (90.9)
11 (50.0)
12 (100.0)
6 (50.0)
46 (97.9)
24 (51.1)
36 (94.7)
23 (60.5)
35 (97.2)
29 (80.6)
20 (90.9)
17 (77.3)
36 (85.7)
31 (73.8)

0.2

21 (95.5)
8 (36.4)

0.56

12 (6.8)
62 (35.2)
3 (6.7)
18 (40.0)

0.594

9 (7.1)
47 (37.0)
6 (6.4)
33 (35.1)

0.593

7 (6.4)
41 (37.3)
8 (7.2)
39 (35.1)

0.313

□
2 (100.0)
3 (13.6)
11 (50.0)
□
6 (50.0)
5 (10.6)
23 (48.9)
4 (10.5)
15 (39.5)
□
7 (19.4)
□
5 (22.7)
3 (7.1)
11 (26.2)

0.936

3 (13.6)
14 (63.6)

Table7.txt

3 (6.5)
45 (79.8)
10 (6.5)
142 (92.8)
0.717

0.002
1 (1.9)
47 (92.2)
13 (7.7)
159 (93.5)
□

□
14 (6.3)
206 (93.2)
□

0.364

0.012
1 (8.3)
9 (75.0)
□
17 (100.0)
□
21 (95.4)
13 (7.7)
159 (93.5)
0.757

0.389
9 (6.4)
131 (92.9)
5 (6.3)
75 (93.8)
0.841

0.119
1 (3.9)
24 (92.3)
13 (6.7)
182 (93.3)
0.967

0.005
3 (3.9)
71 (93.4)
43 (93.5)
25 (54.4)
143 (93.5)
108 (70.6)

0.733

50 (98.1)
23 (45.1)
157 (92.3)
118 (69.4)

□

□

207 (93.7)
141 (63.8)

□

0.052

11 (91.7)
4 (33.3)
17 (100.0)
8 (47.1)
22 (100.0)
11 (50.0)
157 (92.4)
118 (69.4)

0.811

132 (93.6)
87 (61.7)
75 (93.8)
54 (67.5)

0.845

25 (96.2)
13 (50.0)
182 (93.3)
128 (65.6)

0.929

73 (96.1)
39 (51.3)
1 (2.2)
21 (45.6)
11 (7.2)
45 (29.4)
0.144

4 (7.8)
28 (54.9)
11 (6.5)
52 (30.6)
□

15 (6.8)
80 (36.2)
□
□
0.36

3 (25.0)
8 (66.7)
□
9 (52.9)
1 (4.6)
11 (50.0)
11 (6.5)
52 (30.6)
0.969

10 (7.1)
54 (38.3)
5 (6.3)
26 (32.5)
0.579

2 (7.7)
13 (50.0)
13 (6.7)
67 (34.4)
0.291

5 (6.6)
37 (48.7)

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11 (7.6) | 134 (92.4) | 10 (6.9)
135 (93.1) | 102 (70.3) | 43 (29.7)
0.173 | 22 (18–26) | 19 (15–27) | 0.345 | 26 (19–28) | 18 (14–27)
0.044 | 0.059 | 0.262
0.261

0.285

5 (4.5) | 106 (95.5) | 4 (3.6)
107 (96.4) | 67 (60.4) | 44 (39.6)
9 (8.2) | 101 (91.8) | 11 (10.0)
99 (99.0) | 74 (67.3) | 35 (32.7)
0.965 | 4 (2–7) | 2 (1–5) | 0.547 | 3 (1–6) | 0.185 | 4 (0–6) | 1 (0–3)
<0.001 | 0.733 | 0.144
0.717

0.002

1 (1.9) | 50 (98.1) | 4 (7.8)
47 (92.2) | 23 (45.1) | 28 (54.9)
13 (7.7) | 157 (92.3) | 11 (6.5)
159 (93.5) | 118 (69.4) | 52 (30.6)

Table8.txt

Table 8. Summary of KRAS plasma mutations and protein biomarkers identified in 221 PDAC patients

Sample ID #	Plasma DNA Mutant mean allele frequency (%)	Mutant plasma concentration (ng/mL)	Mutation identified in plasma	CA19-9 plasma concentration (U/mL)	CEA plasma concentration (pg/mL)	HGF plasma concentration (pg/mL)	OPN plasma concentration (pg/mL)	Mutation Combination assay result (Postive/Negative)	Tumor AJCC Stage	Size tumor tissue (cm)
PANC 304	5.56	None detected	Not applicable	19	4,367	193	44,946	Negative	IB	6
PANC 305	204.02	None detected	Not applicable	504	1,800	406	104,131	Positive	IIB	1.4
PANC 317	10.36	None detected	Not applicable	52	1,928	166	22,155	Negative	IIB	2.5
PANC 333	58.51	None detected	Not applicable	1,184	3,369	380	98,827	Positive	IIB	5
PANC 335	13.28	KRAS p.G12V, c.35G>T	KRAS p.G12V, c.35G>T	1.306	53.4	562	1,911	188	33,482	Positive	IIB	4
PANC 336	13.67	KRAS p.G12D, c.35G>A	KRAS p.G12D, c.35G>A	0.926	39.0	850	1,451	287	84,651	Positive	IIB	5
PANC 339	41.41	KRAS p.G12V, c.35G>T	KRAS p.G12V, c.35G>T	0.186	23.8	2,867	4,167	171	72,479	Positive	IIB	3.5
PANC 345	27.27	None detected	Not applicable	30	1,394	182	55,337	Negative	IIA	3
PANC 346	22.77	None detected	Not applicable	88	1,386	244	69,136	Negative	IIB	2.5
PANC 347	26.33	None detected	Not applicable	24	950	171	52,809	Negative	IIB	1.5
PANC 348	26.52	KRAS p.G12V, c.35G>T	KRAS p.G12V, c.35G>T	0.195	15.9	82	782	166	41,685	Positive	IIB	3.1
PANC 349	7.10	None detected	Not applicable	17	927	166	10,288	Negative	IIB	2.5

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PANC 350 25.02 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.319 24.6 17 942
301 43,281 Positive IIB 4
PANC 352 19.44 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.536 32.1 101 470
166 40,485 Positive IIB 3.5
PANC 353 50.05 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.038 5.8 17 649
301 22,987 Positive IIA 3.5
PANC 355 16.22 None detected Not applicable
Not applicable Not applicable 104 491
166 29,925 Positive IIB 2.2
PANC 358 19.76 None detected Not applicable
Not applicable Not applicable 153 1,988
182 42,774 Positive IIB 4.7
PANC 359 83.17 None detected Not applicable
Not applicable Not applicable 39 671
166 125,383 Negative IIB 2
PANC 386 16.51 None detected Not applicable
Not applicable Not applicable 21 3,132
166 68,102 Negative IB 3
PANC 387 11.11 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C
0.118 4.0 305 865
193 78,342 Positive IIB 3.5
PANC 389 38.42 None detected Not applicable
Not applicable Not applicable 48 2,230
166 88,144 Negative IIB 4.5
PANC 390 19.48 None detected Not applicable
Not applicable Not applicable 136 1,153
166 44,946 Positive IIA 1.5
PANC 391 28.88 None detected Not applicable
Not applicable Not applicable 123 4,805
471 141,916 Positive IIB 4
PANC 394 49.66 None detected Not applicable
Not applicable Not applicable 19 942
166 27,094 Negative IIB 2
PANC 396 217.52 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.031 20.7 115 4,830
1,161 171,589 Positive IA 1.2
PANC 400 30.05 None detected Not applicable
Not applicable Not applicable 51 7,891
166 61,285 Positive IIB 1.3
PANC 402 43.58 KRAS p.Q61H, c.183A>C KRAS p.Q61H, c.183A>C
0.043 5.8 284 1,779
254 45,704 Positive IIB 4.5
PANC 403 13.51 None detected Not applicable
Not applicable Not applicable 859 2,065
171 22,822 Positive IB 3.2

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PANC 404 26.75 None detected Not applicable
Not applicable Not applicable 37 519
229 72,106 Negative IIA 2.5
PANC 406 59.49 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.050 9.1 319 797
224 98,908 Positive IIB 3
PANC 407 63.44 None detected Not applicable
Not applicable Not applicable 71 888
422 61,686 Negative IIB 1.5
PANC 409 10.58 None detected Not applicable
Not applicable Not applicable 1,765 2,541
153 36,394 Positive IIB 5.5
PANC 464 13.00 None detected Not applicable
Not applicable Not applicable 3,528 6,691
2,314 170,915 Positive IIB 2.5
PANC 465 8.22 None detected Not applicable
Not applicable Not applicable 344 2,071
168 32,069 Positive IIB 2.4
PANC 467 6.76 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C
0.761 15.9 1,059 5,191
220 8,328 Positive IIB 3.5
PANC 468 10.28 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A
0.261 8.3 1,399 13,410
609 25,473 Positive IIB 5
PANC 469 5.98 KRAS p.G12A, c.35G>C KRAS p.G12A, c.35G>C
0.125 2.3 40 2,517
466 38,844 Positive IIB 2
PANC 470 6.49 None detected Not applicable
Not applicable Not applicable 26 715
168 59,706 Negative IA 1.3
PANC 471 13.78 None detected Not applicable
Not applicable Not applicable 256 1,718
392 135,997 Positive IIB 2.5
PANC 485 2.64 None detected Not applicable
Not applicable Not applicable 162 930
153 43,260 Positive IB 3.4
PANC 492 8.99 None detected Not applicable
Not applicable Not applicable 39 1,664
311 25,695 Negative IIB 2.5
PANC 496 11.54 None detected Not applicable
Not applicable Not applicable 1,039 3,693
961 78,977 Positive IIB 3.5
PANC 498 8.89 None detected Not applicable
Not applicable Not applicable 41 616
1,114 199,989 Positive IIB 2.5
PANC 502 13.60 None detected Not applicable
Not applicable Not applicable 94 5,542
1,204 116,386 Positive IB 2.8

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PANC 506 2.71 None detected Not applicable Not applicable Not applicable 205 2,195 153 33,292 Positive IIB 7.5
PANC 507 63.64 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.018 3.5 32 2,964 1,994 172,022 Positive IA 1.2
PANC 508 26.47 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.016 1.3 21 744 244 57,888 Positive IIB 1.5
PANC 509 8.60 None detected Not applicable Not applicable Not applicable 311 2,804 311 38,455 Positive IIB 3.2
PANC 510 9.49 None detected Not applicable Not applicable Not applicable 16 1,312 153 23,441 Negative IIB 2.9
PANC 511 8.94 None detected Not applicable Not applicable Not applicable 240 1,642 1,267 60,977 Positive IIB 2.7
PANC 512 4.21 None detected Not applicable Not applicable Not applicable 768 1,855 153 41,353 Positive IIB 1.9
PANC 513 6.34 None detected Not applicable Not applicable Not applicable 19 1,193 244 54,510 Negative IA 2.1
PANC 514 7.59 None detected Not applicable Not applicable Not applicable 2,200 11,133 1,329 178,169 Positive IA 1.4
PANC 515 5.28 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C 0.235 3.8 2,472 12,039 871 164,018 Positive IIB 5
PANC 520 16.01 None detected Not applicable Not applicable Not applicable 301 2,844 181 114,368 Positive IIB 2.5
PANC 529 6.94 None detected Not applicable Not applicable Not applicable 60 1,071 395 66,301 Negative IIA 4.5
PANC 532 30.19 None detected Not applicable Not applicable Not applicable 91 1,947 585 50,001 Negative IB 3.2
PANC 533 7.37 None detected Not applicable Not applicable Not applicable 27 1,341 649 50,001 Negative IIB 1.5
PANC 534 8.58 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.317 8.4 21 1,061 153 40,392 Positive IIB 2.5
PANC 536 25.27 None detected Not applicable Not applicable Not applicable 120 1,855 332 72,280 Positive IIB 2.3

Table8.txt

PANC 538 15.46 None detected Not applicable Not applicable Not applicable 146 952 711 84,887 Positive IIA 2.4
PANC 539 6.77 None detected Not applicable Not applicable Not applicable 16 1,644 756 140,211 Negative IIB 1.5
PANC 540 8.16 None detected Not applicable Not applicable Not applicable 20 1,158 170 35,144 Negative IIB 2.3
PANC 541 20.74 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.073 4.7 205 2,906 323 25,058 Positive IIB 4.5
PANC 542 5.73 None detected Not applicable Not applicable Not applicable 31 629 571 37,655 Negative IIB 3.5
PANC 543 9.63 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.490 14.5 2,499 13,902 688 63,505 Positive IIB 4.8
PANC 544 3.82 None detected Not applicable Not applicable Not applicable 259 932 161 41,347 Positive IB 2.2
PANC 545 12.23 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.189 7.1 16 9,420 350 38,806 Positive IIB 3.2
PANC 546 6.11 None detected Not applicable Not applicable Not applicable 102 616 369 97,001 Positive IB 3.7
PANC 547 10.73 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.033 1.1 88 689 547 99,692 Positive IIB 3
PANC 548 4.91 None detected Not applicable Not applicable Not applicable 450 5,248 304 40,912 Positive IIB 3
PANC 549 21.33 None detected Not applicable Not applicable Not applicable 3,807 911 879 81,002 Positive IIA 3.7
PANC 550 7.44 None detected Not applicable Not applicable Not applicable 439 1,078 387 243,042 Positive IIA 2.5
PANC 552 10.00 KRAS p.Q61H, c.183A>T KRAS p.Q61H, c.183A>T 0.363 11.2 865 5,884 730 107,142 Positive IIB 2.8
PANC 671 49.52 KRAS p.G12V, c.35G>T Not available 0.035 5.4 146 10,180 2,199 62,382 Positive IIB 5
PANC 676 9.25 None detected Not applicable Not applicable Not applicable 113 2,563 465 161,059 Positive IIB 2.5

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PANC 677 25.79 None detected Not applicable Not applicable Not applicable 316 4,840 439 154,906 Positive IIB 3
PANC 678 25.51 None detected Not applicable Not applicable Not applicable 16 1,424 460 66,699 Negative IIB 2.3
PANC 681 5.31 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C 0.086 1.4 100 483 197 98,462 Positive IIB 4
PANC 682 12.50 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.362 13.9 280 1,260 422 128,365 Positive IIB 3
PANC 683 26.55 None detected Not applicable Not applicable Not applicable 73 2,148 833 121,584 Negative IIB 2.3
PANC 685 2.37 None detected Not applicable Not applicable Not applicable 16 453 161 99,923 Negative IIB 3.5
PANC 686 16.17 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.192 9.6 1,015 3,401 1,170 50,532 Positive IIB 4
PANC 687 5.04 None detected Not applicable Not applicable Not applicable 54 583 161 46,582 Negative IIB 4
PANC 689 11.07 None detected Not applicable Not applicable Not applicable 39 1,267 341 40,125 Negative IIB 1.5
PANC 690 3.32 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.152 1.6 3,059 2,501 161 38,276 Positive IIB 6
PANC 691 3.99 None detected Not applicable Not applicable Not applicable 16 982 631 32,496 Negative IB 2.2
PANC 692 9.83 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.155 4.7 226 2,116 355 63,024 Positive IIB 4
PANC 693 22.56 None detected Not applicable Not applicable Not applicable 16 978 456 71,529 Negative IIB 5
PANC 694 10.64 None detected Not applicable Not applicable Not applicable 228 2,880 341 375,513 Positive IIB 6
PANC 695 10.44 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.022 0.7 475 992 378 64,465 Positive IIB 2.6
PANC 696 44.54 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.023 3.2 717 18,814 1,246 273,534 Positive IIB 5.1

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PANC 697 0.90 None detected Not applicable Not applicable Not applicable Not applicable 522 915 224 107,832 Positive IIB 3.1
PANC 699 7.56 None detected Not applicable Not applicable Not applicable Not applicable 174 1,606 161 43,853 Positive IIB 3.1
PANC 700 20.84 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.048 3.1 21 453 395 49,027 Positive IIB 1.5
PANC 701 18.67 None detected Not applicable Not applicable Not applicable Not applicable 16 557 161 35,235 Negative IA 1.9
PANC 702 11.08 None detected Not applicable Not applicable Not applicable Not applicable 24 763 395 59,316 Negative IIB 3.1
PANC 703 9.18 None detected Not applicable Not applicable Not applicable Not applicable 53 1,071 995 91,996 Positive IIB 1.4
PANC 704 18.37 None detected Not applicable Not applicable Not applicable Not applicable 175 2,423 2,444 97,539 Positive IIB 2.5
PANC 705 3.61 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 1.047 11.7 24 1,323 161 88,445 Positive IIB 4.8
PANC 706 5.23 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.077 1.2 958 3,830 170 76,477 Positive IIB 3.5
PANC 707 6.10 None detected Not applicable Not applicable Not applicable Not applicable 16 3,575 506 61,577 Negative IIB 1.5
PANC 708 3.04 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.137 1.3 156 1,431 627 45,733 Positive IIB 3.8
PANC 709 4.82 None detected Not applicable Not applicable Not applicable Not applicable 79 702 323 39,687 Negative IB 3
PANC 710 2.49 None detected Not applicable Not applicable Not applicable Not applicable 78 1,257 520 119,731 Negative IIB 0.8
PANC 711 3.20 None detected Not applicable Not applicable Not applicable Not applicable 95 2,877 950 60,142 Positive IIB 3.8
PANC 712 9.06 None detected Not applicable Not applicable Not applicable Not applicable 29 823 798 57,233 Negative IIB 2.8
PANC 713 6.71 None detected Not applicable Not applicable Not applicable Not applicable 992 2,610 742 137,147 Positive IIB 4.5

Table8.txt

PANC 714 7.35 None detected Not applicable Not applicable Not applicable 702 1,364 436 130,904 Positive IIB 3.5
PANC 715 1.98 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.105 0.6 980 3,312 159 54,937 Positive IIB 3.8
PANC 716 2.78 None detected Not applicable Not applicable Not applicable 16 789 337 39,212 Negative IA 1.5
PANC 718 13.95 None detected Not applicable Not applicable Not applicable 679 2,275 446 73,885 Positive IIB 3
PANC 719 21.28 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.095 6.2 16 2,549 165 96,616 Positive IIB 5
PANC 720 204.08 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.038 23.6 3,998 4,943 3,346 133,514 Positive IIB 13
PANC 721 5.67 None detected Not applicable Not applicable Not applicable 113 2,397 159 50,472 Positive IB 2.5
PANC 722 16.61 None detected Not applicable Not applicable Not applicable 453 1,027 659 50,874 Positive IIB 3
PANC 723 5.32 None detected Not applicable Not applicable Not applicable 60 1,208 165 44,355 Negative IB 3
PANC 724 22.12 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.681 46.4 2,137 1,120 621 81,074 Positive IIB 3
PANC 725 11.90 None detected Not applicable Not applicable Not applicable 489 2,322 492 108,399 Positive IB 3.2
PANC 726 4.47 None detected Not applicable Not applicable Not applicable 54 1,199 316 43,871 Negative IIB 0.6
PANC 728 8.52 None detected Not applicable Not applicable Not applicable 322 2,397 305 47,738 Positive IIB 2.7
PANC 729 15.76 None detected Not applicable Not applicable Not applicable 83 1,346 203 28,360 Negative IIB 4.9
PANC 730 7.34 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.552 12.5 986 712 717 76,921 Positive IIB 3
PANC 731 6.87 None detected Not applicable Not applicable Not applicable 62 1,803 295 35,198 Negative IIB 2.4

Table8.txt

PANC 732 7.11 None detected Not applicable Not applicable Not applicable 232 918 483 72,023 Positive IIB 2
PANC 734 9.96 None detected Not applicable Not applicable Not applicable 16 1,840 203 65,339 Negative IIB 2.3
PANC 735 3.05 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C 0.191 1.8 16 5,061 159 53,287 Positive IIB 2.5
PANC 736 8.25 None detected Not applicable Not applicable Not applicable 16 729 625 53,206 Negative IA 2.5
PANC 738 85.58 None detected Not applicable Not applicable Not applicable 219 2,294 1,639 103,509 Positive IIB 7
PANC 739 1.36 None detected Not applicable Not applicable Not applicable 17 658 165 22,376 Negative IIB 2.5
PANC 742 11.51 None detected Not applicable Not applicable Not applicable 16 708 203 62,410 Negative IA 1.3
PANC 743 4.35 None detected Not applicable Not applicable Not applicable 16 1,257 250 55,460 Negative IIB 3.7
PANC 744 18.95 None detected Not applicable Not applicable Not applicable 55 623 1,052 53,689 Positive IIB 3.4
PANC 747 11.99 KRAS p.G12D, c.35G>A Not available 0.559 20.6 492 2,677 663 62,573 Positive IIB 1.5
PANC 748 5.88 None detected Not applicable Not applicable Not applicable 17 1,794 407 14,425 Negative IA 2.1
PANC 750 31.50 None detected Not applicable Not applicable Not applicable 369 953 1,353 57,798 Positive IIB 2
PANC 759 20.82 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 0.025 1.6 102 5,464 178 59,616 Positive IIB 5
PANC 760 3.51 None detected Not applicable Not applicable Not applicable 16 3,601 233 48,824 Negative IIB 3
PANC 761 3.59 None detected Not applicable Not applicable Not applicable 72 1,208 203 44,396 Negative IIA 3
PANC 762 18.45 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C 0.052 3.0 2,159 15,443 412 51,759 Positive IIB 4.5

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PANC 765 22.24 KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A
0.062 4.2 983 12,251
2,968 237,322 Positive IIB 3
PANC 766 14.29 None detected Not applicable
Not applicable Not applicable 34 2,070
11,433 39,090 Positive IIB 2.5
PANC 767 3.05 None detected Not applicable
Not applicable Not applicable 40 568
261 64,280 Negative IIB 2.5
PANC 768 3.16 None detected Not applicable
Not applicable Not applicable 16 1,876
159 32,042 Negative IIB 5
PANC 769 5.07 None detected Not applicable
Not applicable Not applicable 41 729
284 50,231 Negative IIB 2.2
PANCA 1001 6.35 None detected Not applicable
Not applicable Not applicable 54 653
357 74,764 Negative IIA 8.1
PANCA 1006 196.38 None detected Not applicable
Not applicable Not applicable 468 1,316
543 336,611 Positive IIB 2.6
PANCA 1009 4.62 KRAS p.Q61H, c.183A>C Not available
1.002 14.2 521 3,941
188 70,449 Positive IIB 3.5
PANCA 1010 7.47 None detected Not applicable
Not applicable Not applicable 18 748
255 50,834 Negative IA 1.5
PANCA 1011 26.58 KRAS p.G12D, c.35G>A Not available
0.054 4.4 367 2,297
799 100,221 Positive IIB 3.5
PANCA 1012 5.43 None detected Not applicable
Not applicable Not applicable 106 1,382
471 51,979 Positive IIB 3.5
PANCA 1014 45.97 KRAS p.G12D, c.35G>A Not available
0.135 19.1 17 7,747
770 127,393 Positive IIB 2.7
PANCA 1018 18.46 None detected Not applicable
Not applicable Not applicable 350 3,362
653 70,298 Positive IIB 2
PANCA 1020 15.47 None detected Not applicable
Not applicable Not applicable 44 1,741
808 83,017 Negative IIB 2.2
PANCA 1022 24.75 None detected Not applicable
Not applicable Not applicable 57 1,208
388 74,679 Negative IIB 2.2
PANCA 1024 2.66 None detected Not applicable
Not applicable Not applicable 17 1,299
225 39,828 Negative IIB 3

Table8.txt

PANCA 1030 23.08 None detected Not applicable Not applicable Not applicable 42 467 425 97,065 Negative IIA 3.5
PANCA 1031 3.53 None detected Not applicable Not applicable Not applicable 885 5,128 270 65,798 Positive IIB 5.1
PANCA 1034 5.64 None detected Not applicable Not applicable Not applicable 56 2,598 539 27,895 Negative IIB 2.5
PANCA 1036 3.95 None detected Not applicable Not applicable Not applicable 16 1,208 471 43,230 Negative IIA 2.1
PANCA 1039 12.31 None detected Not applicable Not applicable Not applicable 221 1,636 304 93,935 Positive IIB 3.5
PANCA 1040 17.85 None detected Not applicable Not applicable Not applicable 38 1,760 407 39,719 Negative IIA 2
PANCA 1042 11.96 KRAS p.G12V, c.35G>T Not available 0.168 6.2 21 723 234 42,484 Positive IIB 9
PANCA 1043 4.31 None detected Not applicable Not applicable Not applicable 172 3,383 363 78,154 Positive IIA 3.9
PANCA 1044 7.59 KRAS p.G12R, c.34G>C Not available 0.240 5.6 57 2,527 516 67,807 Positive IIB 3.5
PANCA 1047 3.55 None detected Not applicable Not applicable Not applicable 68 1,471 263 25,107 Negative IIB 3
PANCA 1050 67.68 KRAS p.G12D, c.35G>A Not available 0.030 6.2 124 1,068 240 69,507 Positive IIB 2.4
PANCA 1051 48.18 None detected Not applicable Not applicable Not applicable 149 1,688 643 124,142 Positive IIB 3.2
PANCA 1052 7.75 None detected Not applicable Not applicable Not applicable 17 774 209 42,915 Negative IIA 3
PANCA 1053 37.23 None detected Not applicable Not applicable Not applicable 1,488 1,945 287 209,138 Positive IIB 2.4
PANCA 1054 14.89 None detected Not applicable Not applicable Not applicable 225 1,212 643 171,694 Positive IIB 2.8
PANCA 1055 3.20 None detected Not applicable Not applicable Not applicable 20 519 166 36,638 Negative IIB 1.5

Table8.txt

PANCA 1056 15.66 None detected Not applicable Not applicable Not applicable 77 1,702 527 79,215 Negative IIA 3.5
PANCA 1057 4.35 None detected Not applicable Not applicable Not applicable 643 1,522 193 35,159 Positive IIB 3.4
PANCA 1058 13.87 None detected Not applicable Not applicable Not applicable 75 4,573 255 131,223 Negative IIB 2
PANCA 1059 5.55 KRAS p.Q61H, c.183A>T Not available 0.139 2.4 511 1,856 225 39,537 Positive IIB 4.6
PANCA 1061 31.05 KRAS p.G12D, c.35G>A Not available 0.293 28.1 497 6,198 693 64,133 Positive IIB 4
PANCA 1063 4.77 None detected Not applicable Not applicable Not applicable 317 2,309 166 23,728 Positive IIB 3.5
PANCA 1068 2.75 None detected Not applicable Not applicable Not applicable 132 3,007 1,351 74,987 Positive IIA 1.5
PANCA 1072 2.97 None detected Not applicable Not applicable Not applicable 346 4,152 351 43,140 Positive IIB 10.7
PANCA 1075 3.28 None detected Not applicable Not applicable Not applicable 53 1,290 437 69,424 Negative IIA 2.7
PANCA 1077 4.94 None detected Not applicable Not applicable Not applicable 149 706 437 38,236 Positive IIB 2.2
PANCA 1081 5.94 None detected Not applicable Not applicable Not applicable 571 887 5,831 61,522 Positive IIA 4.5
PANCA 1082 16.29 KRAS p.G12V, c.35G>T Not available 0.069 3.5 37 672 325 33,631 Positive IIB 2.9
PANCA 1086 11.57 KRAS p.G12D, c.35G>A Not available 0.143 5.1 35 3,621 176 30,480 Positive IIA 3.2
PANCA 1093 25.35 KRAS p.G12V, c.35G>T Not available 0.032 2.5 766 1,019 413 27,440 Positive IIB 2.8
PANCA 1096 12.58 KRAS p.G12R, c.34G>C Not available 0.016 0.6 175 736 159 21,452 Positive IIA 2.3
PANCA 1098 15.31 KRAS p.G12C, c.34G>T Not available 0.164 7.7 17 4,174 193 33,631 Positive IIA 3.5

Table8.txt

PANCA 1099	29.75	None detected	Not applicable	Not applicable	Not applicable	40	576	6,969	38,006
Positive	IIB	2.6							
PANCA 1101	7.29	None detected	Not applicable	Not applicable	Not applicable	144	1,434	351	55,228
Positive	IIB	6.2							
PANCA 1103	56.56	None detected	Not applicable	Not applicable	Not applicable	100	740	623	48,670
Positive	IIB	7							
PANCA 1104	15.77	KRAS p.G12D, c.35G>A	KRAS p.G12D, c.35G>A	0.057	2.8	348	714	209	78,418
Positive	IIB	3.2							
PANCA 1105	11.49	KRAS p.G12D, c.35G>A	KRAS p.G12D, c.35G>A	0.124	4.4	17	1,373	240	31,826
Positive	IA	2							
PANCA 1106	5.97	None detected	Not applicable	Not applicable	Not applicable	23	531	225	39,106
Negative	IB	2.4							
PANCA 1107	19.46	KRAS p.G12D, c.35G>A	KRAS p.G12D, c.35G>A	0.038	2.3	230	1,693	159	46,762
Positive	IIB	6.5							
PANCA 1108	19.29	None detected	Not applicable	Not applicable	Not applicable	128	1,683	255	41,923
Positive	IIB	2.5							
PANCA 1109	27.57	None detected	Not applicable	Not applicable	Not applicable	240	1,645	500	159,902
Positive	IIB	2.6							
PANCA 1112	31.13	None detected	Not applicable	Not applicable	Not applicable	721	18,071	868	69,336
Positive	IIB	4							
PANCA 1114	8.49	None detected	Not applicable	Not applicable	Not applicable	118	1,217	338	29,314
Positive	IB	2.4							
PANCA 1116	11.96	None detected	Not applicable	Not applicable	Not applicable	928	17,570	338	52,155
Positive	IIB	2.4							
PANCA 1117	4.72	None detected	Not applicable	Not applicable	Not applicable	35	2,080	225	27,191
Negative	IIB	1.8							
PANCA 1120	14.63	None detected	Not applicable	Not applicable	Not applicable	18	959	217	99,822
Negative	IB	3							
PANCA 1121	5.03	KRAS p.G12D, c.35G>A	KRAS p.G12D, c.35G>A	0.303	4.7	18	1,084	207	129,675
Positive	IIB	3.7							
PANCA 1122	15.72	None detected	Not applicable	Not applicable	Not applicable	33	600	226	67,353
Negative	IIB	3.1							

Table8.txt

PANCA 1123 9.61 None detected Not applicable
Not applicable Not applicable 602 7,363
165 72,515 Positive IIB 3.7
PANCA 1124 60.56 None detected Not applicable
Not applicable Not applicable 55 1,887
327 49,108 Negative IIB 2.8
PANCA 1125 4.42 None detected Not applicable
Not applicable Not applicable 17 456
188 65,246 Negative IIB 4.5
PANCA 1126 7.41 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C
0.086 2.0 921 1,695
349 27,386 Positive IIB 6.3
PANCA 1128 5.70 None detected Not applicable
Not applicable Not applicable 44 791
279 49,199 Negative IIB 3.9
PANCA 1130 35.65 KRAS p.G12R, c.34G>C KRAS p.G12R, c.34G>C
0.012 1.3 17 456
327 124,862 Positive IIB 3
PANCA 1131 9.85 None detected Not applicable
Not applicable Not applicable 90 2,506
253 74,674 Negative IIB 3.8
PANCA 1132 8.62 KRAS p.G12V, c.35G>T Not available
0.031 0.8 17 697
165 99,541 Positive IIB 3.5
PANCA 1133 4.08 None detected Not applicable
Not applicable Not applicable 76 668
167 47,645 Negative IIB 6
PANCA 1134 4.34 None detected Not applicable
Not applicable Not applicable 230 456
262 81,905 Positive IIB 4.8
PANCA 1135 3.84 KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T
0.070 0.8 113 8,486
188 66,142 Positive IIB 4
PANCA 1136 10.09 None detected Not applicable
Not applicable Not applicable 295 964
167 99,588 Positive IIB 2.4
PANCA 1137 23.59 None detected Not applicable
Not applicable Not applicable 31 673
342 110,202 Negative IIB 3
PANCA 1138 71.54 None detected Not applicable
Not applicable Not applicable 49 456
295 79,503 Negative IIB 6
PANCA 1140 1.72 None detected Not applicable
Not applicable Not applicable 17 456
165 31,215 Negative IIB 4.4
PANCA 1141 7.23 None detected Not applicable
Not applicable Not applicable 91 766
207 67,846 Negative IB 2.4

PANCA 1142 18.82 None detected Not applicable
Not applicable Not applicable 92 619
311 123,668 Negative IIB 3.7

Highlighted values represent protein concentrations below or below the limit of detection of the assay; values set as correspoding lower or upper limit of detection

TNM Staging	Age	Gender
T2N0M0	63	M
T3N1M0	70	M
T3N1M0	53	M
T3N1M0	68	F
T3N1M0	63	F
T3N1M0	73	M
T3N1M0	63	M
T3N0M0	51	M
T2N1M0	82	F
T3N1M0	69	M
T3N1M0	62	M
T2N1M0	69	M
T3N1M0	70	M
T3N1M0	62	F
T3N0M0	50	F
T2N1M0	63	M
T3N1M0	58	M
T3N1M0	65	M
T2N0M0	44	M
T3N1M0	68	M
T2N1M0	72	F
T3N0M0	62	M
T2N1M0	69	M
T1N1M0	40	F
T1N0M0	74	M
T2N1M0	69	F
T3N1M0	86	F
T2N0M0	63	F
T3N0M0	72	M
T3N1M0	73	F
T1N1M0	68	M
T3N1M0	73	M
T3N1M0	56	F
T2N1M0	51	M
T3N1M0	27	M
T3N1M0	67	M

Table8.txt

T3N1M0	64	F
T1N0M0	64	F
T3N1M0	41	M
T2N0M0	78	M
T2N1M0	48	M
T3N1M0	63	F
T3N1M0	85	M
T2N0M0	69	M
T3N1M0	54	F
T1N0M0	56	F
T1N1M0	78	F
T2N1M0	53	F
T3N1M0	72	M
T2N1M0	72	M
T1N1M0	51	M
T1N0M0	83	M
T1N0M0	80	F
T2N1M0	79	M
T3N1M0	67	M
T3N0M0	66	M
T2N0M0	77	F
T3N1M0	76	M
T3N1M0	77	F
T3N1M0	65	M
T3N0M0	70	M
T1N1M0	79	M
T2N1M0	64	F
T3N1M0	70	F
T3N1M0	59	F
T3N1M0	71	F
T2N0M0	59	F
T2N1M0	74	F
T2N0M0	58	M
T3N1M0	57	F
T2N1M0	57	M
T3N0M0	69	M
T3N0M0	80	M
T3N1M0	73	F
T3N1M0	64	M
T3N1M0	65	F
T3N1M0	73	M
T3N1M0	48	M
T2N1M0	61	F
T3N1M0	66	M
T2N1M0	54	F
T2N1M0	72	M
T3N1M0	70	F
T2N1M0	82	F

Table8.txt

T3N1M0	81	F
T3N1M0	44	M
T2N0M0	67	M
T3N1M0	80	M
T3N1M0	80	F
T3N1M0	60	M
T3N1M0	74	M
T3N1M0	79	M
T3N1M0	63	M
T2N1M0	63	M
T1N1M0	68	F
T1N0M0	64	F
T2N1M0	85	F
T3N1M0	62	F
T3N1M0	68	F
T3N1M0	65	F
T3N1M0	68	M
T1N1M0	54	F
T3N1M0	57	M
T2N0M0	81	M
T2N1M0	78	M
T2N1M0	78	M
T3N1M0	76	F
T2N1M0	72	M
T3N1M0	65	M
T3N1M0	75	M
T1N0M0	62	M
T3N1M0	55	M
T3N1M0	68	F
T3N1M0	57	M
T2N0M0	81	M
T2N1M0	91	F
T2N0M0	80	M
T2N1M0	84	F
T2N0M0	76	M
T1N1M0	72	M
T3N1M0	65	F
T3N1M0	73	M
T3N1M0	58	F
T3N1M0	48	M
T3N1M0	61	M
T3N1M0	84	F
T2N1M0	82	M
T1N0M0	64	F
T3N1M0	70	M
T3N1M0	79	F
T1N0M0	56	M
T2N1M0	71	F

Table8.txt

T3N1M0	81	F
T3N1M0	66	F
T1N0M0	83	F
T3N1M0	68	F
T3N1M0	57	F
T3N1M0	49	M
T3N0M0	54	M
T3N1M0	71	F
T3N1M0	48	F
T2N1M0	72	M
T3N1M0	71	M
T3N1M0	60	F
T3N1M0	60	M
T3N0M0	74	M
T3N1M0	78	F
T3N1M0	66	F
T1N0M0	86	M
T3N1M0	72	M
T3N1M0	69	F
T3N1M0	65	M
T1N1M0	53	F
T3N1M0	56	F
T3N1M0	70	M
T3N1M0	58	F
T3N0M0	69	M
T3N1M0	82	F
T3N1M0	63	F
T3N0M0	69	F
T3N1M0	68	M
T3N0M0	63	M
T3N1M0	75	M
T3N0M0	63	M
T3N1M0	56	F
T3N1M0	48	M
T3N1M0	68	F
T3N1M0	62	M
T3N0M0	78	M
T3N1M0	78	F
T3N1M0	75	F
T3N1M0	60	M
T3N0M0	64	M
T3N1M0	71	M
T3N1M0	68	F
T3N1M0	55	M
T3N1M0	67	M
T3N1M0	62	M
T3N0M0	73	F
T3N1M0	76	F

Table8.txt

T3N0M0	78	M
T3N1M0	56	F
T3N0M0	62	F
T3N1M0	62	F
T3N0M0	59	F
T3N1M0	65	M
T3N0M0	59	F
T3N0M0	61	M
T3N1M0	59	F
T3N1M0	81	M
T3N1M0	57	F
T3N1M0	69	F
T1N0M0	84	F
T2N0M0	82	M
T3N1M0	52	M
T3N1M0	53	M
T3N1M0	61	M
T3N1M0	68	F
T2N0M0	61	F
T3N1M0	85	F
T1N1M0	70	F
T2N0M0	85	M
T3N1M0	86	F
T3N1M0	58	F
T3N1M0	74	M
T2N1M0	73	F
T3N1M0	54	M
T3N1M0	63	F
T3N1M0	70	M
T3N1M0	66	M
T3N1M0	81	M
T3N1M0	78	M
T3N1M0	72	M
T3N1M0	67	M
T3N1M0	41	F
T3N1M0	57	F
T3N1M0	74	M
T3N1M0	72	F
T3N1M0	63	F
T2N0M0	74	F
T3N1M0	60	M

Table9.txt

Table 9. Summary of KRAS plasma mutations and protein biomarkers identified in 182 healthy patients

Sample ID #	Plasma DNA Mutant fragment concentration (ng/mL)	CA19-9 plasma concentration (U/mL)	CEA plasma concentration (pg/mL)	Mutation identified in plasma	HGF plasma concentration (pg/mL)	OPN plasma Mutant mean allele concentration (pg/mL)	Mutant allele frequency (%) /mL plasma	Combination assay result (Positive/Negative)	Age	Gender
LCR 588	7.34	21	803	None detected	182	Not applicable	35,610	Negative	63	F
LCR 589	7.48	16	686	None detected	165	Not applicable	17,420	Negative	45	M
LCR 590	8.50	16	426	None detected	247	Not applicable	26,361	Negative	54	M
LCR 591	10.50	16	2,041	None detected	258	Not applicable	55,002	Negative	44	M
LCR 592	5.04	16	432	None detected	203	Not applicable	28,195	Negative	53	F
LCR 593	11.14	16	900	None detected	258	Not applicable	18,755	Negative	65	M
LCR 594	4.84	16	468	None detected	162	Not applicable	14,061	Negative	57	M
LCR 595	3.73	27	1,303	None detected	162	Not applicable	14,183	Negative	65	M
LCR 597	4.77	16	459	None detected	351	Not applicable	38,344	Negative	51	M
LCR 599	3.41	16	1,732	None detected	162	Not applicable	37,623	Negative	51	M
LCR 600	4.65	16	579	None detected	162	Not applicable	37,929	Negative	66	F
LCR 601	3.19	16	696	None detected	185	Not applicable	13,362	Negative	61	M
LCR 602	9.94	16	744	KRAS p.G12C, c.34G>T	217	0.009	10,376	0.3		

Table9.txt

Positive		69		M					
LCR 603		2.92		None detected		Not applicable		Not applicable	28
470		162		10,738					
Negative		60		F					
LCR 604		7.73		None detected		Not applicable		Not applicable	16
506		162		19,584					
Negative		63		F					
LCR 605		5.75		None detected		Not applicable		Not applicable	16
426		162		8,921					
Negative		67		M					
LCR 606		6.06		None detected		Not applicable		Not applicable	16
426		200		15,269					
Negative		55		M					
LCR 607		8.85		None detected		Not applicable		Not applicable	16
426		226		28,984					
Negative		43		F					
LCR 608		3.74		None detected		Not applicable		Not applicable	16
636		241		26,108					
Negative		66		F					
LCR 610		2.05		None detected		Not applicable		Not applicable	16
567		162		20,444					
Negative		51		M					
LCR 611		2.71		None detected		Not applicable		Not applicable	29
699		162		23,243					
Negative		66		F					
LCR 612		4.86		None detected		Not applicable		Not applicable	16
934		235		40,079					
Negative		62		F					
LCR 613		2.46		None detected		Not applicable		Not applicable	16
444		165		16,178					
Negative		48		F					
LCR 614		5.18		None detected		Not applicable		Not applicable	22
975		238		26,919					
Negative		56		F					
LCR 616		9.30		None detected		Not applicable		Not applicable	16
2,137		167		35,610					
Negative		81		F					
LCR 617		8.47		None detected		Not applicable		Not applicable	16
754		270		22,878					
Negative		61		F					
LCR 618		3.18		None detected		Not applicable		Not applicable	16
1,238		162		20,592					
Negative		60		F					
LCR 619		5.61		None detected		Not applicable		Not applicable	16
426		162		9,660					
Negative		55		F					
LCR 620		5.33		None detected		Not applicable		Not applicable	16
549		247		22,200					

Table9.txt

Negative		59		F					
LCR 621		2.80		None detected		Not applicable		Not applicable	16
592		162		40,622					
Negative		79		F					
LCR 622		16.35		None detected		Not applicable		Not applicable	17
790		223		29,486					
Negative		57		F					
LCR 623		5.34		None detected		Not applicable		Not applicable	16
2,241		191		9,963					
Negative		45		F					
LCR 624		3.81		None detected		Not applicable		Not applicable	16
1,131		165		19,490					
Negative		71		F					
LCR 625		17.16		None detected		Not applicable		Not applicable	16
441		302		18,452					
Negative		76		M					
LCR 626		3.95		None detected		Not applicable		Not applicable	16
1,335		162		18,604					
Negative		60		F					
LCR 627		2.76		None detected		Not applicable		Not applicable	16
426		170		29,790					
Negative		69		F					
LCR 628		2.29		None detected		Not applicable		Not applicable	16
777		165		7,349					
Negative		54		F					
LCR 629		7.50		None detected		Not applicable		Not applicable	16
744		794		24,299					
Negative		54		M					
LCR 630		14.32		None detected		Not applicable		Not applicable	19
985		176		36,077					
Negative		79		F					
LCR 631		3.87		None detected		Not applicable		Not applicable	16
876		165		13,279					
Negative		59		F					
LCR 632		7.22		None detected		Not applicable		Not applicable	16
1,089		162		9,543					
Negative		66		F					
LCR 633		10.48		None detected		Not applicable		Not applicable	17
693		194		34,462					
Negative		60		M					
LCR 634		5.81		None detected		Not applicable		Not applicable	23
667		162		42,951					
Negative		62		M					
LCR 635		4.11		None detected		Not applicable		Not applicable	16
462		162		8,799					
Negative		66		M					
LCR 636		4.08		None detected		Not applicable		Not applicable	17
1,357		194		65,503					

Table9.txt

Negative		72		F							
LCR 637		2.56		None detected		Not applicable		Not applicable	16	518	176	18,774
Negative		47		F							
LCR 638		3.27		None detected		Not applicable		Not applicable	16	1,040	229	31,616
Negative		78		F							
LCR 639		5.42		None detected		Not applicable		Not applicable	16	715	206	8,578
Negative		71		M							
LCR 640		9.99		None detected		Not applicable		Not applicable	16	2,041	235	38,236
Negative		73		M							
LCR 641		5.50		None detected		Not applicable		Not applicable	16	503	188	19,809
Negative		56		M							
LCR 642		6.58		None detected		Not applicable		Not applicable	16	836	162	36,364
Negative		63		F							
LCR 643		2.70		None detected		Not applicable		Not applicable	16	1,152	165	10,961
Negative		61		M							
LCR 644		4.70		None detected		Not applicable		Not applicable	16	783	162	17,150
Negative		61		F							
LCR 645		8.55		None detected		Not applicable		Not applicable	16	524	182	8,329
Negative		62		F							
LCR 646		7.59		None detected		Not applicable		Not applicable	16	426	188	29,987
Negative		77		M							
LCR 647		7.61		None detected		Not applicable		Not applicable	16	426	162	34,606
Negative		76		F							
LCR 648		5.30		None detected		Not applicable		Not applicable	16	579	162	32,743
Negative		55		M							
LCR 649		7.69		None detected		Not applicable		Not applicable	16	1,274	162	11,315
Negative		61		F							
LCR 650		4.06		None detected		Not applicable		Not applicable	38	1,660	182	9,870
Negative		51		F							
LCR 652		4.71		None detected		Not applicable		Not applicable	16	426	162	12,882
Negative		58		F							
LCR 653		21.77		None detected		Not applicable		Not applicable	16	426	162	40,550

Table9.txt

Negative		75		F					
LCR 654		3.38		None detected		Not applicable		Not applicable	16
546		165		6,750					
Negative		51		F					
LCR 655		3.34		None detected		Not applicable		Not applicable	16
1,138		162		43,097					
Negative		60		M					
LCR 658		1.80		None detected		Not applicable		Not applicable	16
500		162		19,020					
Negative		57		F					
LCR 659		4.23		None detected		Not applicable		Not applicable	16
426		176		8,726					
Negative		61		F					
LCR 660		1.72		None detected		Not applicable		Not applicable	16
1,064		188		24,843					
Negative		61		M					
LCR 661		1.04		None detected		Not applicable		Not applicable	16
790		162		8,077					
Negative		69		M					
LCR 662		3.35		None detected		Not applicable		Not applicable	16
482		229		30,309					
Negative		59		M					
LCR 663		4.40		None detected		Not applicable		Not applicable	16
450		229		44,524					
Negative		81		M					
LCR 665		8.49		None detected		Not applicable		Not applicable	16
467		285		32,269					
Negative		68		M					
LCR 666		1.95		None detected		Not applicable		Not applicable	18
1,926		229		57,623					
Negative		72		M					
LCR 667		2.13		None detected		Not applicable		Not applicable	16
719		266		39,455					
Negative		50		F					
LCR 668		5.91		None detected		Not applicable		Not applicable	16
975		242		25,239					
Negative		80		F					
LCR 670		2.93		None detected		Not applicable		Not applicable	16
520		229		46,196					
Negative		63		F					
LCR 671		0.90		None detected		Not applicable		Not applicable	16
1,878		185		30,792					
Negative		52		F					
LCR 672		2.56		None detected		Not applicable		Not applicable	31
1,583		248		18,261					
Negative		66		M					
LCR 673		2.67		None detected		Not applicable		Not applicable	24
1,048		235		8,727					

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Negative		58		F					
LCR 674		5.50		None detected		Not applicable		Not applicable	16
1,038		223		33,914					
Negative		63		F					
LCR 675		8.63		None detected		Not applicable		Not applicable	16
884		313		29,085					
Negative		55		M					
LCR 676		3.34		None detected		Not applicable		Not applicable	16
2,123		282		35,973					
Negative		63		M					
LCR 677		12.26		None detected		Not applicable		Not applicable	16
1,104		232		55,870					
Negative		73		M					
LCR 678		3.13		None detected		Not applicable		Not applicable	16
1,190		260		50,299					
Negative		56		F					
LCR 679		5.80		None detected		Not applicable		Not applicable	16
523		165		18,044					
Negative		66		M					
LCR 680		4.18		None detected		Not applicable		Not applicable	18
1,023		183		31,692					
Negative		64		F					
LCR 681		5.83		None detected		Not applicable		Not applicable	16
2,417		322		28,243					
Negative		61		F					
LCR 682		6.17		None detected		Not applicable		Not applicable	16
1,027		164		36,327					
Negative		65		F					
LCR 683		6.17		None detected		Not applicable		Not applicable	16
460		178		24,109					
Negative		82		M					
LCR 684		4.83		None detected		Not applicable		Not applicable	16
460		235		29,522					
Negative		56		F					
LCR 685		8.62		None detected		Not applicable		Not applicable	41
6,031		254		87,258					
Negative		63		F					
LCR 686		4.78		None detected		Not applicable		Not applicable	16
502		242		34,839					
Negative		58		F					
LCR 687		1.96		None detected		Not applicable		Not applicable	20
1,579		164		64,373					
Negative		51		F					
LCR 688		7.42		None detected		Not applicable		Not applicable	37
1,045		279		15,710					
Negative		80		M					
LCR 689		1.99		None detected		Not applicable		Not applicable	16
569		172		21,582					

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Negative		57		M					
LCR 690		6.21		None detected		Not applicable		Not applicable	28
1,094		185		52,982					
Negative		81		M					
LCR 691		3.99		None detected		Not applicable		Not applicable	21
887		216		48,990					
Negative		53		M					
LCR 692		3.42		None detected		Not applicable		Not applicable	18
5,826		304		72,589					
Negative		66		M					
LCR 693		2.57		None detected		Not applicable		Not applicable	16
735		164		41,653					
Negative		61		M					
LCR 694		1.54		None detected		Not applicable		Not applicable	23
713		216		40,538					
Negative		59		F					
LCR 697		12.02		None detected		Not applicable		Not applicable	16
599		254		35,549					
Negative		61		M					
LCR 698		6.49		None detected		Not applicable		Not applicable	38
2,371		341		35,178					
Negative		74		M					
LCR 699		0.90		None detected		Not applicable		Not applicable	19
724		264		29,592					
Negative		71		F					
LCR 700		3.76		None detected		Not applicable		Not applicable	28
1,451		307		96,120					
Negative		78		F					
LCR 701		1.86		None detected		Not applicable		Not applicable	16
539		311		21,619					
Negative		52		M					
LCR 702		3.95		None detected		Not applicable		Not applicable	16
1,650		398		133,358					
Negative		85		F					
LCR 703		0.65		None detected		Not applicable		Not applicable	20
569		223		46,299					
Negative		85		M					
LCR 704		7.32		None detected		Not applicable		Not applicable	16
2,616		406		35,208					
Negative		81		M					
LCR 705		5.14		None detected		Not applicable		Not applicable	33
1,038		273		55,638					
Negative		54		F					
LCR 706		10.62		None detected		Not applicable		Not applicable	32
1,090		273		23,953					
Negative		66		M					
LCR 707		3.90		None detected		Not applicable		Not applicable	16
1,586		365		43,633					

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Negative		82		M							
LCR 709		2.36		None detected		Not applicable		Not applicable	16	1,795	467	28,573
Negative		67		F							
LCR 710		7.20		None detected		Not applicable		Not applicable	16	958	437	24,261
Negative		71		M							
LCR 711		2.26		None detected		Not applicable		Not applicable	16	1,345	298	49,222
Negative		66		M							
LCR 712		11.51		None detected		Not applicable		Not applicable	16	1,823	213	41,932
Negative		61		M							
LCR 713		9.78		None detected		Not applicable		Not applicable	45	3,706	260	31,262
Negative		79		M							
LCR 714		1.93		None detected		Not applicable		Not applicable	16	917	266	48,714
Negative		72		F							
LCR 715		0.50		None detected		Not applicable		Not applicable	16	972	202	23,148
Negative		52		M							
LCR 716		5.21		None detected		Not applicable		Not applicable	16	885	324	25,231
Negative		69		M							
LCR 717		1.27		None detected		Not applicable		Not applicable	41	1,788	670	54,642
Negative		75		F							
LCR 718		3.12		None detected		Not applicable		Not applicable	16	778	238	28,390
Negative		52		M							
LCR 719		3.19		None detected		Not applicable		Not applicable	16	593	169	45,608
Negative		60		M							
LCR 720		3.36		None detected		Not applicable		Not applicable	16	2,475	198	56,420
Negative		61		F							
LCR 721		5.91		None detected		Not applicable		Not applicable	17	1,302	198	60,134
Negative		75		M							
LCR 722		5.16		None detected		Not applicable		Not applicable	16	710	166	71,301
Negative		80		M							
LCR 723		5.22		None detected		Not applicable		Not applicable	20	1,076	175	40,538
Negative		61		F							
LCR 725		2.85		None detected		Not applicable		Not applicable	16	2,492	172	43,981

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Negative		65		F					
LCR 726		1.45		None detected		Not applicable		Not applicable	
16		1,435		307		59,059			
Negative		60		F					
LCR 727		1.80		None detected		Not applicable		Not applicable	
16		1,388		165		12,989			
Negative		65		M					
LCR 728		1.82		None detected		Not applicable		Not applicable	
16		436		510		22,565			
Negative		51		M					
LCR 729		1.61		None detected		Not applicable		Not applicable	
18		2,384		307		38,693			
Negative		67		M					
LCR 730		2.75		None detected		Not applicable		Not applicable	
16		460		164		25,950			
Negative		71		M					
LCR 731		1.45		None detected		Not applicable		Not applicable	
16		436		165		22,922			
Negative		56		M					
LCR 732		0.76		None detected		Not applicable		Not applicable	
16		1,188		255		64,361			
Negative		50		M					
LCR 733		3.81		None detected		Not applicable		Not applicable	
26		1,567		172		17,531			
Negative		80		M					
LCR 734		3.43		None detected		Not applicable		Not applicable	
16		1,310		260		66,017			
Negative		77		F					
LCR 736		2.97		None detected		Not applicable		Not applicable	
22		2,152		178		84,797			
Negative		59		M					
LCR 737		2.65		None detected		Not applicable		Not applicable	
17		1,068		242		97,150			
Negative		81		M					
LCR 738		7.94		None detected		Not applicable		Not applicable	
16		2,501		383		122,519			
Negative		84		F					
LCR 739		1.95		None detected		Not applicable		Not applicable	
16		1,306		235		109,025			
Negative		36		M					
LCR 740		3.11		None detected		Not applicable		Not applicable	
27		1,863		172		82,561			
Negative		81		M					
LCR 741		100.42		None detected		Not applicable		Not applicable	
16		1,027		297		121,739			
Negative		65		M					
LCR 742		5.67		None detected		Not applicable		Not applicable	
32		615		316		60,066			

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Negative		50		M							
LCR 743		4.22		None detected		Not applicable		Not applicable	26	1,792	488	147,000
Negative		77		M							
LCR 744		4.06		None detected		Not applicable		Not applicable	47	3,195	201	43,356
Negative		68		M							
LCR 745		1.30		None detected		Not applicable		Not applicable	31	744	183	22,467
Negative		60		F							
LCR 746		1.53		None detected		Not applicable		Not applicable	16	2,197	346	69,390
Negative		53		M							
LCR 747		1.78		None detected		Not applicable		Not applicable	16	4,709	165	52,773
Negative		80		M							
LCR 749		1.32		None detected		Not applicable		Not applicable	19	1,062	337	60,685
Negative		70		F							
LCR 750		1.36		None detected		Not applicable		Not applicable	16	2,957	183	30,706
Negative		78		M							
LCR 751		2.10		None detected		Not applicable		Not applicable	16	1,049	220	18,994
Negative		76		M							
LCR 752		9.31		None detected		Not applicable		Not applicable	16	965	183	157,671
Negative		88		M							
LCR 753		1.52		None detected		Not applicable		Not applicable	16	717	349	61,187
Negative		80		M							
LCR 754		2.21		None detected		Not applicable		Not applicable	16	649	211	31,323
Negative		40		M							
LCR 755		1.39		None detected		Not applicable		Not applicable	21	1,060	251	19,701
Negative		55		F							
LCR 757		1.62		None detected		Not applicable		Not applicable	59	2,893	430	90,072
Negative		75		F							
LCR 758		67.40		None detected		Not applicable		Not applicable	52	2,628	266	25,239
Negative		73		M							
LCR 759		1.97		None detected		Not applicable		Not applicable	19	2,415	556	113,487
Negative		55		M							
LCR 760		0.65		None detected		Not applicable		Not applicable	16	436	193	77,203

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Negative		55		F					
LCR 761		0.94		None detected		Not applicable		Not applicable	16
1,490		246		13,138					
Negative		62		M					
LCR 762		135.67		None detected		Not applicable		Not applicable	16
538		300		27,765					
Negative		73		M					
LCR 763		37.22		None detected		Not applicable		Not applicable	16
460		188		26,953					
Negative		60		M					
LCR 764		71.68		None detected		Not applicable		Not applicable	18
544		178		43,842					
Negative		72		F					
LCR 765		64.69		None detected		Not applicable		Not applicable	16
2,379		229		41,584					
Negative		51		M					
LCR 766		6.85		None detected		Not applicable		Not applicable	16
1,045		174		14,859					
Negative		76		F					
LCR 768		4.67		None detected		Not applicable		Not applicable	25
5,365		430		33,531					
Negative		56		M					
LCR 769		4.49		None detected		Not applicable		Not applicable	16
1,256		229		20,133					
Negative		51		M					
LCR 770		3.25		None detected		Not applicable		Not applicable	16
2,093		255		16,594					
Negative		34		M					
LCR 771		100.85		None detected		Not applicable		Not applicable	43
1,262		291		37,877					
Negative		70		M					
LCR 772		7.79		None detected		Not applicable		Not applicable	16
1,682		198		28,353					
Negative		73		M					
LCR 773		5.23		None detected		Not applicable		Not applicable	22
461		182		19,383					
Negative		44		M					
LCR 774		7.43		None detected		Not applicable		Not applicable	16
460		210		18,985					
Negative		67		F					
LCR 775		5.50		None detected		Not applicable		Not applicable	37
1,041		502		38,859					
Negative		51		F					
LCR 776		2.82		None detected		Not applicable		Not applicable	16
1,934		164		31,262					
Negative		50		M					
LCR 777		4.78		None detected		Not applicable		Not applicable	17
7,378		341		32,736					

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Negative		86		F			
LCR 778		3.11		None detected		Not applicable	Not applicable
27		2,055		332		23,600	
Negative		57		M			
LCR 779		11.52		None detected		Not applicable	Not applicable
42		1,439		264		22,109	
Negative		65		F			
LCR 780		5.49		None detected		Not applicable	Not applicable
20		1,427		281		28,847	
Negative		65		F			
LCR 781		3.34		None detected		Not applicable	Not applicable
24		779		298		34,569	
Negative		71		F			
LCR 782		3.10		None detected		Not applicable	Not applicable
48		1,083		164		56,076	
Negative		56		F			
LCR 783		4.26		None detected		Not applicable	Not applicable
29		460		185		6,296	
Negative		68		M			
LCR 784		4.30		None detected		Not applicable	Not applicable
16		5,715		229		26,211	
Negative		62		F			
LCR 785		6.71		None detected		Not applicable	Not applicable
16		2,530		322		93,629	
Negative		55		M			
LCR 786		5.05		None detected		Not applicable	Not applicable
16		2,921		235		51,194	
Negative		75		F			

Highlighted values represent protein concentrations below or below the limit of detection of the assay; values set as correspoding lower or upper limit of detection

Table10.txt

Table 10. Examples tumor-specific mutations detected in PaCan patients

Sample ID #	Mutation identified in tumor tissue	Cancer Type	Mutant mean allele frequency (%)	Mutation identified in plasma
INDI 006 PLS 1	TP53 p.R280S, c.840A>T	Lung	11.230	TP53 p.R280S, c.840A>T
INDI 008 PLS 1	FBXW7 p.R479G, c.1435C>G	Lung	1.705	FBXW7 p.R479G, c.1435C>G
INDI 008 PLS 1	TP53 p.E258*, c.772G>T	Lung	1.429	TP53 p.E258*, c.772G>T
INDI 009 PLS 1	TP53 p.C176F, c.527G>T	Lung	1.061	TP53 p.C176F, c.527G>T
INDI 014 PLS 1	TP53 p.E298*, c.892G>T	Lung	1.360	TP53 p.E298*, c.892G>T
INDI 021 PLS 1	TP53 p.A88fs, c.263C>	Lung	5.431	TP53 p.A88fs, c.263C>
INDI 023 PLS 1	TP53 p.G266V, c.797G>T	Lung	0.904	TP53 p.G266V, c.797G>T
INDI 027 PLS 1	TP53 p.R175H, c.524G>A	CRC	2.486	TP53 p.R175H, c.524G>A
INDI 034 PLS 1	TP53 p.R175H, c.524G>A	CRC	0.130	TP53 p.R175H, c.524G>A
INDI 070 PLS 1	PTEN p.C136R, c.406T>C	Breast	0.749	PTEN p.C136R, c.406T>C
INDI 075 PLS 1	TP53 p.Y220C, c.659A>G	Ovarian	8.472	TP53 p.Y220C, c.659A>G
INDI 077 PLS 1	TP53 p.K132R, c.395A>G	Liver	4.396	TP53 p.K132R, c.395A>G
INDI 081 PLS 1	TP53 p.W53*, c.158G>A	CRC	0.232	TP53 p.W53*, c.158G>A
INDI 091 PLS 1	TP53 p.R248Q, c.743G>A	Gastric	7.420	TP53 p.R248Q, c.743G>A
INDI 109 PLS 1	TP53 p.R248Q, c.743G>A	CRC	4.869	TP53 p.R248Q, c.743G>A
INDI 116 PLS 1	TP53 p.S260Y, c.779C>A	Gastric	40.923	TP53 p.S260Y, c.779C>A
INDI 119 PLS 1	TP53 p.H179R, c.536A>G	Esophagus	2.175	TP53 p.H179R, c.536A>G
INDI 119 PLS 1	APC p.N1455fs, c.4364A>	Esophagus	1.078	APC p.N1455fs, c.4364A>
INDI 124 PLS 1	TP53 p.A63V, c.188C>T	CRC	46.229	TP53 p.A63V, c.188C>T
INDI 126 PLS 1	TP53 p.K132R, c.395A>G	Gastric	0.634	TP53 p.K132R, c.395A>G
INDI 128 PLS 1	CTNNB1 p.S45F, c.134C>T	CRC	0.434	CTNNB1 p.S45F, c.134C>T

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INDI 139 PLS 1 Gastric GNAS p.R201H, c.602G>A GNAS p.R201H, c.602G>A 19.853
INDI 150 PLS 1 CRC KRAS p.G12C, c.34G>T KRAS p.G12C, c.34G>T 3.448
INDI 150 PLS 1 CRC TP53 g.7578176C>T (splice site) TP53 g.7578176C>T (splice site) 2.429
INDI 154 PLS 1 Small Intestine KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 0.975
INDI 156 PLS 1 CRC KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T 7.212
INDI 156 PLS 1 CRC TP53 p.P190fs, c.570CCT> TP53 p.P190fs, c.570CCT> 6.150
INDI 157 PLS 1 CRC TP53 p.R282W, c.844C>T TP53 p.R282W, c.844C>T 54.847
INDI 172 PLS 1 Gastric TP53 p.R248Q, c.743G>A TP53 p.R248Q, c.743G>A 2.950
INDI 185 PLS 1 Gastric TP53 p.S183fs, c.549>A TP53 p.S183fs, c.549>A 1.404
INDI 190 PLS 1 Liver TP53 p.P151fs, c.451>C TP53 p.P151fs, c.451>C 0.273
INDI 198 PLS 1 Gastric TP53 p.V274F, c.820G>T TP53 p.V274F, c.820G>T 1.669
INDI 210 PLS 1 Gastric TP53 p.C135*, c.405C>A TP53 p.C135*, c.405C>A 1.050
INDI 211 PLS 1 CRC TP53 p.R175H, c.524G>A TP53 p.R175H, c.524G>A 0.253
INDI 212 PLS 1 CRC BRAF p.V600E, c.1799T>A BRAF p.V600E, c.1799T>A 2.627
INDI 217 PLS 1 CRC BRAF p.D594G, c.1781A>G BRAF p.D594G, c.1781A>G 1.237
INDI 219 PLS 1 Liver KRAS p.G12C, c.34G>T KRAS p.G12C, c.34G>T 0.395
INDI 222 PLS 1 CRC TP53 p.G266E, c.797G>A TP53 p.G266E, c.797G>A 7.385
INDI 222 PLS 1 CRC KRAS p.G13D, c.38G>A KRAS p.G13D, c.38G>A 6.933
INDI 231 PLS 1 Lung KRAS p.G12D, c.35G>A KRAS p.G12D, c.35G>A 9.384
INDI 240 PLS 1 CRC TP53 p.E224E, c.672G>A (Exon End) TP53 p.E224E, c.672G>A (Exon End) 19.758
INDI 240 PLS 1 CRC NRAS p.Q61K, c.181C>A NRAS p.Q61K, c.181C>A 9.620
INDI 242 PLS 1 Lung TP53 p.R290fs, c.869G> TP53 p.R290fs, c.869G> 0.297
INDI 243 PLS 1 CRC APC p.E1309fs, c.3927AAAGA> APC p.E1309fs, c.3927AAAGA> 2.958
INDI 244 PLS 1 CRC KRAS p.G12C, c.34G>T KRAS p.G12C, c.34G>T 0.654

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INDI 245 PLS 1	CRC	KRAS p.Q61K, c.181C>A	KRAS p.Q61K, c.181C>A 1.191
INDI 255 PLS 1	CRC	PIK3CA p.H1047R, c.3140A>G	PIK3CA p.H1047R, c.3140A>G 1.121
INDI 255 PLS 1	CRC	KRAS p.G13V, c.38G>T	KRAS p.G13V, c.38G>T 0.574
INDI 256 PLS 1	CRC	KRAS p.G12S, c.34G>A	KRAS p.G12S, c.34G>A 3.966
INDI 256 PLS 1	CRC	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A 2.050
INDI 263 PLS 1	CRC	TP53 p.D281N, c.841G>A	TP53 p.D281N, c.841G>A 50.972
INDI 263 PLS 1	CRC	BRAF p.V600E, c.1799T>A	BRAF p.V600E, c.1799T>A 31.738
INDI 268 PLS 1	CRC	NRAS p.Q61R, c.182A>G	NRAS p.Q61R, c.182A>G 3.337
INDI 284 PLS 1	CRC	APC p.E1309fs, c.3927AAAGA>	APC p.E1309fs, c.3927AAAGA> 0.122
INDI 285 PLS 1	Lung	TP53 p.E339*, c.1015G>T	TP53 p.E339*, c.1015G>T 1.293
INDI 287 PLS 1	Breast	TP53 p.S94*, c.281C>G	TP53 p.S94*, c.281C>G 1.429
INDI 288 PLS 1	Lung	TP53 p.T125T, c.375G>T (Exon End)	TP53 p.T125T, c.375G>T (Exon End) 8.374
INDI 306 PLS 1	CRC	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A 46.107
INDI 306 PLS 1	CRC	APC p.E1309fs, c.3927AAAGA>	APC p.E1309fs, c.3927AAAGA> 36.318
INDI 310 PLS 1	CRC	PIK3CA p.E545A, c.1634A>C	PIK3CA p.E545A, c.1634A>C 0.694
INDI 329 PLS 1	CRC	BRAF p.V600E, c.1799T>A	BRAF p.V600E, c.1799T>A 10.039
INDI 329 PLS 1	CRC	PIK3CA p.E542K, c.1624G>A	PIK3CA p.E542K, c.1624G>A 5.058
INDI 331 PLS 1A	Lung	KRAS p.G12C, c.34G>T	KRAS p.G12C, c.34G>T 10.876
INDI 340 PLS 1	CRC	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A 1.319
INDI 345 PLS 1	CRC	TP53 p.M160fs, c.479>TGGCC	TP53 p.M160fs, c.479>TGGCC 38.114
INDI 345 PLS 1	CRC	KRAS p.Q61K, c.181C>A	KRAS p.Q61K, c.181C>A 23.235
INDI 349 PLS 1	CRC	KRAS p.G12C, c.34G>T	KRAS p.G12C, c.34G>T 0.977
INDI 349 PLS 1	CRC	TP53 p.R248Q, c.743G>A	TP53 p.R248Q, c.743G>A 0.925
INDI 353 PLS 1A	Lung	TP53 p.M133L, c.397A>T	TP53 p.M133L, c.397A>T 0.235

Table10.txt

INDI 365 PLS 1	CRC	APC p.E1309fs, c.3927AAAGA> APC p.E1309fs, c.3927AAAGA>	0.596	
INDI 367 PLS 1	Liver	CTNNB1 p.I35S, c.104T>G CTNNB1 p.I35S, c.104T>G	0.284	
INDI 370 PLS 1	CRC	TP53 p.A161T, c.481G>A TP53 p.A161T, c.481G>A	42.557	
INDI 370 PLS 1	CRC	KRAS p.A146V, c.437C>T KRAS p.A146V, c.437C>T	42.018	
INDI 371 PLS 1A	Lung	KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T	7.711	
INDI 381 PLS 1A	Lung	PIK3CA p.H1047L, c.3140A>T PIK3CA p.H1047L, c.3140A>T	2.035	
INDI 400 PLS 1	CRC	TP53 p.R175H, c.524G>A TP53 p.R175H, c.524G>A	2.962	
INDI 435 PLS 1	CRC	KRAS p.G12C, c.34G>T KRAS p.G12C, c.34G>T	0.706	
INDI 435 PLS 1	CRC	TP53 p.Y163N, c.487T>A TP53 p.Y163N, c.487T>A	0.554	
INDI 439 PLS 1	CRC	KRAS p.G12C, c.34G>T KRAS p.G12C, c.34G>T	0.931	
INDI 439 PLS 1	CRC	BRAF p.F595L, c.1785T>G BRAF p.F595L, c.1785T>G	0.901	
INDI 445 PLS 1	Breast	TP53 p.E171fs, c.513GACGGAG> TP53 p.E171fs, c.513GACGGAG>	0.695	
INDI 447 PLS 1	Breast	TP53 p.F113S, c.338T>C TP53 p.F113S, c.338T>C	23.948	
INDI 447 PLS 1	Breast	PIK3CA p.G1049R, c.3145G>C PIK3CA p.G1049R, c.3145G>C	21.723	
INDI 457 PLS 1	Esophagus	TP53 p.E221*, c.661G>T TP53 p.E221*, c.661G>T	1.375	
INDI 457 PLS 1	Esophagus	TP53 p.G266V, c.797G>T TP53 p.G266V, c.797G>T	1.104	
INDI 459 PLS 1	Breast	PIK3CA p.H1047R, c.3140A>G PIK3CA p.H1047R, c.3140A>G	60.444	
INDI 459 PLS 1	Breast	TP53 p.E285K, c.853G>A TP53 p.E285K, c.853G>A	58.047	
INDI 461 PLS 1	CRC	TP53 p.V172F, c.514G>T TP53 p.V172F, c.514G>T	0.308	
INDI 462 PLS 1	Breast	TP53 g.7578176C>A (splice site) TP53 g.7578176C>A (splice site)	65.428	
INDI 464 PLS 1	Liver	TP53 p.K132*, c.394A>T TP53 p.K132*, c.394A>T	0.297	
INDI 466 PLS 1	CRC	KRAS p.G12V, c.35G>T KRAS p.G12V, c.35G>T	0.265	
INDI 509 PLS 1	Breast	TP53 p.P278T, c.832C>A TP53 p.P278T, c.832C>A	38.691	
INDI 518 PLS 1	CRC	TP53 p.N131fs, c.392CAA> TP53 p.N131fs, c.392CAA>	0.175	

Table10.txt

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   INDI 536 PLS 1            CRC                KRAS p.G13D, c.38G>A
 KRAS p.G13D, c.38G>A               57.820
   INDI 536 PLS 1            CRC               TP53 p.C135R, c.403T>C
TP53 p.C135R, c.403T>C             57.647
   INDI 539 PLS 1            CRC               PTEN p.D92A, c.275A>C
 PTEN p.D92A, c.275A>C              0.492
   INDI 539 PLS 1            CRC              BRAF p.V600E, c.1799T>A
BRAF p.V600E, c.1799T>A            0.396
   INDI 542 PLS 1            CRC                KRAS p.G12C, c.34G>T
 KRAS p.G12C, c.34G>T               36.797
   INDI 543 PLS 1           Lung               TP53 p.G105A, c.314G>C
TP53 p.G105A, c.314G>C             2.993
   INDI 544 PLS 1            CRC              TP53 p.G334R, c.1000G>C
TP53 p.G334R, c.1000G>C            52.811
   INDI 552 PLS 1           Lung               TP53 p.C238F, c.713G>T
TP53 p.C238F, c.713G>T             6.014
   INDI 555 PLS 1            CRC            APC p.E1309fs, c.3927AAAGA>
APC p.E1309fs, c.3927AAAGA>          0.779
   INDI 567 PLS 1            CRC               TP53 p.R175H, c.524G>A
TP53 p.R175H, c.524G>A             2.632
   INDI 567 PLS 1            CRC                KRAS p.G12A, c.35G>C
 KRAS p.G12A, c.35G>C               2.594
   INDI 567 PLS 1            CRC             PIK3CA p.E545K, c.1633G>A
PIK3CA p.E545K, c.1633G>A           0.880
   INDI 580 PLS 1            CRC                KRAS p.G12D, c.35G>A
 KRAS p.G12D, c.35G>A               27.279
   INDI 580 PLS 1            CRC               TP53 p.M237I, c.711G>A
TP53 p.M237I, c.711G>A             24.892
   INDI 581 PLS 1            CRC                KRAS p.G13D, c.38G>A
 KRAS p.G13D, c.38G>A               3.409
   INDI 581 PLS 1            CRC          TP53 g.7579311C>A (splice site)
TP53 g.7579311C>A (splice site)        1.358
   INDI 585 PLS 1         Esophagus            TP53 p.E343*, c.1027G>T
TP53 p.E343*, c.1027G>T            0.519
   INDI 601 PLS 1          Breast              TP53 p.R213*, c.637C>T
TP53 p.R213*, c.637C>T             9.270
   INDI 618 PLS 1            CRC               TP53 p.A63V, c.188C>T
 TP53 p.A63V, c.188C>T             47.323
   INDI 623 PLS 1          Breast              TP53 p.R273P, c.818G>C
TP53 p.R273P, c.818G>C             2.140
   INDI 628 PLS 1            CRC               TP53 p.A63V, c.188C>T
 TP53 p.A63V, c.188C>T             47.184
   INDI 636 PLS 1           Liver              CTNNB1 p.T41A, c.121A>G
CTNNB1 p.T41A, c.121A>G            3.966
   INDI 645 PLS 1           Liver               TP53 p.R249S, c.747G>T
TP53 p.R249S, c.747G>T             7.169
   INDI 648 PLS 1            CRC               TP53 p.E258G, c.773A>G
TP53 p.E258G, c.773A>G             28.968
```

Table10.txt

INDI 648 PLS 1	CRC	KRAS p.G12V, c.35G>T	KRAS p.G12V, c.35G>T 24.217
INDI 665 PLS 1	Esophagus	FGFR2 p.P253R, c.758C>G	FGFR2 p.P253R, c.758C>G 0.354
INDI 665 PLS 1	Esophagus	TP53 p.C135F, c.404G>T	TP53 p.C135F, c.404G>T 0.275
INDI 670 PLS 1	CRC	TP53 p.G117fs, c.350>GGAC	TP53 p.G117fs, c.350>GGAC 14.282
INDI 675 PLS 1	CRC	BRAF p.I592V, c.1774A>G	BRAF p.I592V, c.1774A>G 56.661
INDI 678 PLS 1	CRC	KRAS p.Q61H, c.183A>T	KRAS p.Q61H, c.183A>T 1.164
INDI 678 PLS 1	CRC	TP53 p.E224fs, c.670>G	TP53 p.E224fs, c.670>G 1.096
INDI 687 PLS 1	Lung	KRAS p.G12V, c.35G>T	KRAS p.G12V, c.35G>T 5.151
INDI 687 PLS 1	Lung	TP53 p.R273L, c.818G>T	TP53 p.R273L, c.818G>T 0.519
INDI 693 PLS 1	Lung	TP53 p.H193Y, c.577C>T	TP53 p.H193Y, c.577C>T 22.235
INDI 701 PLS 1	CRC	BRAF p.V600E, c.1799T>A	BRAF p.V600E, c.1799T>A 0.170
INDI 702 PLS 1	Lung	TP53 p.E298*, c.892G>T	TP53 p.E298*, c.892G>T 0.138
INDI 708 PLS 1	CRC	KRAS p.G12C, c.34G>T	KRAS p.G12C, c.34G>T 0.257
INDI 710 PLS 1	CRC	PIK3CA p.Q546R, c.1637A>G	PIK3CA p.Q546R, c.1637A>G 0.163
INDI 714 PLS 1	Breast	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A 2.123
INDI 748 PLS 1	CRC	TP53 p.S241fs, c.722C>	TP53 p.S241fs, c.722C> 0.261
INDI 751 PLS 1	CRC	PIK3CA p.N345K, c.1035T>A	PIK3CA p.N345K, c.1035T>A 8.228
INDI 752 PLS 1	CRC	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A 0.659
INDI 753 PLS 1	Esophagus	TP53 p.Y220C, c.659A>G	TP53 p.Y220C, c.659A>G 3.457
INDI 764 PLS 1	CRC	TP53 p.E51fs, c.151G>	TP53 p.E51fs, c.151G> 1.779
INDI 769 PLS 1	CRC	TP53 p.I251V, c.751A>G	TP53 p.I251V, c.751A>G 50.294
INDI 770 PLS 1	CRC	TP53 p.E285K, c.853G>A	TP53 p.E285K, c.853G>A 0.152
INDI 778 PLS 1	Liver	CTNNB1 p.I35S, c.104T>G	CTNNB1 p.I35S, c.104T>G 0.084
INDI 779 PLS 1	CRC	TP53 p.E11Q, c.31G>C	TP53 p.E11Q, c.31G>C 50.219

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INDI 782 PLS 1	CRC	BRAF p.V600E, c.1799T>A	BRAF p.V600E, c.1799T>A	2.885
INDI 786 PLS 1	Liver	TP53 p.C135F, c.404G>T	TP53 p.C135F, c.404G>T	1.135
INDI 796 PLS 1	Liver	PIK3CA p.H1047R, c.3140A>G	PIK3CA p.H1047R, c.3140A>G	0.521
INDI 798 PLS 1	Ovarian	TP53 p.Y163C, c.488A>G	TP53 p.Y163C, c.488A>G	7.314
INDI 804 PLS 1	CRC	KRAS p.G12R, c.34G>C	KRAS p.G12R, c.34G>C	30.128
INDI 804 PLS 1	CRC	APC p.E1309fs, c.3927AAAGA>	APC p.E1309fs, c.3927AAAGA>	23.715
INDI 812 PLS 1	Ovarian	KRAS p.G12C, c.34G>T	KRAS p.G12C, c.34G>T	3.472
INDI 812 PLS 1	Ovarian	CTNNB1 p.T41A, c.121A>G	CTNNB1 p.T41A, c.121A>G	3.184
INDI 813 PLS 1	Liver	TP53 p.K381fs, c.1141A>	TP53 p.K381fs, c.1141A>	0.763
INDI 815 PLS 1	CRC	BRAF p.V600E, c.1799T>A	BRAF p.V600E, c.1799T>A	0.224
INDI 817 PLS 1	Liver	CTNNB1 p.I35S, c.104T>G	CTNNB1 p.I35S, c.104T>G	0.099
INDI 818 PLS 1	Ovarian	TP53 p.G154fs, c.460G>	TP53 p.G154fs, c.460G>	2.827
INDI 819 PLS 1	Breast	AKT1 p.E17K, c.49G>A	AKT1 p.E17K, c.49G>A	6.061
INDI 819 PLS 1	Breast	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A	4.100
INDI 827 PLS 1	CRC	TP53 p.R175H, c.524G>A	TP53 p.R175H, c.524G>A	0.370
INDI 834 PLS 1	Ovarian	TP53 g.7578290C>A (splice site)	TP53 g.7578290C>A (splice site)	2.801
INDI 845 PLS 1	CRC	TP53 p.E258*, c.772G>T	TP53 p.E258*, c.772G>T	0.208
INDI 850 PLS 1	Esophagus	TP53 p.H193P, c.578A>C	TP53 p.H193P, c.578A>C	21.370
INDI 859 PLS 1	Esophagus	TP53 p.Y234N, c.700T>A	TP53 p.Y234N, c.700T>A	0.591
INDI 866 PLS 1	Breast	TP53 p.R110H, c.329G>A	TP53 p.R110H, c.329G>A	40.819
INDI 872 PLS 1	Breast	PIK3CA p.H1047L, c.3140A>T	PIK3CA p.H1047L, c.3140A>T	0.902
INDI 872 PLS 1	Breast	TP53 p.H179Y, c.535C>T	TP53 p.H179Y, c.535C>T	0.490
INDI 884 PLS 1	Breast	TP53 p.Y220C, c.659A>G	TP53 p.Y220C, c.659A>G	11.696
INDI 906 PLS 1	Pancreas	TP53 p.F134fs, c.400>T	TP53 p.F134fs, c.400>T	0.245

Table10.txt

INDI 906 PLS 1	Pancreas	KRAS p.Q61H, c.183A>T	KRAS p.Q61H, c.183A>T
0.241			
INDI 910 PLS 1	Esophagus	TP53 p.H193L, c.578A>T	TP53 p.H193L, c.578A>T
0.096			
INDI 925 PLS 1	Gastric	TP53 p.R196*, c.586C>T	TP53 p.R196*, c.586C>T
17.732			
INDI 932 PLS 1	Ovarian	TP53 p.L252fs, c.754TCC>	TP53 p.L252fs, c.754TCC>
10.810			

Table11.txt

Table 11. PlasmaSeqS with 5718 Matched White Blood Cell Summary.

Sample											MAF	MAF
Experiment	Patient	Template	Type	ampMatchName	Chrom	Position	MutType	BaseFrom	BaseTo	Gene	ntStart	codonStart	aaRef	aaVar	in Plasma	in PT	in WBCs
5578	CRC 458	CRC 458 PLS	CRC	TP53_0248_0261	chr17	7577538	SBS	C	T	TP53	743	248	R	Q	0.156	53.883	0.082
5578	CRC 468	CRC 468 PLS	CRC	TP53_0272_0283	chr17	7577105	SBS	G	C	TP53	833	278	P	R	5.573	1.613	7.638
5578	CRC 469	CRC 469 PLS	CRC	TP53_0248_0261	chr17	7577538	SBS	C	T	TP53	743	248	R	Q	4.181	Not found	4.015
5578	CRC 470	CRC 470 PLS	CRC	TP53_342	chr17	7574003	SBS	G	A	TP53	1024	342	R	*	0.859	72.662	Not found
5578	CRC 471	CRC 471 PLS	CRC	TP53_0196_0205	chr17	7578263	SBS	G	A	TP53	586	196	R	*	1.842	67.010	Not found
5578	CRC 473	CRC 473 PLS	CRC	TP53_219_224	chr17	7578190	SBS	T	C	TP53	659	220	Y	C	2.561	Not found	0.290
5578	CRC 476	CRC 476 PLS	CRC	TP53_0248_0261	chr17	7577536	SBS	T	C	TP53	745	249	R	G	7.207	62.896	Not found
5578	CRC 477	CRC 477 PLS	CRC	TP53_113_125	chr17	7579332	SBS	C	T	TP53	355	119	A	T	0.101	Not found	Not found
5578	CRC 483	CRC 483 PLS	CRC	TP53_172A	chr17	7578394	SBS	T	C	TP53	536	179	H	R	0.622	Not found	1.018
5578	CRC 489	CRC 489 PLS	CRC	KRAS_0057_0064	chr12	25380277	SBS	G	T	KRAS	181	61	Q	K	0.169	23.333	Not found
5578	CRC 494	CRC 494 PLS	CRC	APC_1450_1458	chr5	112175639	SBS	C	T	APC	4348	1450	R	*	0.473	27.418	Not found
5578	CRC 494	CRC 494 PLS	CRC	TP53_0248_0261	chr17	7577538	SBS	C	T	TP53	743	248	R	Q	0.836	76.451	0.203
5578	CRC 494	CRC 494 PLS	CRC	TP53_0272_0283	chr17	7577120	SBS	C	T	TP53	818	273	R	H	0.170	Not found	Not found
5578	CRC 521	CRC 521 PLS	CRC	KRAS_144_147A	chr12	25378561											

Table11.txt

SBS	G	A	KRAS	437	146	A	V	0.440	48.106	Not found
5578	CRC 523	CRC 523 PLS	CRC	TP53_172A	chr17	7578394			
SBS	T	C	TP53	536	179	H	R	0.657	Not found	0.856
5578	CRC 524	CRC 524 PLS	CRC	KRAS_0057_0064	chr12	25380282			
SBS	G	T	KRAS	176	59	A	E	0.155	Not found	0.754
5578	CRC 524	CRC 524 PLS	CRC	PIK3CA_1039_1050	chr3	178952085			
SBS	A	G	PIK3CA	3140	1047	H	R	0.182	40.747	Not found
5578	CRC 527	CRC 527 PLS	CRC	KRAS_144_147A	chr12	25378562			
SBS	C	T	KRAS	436	146	A	T	2.200	32.549	Not found
5578	CRC 531	CRC 531 PLS	CRC	TP53_0227_0236	chr17	7577580			
SBS	T	C	TP53	701	234	Y	C	0.306	Not found	0.178
5578 and 557	CRC 456	CRC 456 PLS	CRC	CTNNB1_0039_0046	chr3	41266121			
SBS	A	G	CTNNB1	118	40	T	A	0.105	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	PIK3CA_0542_0551	chr3	178936083			
SBS	A	C	PIK3CA	1625	542	E	A	0.108	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_026	chr17	7579707			
SBS	T	C	TP53	89	30	N	S	0.108	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_033_040	chr17	7579574			
SBS	T	C	TP53	113	38	Q	R	0.118	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_113_125	chr17	7579338			
SBS	C	G	TP53	349	117	G	R	0.101	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_208_218	chr17	7578221			
SBS	T	C	TP53	628	210	N	D	0.101	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_219_224	chr17	7578191			
SBS	A	G	TP53	658	220	Y	H	0.159	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_233_245	chr17	7577551			
SBS	C	T	TP53	730	244	G	S	0.103	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_345	chr17	7573972			
SBS	T	G	TP53	1055	352	D	A	0.103	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_345	chr17	7573991			
SBS	C	G	TP53	1036	346	E	Q	0.103	Not found	Not found
5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_374_385	chr17	7572985			

Table11.txt

SBS T G TP53 1124 375 Q P 0.132
Not found Not found
5578 and 557 CRC 460 CRC 460 PLS CRC CDKN2A_7_88 chr9 21971098
SBS C T CDKN2A 260 87 R Q 0.130
Not found Not found
5578 and 557 CRC 460 CRC 460 PLS CRC TP53_0196_0205 chr17 7578255
SBS T G TP53 594 198 E D 0.101
Not found Not found
5578 and 557 CRC 460 CRC 460 PLS CRC TP53_233_245 chr17 7577551
SBS C T TP53 730 244 G S 0.344
Not found Not found
5578 and 557 CRC 461 CRC 461 PLS CRC TP53_219_224 chr17 7578191
SBS A G TP53 658 220 Y H 0.117
Not found Not found
5578 and 557 CRC 474 CRC 474 PLS CRC TP53_113_125 chr17 7579349
SBS A C TP53 338 113 F C 0.116
Not found Not found
5578 and 557 CRC 481 CRC 481 PLS CRC FBXW7_464_472A chr4 153249366
Indel NULL T FBXW7 1412 471 E fs 0.171
15.621 Not found
5578 and 557 CRC 481 CRC 481 PLS CRC PIK3CA_1039_1050 chr3 178952085
SBS A G PIK3CA 3140 1047 H R 0.267
32.437 Not found
5578 and 557 CRC 491 CRC 491 PLS CRC FBXW7_464_472A chr4 153249384
SBS C T FBXW7 1394 465 R H 0.153
24.088 Not found
5578 and 557 CRC 497 CRC 497 PLS CRC APC_1304_1310 chr5 112175216
SBS G T APC 3925 1309 E * 0.316
29.560 Not found
5578 and 557 CRC 497 CRC 497 PLS CRC FBXW7_474_482 chr4 153247366
SBS C T FBXW7 1436 479 R Q 0.505
27.814 Not found
5578 and 557 CRC 504 CRC 504 PLS CRC APC_1304_1310 chr5 112175218
Indel AAAGA NULL APC 3927 1309 E fs 1.619
64.283 Not found
5578 and 557 CRC 504 CRC 504 PLS CRC TP53_0272_0283 chr17 7577121
SBS G A TP53 817 273 R C 0.922
60.499 Not found
5578 and 557 CRC 512 CRC 512 PLS CRC KRAS_012_+13_-4 chr12 25398284
SBS C T KRAS 35 12 G D 0.211
38.645 Not found
5578 and 557 CRC 512 CRC 512 PLS CRC TP53_132_142 chr17 7578536
SBS T G TP53 394 132 K Q 0.135
Not found Not found
5578 and 557 CRC 516 CRC 516 PLS CRC TP53_172A chr17 7578395
SBS G C TP53 535 179 H D 0.183
Not found Not found
5578 and 557 CRC 517 CRC 517 PLS CRC TP53_233_245 chr17 7577548

Table11.txt

```
SBS         C         T       TP53     733       245         G       S         0.430
 79.836     Not found
5578 and 557 CRC 518 CRC 518 PLS      CRC       TP53_208_218     chr17   7578205
Indel      NULL      CAC      TP53     644       215         S      fs         8.816
  75.000     Not found
5578 and 557 CRC 522 CRC 522 PLS      CRC       TP53_219_224     chr17   7578191
SBS         A         G       TP53     658       220         Y       H         0.132
Not found   Not found
5578 and 557 CRC 526 CRC 526 PLS      CRC      AKT1_0016_0017    chr14  105246551
SBS         C         T       AKT1      49        17         E       K         0.101
 42.495     Not found
    5579     CRC 457 CRC 457 PLS      CRC       TP53_188_195     chr17   7578265
SBS         A         G       TP53     584       195         I       T         0.120
Not found     0.563
    5579     CRC 468 CRC 468 PLS      CRC      TP53_0280_0289    chr17   7577081
SBS         T         C       TP53     857       286         E       G         0.358
 74.714     Not found
    5579     CRC 468 CRC 468 PLS      CRC       TP53_188_195     chr17   7578268
SBS         A         C       TP53     581       194         L       R         0.347
Not found     0.391
    5579     CRC 470 CRC 470 PLS      CRC      NRAS_0055_0062     chr1  115256529
SBS         T         A       NRAS     182        61         Q       L         0.369
 55.290     Not found
    5579     CRC 473 CRC 473 PLS      CRC      KRAS_012_+13_-4   chr12  25398281
SBS         C         T       KRAS      38        13         G       D         3.840
 51.923     Not found
    5579     CRC 477 CRC 477 PLS      CRC       TP53_262_267     chr17   7577139
SBS         G         A       TP53     799       267         R       W         2.700
  1.405       3.604
    5579     CRC 480 CRC 480 PLS      CRC     CTNNB1_0039_0046    chr3  41266124
SBS         A         G     CTNNB1     121        41         T       A         0.774
 33.306     Not found
    5579     CRC 480 CRC 480 PLS      CRC      KRAS_012_+13_-4   chr12  25398284
SBS         C         T       KRAS      35        12         G       D         0.494
 49.603     Not found
    5579     CRC 480 CRC 480 PLS      CRC       TP53_167_177     chr17   7578427
SBS         T         C       TP53     503       168         H       R         0.782
 28.687     Not found
    5579     CRC 489 CRC 489 PLS      CRC       TP53_233_245     chr17   7577548
SBS         C         T       TP53     733       245         G       S         0.472
Not found     0.752
    5579     CRC 505 CRC 505 PLS      CRC       TP53_233_245     chr17   7577568
SBS         C         T       TP53     713       238         C       Y         0.360
Not found     0.610
    5579     CRC 506 CRC 506 PLS      CRC       APC_1304_1310     chr5  112175222
Indel      NULL       A       APC     3931      1311         I      fs         0.180
  95.164     Not found
    5579     CRC 507 CRC 507 PLS      CRC     CTNNB1_0039_0046    chr3  41266137
```

Table11.txt

SBS	C	T	CTNNB1	134	45	S	F	0.109	73.257
Not found	5579	CRC 520	CRC 520 PLS	CRC	KRAS_012_+13_-4	chr12	25398284	SBS	C
A	KRAS	35	12	G	V	0.471	76.048	Not found	5579
CRC 521	CRC 521 PLS	CRC	FBXW7_361_371	chr4	153251907	SBS	G	A	FBXW7
1099	367	R	*	0.267	65.306	Not found	5579	CRC 521	CRC 521 PLS
CRC	PIK3CA_0542_0551	chr3	178936091	SBS	G	A	PIK3CA	1633	545
E	K	0.119	29.290	Not found	5579	CRC 524	CRC 524 PLS	CRC	KRAS_012_+13_-4
chr12	25398284	SBS	C	A	KRAS	35	12	G	V
0.358	41.673	Not found	5579	CRC 531	CRC 531 PLS	CRC	KRAS_012_+13_-4	chr12	25398284
SBS	C	A	KRAS	35	12	G	V	0.144	37.804
Not found	5579	CRC 531	CRC 531 PLS	CRC	TP53_233_245	chr17	7577580	SBS	T
C	TP53	701	234	Y	C	0.246	Not found	Not found	5578
CRC 482	CRC 482 PLS	CRC	TP53_172A	chr17	7578406	SBS	C	T	TP53
524	175	R	H	0.143	82.996	Not found	5578 and 557	CRC 456	CRC 456 PLS
CRC	TP53_053	chr17	7579520	SBS	T	C	TP53	167	56
E	G	0.122	Not found	Not found	5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_132_142
chr17	7578535	SBS	T	G	TP53	395	132	K	T
0.159	Not found	Not found	5578 and 557	CRC 456	CRC 456 PLS	CRC	TP53_151_163	chr17	7578475
SBS	G	A	TP53	455	152	P	L	0.107	Not found
0.063	5578 and 557	CRC 474	CRC 474 PLS	CRC	TP53_033_040	chr17	7579574	SBS	T
A	TP53	113	38	Q	L	0.110	Not found	Not found	5578 and 557
CRC 474	CRC 474 PLS	CRC	TP53_345	chr17	7573974	SBS	C	G	TP53
1053	351	K	N	0.111	Not found	Not found	5578 and 557	CRC 491	CRC 491 PLS
CRC	TP53_0248_0261	chr17	7577538	SBS	C	T	TP53	743	248
R	Q	0.186	59.012	0.059	5578 and 557	CRC 512	CRC 512 PLS	CRC	NRAS_0055_0062
chr1	115256529	SBS	T	G	NRAS	182	61	Q	P
0.103	Not found	Not found	5578 and 557	CRC 512	CRC 512 PLS	CRC	TP53_374_385	chr17	7572977
SBS	A	C	TP53	1132	378	S	A	0.111	Not found
Not found	5578 and 557	CRC 526	CRC 526 PLS	CRC	TP53_0196_0205	chr17	7578245		

Table11.txt

SBS	G	A	TP53	604	202	R	C	0.108	Not found	Not found
5579	CRC 470	CRC 470 PLS	CRC	APC_1304_1310	chr5	112175207			
SBS	G	T	APC	3916	1306	E	*	0.344	56.466	Not found
5579	CRC 482	CRC 482 PLS	CRC	TP53_167_177	chr17	7578406			
SBS	C	T	TP53	524	175	R	H	0.136	80.375	Not found
5578	CRC 464	CRC 464 PLS	CRC	PPP2R1A_176_187	chr19	52715982			
SBS	C	T	PPP2R1A	547	183	R	W	0.126	Not found	Not found
5578 and 557	CRC 512	CRC 512 PLS	CRC	TP53_342	chr17	7573997			
SBS	G	C	TP53	1030	344	L	V	0.120	Not found	Not found
5578 and 557	CRC 512	CRC 512 PLS	CRC	TP53_342	chr17	7574003			
SBS	G	A	TP53	1024	342	R	*	0.154	53.715	Not found
5578 and 557	CRC 512	CRC 512 PLS	CRC	TP53_342	chr17	7574005			
SBS	A	G	TP53	1022	341	F	S	0.103	Not found	Not found
5578	CRC 465	CRC 465 PLS	CRC	TP53_0227_0236	chr17	7577580			
SBS	T	C	TP53	701	234	Y	C	0.115	Not found	Not found
5578	CRC 530	CRC 530 PLS	CRC	TP53_113_125	chr17	7579316			
Indel	NULL	GAC	TP53	371	124	C	fs	0.135	Not found	Not found
5579	CRC 465	CRC 465 PLS	CRC	TP53_188_195	chr17	7578280			
SBS	G	C	TP53	569	190	P	R	0.148	Not found	Not found

Table12.txt

Table 12. PlasmaSeqS with 5502 Matched White Blood Cell Summary.

Experiment	Patient	Template	Sample Type	ampMatchName	Chrom	Position	MutType	BaseFrom	BaseTo	Gene	ntStart	codonStart	aaRef	aaVar	MAF in Plasma	MAF in WBCs	MAF in PT
4946	LCR 600	LCR 600 PLS1	Normal control	TP53_151_163	chr17	7578457	SBS	C	T	TP53	473	158	R	H	0.115	0.007	Not applicable
4958	LCR 627	LCR 627 PLS1	Normal control	TP53_172A	chr17	7578406	SBS	C	T	TP53	524	175	R	H	0.180	0.161	Not applicable
4958	LCR 628	LCR 628 PLS1	Normal control	TP53_151_163	chr17	7578461	SBS	C	T	TP53	469	157	V	I	0.146	0.027	Not applicable
4959	LCR 634	LCR 634 PLS1	Normal control	TP53_0248_0261	chr17	7577538	SBS	C	T	TP53	743	248	R	Q	0.110	0.015	Not applicable
4959	LCR 636	LCR 636 PLS1	Normal control	PIK3CA_1039_1050	chr3	178952076	SBS	A	G	PIK3CA	3131	1044	N	S	0.200	Not found	Not applicable
4959	LCR 636	LCR 636 PLS1	Normal control	TP53_0272_0283	chr17	7577094	SBS	G	A	TP53	844	282	R	W	0.150	0.002	Not applicable
4965	LCR 667	LCR 667 PLS1	Normal control	TP53_233_245	chr17	7577547	SBS	C	T	TP53	734	245	G	D	0.128	0.037	Not applicable
4984	LCR 700	LCR 700 PLS1	Normal control	TP53_113_125	chr17	7579328	SBS	T	C	TP53	359	120	K	R	0.281	0.459	Not applicable
4984	LCR 701	LCR 701 PLS1	Normal control	TP53_233_245	chr17	7577586	SBS	A	G	TP53	695	232	I	T	0.895	0.433	Not applicable
4984	LCR 701	LCR 701 PLS1	Normal control	TP53_172A	chr17	7578406	SBS	C	T	TP53	524	175	R	H	0.140	0.017	Not applicable
4971	LCR 721	LCR 721 PLS1	Normal control	TP53_0248_0261	chr17	7577539	SBS	G	A	TP53	742	248	R	W	0.179	0.137	Not applicable
4971	LCR 730	LCR 730 PLS1	Normal control	TP53_167_177	chr17	7578406	SBS	C	T	TP53	524	175	R	H	0.160	0.026	Not applicable
4971	LCR 738	LCR 738 PLS1	Normal control	TP53_0227_0236	chr17	7577574	SBS	T	C	TP53	707	236	Y	C	12.230	3.489	Not applicable
4971	LCR 738	LCR 738 PLS1	Normal control	TP53_167_177	chr17	7578413											

Table12.txt

SBS C G TP53 517 173 V L 6.876
7.333 Not applicable
4971 LCR 738 LCR 738 PLS1 Normal control TP53_0272_0283 chr17 7577111
SBS G T TP53 827 276 A D 5.810
5.512 Not applicable
4985 LCR 760 LCR 760 PLS1 Normal control TP53_0272_0283 chr17 7577094
SBS G A TP53 844 282 R W 0.113
0.017 Not applicable
4977 LCR 764 LCR 764 PLS1 Normal control TP53_0272_0283 chr17 7577120
SBS C T TP53 818 273 R H 0.176
0.008 Not applicable
4978 LCR 782 LCR 782 PLS1 Normal control TP53_0248_0261 chr17 7577538
SBS C T TP53 743 248 R Q 0.110
Not found Not applicable
4866 PANC 317 PANC 317 PLS 2 PDAC TP53_0272_0283 chr17 7577105
SBS G C TP53 833 278 P R 0.348
0.679 Not found
4866 PANC 317 PANC 317 PLS 2 PDAC TP53_368_to_374 chr17 7572995
Indel T TP53 1114 372 K fs 0.100
0.039 Not found
4866 PANC 317 PANC 317 PLS1 PDAC TP53_0272_0283 chr17 7577105
SBS G C TP53 833 278 P R 0.943
0.679 Not found
4868 PANC 355 PANC 355 PLS1 PDAC TP53_0248_0261 chr17 7577517
SBS A C TP53 764 255 I S 0.116
Not found Not found
4868 PANC 355 PANC 355 PLS1 PDAC TP53_208_218 chr17 7578203
SBS C T TP53 646 216 V M 0.102
0.020 Not found
4869 PANC 387 PANC 387 PLS PDAC TP53_172A chr17 7578406
SBS C T TP53 524 175 R H 0.153
0.008 39.5883777
4869 PANC 387 PANC 387 PLS PDAC KRAS_012_+13_-4 chr12 25398285
SBS C G KRAS 34 12 G R 0.118
Not found 30.56
4869 PANC 389 PANC 389 PLS PDAC TP53_0248_0261 chr17 7577517
SBS A C TP53 764 255 I S 0.101
Not found Not found
4870 PANC 400 PANC 400 PLS 1 PDAC TP53_0248_0261 chr17 7577536
SBS T A TP53 745 249 R W 0.791
0.675 Not found
4870 PANC 400 PANC 400 PLS 1 PDAC TP53_0272_0283 chr17 7577120
SBS C T TP53 818 273 R H 0.133
0.070 Not found
4880 PANC 462 PANC 462 PLS1 PDAC KRAS_012_+13_-4 chr12 25398285
SBS C G KRAS 34 12 G R 2.223
Not found 39.7744361
4880 PANC 462 PANC 462 PLS1 PDAC TP53_233_245 chr17 7577556

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SBS C A TP53 725 242 C F 1.741
Not found 59.2592593
4999 PANC 469 PANC 469 PLS1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C G KRAS 35 12 G A 0.125
Not found 23.9110287
5007 PANC 485 PANC 485 PLS 1 PDAC TP53_208_218 chr17 7578212
SBS G A TP53 637 213 R * 0.118
Not found Not found
5019 PANC 509 PANC 509 PLS 1 PDAC TP53_0248_0261 chr17 7577538
SBS C T TP53 743 248 R Q 0.146
0.227 Not found
5019 PANC 509 PANC 509 PLS 1 PDAC TP53_172A chr17 7578393
SBS A T TP53 537 179 H Q 0.121
0.040 Not found
5019 PANC 513 PANC 513 PLS 1 PDAC TP53_219_224 chr17 7578190
SBS T C TP53 659 220 Y C 0.124
0.028 Not found
5098 PANC 552 PANC 552 PLS 1 PDAC KRAS_0057_0064 chr12 25380275
SBS T A KRAS 183 61 Q H 0.363
Not found 16.0069849
5098 PANC 552 PANC 552 PLS 1 PDAC GNAS_201 chr20 57484421
SBS G A GNAS 602 201 R H 0.318
0.035 9.232715
5098 PANC 552 PANC 552 PLS 1 PDAC TP53_233_245 chr17 7577568
SBS C T TP53 713 238 C Y 0.317
0.002 12.9032258
5098 PANC 552 PANC 552 PLS 1 PDAC CDKN2A_7_88 chr9 21971107
SBS T C CDKN2A 251 84 D G 0.167
Not found 10.5439893
5023 PANC 686 PANC 686 PLS 1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C A KRAS 35 12 G V 0.192
Not found 38.7512676
5023 PANC 691 PANC 691 PLS 1 PDAC TP53_0280_0289 chr17 7577094
SBS G A TP53 844 282 R W 0.116
0.273 Not found
5023 PANC 691 PANC 691 PLS 2 PDAC TP53_167_177 chr17 7578413
SBS C G TP53 517 173 V L 0.140
0.145 3.2258065
5023 PANC 691 PANC 691 PLS 3 PDAC TP53_167_177 chr17 7578413
SBS C G TP53 517 173 V L 0.121
0.145 3.2258065
5024 PANC 692 PANC 692 PLS 1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C T KRAS 35 12 G D 0.155
Not found 71.5549482
5024 PANC 692 PANC 692 PLS 1 PDAC TP53_233_245 chr17 7577580
SBS T C TP53 701 234 Y C 0.132
0.064 Not found
5024 PANC 692 PANC 692 PLS 1 PDAC TP53_0272_0283 chr17 7577124

Table12.txt

SBS C T TP53 814 272 V M 0.101
Not found 27.7915633
5024 PANC 694 PANC 694 PLS1 PDAC TP53_172A chr17 7578406
SBS C T TP53 524 175 R H 0.176
Not found Not found
5024 PANC 697 PANC 697 PLS 1 PDAC TP53_151_163 chr17 7578457
SBS C T TP53 473 158 R H 0.135
0.019 Not found
5041 PANC 708 PANC 708 PLS 1 PDAC TP53_151_163 chr17 7578478
SBS G T TP53 452 151 P H 0.169
Not found 19.930975
5041 PANC 708 PANC 708 PLS 1 PDAC TP53_0248_0261 chr17 7577539
SBS G A TP53 742 248 R W 0.154
0.043 Not found
5041 PANC 708 PANC 708 PLS 1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C T KRAS 35 12 G D 0.137
Not found 16.9190826
5041 PANC 715 PANC 715 PLS 1 PDAC TP53_172A chr17 7578406
SBS C T TP53 524 175 R H 0.274
0.235 Not found
5041 PANC 715 PANC 715 PLS 1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C T KRAS 35 12 G D 0.105
Not found 35.971223
5042 PANC 717 PANC 717 PLS 1 PDAC TP53_151_163 chr17 7578457
SBS C T TP53 473 158 R H 0.118
0.055 Not found
5042 PANC 717 PANC 717 PLS 1 PDAC KRAS_012_+13_-4 chr12 25398284
SBS C T KRAS 35 12 G D 0.117
Not found 12.4012367
5040 PANC 725 PANC 725 PLS 1 PDAC TP53_298_306 chr17 7577022
SBS G A TP53 916 306 R * 0.451
0.460 Not found
5048 PANC 759 PANC 759 PLS 1 PDAC TP53_172A chr17 7578403
SBS C T TP53 527 176 C Y 0.357
0.233 Not found
5048 PANC 759 PANC 759 PLS 1 PDAC TP53_132_142 chr17 7578535
SBS T C TP53 395 132 K R 0.105
0.144 Not found
5048 PANC 759 PANC 759 PLS 2 PDAC TP53_172A chr17 7578403
SBS C T TP53 527 176 C Y 0.723
0.233 Not found
5048 PANC 759 PANC 759 PLS 2 PDAC TP53_132_142 chr17 7578535
SBS T C TP53 395 132 K R 0.148
0.144 Not found
5048 PANC 760 PANC 760 PLS 1 PDAC TP53_233_245 chr17 7577559
SBS G A TP53 722 241 S F 2.865
3.014 Not found
5048 PANC 760 PANC 760 PLS 1 PDAC TP53_0272_0283 chr17 7577120

Table12.txt

SBS C T TP53 818 273 R H 0.358
0.089 Not found
5048 PANC 760 PANC 760 PLS 2 PDAC TP53_233_245 chr17 7577559
SBS G A TP53 722 241 S F 3.418
3.014 Not found
5049 PANC 768 PANC 768 PLS 1 PDAC TP53_0272_0283 chr17 7577120
SBS C T TP53 818 273 R H 0.186
0.167 Not found
5049 PANC 768 PANC 768 PLS 2 PDAC TP53_0272_0283 chr17 7577120
SBS C T TP53 818 273 R H 0.234
0.167 Not found

Table13.txt

Table 13. Patient and tumor characteristics.

Patient ID	Age	Race	Cancer Type	Histopathologic Diagnosis	Stage	Pap Brush Sample	Tao Brush Sample	Plasma Sample
PAP 001	45	NA	Endometrial	Well to moderately differentiated endometrioid adenocarcinoma	I	Positive	Not tested	Not tested
PAP 002	53	NA	Ovarian	Moderately to poorly differentiated serous adenocarcinoma	III	Positive	Not tested	Not tested
PAP 003	53	NA	Endometrial	Moderately differentiated endometrial adenocarcinoma	I	Positive	Not tested	Not tested
PAP 006	57	NA	Ovarian	Moderately to poorly differentiated ovarian serous papillary a	III	Negative	Not tested	Not tested
PAP 007	63	NA	Ovarian	Moderately to poorly differentiated ovarian serous papillary a	III	Negative	Not tested	Not tested
PAP 010	73	NA	Endometrial	Well differentiated endometrial adenocarcinoma	I	Positive	Not tested	Not tested
PAP 011	58	NA	Endometrial	Well differentiated endometrial adenocarcinoma	I	Positive	Not tested	Not tested
PAP 024	56	Caucasian	Endometrial	Endometrioid carcinoma with squamous differentiation	I	Negative	Not tested	Not tested
PAP 025	75	African	Endometrial	High-grade Serous carcinoma	I	Positive	Not tested	Not tested
PAP 026	86	Caucasian	Endometrial	Endometrioid adenocarcinoma	I	Negative	Not tested	Not tested
PAP 027	NA	NA	Ovarian	NA	NA	Negative	Not tested	Not tested
PAP 030	73	NA	Endometrial	Endometrioid adenocarcinoma	I	Negative	Not tested	Not tested
PAP 032	82	NA	Endometrial	Endometrioid adenocarcinoma	I	Negative	Not tested	Not tested
PAP 033	68	Caucasian	Endometrial	Endometrioid adenocarcinoma with squamous differentiation	I	Positive	Not tested	Not tested
PAP 034	55	Caucasian	Endometrial	Endometrioid adenocarcinoma	I	Positive	Not tested	Not tested
PAP 035	50	Caucasian	Endometrial	Endometrioid adenocarcinoma	IV	Positive	Not tested	Not tested
PAP 036	57	Caucasian	Ovarian	Low-grade serous carcinoma	I	Negative	Not tested	Not tested
PAP 037	64	Asian	Endometrial	Endometrial papillary carcinoma	I	Positive	Not tested	Not tested
PAP 038	46	Asian	Ovarian	NA	I	Negative	Not tested	Not tested
PAP 039	72	Asian	Ovarian	Serous adenocarcinoma	I	Positive	Not tested	Not tested
PAP 040	56	Asian	Endometrial	Endometrial adenocarcinoma	I	Negative	Not tested	Not tested
PAP 041	65	Asian	Endometrial	Papillary endometrial carcinoma				

Table13.txt

			I	Negative	Not tested	Not tested	
PAP 042	45	Asian		Ovarian	Adenosquamous Cell Carcinoma		
			III	Positive	Not tested	Not tested	
PAP 058	NA	NA		Ovarian	NA		
			NA	Negative	Not tested	Not tested	
PAP 059	NA	NA		Ovarian	NA		
			NA	Positive	Not tested	Not tested	
PAP 060	NA	NA		Ovarian	NA		
			III	Negative	Not tested	Not tested	
PAP 061	NA	NA		Ovarian	NA		
			III	Negative	Not tested	Not tested	
PAP 062	NA	NA		Ovarian	NA		
			III	Positive	Not tested	Not tested	
PAP 063	NA	NA		Ovarian	NA		
			III	Negative	Not tested	Not tested	
PAP 065	58	Asian		Endometrial	Endometrioid adenocarcinoma, villoglandular type		
			I	Positive	Not tested	Not tested	
PAP 066	70	Asian		Endometrial	Endometrial Clear Cell Carcinoma		
			III	Positive	Not tested	Not tested	
PAP 067	61	Asian		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested	
PAP 068	63	Asian		Endometrial	Endometrioid adenocarcinoma with mucinous differentiation		
			I	Negative	Not tested	Not tested	
PAP 069	51	Asian		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested	
PAP 070	49	Asian		Endometrial	Endometrial adenocarcinoma		
			II	Positive	Not tested	Not tested	
PAP 071	56	Caucasian		Endometrial	Endometrioid carcinoma with mucinous differentiation		
			I	Negative	Not tested	Not tested	
PAP 072	64	NA		Ovarian	Serous adenocarcinoma		
			IV	Negative	Not tested	Not tested	
PAP 073	64	NA		Ovarian	Serous adenocarcinoma		
			III	Negative	Not tested	Not tested	
PAP 074	73	NA		Ovarian	Serous adenocarcinoma		
			IV	Negative	Not tested	Not tested	
PAP 075	54	NA		Ovarian	Serous adenocarcinoma		
			III	Negative	Not tested	Not tested	
PAP 076	53	NA		Ovarian	Serous adenocarcinoma		
			III	Negative	Not tested	Not tested	
PAP 078	53	NA		Ovarian	Serous adenocarcinoma		
			III	Negative	Not tested	Not tested	
PAP 079	66	NA		Ovarian	Serous adenocarcinoma		
			IV	Positive	Not tested	Not tested	
PAP 080	94	NA		Endometrial	NA		
			III	Positive	Not tested	Not tested	
PAP 081	59	NA		Ovarian	NA		
			NA	Negative	Not tested	Not tested	

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PAP 083 51 NA Endometrial NA
I Negative Not tested Not tested
PAP 084 66 NA Endometrial NA
III Positive Not tested Not tested
PAP 119 58 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Positive Not tested Not tested
PAP 120 57 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Positive Not tested Not tested
PAP 121 61 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Positive Not tested Not tested
PAP 122 54 Asian Endometrial Endometrioid adenocarcinoma, mixed
solid-villoglandular PatterI Positive Not tested Not tested
PAP 123 47 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Negative Not tested Not tested
PAP 125 62 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Negative Not tested Not tested
PAP 126 53 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Negative Not tested Not tested
PAP 128 54 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Positive Not tested Not tested
PAP 129 50 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Negative Not tested Not tested
PAP 131 56 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular pattern I Positive Not tested Not tested
PAP 132 62 Asian Endometrial Endometrioid adenocarcinoma, solid
pattern I Positive Not tested Not tested
PAP 168 39 Asian Ovarian Adenocarcinoma (likely high-grade
serous) IV Positive Not tested Not tested
PAP 169 48 Asian Ovarian Carcinosarcoma
IV Positive Not tested Not tested
PAP 172 42 Asian Ovarian Adenocarcinoma (likely high-grade
serous) I Negative Not tested Not tested
PAP 173 51 Asian Ovarian Clear cell carcinoma
I Positive Not tested Not tested
PAP 174 42 Asian Ovarian Adenoacanthoma
I Negative Not tested Not tested
PAP 175 61 Asian Endometrial Adenosquamous Cell Carcinoma
IV Positive Not tested Not tested
PAP 176 57 Asian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 177 59 Asian Endometrial Villoglandular endometrioid
adenocarcinoma I Positive Not tested Not
tested
PAP 178 53 Asian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 179 67 Asian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 180 52 Asian Endometrial Villoglandular endometrioid

Table13.txt

adenocarcinoma I Positive Not tested Not tested
PAP 181 78 Asian Endometrial Villoglandular endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 182 56 Asian Ovarian Adenosquamous Cell Carcinoma I Negative Not tested Negative
PAP 183 56 Asian Endometrial Villoglandular endometrioid adenocarcinoma III Negative Not tested Not tested
PAP 184 25 Asian Ovarian Villoglandular Endometrioid Adenocarcinoma I Positive Not tested Positive
PAP 185 54 Asian Ovarian Papillary serous adenocarcinoma (likely high-grade serous) I Negative Not tested Negative
PAP 186 48 Asian Ovarian Papillary transitional cell carcinoma II Positive Not tested Positive
PAP 193 53 Asian Ovarian Papillary serous cystadenocarcinoma (likely high-grade serous)III Negative Not tested Positive
PAP 194 45 Asian Ovarian Endometrioid adenocarcinoma, villoglandular type I Positive Not tested Not tested
PAP 195 55 Asian Ovarian Papillary serous adenocarcinoma (likely high-grade serous) III Positive Not tested Negative
PAP 196 54 Asian Ovarian Mixed carcinoma (likely high-grade serous) I Negative Not tested Positive
PAP 197 54 Asian Ovarian Serous adenocarcinoma (likely high-grade serous) I Negative Not tested Positive
PAP 198 44 Asian Ovarian Clear cell carcinoma III Negative Not tested Positive
PAP 199 51 Asian Ovarian Serous adenocarcinoma (likely high-grade serous) I Positive Not tested Positive
PAP 200 56 Asian Endometrial Endometrioid adenocarcinoma, villoglandular type with mucinousI Positive Not tested Not tested
PAP 201 59 Asian Endometrial Endometrioid adenocarcinoma, macroglandular type I Positive Not tested Not tested
PAP 202 57 Asian Endometrial Carcinosarcoma I Positive Not tested Not tested
PAP 203 71 Asian Endometrial Endometrioid adenocarcinoma, mixed type I Positive Not tested Not tested
PAP 204 52 Asian Endometrial Endometrioid adenocarcinoma, villoglandular type with squamousI Positive Not tested Not tested
PAP 205 54 Asian Endometrial Endometrioid adenocarcinoma with squamous metaplasia I Positive Not tested Not tested
PAP 206 58 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type III Positive Not tested Not tested
PAP 207 59 Asian Endometrial Endometrioid adenocarcinoma, villoglandular type I Positive Not tested Not tested
PAP 208 61 NA Endometrial Endometrioid adenocarcinoma

Table13.txt

			I	Positive	Not tested	Not tested
PAP 209	62	NA		Endometrial	Endometrioid adenocarcinoma		
			II	Positive	Not tested	Not tested
PAP 210	50	NA		Ovarian	Mucinous adenocarcinoma		
			I	Negative	Not tested	Positive
PAP 212	61	NA		Endometrial	Endometrioid adenocarcinoma		
			NA	Negative	Not tested	Not tested
PAP 213	70	NA		Endometrial	Endometrioid adenocarcinoma		
			II	Positive	Not tested	Not tested
PAP 214	56	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 215	62	NA		Endometrial	Serous Adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 216	58	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 217	64	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Negative	Not tested	Not tested
PAP 218	80	NA		Endometrial	Serous Adenocarcinoma		
			IV	Positive	Not tested	Not tested
PAP 219	64	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 220	70	NA		Endometrial	Clear cell adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 221	57	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 222	68	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 224	71	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 225	61	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 226	69	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Negative	Not tested	Not tested
PAP 227	63	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 228	75	NA		Endometrial	Endometrioid adenocarcinoma		
			II	Positive	Not tested	Not tested
PAP 229	54	NA		Endometrial	Endometrioid adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 230	79	NA		Ovarian	Low-grade serous carcinoma		
			III	Positive	Not tested	Negative
PAP 231	82	NA		Endometrial	Serous Adenocarcinoma		
			I	Positive	Not tested	Not tested
PAP 232	77	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 233	54	NA		Endometrial	Endometrioid adenocarcinoma		
			III	Positive	Not tested	Not tested
PAP 234	49	NA		Endometrial	Endometrioid adenocarcinoma		

Table13.txt

			I	Positive	Not tested	Not tested
PAP 235	61	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 236	64	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 237	64	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 238	48	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 239	68	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 240	57	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 241	82	NA		Ovarian	NA		
			NA	Negative	Not tested	Negative
PAP 242	65	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 243	51	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 244	63	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 245	63	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 246	63	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 247	58	NA		Endometrial	NA		
			NA	Positive	Not tested	Not tested
PAP 248	59	Asian		Ovarian	Serous papillary carcinoma		
			III	Negative	Not tested	Negative
PAP 250	53	Asian		Ovarian	Endometrioid adenocarcinoma, villoglandular type		
			IV	Positive	Not tested	Positive
PAP 251	79	Asian		Ovarian	Endometrioid adenocarcinoma, solid type		
			I	Negative	Not tested	Positive
PAP 252	42	Asian		Ovarian	Mucinous Cystadenocarcinoma		
			I	Negative	Not tested	Negative
PAP 253	60	Asian		Ovarian	Serous papillary cystadenocarcinoma (likely high-grade serous)		
			III	Negative	Not tested	Negative
PAP 254	46	Asian		Ovarian	Serous papillary cystadenocarcinoma		
			I	Positive	Not tested	Negative
PAP 255	62	Asian		Ovarian	Mucinous adenocarcinoma		
			III	Positive	Not tested	Positive
PAP 257	45	Asian		Ovarian	Serous papillary cystadenocarcinoma		
			I	Negative	Not tested	Negative
PAP 258	56	Asian		Ovarian	Mucinous adenocarcinoma		
			I	Negative	Not tested	Negative
PAP 259	57	Asian		Ovarian	Clear cell carcinoma		
			I	Negative	Not tested	Negative
PAP 261	53	Asian		Ovarian	Mucinous adenocarcinoma		

Table13.txt

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                          I       Negative        Not tested      Positive
PAP 262    49      Asian       Ovarian         Serous adenocarcinoma (likely
high-grade serous)              III     Positive        Not tested      Positive
PAP 263    55      Asian       Ovarian         Clear cell carcinoma
                          I       Negative        Not tested      Negative
PAP 264    56      Asian       Ovarian         Serous adenocarcinoma
                          I       Positive        Not tested      Negative
PAP 265    46      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              II      Positive        Not tested      Not tested
PAP 266    51      Asian       Endometrial     Mucinous adenocarcinoma
                          I       Positive        Not tested      Not tested
PAP 267    46      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 268    70      Asian       Endometrial     Carcino-Sarcoma (Malignant
Mullerian Mixed Tumor)           I       Positive        Not tested      Not
tested
PAP 269    55      Asian       Endometrial     Carcino-Sarcoma (Malignant
Mullerian Mixed Tumor)           I       Positive        Not tested      Not
tested
PAP 270    56      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 271    53      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 272    54      Asian       Endometrial     Endometrial stromal sarcoma
                          II      Positive        Not tested      Not tested
PAP 273    57      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 274    59      Asian       Endometrial     Mucinous adenocarcinoma
                          I       Positive        Not tested      Not tested
PAP 275    37      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 276    65      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 277    61      Asian       Endometrial     Endometrioid adenocarcinoma,
villoglandular type              I       Positive        Not tested      Not tested
PAP 524    64      NA          Ovarian         Serous adenocarcinoma (likely
high-grade serous)              III     Positive        Not tested      Not tested
PAP 525    65      NA          Ovarian         Serous adenocarcinoma
                          III     Negative        Not tested      Not tested
PAP 526    69      NA          Ovarian         Serous adenocarcinoma (likely
high-grade serous)              IV      Negative        Not tested      Not tested
PAP 527    58      NA          Ovarian         Serous adenocarcinoma (likely
high-grade serous)              III     Negative        Not tested      Not tested
PAP 528    68      NA          Ovarian         Serous adenocarcinoma (likely
high-grade serous)              III     Positive        Not tested      Not tested
PAP 529    70      NA          Ovarian         Serous adenocarcinoma (likely
high-grade serous)              III     Negative        Not tested      Not tested
PAP 530    68      NA          Ovarian         Serous adenocarcinoma (likely
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Table13.txt

high-grade serous) III Positive Not tested Not tested
PAP 531 62 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) II Positive Not tested Not tested
PAP 532 51 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 533 48 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 535 65 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 536 67 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) IV Positive Not tested Not tested
PAP 537 45 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) IV Negative Not tested Not tested
PAP 540 69 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 541 65 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) IV Positive Not tested Not tested
PAP 542 64 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 544 45 NA Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 549 72 NA Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 550 60 NA Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 551 49 NA Ovarian Serous adenocarcinoma
III Negative Not tested Not tested
PAP 552 56 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Positive Not tested Not tested
PAP 554 59 NA Endometrial Mixed adenocarcinoma with clear
cell & serous features IV Positive Not tested Not tested
PAP 555 71 NA Endometrial Endometrioid adenocarcinoma
IV Positive Not tested Not tested
PAP 556 62 NA Endometrial Endometrioid adenocarcinoma
III Positive Not tested Not tested
PAP 557 79 NA Endometrial NA
IV Positive Not tested Not tested
PAP 558 59 NA Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 560 59 NA Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 561 66 NA Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 562 73 NA Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 563 68 NA Ovarian Serous adenocarcinoma
III Negative Not tested Not tested
PAP 564 65 NA Endometrial Serous Adenocarcinoma

Table13.txt

			IV	Positive	Not tested	Not tested		
PAP 565	56	NA	Endometrial	Well differentiated endometrioid adenocarcinoma and undifferenI	Positive	Not tested	Not tested	
PAP 566	60	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	IV	Negative	Not tested	Not tested
PAP 567	58	NA	Ovarian	Serous adenocarcinoma				
			IV	Negative	Not tested	Not tested		
PAP 568	53	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	III	Negative	Not tested	Not tested
PAP 569	45	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	IV	Positive	Not tested	Not tested
PAP 570	60	NA	Endometrial	Carcinosarcoma				
			III	Positive	Not tested	Not tested		
PAP 572	68	NA	Endometrial	Serous Adenocarcinoma				
			III	Positive	Not tested	Not tested		
PAP 573	69	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	IV	Negative	Not tested	Not tested
PAP 574	52	NA	Endometrial	Endometrioid adenocarcinoma				
			III	Positive	Not tested	Not tested		
PAP 575	42	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	III	Negative	Not tested	Not tested
PAP 576	69	NA	Ovarian	Serous adenocarcinoma (likely high-grade serous)	III	Positive	Not tested	Not tested
PAP 579	43	Asian	Ovarian	Papillary serous cystadenocarcinoma (likely high-grade serous)I	Negative	Not tested	Negative	
PAP 581	53	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 582	64	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 583	58	Asian	Endometrial	Endometrioid adenocarcinoma, cribriform type	I	Positive	Not tested	Not tested
PAP 584	66	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 585	65	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 587	41	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 588	62	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 589	74	Asian	Endometrial	Endometrioid adenocarcinoma, poorly differentiated	IV	Positive	Not tested	Not tested
PAP 590	56	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Positive	Not tested	Not tested
PAP 591	63	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type	I	Negative	Not tested	Not tested
PAP 592	56	Asian	Ovarian	Adenosquamous Cell Carcinoma				
			II	Positive	Not tested	Not tested		
PAP 593	68	Asian	Endometrial	Endometrioid adenocarcinoma,				

Table13.txt

villoglandular type I Positive Not tested Not tested
PAP 594 51 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular type I Positive Not tested Not tested
PAP 595 60 Asian Endometrial Endometrioid adenocarcinoma,
villoglandular type I Positive Not tested Not tested
PAP 596 50 Asian Endometrial Endometrioid adenocarcinoma,
secretory type I Positive Not tested Not tested
PAP 599 79 Caucasian Endometrial Endometrioid adenocarcinoma
II Positive Not tested Not tested
PAP 600 69 Caucasian Endometrial clear cell adenocarcinoma
III Negative Not tested Not tested
PAP 601 59 Caucasian Endometrial Serous-papillary adenocarcinoma
II Positive Not tested Not tested
PAP 604 69 Caucasian Endometrial Endometrioid adenocarcinoma with
clear cell component I Positive Not tested Not tested
PAP 606 56 Caucasian Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 607 60 Caucasian Ovarian serous papillary adenocarcinoma
(likely high-grade serous) III Negative Not tested Not tested
PAP 608 73 Caucasian Ovarian Serous adenocarcinoma (likely
high-grade serous) III Negative Not tested Not tested
PAP 609 90 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 610 49 Caucasian Endometrial Endometrioid adenocarcinoma with
clear cell component III Positive Not tested Not tested
PAP 612 59 Caucasian Ovarian serous papillary adenocarcinoma
(likely high-grade serous) III Negative Not tested Not tested
PAP 613 57 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 616 68 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 617 74 Caucasian Endometrial Serous-papillary adenocarcinoma
III Positive Not tested Not tested
PAP 618 76 Caucasian Endometrial Endometroid Adenocarcinoma
I Positive Not tested Not tested
PAP 619 59 Caucasian Endometrial Endometrioid adenocarcinoma
III Positive Not tested Not tested
PAP 621 56 Caucasian Endometrial Serous-papillary adenocarcinoma
I Positive Not tested Not tested
PAP 622 56 Caucasian Ovarian serous papillary adenocarcinoma
III Negative Not tested Not tested
PAP 625 59 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 627 77 Caucasian Endometrial Endometroid adenocarcinoma
I Negative Not tested Not tested
PAP 628 53 Caucasian Ovarian Serous papillary carcinoma (likely
high-grade serous) I Negative Not tested Not tested
PAP 629 56 Caucasian Endometrial Endometrioid adenocarcinoma

Table13.txt

			I	Positive	Not tested	Not tested	
PAP 632	66	Caucasian	Endometrial	Carcinosarcoma			
			I	Positive	Not tested	Not tested	
PAP 633	71	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 636	63	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Negative	Negative	Not tested	
PAP 637	77	NA	Endometrial	High-grade serous carcinoma			
			I	Negative	Positive	Not tested	
PAP 638	67	NA	Endometrial	High-grade serous carcinoma			
			IV	Positive	Positive	Not tested	
PAP 641	53	Asian	Ovarian	Clear cell carcinoma			
			II	Negative	Not tested	Negative	
PAP 642	53	Asian	Ovarian	Serous adenocarcinoma			
			I	Negative	Not tested	Positive	
PAP 643	46	Asian	Ovarian	Endometrioid adenocarcinoma			
			I	Negative	Not tested	Positive	
PAP 644	63	Asian	Ovarian	Carcinosarcoma			
			II	Negative	Not tested	Positive	
PAP 645	63	Asian	Ovarian	Mucinous Cystadenocarcinoma			
			I	Negative	Not tested	Positive	
PAP 646	73	Asian	Endometrial	Endometrioid adenocarcinoma, solid type			
			II	Positive	Not tested	Not tested	
PAP 647	49	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Not tested	
PAP 648	29	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Not tested	
PAP 649	60	Asian	Endometrial	Papillary Serous Adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 650	59	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Not tested	
PAP 651	66	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Negative	Not tested	Not tested	
PAP 652	43	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Not tested	
PAP 653	63	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			II	Negative	Not tested	Not tested	
PAP 654	54	Asian	Endometrial	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Not tested	
PAP 655	74	Asian	Endometrial	Mucinous adenocarcinoma			
			II	Negative	Not tested	Not tested	
PAP 663	53	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 665	81	Caucasian	Ovarian	Mucinous adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAP 667	68	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 668	68	Caucasian	Endometrial	Endometrioid adenocarcinoma			

Table13.txt

			II	Positive	Not tested	Not tested	
PAP 669	75	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 670	57	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAP 671	56	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 672	64	Caucasian	Ovarian	Serous adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAP 674	59	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			IV	Negative	Not tested	Not tested	
PAP 675	60	Caucasian	Endometrial	serous-papillary adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 676	83	Caucasian	Endometrial	Serous Adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAP 678	48	Caucasian	Ovarian	Clear cell carcinoma			
			III	Negative	Not tested	Not tested	
PAP 679	72	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 681	64	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 684	68	Caucasian	Endometrial	Endometroid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAP 685	61	Caucasian	Endometrial	Endometrial cancer			
			I	Positive	Positive	Not tested	
PAP 686	57	Caucasian	Endometrial	Endometrial endometrioid adenocarcinoma w extensive mucinous dI			
				Negative	Positive	Not tested	
PAP 687	86	Caucasian	Endometrial	High-grade endometrioid carcinoma			
			I	Positive	Positive	Not tested	
PAP 688	59	NA	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Positive	Not tested	
PAP 689	76	NA	Endometrial	High-grade serious carcinoma of the endometrium with metastasiIII			
				Positive	Positive	Not tested	
PAP 690	56	Caucasian	Endometrial	Low-grade endometrioid adenicarcinoma			
			I	Positive	Positive	Not tested	
PAP 691	60	Caucasian	Endometrial	High-grade endometrioid carcinoma			
			I	Positive	Positive	Not tested	
PAP 692	58	African	Ovarian	Papillary thyroid caricnoma (right); mature cystic teratoma (lI			
				Negative	Negative	Not tested	
PAP 694	62	Asian	Endometrial	Endometrioid Adenocarcinona, Villoglandular Type			
			I	Negative	Not tested	Not tested	
PAP 695	66	Asian	Endometrial	Serous Adenocarcinoma			
			II	Positive	Not tested	Not tested	
PAP 696	71	Asian	Endometrial	Endometrioid Adenocarcinona, Villoglandular Type			
			III	Positive	Not tested	Not tested	

Table13.txt

PAP 697 56 Asian Endometrial Endometrioid Adenocarcinona, Villoglandular Type I Positive Not tested Not tested
PAP 698 55 Asian Endometrial Endometrioid Adenocarcinona, Villoglandular Type I Negative Not tested Not tested
PAP 699 59 Asian Endometrial Endometrioid Adenocarcinona, Villoglandular Type I Positive Not tested Not tested
PAP 701 51 Asian Ovarian Papillary serous cystadenocarcinoma (likely high-grade serous)I Negative Not tested Negative
PAP 702 59 Asian Endometrial Endometrioid adenocarcinoma I Negative Not tested Not tested
PAP 704 59 Asian Ovarian Clear cell carcinoma I Negative Not tested Negative
PAP 705 53 Asian Ovarian Clear cell carcinoma I Positive Not tested Negative
PAP 707 54 Asian Ovarian Papillary serous adenocarcinoma (likely high-grade serous) III Positive Not tested Positive
PAP 708 49 Asian Ovarian Clear cell carcinoma II Negative Not tested Negative
PAP 709 52 Asian Ovarian Mucinous adenocarcinoma II Negative Not tested Negative
PAP 710 51 Asian Ovarian Clear cell carcinoma III Positive Not tested Negative
PAP 711 57 Asian Ovarian Papillary serous adenocarcinoma (likely high-grade serous) III Positive Not tested Positive
PAP 715 64 Asian Ovarian Poorly differentiated adenocarcinoma (likely high-grade serousI Negative Not tested Negative
PAP 717 51 Asian Endometrial Endometrioid adenocarcinoma III Positive Not tested Not tested
PAP 719 76 African Endometrial Endometrioid carcinoma with mucinous differentiation I Positive Not tested Not tested
PAP 721 75 Caucasian Ovarian High-grade serous adenocarcinoma III Positive Not tested Not tested
PAP 722 70 African Ovarian High-grade serous adenocarcinoma III Negative Not tested Not tested
PAP 726 67 Caucasian Endometrial Endometrioid carcinoma with mucinous features I Positive Not tested Not tested
PAP 727 34 Caucasian Endometrial Endometrioid with squamous morular metaplasia and treatment efI Negative Not tested Not tested
PAP 728 61 Caucasian Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 730 7?? Other Endometrial Endometrioid carcinoma metastatic to multiple lymph nodes III Positive Not tested Not tested
PAP 735 65 Caucasian Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 736 62 African Endometrial Endometrioid carcinoma with focal

Table13.txt

squamous differentiation I Positive Not tested Not tested
PAP 742 72 Caucasian Ovarian High-grade serous carcinoma
IV Positive Not tested Not tested
PAP 744 59 African Endometrial Endometrioid carcinoma metastatic
to multiple lymph nodes III Positive Not tested Not tested
PAP 746 56 Asian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Not tested
PAP 748 57 Caucasian Endometrial High-grade Serous carcinoma
I Positive Not tested Not tested
PAP 749 75 Caucasian Ovarian Low-grade serous carcinoma
I Positive Not tested Not tested
PAP 751 63 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Not tested
PAP 753 72 Caucasian Endometrial High-grade serous carcinoma
IV Positive Not tested Not tested
PAP 754 71 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 757 56 Caucasian Endometrial Endometrioid carcinoma with focal
squamous differentiation III Positive Not tested Not tested
PAP 758 45 Caucasian Endometrial Endometrial carcinoma
I Negative Not tested Not tested
PAP 761 79 African Endometrial High-grade Serous carcinoma
I Positive Not tested Not tested
PAP 763 50 Caucasian Ovarian High-grade serous adenocarcinoma
III Positive Not tested Not tested
PAP 767 57 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Not tested
PAP 768 68 Caucasian Endometrial High-grade Serous carcinoma with
focal endometrioid differentiI Positive Not tested Not tested
PAP 770 76 African Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 775 79 African Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAP 777 65 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Not tested
PAP 778 35 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 787 78 Other Ovarian NA
IV Negative Not tested Not tested
PAP 789 61 Caucasian Endometrial Endometrioid adenocarcinoma with
squamous differentiation III Positive Not tested Not tested
PAP 790 60 African Endometrial Carcinosarcoma
III Positive Not tested Not tested
PAP 791 64 Caucasian Endometrial Endometrioid adenocarcinoma
III Positive Not tested Not tested
PAP 799 39 Asian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAP 800 56 Caucasian Endometrial Endometrioid carcinoma with

Table13.txt

squamous differentiation IV Positive Not tested Not tested
PAP 802 68 African Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 804 59 Caucasian Endometrial Endometrioid carcinoma with squamous differentiation I Positive Not tested Not tested
PAP 805 50 African Endometrial Endometrioid carcinoma with squamous differentiation I Positive Not tested Not tested
PAP 807 65 Other Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 809 38 Caucasian Ovarian High-grade adenocarcinoma with clear cell features III Negative Not tested Not tested
PAP 812 77 Caucasian Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 813 64 Caucasian Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 815 67 Caucasian Ovarian Low-grade serous carcinoma III Negative Not tested Negative
PAP 816 61 Caucasian Endometrial Endometrioid adenocarcinoma I Positive Not tested Not tested
PAP 824 64 NA Endometrial Endometrioid adenocarcinoma I Positive Positive Not tested
PAP 829 75 Asian Endometrial Endometrioid adenocarcinoma I Positive Negative Not tested
PAP 830 69 Asian Ovarian Endometrioid adenocarcinoma I Negative Positive Not tested
PAP 831 68 Arabic Endometrial High-grade Serous Carcinoma of the endometrium III Positive Positive Not tested
PAP 832 81 Caucasian Endometrial High-grade uterine leiomyosarcoma I Negative Positive Not tested
PAP 835 73 NA Endometrial High-grade seroius carcinoma with metastasis to lymph nodes III Positive Positive Not tested
PAP 836 76 NA Endometrial Endometrioid adenocarcinoma I Negative Positive Not tested
PAP 837 74 NA Endometrial Endometrioid adenocarcinoma I Negative Positive Not tested
PAP 839 68 Arabic Endometrial High-grade serous endometrial carcinoma III Positive Positive Not tested
PAP 841 66 NA Endometrial Endometrioid adenocarcinoma III Positive Positive Not tested
PAP 842 70 NA Endometrial High-grade endometrioid carcinoma III Positive Positive Not tested
PAP 845 67 Caucasian Ovarian High-grade serous adenocarcinoma IV Negative Positive Not tested
PAP 850 63 Asian Endometrial High-grade endometrioid carcinoma IV Positive Positive Not tested

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PAP 851 72 Caucasian Endometrial Well differentiated endometrioid adenocarcinoma with squamous III Positive Positive Not tested
PAP 853 53 NA Endometrial Endometrioid adenocarcinoma I Negative Positive Not tested
PAP 858 66 Asian Endometrial High-grade serous carcinoma III Negative Positive Not tested
PAP 860 65 NA Endometrial Endometrioid adenocarcinoma I Positive Positive Not tested
PAP 862 66 Caucasian Endometrial High-grade serous carcinoma III Not tested Positive Not tested
PAP 865 73 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 866 61 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 867 64 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 868 53 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 869 62 Asian Endometrial Endometrial adenocarcinoma, mixed solid and villoglandular typI Positive Not tested Not tested
PAP 870 56 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 871 67 Asian Endometrial Endometrial adenocarcinoma, solid type II Positive Not tested Not tested
PAP 873 58 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Negative Not tested Not tested
PAP 874 64 Asian Endometrial Squamous cell carcinoma, clear cell type I Positive Not tested Not tested
PAP 875 64 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 876 76 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 877 45 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not tested
PAP 878 62 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type II Positive Not tested Not tested
PAP 879 75 Asian Endometrial Endometrial Adenocarcinoma, Villoglandular Type I Positive Not tested Not

Table13.txt

tested
PAP 881 60 African Endometrial Endometrioid adenocarcinoma
III Positive Not tested Not tested
PAP 884 57 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAP 889 53 NA Endometrial Endometrium adenocarcinoma,
endometrioid type, well-differentiI Negative Negative Not
tested
PAP 891 51 NA Ovarian High-grade serous adenocarcinoma
III Negative Negative Not tested
PAP 892 61 NA Endometrial Endometrial adenocarcinoma,
endometrioid-type, well-differentiIII Positive Positive Not
tested
PAP 894 59 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAP 897 81 Caucasian Endometrial Endometrioid adenocarcinoma
III Positive Positive Not tested
PAP 900 45 Caucasian Ovarian High-grade mullerian carcinoma
undifferentiated III Negative Not tested Not tested
PAP 901 55 Caucasian Endometrial Endometrial adenocarcinoma,
endometrioid type with squamous anII Positive Positive Not
tested
PAP 902 61 NA Endometrial Endometrioid adenocarcinoma
III Positive Positive Not tested
PAP 904 63 Asian Endometrial High-grade serous adenocarcinoma
III Positive Positive Not tested
PAP 907 69 Caucasian Endometrial Endometrial carcinoma, endometrioid
type with squamous and mucIII Positive Positive Not tested
PAP 910 81 NA Endometrial Endometrioid adenocarcinoma
III Positive Positive Not tested
PAP 914 68 Arabic Ovarian High-grade serous carcinoma
I Negative Positive Not tested
PAP 919 57 NA Ovarian Endometrioid adenocarcinoma, well
differentiated II Negative Negative Not tested
PAP 922 54 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAP 925 51 Asian Ovarian High-grade serous carcinoma of
tubo-ovarian origin III Negative Positive Not tested
PAP 926 57 NA Endometrial Well differentiated endometrioid
adenocarcinoma I Positive Positive Not tested
PAP 927 56 NA Endometrial Endometrium: FIGO grade I
Well-differentiated endometrial adenI Positive Positive Not
tested
PAP 928 64 Latino Ovarian High-grade serous carcinoma of
tubo-ovarian origin II Positive Positive Not tested
PAP 931 61 Caucasian Endometrial Endometrioid adenocarcinoma of the
endometrium with squamous dII Positive Positive Not tested
PAP 934 59 Caucasian Endometrial Endometrioid adenocarcinoma

Table13.txt

			I	Positive	Positive	Not tested	
PAP 936	61	NA	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Positive	Not tested	
PAP 937	55	NA	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Negative	Not tested	
PAP 989	74	NA	Endometrial	Uterine Carcinosarcoma			
			II	Positive	Positive	Not tested	
PAP 990	63	Arabic	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Positive	Not tested	
PAP 991	63	Asian	Endometrial	Endometrial carcinoma, endometrioid			
with squamous differentiat			III	Positive	Positive	Not tested	
PAP 993	75	Arabic	Ovarian	High-grade serous carcinoma arising			
from fallopian tube			III	Positive	Positive	Not tested	
PAP 994	65	Asian	Endometrial	Endometrial adenocarcinoma,			
endometrioid type with foci of squ			I	Positive	Negative	Not	
tested							
PAP 995	58	Caucasian	Endometrial	Endometrial carcinoma, endometrioid			
90% with 10% clear cell co			II	Positive	Positive	Not tested	
PAP 996	68	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Positive	Not tested	
PAP 998	71	NA	Endometrial	Endometrial adenocarcinoma,			
mucinous type			I	Positive	Positive	Not	
tested							
PAP 999	66	NA	Endometrial	Endometrial High-grade serious			
carcinoma			III	Positive	Positive	Not tested	
PAPA 1001	53	Asian	Endometrial	Endometrial adenocarcinoma,			
endometrioid type with mucinous di			III	Positive	Positive	Not	
tested							
PAPA 1002	68	NA	Endometrial	Endometrioid adenocarcinoma with			
mucinous and squamous differe			I	Positive	Positive	Not tested	
PAPA 1003	49	NA	Endometrial	Endometrioid adenocarcinoma w			
squamous differentiation			III	Positive	Positive	Not tested	
PAPA 1005	72	Caucasian	Endometrial	High-grade serious with			
endometrioid and squamous features			II	Positive	Positive	Not	
tested							
PAPA 1010	55	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			III	Positive	Positive	Not tested	
PAPA 1011	64	Asian	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Positive	Not tested	
PAPA 1012	73	Caucasian	Endometrial	Endometrial Carcinoma,			
undifferentiated			III	Positive	Positive	Not	
tested							
PAPA 1013	80	Caucasian	Endometrial	High-grade serous carcinoma			
			III	Positive	Positive	Not tested	
PAPA 1016	77	Other	Endometrial	Endometrioid endometrial			
adenocarcinoma with squamous metaplas			I	Positive	Positive	Not	
tested							
PAPA 1019	63	NA	Endometrial	Endometrioid adenocarcinoma with			

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papillary villous and focal mIII Positive Positive Not tested
PAPA 1026 59 African Endometrial High-grade Serous carcinoma
I Negative Not tested Not tested
PAPA 1033 76 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Not tested
PAPA 1035 65 Caucasian Endometrial High-grade Serous carcinoma
II Positive Not tested Not tested
PAPA 1037 60 Caucasian Ovarian High-grade serous adenocarcinoma
III Positive Not tested Positive
PAPA 1040 79 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAPA 1043 57 Asian Endometrial Endometrioid carcinoma with
mucinous differentiation I Positive Not tested Not
tested
PAPA 1048 74 African Endometrial High-grade Serous carcinoma
I Positive Not tested Not tested
PAPA 1057 73 Caucasian Endometrial High-grade Serous carcinoma
I Positive Not tested Not tested
PAPA 1058 48 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAPA 1059 56 Caucasian Endometrial Endometrioid carcinoma with
mucinous and secretory differentiaI Positive Not tested Not
tested
PAPA 1062 66 Caucasian Ovarian High-grade serous adenocarcinoma
IV Negative Not tested Negative
PAPA 1065 50 Other Endometrial Endometrial adenocarcinoma
NA Negative Not tested Not tested
PAPA 1066 66 Caucasian Endometrial Endometrioid carcinoma with
squamous differentiation I Positive Not tested Not
tested
PAPA 1069 56 Caucasian Endometrial Endometrioid carcinoma with
prominent squamous differentiationI Positive Not tested Not
tested
PAPA 1072 39 Caucasian Ovarian Low-grade serous carcinoma
III Negative Not tested Negative
PAPA 1074 48 Caucasian Ovarian Poorly differentiated High-grade
serous carcinoma III Negative Not tested Negative
PAPA 1076 58 African Endometrial Endometrioid carcinoma with
secretory and metaplastic changes III Positive Not tested Not
tested
PAPA 1077 53 Caucasian Endometrial Endometrioid carcinoma with
mucinous differentiation I Positive Not tested Not
tested
PAPA 1078 40 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAPA 1080 63 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAPA 1081 73 Caucasian Endometrial Endometrioid adenocarcinoma

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			III	Positive	Not tested	Not tested	
PAPA 1084	40	Caucasian	Ovarian	High-grade mucinous adenocarcinoma			
			II	Negative	Not tested	Negative	
PAPA 1086	64	African	Endometrial	Multifocal serous endometrial intraepithelial carcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1092	63	African	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1094	52	African	Ovarian	High-grade serous adenocarcinoma			
			IV	Positive	Not tested	Negative	
PAPA 1095	70	Caucasian	Endometrial	Endometrioid carcinoma with prominent mucinous differentiation			
			I	Positive	Not tested	Not tested	
PAPA 1096	60	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Negative	Not tested	Positive	
PAPA 1097	55	Caucasian	Endometrial	Endometrioid carcinoma, undifferentiated carcinoma			
			IV	Positive	Not tested	Not tested	
PAPA 1098	31	Caucasian	Ovarian	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Negative	
PAPA 1099	58	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1100	65	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1103	51	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1106	51	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1110	55	Asian	Ovarian	Undifferentiated carcinoma (likely high-grade serous)			
			II	Positive	Not tested	Negative	
PAPA 1112	52	Asian	Ovarian	Mucinous Cystadenocarcinoma			
			I	Positive	Not tested	Negative	
PAPA 1113	60	Asian	Ovarian	Papillary serous adenocarcinoma (likely high-grade serous)			
			III	Positive	Not tested	Positive	
PAPA 1115	57	Asian	Ovarian	Serous adenocarcinoma-fibroma (likely high-grade serous)			
			III	Positive	Not tested	Positive	
PAPA 1116	48	Asian	Ovarian	Clear cell carcinoma, mixed type			
			I	Negative	Not tested	Negative	
PAPA 1117	67	Asian	Ovarian	Papillary serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Positive	
PAPA 1118	37	Asian	Ovarian	Endometrioid adenocarcinoma, villoglandular type			
			I	Positive	Not tested	Negative	
PAPA 1119	41	Asian	Ovarian	Mucinous Cystadenocarcinoma			
			I	Negative	Not tested	Negative	
PAPA 1120	62	Asian	Ovarian	Endometrioid adenocarcinoma, mixed type			
			I	Positive	Not tested	Negative	
PAPA 1121	53	Asian	Ovarian	Clear cell carcinoma, tubulo-cystic type			
			I	Negative	Not tested	Negative	
PAPA 1122	56	Asian	Ovarian	Clear cell carcinoma, papillary			

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type			I	Negative	Not tested	Positive	
PAPA 1126	72	Caucasian	Endometrial	Adenocarcinoma, endometrioid type, well to moderately differen	III	Positive	Positive	Not tested
PAPA 1128	54	Caucasian	Endometrial	Endometrioid adenocarcinoma	I	Negative	Positive	Not tested
PAPA 1129	68	NA	Endometrial	Endometrioid adenocarcinoma	III	Negative	Positive	Not tested
PAPA 1130	51	NA	Endometrial	Endometrioid adenocarcinoma with mucinous differentiation	I	Positive	Positive	Not tested
PAPA 1131	39	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1132	59	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1133	52	NA	Endometrial	Endometrioid adenocarcinoma	III	Positive	Positive	Not tested
PAPA 1134	58	NA	Endometrial	Endometrioid endometrial carcinoma with papillary and squamous	I	Positive	Positive	Not tested
PAPA 1135	57	NA	Endometrial	High-grade serious carcinoma	IV	Positive	Positive	Not tested
PAPA 1136	60	Caucasian	Ovarian	High-grade serous adenocarcinoma	IV	Positive	Positive	Not tested
PAPA 1137	73	Other	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1138	56	Caucasian	Ovarian	Clear cell carcinoma	III	Negative	Negative	Not tested
PAPA 1139	70	NA	Endometrial	Endometrioid adenocarcinoma	I	Negative	Negative	Not tested
PAPA 1140	75	Caucasian	Endometrial	Endometrioid adenocarcinoma	III	Positive	Positive	Not tested
PAPA 1141	71	African	Endometrial	Endometrial adenocarcinoma, clear cell, poorly differentiated	IV	Positive	Positive	Not tested
PAPA 1142	63	NA	Endometrial	Endometrioid adenocarcinoma, with squamous differentiation	I	Positive	Positive	Not tested
PAPA 1143	63	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1144	65	Caucasian	Ovarian	NA	IV	Negative	Negative	Not tested
PAPA 1145	53	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1146	60	NA	Endometrial	Endometrioid adenocarcinoma	I	Negative	Positive	Not tested
PAPA 1147	56	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested
PAPA 1148	65	NA	Endometrial	Endometrial carcinoma with endometrioid and serous differentia	III	Positive	Positive	Not tested
PAPA 1149	67	NA	Endometrial	Endometrioid adenocarcinoma	I	Positive	Positive	Not tested

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PAPA 1150 63 Arabic Endometrial High-grade serous adenocarcinoma
I Positive Positive Not tested
PAPA 1152 53 Arabic Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1153 83 Caucasian Endometrial Endometrial carcinoma, clear cell type III Positive Positive Not tested
PAPA 1154 70 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1155 50 Asian Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1157 80 Asian Endometrial High-grade serous endometrial cancer III Positive Positive Not tested
PAPA 1158 56 NA Endometrial Endometrioid adenocarcinoma
I Positive Negative Not tested
PAPA 1159 75 NA Ovarian Serous adenocarcinoma
III Negative Positive Not tested
PAPA 1160 52 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1161 60 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1162 62 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1164 64 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1167 47 NA Ovarian High-grade serous adenocarcinoma
III Negative Negative Not tested
PAPA 1169 59 Arabic Endometrial Mullerian adenosarcoma of the endometrium with sarcomatous oveI Negative Negative Not tested
PAPA 1172 57 NA Ovarian High-grade serous adenocarcinoma
III Positive Not tested Not tested
PAPA 1176 57 NA Ovarian High-grade serous adenocarcinoma
III Negative Negative Not tested
PAPA 1177 54 Caucasian Endometrial Well differentiated endometrial carcinoma, endometrioid type I Positive Positive Not tested
PAPA 1180 50 Other Ovarian High-grade serous (40%) and endometrioid (60%) carcinoma I Negative Negative Not tested
PAPA 1181 56 Asian Endometrial Carcinosarcoma with sarcomatous overgrowth. 15% endometrioid aIV Negative Negative Not tested
PAPA 1184 61 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Positive Not tested
PAPA 1185 74 Other Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1188 77 NA Endometrial High-grade mixed type endometrial cancer (serous 90% and endomI Positive Positive Not tested
PAPA 1189 81 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Positive Not tested
PAPA 1191 63 Asian Endometrial Endometrioid adenocarcinoma

Table13.txt

			I	Positive	Not tested	Not tested	
PAPA 1192	73	Asian	Endometrial	Endometrioid adenocarcinoma			
			II	Positive	Not tested	Not tested	
PAPA 1193	69	Asian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1194	68	Asian	Endometrial	NA			
			I	Positive	Not tested	Not tested	
PAPA 1198	61	African	Endometrial	High-grade carcinoma with mixed features of serous carcinoma aI	Positive	Not tested	Not tested
PAPA 1200	46	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1202	55	Caucasian	Endometrial	High-grade Serous carcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1204	72	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1207	66	Caucasian	Endometrial	Endometroid carcinoma with metaplastic features	III	Positive	Not tested	Not tested
PAPA 1208	30	Caucasian	Ovarian	Well differentiated mucinous carcinoma	I	Positive	Not tested	Negative
PAPA 1209	64	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1210	67	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1211	58	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1213	67	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Positive	Not tested	Positive	
PAPA 1214	33	African	Endometrial	Endometrioid adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1215	51	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Negative	Not tested	Negative	
PAPA 1217	68	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1218	52	African	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1221	60	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1222	57	Caucasian	Endometrial	Endometrioid carcinoma with mucinous differentiation	I	Negative	Not tested	Not tested
PAPA 1223	65	Caucasian	Endometrial	Endometrioid carcinoma with mucinous differentiation	I	Positive	Not tested	Not tested
PAPA 1224	61	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1225	60	Caucasian	Ovarian	High-grade clear cell carcinoma			
			I	Negative	Not tested	Not tested	

Table13.txt

PAPA 1226 75 African Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAPA 1230 43 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAPA 1232 60 Caucasian Endometrial Endometrioid carcinoma with focal mucinous differentiation I Positive Not tested Not tested
PAPA 1233 41 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Not tested Not tested
PAPA 1235 42 Caucasian Ovarian Low-grade serous carcinoma
III Positive Not tested Negative
PAPA 1237 43 Caucasian Ovarian High-grade serous adenocarcinoma
III Negative Not tested Positive
PAPA 1239 63 Caucasian Endometrial High-grade endometrial adenocarcinoma I Positive Not tested Not tested
PAPA 1240 70 African Ovarian High-grade serous adenocarcinoma
III Negative Not tested Positive
PAPA 1242 64 Caucasian Endometrial High-grade adenocarcinoma with endometrioid features I Positive Not tested Not tested
PAPA 1243 41 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Not tested Not tested
PAPA 1246 29 Asian Ovarian Well differentiated mucinous carcinoma I Negative Not tested Negative
PAPA 1247 59 African Endometrial High-grade Serous carcinoma
I Negative Not tested Not tested
PAPA 1249 58 Caucasian Endometrial Endometrioid adenocarcinoma
I Negative Positive Not tested
PAPA 1251 64 NA Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1253 77 NA Ovarian High-grade serous adenocarcinoma
III Negative Positive Not tested
PAPA 1254 70 NA Endometrial Endometrioid adenocarcinoma
I Negative Positive Not tested
PAPA 1255 67 Caucasian Endometrial Endometrioid adenocarcinoma
I Positive Positive Not tested
PAPA 1256 70 Caucasian Endometrial High-grade serous endometrial cancer I Positive Negative Not tested
PAPA 1257 80 NA Ovarian High-grade serous carcinoma of the fallopian tube III Positive Negative Not tested
PAPA 1258 63 Other Ovarian High-grade serous adenocarcinoma
IV Negative Positive Not tested
PAPA 1259 77 Other Ovarian High-grade serous ovarian cancer from fimbria TIC III Negative Positive Not tested
PAPA 1260 64 NA Ovarian Endometrioid (60%) and sex cord like (40%) I Negative Negative Not tested
PAPA 1262 38 Caucasian Ovarian Heterogenous mucinous ovarian tumor, intestinal type I Negative Negative Not tested
PAPA 1263 45 Caucasian Ovarian High-grade serous adenocarcinoma

Table13.txt

			IV	Negative	Positive	Not tested	
PAPA 1264	56	NA	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Positive	Not tested	
PAPA 1284	41	Other	Endometrial	Endometrioid adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1286	72	Caucasian	Endometrial	Serous endometrial intraepithelial carcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1292	65	Caucasian	Ovarian	Clear cell carcinoma			
			III	Positive	Not tested	Positive	
PAPA 1293	62	African	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1295	52	Caucasian	Endometrial	Endometrioid carcinoma with prominent mucinous differentiation	I	Negative	Not tested Not tested
PAPA 1296	50	Caucasian	Ovarian	High-grade serous adenocarcinoma			
			III	Positive	Not tested	Negative	
PAPA 1297	41	Other	Ovarian	High-grade serous adenocarcinoma			
			III	Positive	Not tested	Positive	
PAPA 1298	73	Caucasian	Ovarian	High-grade serous adenocarcinoma of the fallopian tube			
			III	Positive	Not tested	Positive	
PAPA 1299	51	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1300	63	Caucasian	Endometrial	High-grade adenocarcinoma with endometrioid features	I	Positive	Not tested Not tested
PAPA 1301	65	Caucasian	Ovarian	High-grade endometrioid carcinoma			
			I	Negative	Not tested	Negative	
PAPA 1302	72	Caucasian	Ovarian	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1303	72	African	Endometrial	High-grade Serous carcinoma			
			IV	Positive	Not tested	Not tested	
PAPA 1307	79	African	Endometrial	High-grade Clear cell carcinoma			
			IV	Negative	Not tested	Not tested	
PAPA 1308	65	Caucasian	Endometrial	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1309	34	African	Endometrial	Mucinous carcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1315	39	Asian	Ovarian	Clear cell carcinoma			
			III	Negative	Not tested	Negative	
PAPA 1320	52	Asian	Ovarian	High-grade serous adenocarcinoma			
			IV	Negative	Not tested	Positive	
PAPA 1321	50	Asian	Ovarian	Transitional Cell Carcinoma			
			III	Negative	Not tested	Positive	
PAPA 1322	53	Asian	Ovarian	Transitional Cell Carcinoma			
			II	Positive	Not tested	Positive	
PAPA 1323	53	Asian	Ovarian	High-grade serous adenocarcinoma			
			II	Negative	Not tested	Negative	
PAPA 1325	57	Asian	Ovarian	Low-grade Serous cystadenocarcinoma			
			III	Negative	Not tested	Negative	

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PAPA 1326	47	Asian	I	Ovarian	Positive	Mucinous adenocarcinoma Not tested	Positive
PAPA 1327	46	Asian	I	Ovarian	Negative	Endometrioid adenocarcinoma Not tested	Positive
PAPA 1328	56	Asian	III	Ovarian	Positive	Endometrioid adenocarcinoma Not tested	Negative
PAPA 1329	73	Asian	I	Endometrial	Negative	Villoglandular endometrioid adenocarcinoma Not tested	Not tested
PAPA 1359	78	NA	IV	Ovarian	Negative	High-grade serous adenocarcinoma Negative	Not tested
PAPA 1361	61	Other	II	Ovarian	Negative	High-grade serous adenocarcinoma of the fallopian tube Positive	Not tested
PAPA 1362	45	Caucasian	II	Ovarian	Not tested	Clear cell carcinoma Negative	Not tested
PAPA 1363	63	NA	III	Ovarian	Negative	High-grade serous adenocarcinoma Negative	Not tested
PAPA 1364	49	Caucasian	II	Ovarian	Positive	High-grade endometrioid carcinoma with foci of clear cell type Not tested	Not tested
PAPA 1365	50	NA	III	Ovarian	Negative	High-grade serous adenocarcinoma Negative	Not tested
PAPA 1369	37	Caucasian	II	Ovarian	Negative	Mucinous adenocarcinoma Negative	Not tested
PAPA 1370	73	Caucasian	III	Ovarian	Negative	High-grade serous adenocarcinoma Negative	Not tested
PAPA 1371	67	NA	III	Ovarian	Negative	High-grade serous adenocarcinoma Negative	Not tested
PAPA 1695	65	Caucasian	IV	Ovarian	Positive	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1696	69	Caucasian	III	Ovarian	Positive	Tubal cancer Not tested	Not tested
PAPA 1697	54	Caucasian	III	Ovarian	Positive	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1698	58	Caucasian	II	Ovarian	Negative	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1699	64	Caucasian	IV	Ovarian	Positive	Tubal cancer (likely high-grade serous) Not tested	Not tested
PAPA 1700	62	Caucasian	II	Ovarian	Positive	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1701	53	Caucasian	III	Ovarian	Negative	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1702	65	Caucasian	III	Ovarian	Negative	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1703	55	Caucasian	III	Ovarian	Negative	Serous adenocarcinoma (likely high-grade serous) Not tested	Not tested
PAPA 1705	76	Caucasian	I	Ovarian	Positive	Endometrioid adenocarcinoma Not tested	Not tested
PAPA 1706	60	Caucasian	Ovarian			Mixed serous and carcinosarcoma	

Table13.txt

subtypes			II	Positive	Not tested	Not tested	
PAPA 1707	78	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1710	71	Caucasian	Ovarian	Serous adenocarcinoma			
			III	Positive	Not tested	Not tested	
PAPA 1712	65	Caucasian	Ovarian	Tubal cancer (likely high-grade serous)			
			I	Negative	Not tested	Not tested	
PAPA 1713	59	Caucasian	Ovarian	Serous adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAPA 1714	48	Caucasian	Ovarian	Mucinous adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAPA 1715	62	Caucasian	Ovarian	Serous adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1716	74	Caucasian	Ovarian	Serous adenocarcinoma			
			II	Positive	Not tested	Not tested	
PAPA 1717	66	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1720	69	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1721	78	Caucasian	Ovarian	Serous adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAPA 1722	83	Caucasian	Ovarian	Serous adenocarcinoma			
			IV	Negative	Not tested	Not tested	
PAPA 1724	68	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1725	55	Caucasian	Ovarian	Endometrioid adenocarcinoma			
			I	Positive	Not tested	Not tested	
PAPA 1727	56	Caucasian	Ovarian	Serous adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1728	51	Caucasian	Ovarian	Clear cell carcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1730	71	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1732	65	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			II	Negative	Not tested	Not tested	
PAPA 1734	72	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			IV	Positive	Not tested	Not tested	
PAPA 1735	57	Caucasian	Ovarian	Serous adenocarcinoma			
			III	Negative	Not tested	Not tested	
PAPA 1736	70	Caucasian	Ovarian	Endometrioid adenocarcinoma			
			II	Positive	Not tested	Not tested	
PAPA 1737	59	Caucasian	Ovarian	Mixed endometrioid and clear cell			
			II	Negative	Not tested	Not tested	
PAPA 1738	70	Caucasian	Ovarian	Serous adenocarcinoma (likely high-grade serous)			
			III	Negative	Not tested	Not tested	
PAPA 1739	57	Caucasian	Ovarian	Mucinous adenocarcinoma			
			I	Negative	Not tested	Not tested	
PAPA 1816	54	Caucasian	Ovarian	Endometrioid adenocarcinoma with			

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squamous differentiation I Negative Negative Not tested
PAPA 1817 67 NA Ovarian High-grade serous adenocarcinoma of the fallopian tube III Negative Negative Not tested
PAPA 1819 53 Asian Ovarian High-grade carcinoma of fallopian tube III Positive Positive Not tested
PAPA 1820 82 NA Endometrial carcinosarcoma, mullerian type, carcinomatous component 20-25%III Positive Positive Not tested
PAPA 1821 73 NA Ovarian Tubal cancer, endometrial atypical hyperplasia and tumor on thII Negative Positive Not tested
PAPA 1823 83 Caucasian Ovarian High-grade serous carcinoma of the fallopian tube IV Negative Positive Not tested
PAPA 1826 56 Asian Ovarian Endometrioid adenocarcinoma; endometriosis, endometrial hyperpI Positive Positive Not tested
PAPA 1828 55 Caucasian Ovarian High-grade serous adenocarcinoma III Positive Negative Not tested
PAPA 1829 67 Arabic Ovarian High-grade serous adenocarcinoma; endoetriosis, leiomyoma and III Negative Negative Not tested
PAPA 1832 70 Caucasian Ovarian High-grade serous adenocarcinoma III Not tested Positive Not tested
PAPA 1833 51 NA Ovarian Clear cell carcinoma III Negative Negative Not tested
PAPA 1834 65 Other Ovarian Papillary thyroid carcinoma, follicular variant, encapsulated,I Negative Positive Not tested
PAPA 1836 60 NA Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1837 57 Caucasian Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1838 34 NA Ovarian Low-grade serous carcinoma III Not tested Negative Not tested
PAPA 1839 70 NA Endometrial Endometrium adenocarcinoma, endometrioid type I Not tested Positive Not tested
PAPA 1840 82 Caucasian Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1842 70 Caucasian Endometrial Endometrial endometrioid adenocarcinoma, with papillary viliouI Not tested Positive Not tested
PAPA 1843 64 NA Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1844 60 NA Ovarian High-grade serous adenocarcinoma III Not tested Positive Not tested
PAPA 1845 57 NA Ovarian High-grade serous adenocarcinoma III Not tested Positive Not tested
PAPA 1847 55 NA Endometrial Endometrioid carcinoma with papillary villous differentiation III Not tested Positive Not tested
PAPA 1848 51 Caucasian Endometrial Endometrial adenocarcinoma, endometrioid type, small foci of mIII Not tested Positive Not

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tested
PAPA 1849 55 NA Endometrial Endometrial endometriod adenocarcinoma I Not tested Positive Not tested
PAPA 1850 59 NA Ovarian High-grade serous adenocarcinoma III Not tested Positive Not tested
PAPA 1852 56 NA Endometrial High-grade carcinoma of the endometrium, mixed (80% clear cellIII Not tested Positive Not tested
PAPA 1855 55 NA Endometrial Endometrial endometriod adenocarcinoma I Not tested Positive Not tested
PAPA 1856 45 Other Ovarian High-grade serous adenocarcinoma of the fallopian tube III Not tested Negative Not tested
PAPA 1857 75 NA Endometrial Carcinosarcoma III Not tested Positive Not tested
PAPA 1858 66 NA Endometrial High-grade endometrial cancer, endometrioid and undifferentiatIII Not tested Positive Not tested
PAPA 1859 67 NA Endometrial Endometrial adenocarcinoma endometrioid type, well differentiaI Not tested Positive Not tested
PAPA 1860 57 NA Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1861 69 NA Endometrial Endometrioid adenocarcinoma IV Not tested Positive Not tested
PAPA 1862 74 NA Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
PAPA 1864 62 NA Ovarian High-grade serous adenocarcinoma III Not tested Negative Not tested
PAPA 1865 65 NA Endometrial carcinosarcoma leiomyomata&adenomyosis,LO stromal Hyperplasia,I Not tested Positive Not tested
PAPA 1866 38 Asian Ovarian Low-grade serous carcinoma III Not tested Negative Not tested
PAPA 1867 34 NA Endometrial Endometrioid adenocarcinoma I Not tested Positive Not tested
NA: Not available

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Table 14. Samples tested with PapSEEK for somatic mutations and aneuploidy.

Sample ID	Patient ID	Cancer Type	Stage	Sample Type	Somatic Mutations	Aneuploidy	Combined Assay
PAP 001 S	PAP 001	Endometrial	I	Pap brush sample	Positive	Positive	Positive
PAP 002 S	PAP 002	Ovarian	III	Pap brush sample	Positive	Negative	Positive
PAP 003 S	PAP 003	Endometrial	I	Pap brush sample	Positive	Positive	Positive
PAP 006 S	PAP 006	Ovarian	III	Pap brush sample	Negative	Negative	Negative
PAP 007 S	PAP 007	Ovarian	III	Pap brush sample	Negative	Negative	Negative
PAP 010 S	PAP 010	Endometrial	I	Pap brush sample	Positive	Positive	Positive
PAP 011 S	PAP 011	Endometrial	I	Pap brush sample	Positive	Negative	Positive
PAP 024 S	PAP 024	Endometrial	I	Pap brush sample	Negative	Negative	Negative
PAP 025 S	PAP 025	Endometrial	I	Pap brush sample	Positive	Negative	Positive
PAP 026 S	PAP 026	Endometrial	I	Pap brush sample	Negative	Negative	Negative
PAP 034 S	PAP 034	Endometrial	I	Pap brush sample	Positive	Positive	Positive
PAP 036 S	PAP 036	Ovarian	I	Pap brush sample	Negative	Negative	Negative
PAP 037 S	PAP 037	Endometrial	I	Pap brush sample	Positive	Negative	Positive
PAP 038 S	PAP 038	Ovarian	I	Pap brush sample	Negative	Negative	Negative
PAP 039 S	PAP 039	Ovarian	I	Pap brush sample	Positive	Negative	Positive
PAP 040 S	PAP 040	Endometrial	I	Pap brush sample	Negative	Negative	Negative
PAP 041 S	PAP 041	Endometrial	I	Pap brush sample	Negative	Negative	Negative
PAP 058 S	PAP 058	Ovarian	NA	Pap brush sample	Negative	Negative	Negative
PAP 060 S	PAP 060	Ovarian	III	Pap brush sample	Negative	Negative	Negative
PAP 061 S	PAP 061	Ovarian	III	Pap brush sample	Negative	Negative	Negative
PAP 062 S	PAP 062	Ovarian	III	Pap brush sample	Positive	Negative	Positive
PAP 063 S	PAP 063	Ovarian	III	Pap brush sample	Negative	Negative	Negative
PAP 065 S	PAP 065	Endometrial	I	Pap brush sample			

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Positive		Positive	Positive			
PAP 066 S	PAP 066	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 067 S	PAP 067	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 068 S	PAP 068	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 069 S	PAP 069	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 070 S	PAP 070	Endometrial		II	Pap brush sample	
Positive		Positive	Positive			
PAP 071 S	PAP 071	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 072 S	PAP 072	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 073 S	PAP 073	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 074 S	PAP 074	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 075 S	PAP 075	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 076 S	PAP 076	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 078 S	PAP 078	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 079 S	PAP 079	Ovarian		IV	Pap brush sample	
Positive		Negative	Positive			
PAP 080 S	PAP 080	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 081 S	PAP 081	Ovarian		NA	Pap brush sample	
Negative		Negative	Negative			
PAP 084 S	PAP 084	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 119 S	PAP 119	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 120 S	PAP 120	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 121 S	PAP 121	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 122 S	PAP 122	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 123 S	PAP 123	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 125 S	PAP 125	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 126 S	PAP 126	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 128 S	PAP 128	Endometrial		I	Pap brush sample	

Table14.txt

Positive		Positive	Positive		
PAP 129 S	PAP 129	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 131 S	PAP 131	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 132 S	PAP 132	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 168 S	PAP 168	Ovarian		IV	Pap brush sample
Positive		Positive	Positive		
PAP 169 S	PAP 169	Ovarian		IV	Pap brush sample
Positive		Positive	Positive		
PAP 172 S	PAP 172	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 176 S	PAP 176	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 177 S	PAP 177	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 178 S	PAP 178	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 179 S	PAP 179	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 180 S	PAP 180	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 181 S	PAP 181	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 182 S	PAP 182	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 183 S	PAP 183	Endometrial		III	Pap brush sample
Negative		Negative	Negative		
PAP 185 S	PAP 185	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 193 S	PAP 193	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 195 S	PAP 195	Ovarian		III	Pap brush sample
Positive		Positive	Positive		
PAP 196 S	PAP 196	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 197 S	PAP 197	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 198 S	PAP 198	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 199 S	PAP 199	Ovarian		I	Pap brush sample
Positive		Positive	Positive		
PAP 200 S	PAP 200	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 201 S	PAP 201	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 202 S	PAP 202	Endometrial		I	Pap brush sample

Table14.txt

Positive		Positive	Positive			
PAP 203 S	PAP 203	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 204 S	PAP 204	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 205 S	PAP 205	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 207 S	PAP 207	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 209 S	PAP 209	Endometrial		II	Pap brush sample	
Positive		Positive	Positive			
PAP 210 S	PAP 210	Ovarian		I	Pap brush sample	
Negative		Negative	Negative			
PAP 212 S	PAP 212	Endometrial		NA	Pap brush sample	
Negative		Negative	Negative			
PAP 213 S	PAP 213	Endometrial		II	Pap brush sample	
Positive		Positive	Positive			
PAP 214 S	PAP 214	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 215 S	PAP 215	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 216 S	PAP 216	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 217 S	PAP 217	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 219 S	PAP 219	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAP 221 S	PAP 221	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAP 222 S	PAP 222	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 224 S	PAP 224	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 225 S	PAP 225	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 226 S	PAP 226	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 227 S	PAP 227	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 228 S	PAP 228	Endometrial		II	Pap brush sample	
Positive		Positive	Positive			
PAP 229 S	PAP 229	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 230 S	PAP 230	Ovarian		III	Pap brush sample	
Positive		Negative	Positive			
PAP 231 S	PAP 231	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 232 S	PAP 232	Endometrial		III	Pap brush sample	

Table14.txt

Positive		Positive	Positive		
PAP 233 S	PAP 233	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 234 S	PAP 234	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 235 S	PAP 235	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 236 S	PAP 236	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 237 S	PAP 237	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 238 S	PAP 238	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 239 S	PAP 239	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 240 S	PAP 240	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 242 S	PAP 242	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 243 S	PAP 243	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 244 S	PAP 244	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 245 S	PAP 245	Endometrial	NA	Pap brush sample	
Positive		Positive	Positive		
PAP 246 S	PAP 246	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 247 S	PAP 247	Endometrial	NA	Pap brush sample	
Positive		Negative	Positive		
PAP 248 S	PAP 248	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 250 S	PAP 250	Ovarian	IV	Pap brush sample	
Positive		Negative	Positive		
PAP 251 S	PAP 251	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 252 S	PAP 252	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 253 S	PAP 253	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 254 S	PAP 254	Ovarian	I	Pap brush sample	
Positive		Positive	Positive		
PAP 255 S	PAP 255	Ovarian	III	Pap brush sample	
Positive		Negative	Positive		
PAP 257 S	PAP 257	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 258 S	PAP 258	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 259 S	PAP 259	Ovarian	I	Pap brush sample	

Table14.txt

Negative		Negative	Negative		
PAP 262 S	PAP 262	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 263 S	PAP 263	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 264 S	PAP 264	Ovarian		I	Pap brush sample
Positive		Positive	Positive		
PAP 266 S	PAP 266	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 267 S	PAP 267	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 268 S	PAP 268	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 269 S	PAP 269	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 270 S	PAP 270	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 271 S	PAP 271	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 272 S	PAP 272	Endometrial		II	Pap brush sample
Positive		Positive	Positive		
PAP 273 S	PAP 273	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 274 S	PAP 274	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 276 S	PAP 276	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 277 S	PAP 277	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 524 S	PAP 524	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 525 S	PAP 525	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 526 S	PAP 526	Ovarian		IV	Pap brush sample
Negative		Negative	Negative		
PAP 527 S	PAP 527	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 528 S	PAP 528	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 529 S	PAP 529	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 530 S	PAP 530	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 531 S	PAP 531	Ovarian		II	Pap brush sample
Positive		Negative	Positive		
PAP 535 S	PAP 535	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 536 S	PAP 536	Ovarian		IV	Pap brush sample

Table14.txt

Positive		Negative	Positive			
PAP 537 S	PAP 537	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 540 S	PAP 540	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 541 S	PAP 541	Ovarian		IV	Pap brush sample	
Positive		Negative	Positive			
PAP 542 S	PAP 542	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 549 S	PAP 549	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 550 S	PAP 550	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 551 S	PAP 551	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 552 S	PAP 552	Ovarian		III	Pap brush sample	
Positive		Positive	Positive			
PAP 554 S	PAP 554	Endometrial		IV	Pap brush sample	
Positive		Negative	Positive			
PAP 556 S	PAP 556	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAP 557 S	PAP 557	Endometrial		IV	Pap brush sample	
Positive		Negative	Positive			
PAP 558 S	PAP 558	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 560 S	PAP 560	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 561 S	PAP 561	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 563 S	PAP 563	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 564 S	PAP 564	Endometrial		IV	Pap brush sample	
Positive		Positive	Positive			
PAP 565 S	PAP 565	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 566 S	PAP 566	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 567 S	PAP 567	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 568 S	PAP 568	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 569 S	PAP 569	Ovarian		IV	Pap brush sample	
Positive		Negative	Positive			
PAP 572 S	PAP 572	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 573 S	PAP 573	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 574 S	PAP 574	Endometrial		III	Pap brush sample	

Table14.txt

Positive		Negative	Positive		
PAP 575 S	PAP 575	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 576 S	PAP 576	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 579 S	PAP 579	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 581 S	PAP 581	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 583 S	PAP 583	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 584 S	PAP 584	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 585 S	PAP 585	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 587 S	PAP 587	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 589 S	PAP 589	Endometrial		IV	Pap brush sample
Positive		Negative	Positive		
PAP 592 S	PAP 592	Ovarian		II	Pap brush sample
Negative		Positive	Positive		
PAP 593 S	PAP 593	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 594 S	PAP 594	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 595 S	PAP 595	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 596 S	PAP 596	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 599 S	PAP 599	Endometrial		II	Pap brush sample
Positive		Negative	Positive		
PAP 600 S	PAP 600	Endometrial		III	Pap brush sample
Negative		Negative	Negative		
PAP 604 S	PAP 604	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 606 S	PAP 606	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 607 S	PAP 607	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 609 S	PAP 609	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 610 S	PAP 610	Endometrial		III	Pap brush sample
Negative		Positive	Positive		
PAP 612 S	PAP 612	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 613 S	PAP 613	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 617 S	PAP 617	Endometrial		III	Pap brush sample

Table14.txt

Positive		Negative	Positive		
PAP 619 S	PAP 619	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 621 S	PAP 621	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 622 S	PAP 622	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 625 S	PAP 625	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 628 S	PAP 628	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 629 S	PAP 629	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 632 S	PAP 632	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 633 S	PAP 633	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 636 S1	PAP 636	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 636 S2	PAP 636	Ovarian	III	Tao brush sample	
Negative		Negative	Negative		
PAP 637 S1	PAP 637	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 637 S2	PAP 637	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAP 638 S1	PAP 638	Endometrial	IV	Pap brush sample	
Positive		Positive	Positive		
PAP 638 S2	PAP 638	Endometrial	IV	Tao brush sample	
Positive		Positive	Positive		
PAP 641 S1	PAP 641	Ovarian	II	Pap brush sample	
Negative		Negative	Negative		
PAP 642 S1	PAP 642	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 643 S1	PAP 643	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 644 S1	PAP 644	Ovarian	II	Pap brush sample	
Negative		Negative	Negative		
PAP 646 S1	PAP 646	Endometrial	II	Pap brush sample	
Positive		Negative	Positive		
PAP 647 S1	PAP 647	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 648 S1	PAP 648	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 649 S1	PAP 649	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 650 S1	PAP 650	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 652 S1	PAP 652	Endometrial	I	Pap brush sample	

Table14.txt

Positive		Positive	Positive		
PAP 654 S1	PAP 654	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 663 S1	PAP 663	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 665 S1	PAP 665	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 667 S1	PAP 667	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 668 S1	PAP 668	Endometrial		II	Pap brush sample
Positive		Negative	Positive		
PAP 669 S1	PAP 669	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 670 S1	PAP 670	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 671 S1	PAP 671	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 672 S1	PAP 672	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 674 S1	PAP 674	Ovarian		IV	Pap brush sample
Negative		Negative	Negative		
PAP 676 S1	PAP 676	Endometrial		III	Pap brush sample
Negative		Negative	Negative		
PAP 678 S1	PAP 678	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 679 S1	PAP 679	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 681 S1	PAP 681	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 684 S1	PAP 684	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 685 S1	PAP 685	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 685 S2	PAP 685	Endometrial		I	Tao brush sample
Positive		Negative	Positive		
PAP 686 S1	PAP 686	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 686 S2	PAP 686	Endometrial		I	Tao brush sample
Positive		Negative	Positive		
PAP 687 S1	PAP 687	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 687 S2	PAP 687	Endometrial		I	Tao brush sample
Positive		Negative	Positive		
PAP 688 S1	PAP 688	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 688 S2	PAP 688	Endometrial		I	Tao brush sample
Positive		Positive	Positive		
PAP 689 S1	PAP 689	Endometrial		III	Pap brush sample

Table14.txt

Positive		Positive	Positive		
PAP 689 S2	PAP 689	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 690 S1	PAP 690	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 690 S2	PAP 690	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAP 691 S1	PAP 691	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 691 S2	PAP 691	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAP 692 S1	PAP 692	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 692 S2	PAP 692	Ovarian	I	Tao brush sample	
Negative		Negative	Negative		
PAP 694 S1	PAP 694	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 695 S1	PAP 695	Endometrial	II	Pap brush sample	
Positive		Positive	Positive		
PAP 696 S1	PAP 696	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAP 697 S1	PAP 697	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 698 S1	PAP 698	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 699 S1	PAP 699	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 701 S1	PAP 701	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 702 S1	PAP 702	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 704 S1	PAP 704	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 705 S1	PAP 705	Ovarian	I	Pap brush sample	
Positive		Negative	Positive		
PAP 707 S1	PAP 707	Ovarian	III	Pap brush sample	
Positive		Negative	Positive		
PAP 709 S1	PAP 709	Ovarian	II	Pap brush sample	
Negative		Negative	Negative		
PAP 710 S1	PAP 710	Ovarian	III	Pap brush sample	
Negative		Positive	Positive		
PAP 711 S1	PAP 711	Ovarian	III	Pap brush sample	
Positive		Negative	Positive		
PAP 715 S1	PAP 715	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 717 S1	PAP 717	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAP 719 S1	PAP 719	Endometrial	I	Pap brush sample	

Table14.txt

Positive		Negative	Positive		
PAP 721 S1	PAP 721	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 722 S1	PAP 722	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 726 S1	PAP 726	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 727 S1	PAP 727	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 728 S1	PAP 728	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 730 S1	PAP 730	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 735 S1	PAP 735	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 736 S1	PAP 736	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 742 S1	PAP 742	Ovarian		IV	Pap brush sample
Positive		Negative	Positive		
PAP 744 S1	PAP 744	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 746 S1	PAP 746	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 748 S1	PAP 748	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 749 S1	PAP 749	Ovarian		I	Pap brush sample
Positive		Negative	Positive		
PAP 751 S1	PAP 751	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 754 S1	PAP 754	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 758 S1	PAP 758	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 761 S1	PAP 761	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 763 S1	PAP 763	Ovarian		III	Pap brush sample
Positive		Negative	Positive		
PAP 767 S1	PAP 767	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 768 S1	PAP 768	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 770 S1	PAP 770	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 775 S1	PAP 775	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 777 S1	PAP 777	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 778 S1	PAP 778	Endometrial		I	Pap brush sample

Table14.txt

Negative		Negative	Negative			
PAP 787 S1	PAP 787	Ovarian		IV	Pap brush sample	
Negative		Negative	Negative			
PAP 789 S1	PAP 789	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 790 S1	PAP 790	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 791 S1	PAP 791	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAP 802 S1	PAP 802	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 804 S1	PAP 804	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 805 S1	PAP 805	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 807 S1	PAP 807	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 809 S1	PAP 809	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 812 S1	PAP 812	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 813 S1	PAP 813	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 815 S1	PAP 815	Ovarian		III	Pap brush sample	
Negative		Negative	Negative			
PAP 816 S1	PAP 816	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAP 824 S1	PAP 824	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 824 S2	PAP 824	Endometrial		I	Tao brush sample	
Positive		Positive	Positive			
PAP 829 S1	PAP 829	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAP 829 S2	PAP 829	Endometrial		I	Tao brush sample	
Negative		Negative	Negative			
PAP 830 S1	PAP 830	Ovarian		I	Pap brush sample	
Negative		Negative	Negative			
PAP 830 S2	PAP 830	Ovarian		I	Tao brush sample	
Negative		Positive	Positive			
PAP 831 S1	PAP 831	Endometrial		III	Pap brush sample	
Positive		Positive	Positive			
PAP 831 S2	PAP 831	Endometrial		III	Tao brush sample	
Positive		Negative	Positive			
PAP 832 S1	PAP 832	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAP 832 S2	PAP 832	Endometrial		I	Tao brush sample	
Positive		Negative	Positive			
PAP 835 S1	PAP 835	Endometrial		III	Pap brush sample	

Table14.txt

Positive		Negative	Positive		
PAP 835 S2	PAP 835	Endometrial	III	Tao brush sample	
Positive		Negative	Positive		
PAP 836 S1	PAP 836	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 836 S2	PAP 836	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAP 837 S1	PAP 837	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 837 S2	PAP 837	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAP 839 S1	PAP 839	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 839 S2	PAP 839	Endometrial	III	Tao brush sample	
Positive		Negative	Positive		
PAP 841 S1	PAP 841	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 841 S2	PAP 841	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 842 S1	PAP 842	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 842 S2	PAP 842	Endometrial	III	Tao brush sample	
Positive		Negative	Positive		
PAP 845 S1	PAP 845	Ovarian	IV	Pap brush sample	
Negative		Negative	Negative		
PAP 845 S2	PAP 845	Ovarian	IV	Tao brush sample	
Positive		Negative	Positive		
PAP 850 S1	PAP 850	Endometrial	IV	Pap brush sample	
Positive		Positive	Positive		
PAP 850 S2	PAP 850	Endometrial	IV	Tao brush sample	
Positive		Positive	Positive		
PAP 851 S1	PAP 851	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 851 S2	PAP 851	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 853 S1	PAP 853	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAP 853 S2	PAP 853	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAP 858 S1	PAP 858	Endometrial	III	Pap brush sample	
Negative		Negative	Negative		
PAP 858 S2	PAP 858	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 860 S1	PAP 860	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 860 S2	PAP 860	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAP 862 S2	PAP 862	Endometrial	III	Tao brush sample	

Table14.txt

Positive		Positive	Positive			
PAP 867 S1	PAP 867	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 868 S1	PAP 868	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 869 S1	PAP 869	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 870 S1	PAP 870	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 871 S1	PAP 871	Endometrial		II		Pap brush sample
Positive		Positive	Positive			
PAP 873 S1	PAP 873	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAP 874 S1	PAP 874	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 875 S1	PAP 875	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 876 S1	PAP 876	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 877 S1	PAP 877	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 878 S1	PAP 878	Endometrial		II		Pap brush sample
Positive		Positive	Positive			
PAP 879 S1	PAP 879	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 881 S1	PAP 881	Endometrial		III		Pap brush sample
Positive		Positive	Positive			
PAP 884 S1	PAP 884	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 884 S2	PAP 884	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAP 889 S1	PAP 889	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAP 889 S2	PAP 889	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAP 891 S1	PAP 891	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAP 891 S2	PAP 891	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAP 892 S1	PAP 892	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAP 892 S2	PAP 892	Endometrial		III		Tao brush sample
Positive		Negative	Positive			
PAP 894 S1	PAP 894	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 894 S2	PAP 894	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 897 S1	PAP 897	Endometrial		III		Pap brush sample

Table14.txt

Positive		Negative	Positive		
PAP 897 S2	PAP 897	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 900 S1	PAP 900	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 901 S1	PAP 901	Endometrial	II	Pap brush sample	
Positive		Positive	Positive		
PAP 901 S2	PAP 901	Endometrial	II	Tao brush sample	
Positive		Positive	Positive		
PAP 902 S1	PAP 902	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAP 902 S2	PAP 902	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 904 S1	PAP 904	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAP 904 S2	PAP 904	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 907 S1	PAP 907	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 907 S2	PAP 907	Endometrial	III	Tao brush sample	
Positive		Negative	Positive		
PAP 910 S1	PAP 910	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAP 910 S2	PAP 910	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAP 914 S1	PAP 914	Ovarian	I	Pap brush sample	
Negative		Negative	Negative		
PAP 914 S2	PAP 914	Ovarian	I	Tao brush sample	
Positive		Negative	Positive		
PAP 919 S1	PAP 919	Ovarian	II	Pap brush sample	
Negative		Negative	Negative		
PAP 919 S2	PAP 919	Ovarian	II	Tao brush sample	
Negative		Negative	Negative		
PAP 922 S1	PAP 922	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 922 S2	PAP 922	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAP 925 S1	PAP 925	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAP 925 S2	PAP 925	Ovarian	III	Tao brush sample	
Positive		Positive	Positive		
PAP 926 S1	PAP 926	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAP 926 S2	PAP 926	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAP 927 S1	PAP 927	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAP 927 S2	PAP 927	Endometrial	I	Tao brush sample	

Table14.txt

Positive		Positive	Positive			
PAP 928 S1	PAP 928	Ovarian		II		Pap brush sample
Positive		Negative	Positive			
PAP 928 S2	PAP 928	Ovarian		II		Tao brush sample
Positive		Negative	Positive			
PAP 931 S1	PAP 931	Endometrial		II		Pap brush sample
Positive		Positive	Positive			
PAP 931 S2	PAP 931	Endometrial		II		Tao brush sample
Positive		Positive	Positive			
PAP 934 S1	PAP 934	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 934 S2	PAP 934	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 936 S2	PAP 936	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 937 S2	PAP 937	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAP 989 S1	PAP 989	Endometrial		II		Pap brush sample
Positive		Positive	Positive			
PAP 989 S2	PAP 989	Endometrial		II		Tao brush sample
Positive		Positive	Positive			
PAP 990 S1	PAP 990	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 990 S2	PAP 990	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 991 S1	PAP 991	Endometrial		III		Pap brush sample
Positive		Positive	Positive			
PAP 991 S2	PAP 991	Endometrial		III		Tao brush sample
Positive		Negative	Positive			
PAP 993 S1	PAP 993	Ovarian		III		Pap brush sample
Positive		Positive	Positive			
PAP 993 S2	PAP 993	Ovarian		III		Tao brush sample
Positive		Positive	Positive			
PAP 994 S1	PAP 994	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 994 S2	PAP 994	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAP 995 S1	PAP 995	Endometrial		II		Pap brush sample
Positive		Positive	Positive			
PAP 995 S2	PAP 995	Endometrial		II		Tao brush sample
Positive		Positive	Positive			
PAP 996 S1	PAP 996	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAP 996 S2	PAP 996	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 998 S1	PAP 998	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 998 S2	PAP 998	Endometrial		I		Tao brush sample

Table14.txt

Positive		Negative	Positive		
PAP 999 S1	PAP 999	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAP 999 S2	PAP 999	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1001 S1	PAPA 1001	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAPA 1001 S2	PAPA 1001	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1002 S1	PAPA 1002	Endometrial	I	Pap brush sample	
Positive		Negative	Positive		
PAPA 1002 S2	PAPA 1002	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAPA 1003 S1	PAPA 1003	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAPA 1003 S2	PAPA 1003	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1005 S1	PAPA 1005	Endometrial	II	Pap brush sample	
Positive		Positive	Positive		
PAPA 1005 S2	PAPA 1005	Endometrial	II	Tao brush sample	
Positive		Negative	Positive		
PAPA 1010 S1	PAPA 1010	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAPA 1010 S2	PAPA 1010	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1011 S1	PAPA 1011	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAPA 1011 S2	PAPA 1011	Endometrial	I	Tao brush sample	
Positive		Negative	Positive		
PAPA 1012 S2	PAPA 1012	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1013 S1	PAPA 1013	Endometrial	III	Pap brush sample	
Positive		Positive	Positive		
PAPA 1013 S2	PAPA 1013	Endometrial	III	Tao brush sample	
Positive		Positive	Positive		
PAPA 1016 S1	PAPA 1016	Endometrial	I	Pap brush sample	
Positive		Positive	Positive		
PAPA 1016 S2	PAPA 1016	Endometrial	I	Tao brush sample	
Positive		Positive	Positive		
PAPA 1019 S1	PAPA 1019	Endometrial	III	Pap brush sample	
Positive		Negative	Positive		
PAPA 1019 S2	PAPA 1019	Endometrial	III	Tao brush sample	
Positive		Negative	Positive		
PAPA 1026 S1	PAPA 1026	Endometrial	I	Pap brush sample	
Negative		Negative	Negative		
PAPA 1033 S1	PAPA 1033	Ovarian	III	Pap brush sample	
Negative		Negative	Negative		
PAPA 1035 S1	PAPA 1035	Endometrial	II	Pap brush sample	

Table14.txt

Positive		Positive	Positive				
PAPA 1037 S1	PAPA 1037	Ovarian		III	Pap brush sample		
Positive		Negative	Positive				
PAPA 1040 S1	PAPA 1040	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1043 S1	PAPA 1043	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1048 S1	PAPA 1048	Endometrial		I	Pap brush sample		
Positive		Positive	Positive				
PAPA 1057 S1	PAPA 1057	Endometrial		I	Pap brush sample		
Positive		Positive	Positive				
PAPA 1058 S1	PAPA 1058	Endometrial		I	Pap brush sample		
Negative		Negative	Negative				
PAPA 1059 S1	PAPA 1059	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1062 S1	PAPA 1062	Ovarian		IV	Pap brush sample		
Negative		Negative	Negative				
PAPA 1065 S1	PAPA 1065	Endometrial		NA	Pap brush sample		
Negative		Negative	Negative				
PAPA 1066 S1	PAPA 1066	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1069 S1	PAPA 1069	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1072 S1	PAPA 1072	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1074 S1	PAPA 1074	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1076 S1	PAPA 1076	Endometrial		III	Pap brush sample		
Positive		Positive	Positive				
PAPA 1077 S1	PAPA 1077	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1078 S1	PAPA 1078	Endometrial		I	Pap brush sample		
Negative		Negative	Negative				
PAPA 1081 S1	PAPA 1081	Endometrial		III	Pap brush sample		
Positive		Negative	Positive				
PAPA 1084 S1	PAPA 1084	Ovarian		II	Pap brush sample		
Negative		Negative	Negative				
PAPA 1092 S1	PAPA 1092	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1094 S1	PAPA 1094	Ovarian		IV	Pap brush sample		
Positive		Negative	Positive				
PAPA 1095 S1	PAPA 1095	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1096 S1	PAPA 1096	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1097 S1	PAPA 1097	Endometrial		IV	Pap brush sample		
Positive		Positive	Positive				
PAPA 1098 S1	PAPA 1098	Ovarian		I	Pap brush sample		

Table14.txt

Positive		Negative	Positive			
PAPA 1099 S1	PAPA 1099	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1100 S1	PAPA 1100	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1103 S1	PAPA 1103	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1106 S1	PAPA 1106	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1110 S1	PAPA 1110	Ovarian		II		Pap brush sample
Positive		Negative	Positive			
PAPA 1112 S1	PAPA 1112	Ovarian		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1113 S1	PAPA 1113	Ovarian		III		Pap brush sample
Positive		Positive	Positive			
PAPA 1115 S1	PAPA 1115	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1116 S1	PAPA 1116	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1117 S1	PAPA 1117	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1118 S1	PAPA 1118	Ovarian		I		Pap brush sample
Negative		Positive	Positive			
PAPA 1119 S1	PAPA 1119	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1120 S1	PAPA 1120	Ovarian		I		Pap brush sample
Negative		Positive	Positive			
PAPA 1121 S1	PAPA 1121	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1122 S1	PAPA 1122	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1126 S1	PAPA 1126	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1126 S2	PAPA 1126	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1128 S1	PAPA 1128	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1128 S2	PAPA 1128	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1129 S1	PAPA 1129	Endometrial		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1129 S2	PAPA 1129	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1130 S1	PAPA 1130	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1130 S2	PAPA 1130	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1131 S1	PAPA 1131	Endometrial		I		Pap brush sample

Table14.txt

Positive		Positive	Positive			
PAPA 1131 S2	PAPA 1131	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1132 S1	PAPA 1132	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1132 S2	PAPA 1132	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1133 S1	PAPA 1133	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1133 S2	PAPA 1133	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1134 S1	PAPA 1134	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1134 S2	PAPA 1134	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1135 S1	PAPA 1135	Endometrial		IV		Pap brush sample
Positive		Negative	Positive			
PAPA 1135 S2	PAPA 1135	Endometrial		IV		Tao brush sample
Positive		Positive	Positive			
PAPA 1136 S1	PAPA 1136	Ovarian		IV		Pap brush sample
Positive		Negative	Positive			
PAPA 1136 S2	PAPA 1136	Ovarian		IV		Tao brush sample
Negative		Positive	Positive			
PAPA 1137 S1	PAPA 1137	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1137 S2	PAPA 1137	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1138 S1	PAPA 1138	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1138 S2	PAPA 1138	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1139 S1	PAPA 1139	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1139 S2	PAPA 1139	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAPA 1140 S1	PAPA 1140	Endometrial		III		Pap brush sample
Positive		Positive	Positive			
PAPA 1140 S2	PAPA 1140	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1141 S1	PAPA 1141	Endometrial		IV		Pap brush sample
Positive		Positive	Positive			
PAPA 1141 S2	PAPA 1141	Endometrial		IV		Tao brush sample
Positive		Positive	Positive			
PAPA 1142 S1	PAPA 1142	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1142 S2	PAPA 1142	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1143 S1	PAPA 1143	Endometrial		I		Pap brush sample

Table14.txt

Positive		Negative	Positive			
PAPA 1143 S2	PAPA 1143	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1144 S1	PAPA 1144	Ovarian		IV		Pap brush sample
Negative		Negative	Negative			
PAPA 1144 S2	PAPA 1144	Ovarian		IV		Tao brush sample
Negative		Negative	Negative			
PAPA 1145 S1	PAPA 1145	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1145 S2	PAPA 1145	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1146 S1	PAPA 1146	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1146 S2	PAPA 1146	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1147 S1	PAPA 1147	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1147 S2	PAPA 1147	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1148 S1	PAPA 1148	Endometrial		III		Pap brush sample
Positive		Positive	Positive			
PAPA 1148 S2	PAPA 1148	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1149 S1	PAPA 1149	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1149 S2	PAPA 1149	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1150 S1	PAPA 1150	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1150 S2	PAPA 1150	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1152 S1	PAPA 1152	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1152 S2	PAPA 1152	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1153 S1	PAPA 1153	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1153 S2	PAPA 1153	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1154 S1	PAPA 1154	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1154 S2	PAPA 1154	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1155 S1	PAPA 1155	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1155 S2	PAPA 1155	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1157 S1	PAPA 1157	Endometrial		III		Pap brush sample

Table14.txt

Positive		Positive	Positive			
PAPA 1157 S2	PAPA 1157	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1158 S1	PAPA 1158	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1158 S2	PAPA 1158	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAPA 1159 S1	PAPA 1159	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1159 S2	PAPA 1159	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1160 S1	PAPA 1160	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1160 S2	PAPA 1160	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1161 S1	PAPA 1161	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1161 S2	PAPA 1161	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1162 S1	PAPA 1162	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1162 S2	PAPA 1162	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1164 S1	PAPA 1164	Endometrial		I		Pap brush sample
Negative		Positive	Positive			
PAPA 1164 S2	PAPA 1164	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1167 S1	PAPA 1167	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1167 S2	PAPA 1167	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1169 S1	PAPA 1169	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1169 S2	PAPA 1169	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAPA 1172 S1	PAPA 1172	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1176 S1	PAPA 1176	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1176 S2	PAPA 1176	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1177 S1	PAPA 1177	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1177 S2	PAPA 1177	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1180 S1	PAPA 1180	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1180 S2	PAPA 1180	Ovarian		I		Tao brush sample

Table14.txt

Negative		Negative	Negative			
PAPA 1181 S2	PAPA 1181	Endometrial		IV	Tao brush sample	
Negative		Negative	Negative			
PAPA 1184 S1	PAPA 1184	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAPA 1184 S2	PAPA 1184	Endometrial		I	Tao brush sample	
Positive		Positive	Positive			
PAPA 1185 S1	PAPA 1185	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAPA 1185 S2	PAPA 1185	Endometrial		I	Tao brush sample	
Positive		Positive	Positive			
PAPA 1188 S1	PAPA 1188	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAPA 1188 S2	PAPA 1188	Endometrial		I	Tao brush sample	
Positive		Positive	Positive			
PAPA 1189 S2	PAPA 1189	Ovarian		III	Tao brush sample	
Positive		Negative	Positive			
PAPA 1191 S1	PAPA 1191	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAPA 1192 S1	PAPA 1192	Endometrial		II	Pap brush sample	
Positive		Positive	Positive			
PAPA 1193 S1	PAPA 1193	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAPA 1194 S1	PAPA 1194	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAPA 1198 S1	PAPA 1198	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAPA 1200 S1	PAPA 1200	Endometrial		I	Pap brush sample	
Negative		Negative	Negative			
PAPA 1202 S1	PAPA 1202	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAPA 1204 S1	PAPA 1204	Endometrial		I	Pap brush sample	
Positive		Negative	Positive			
PAPA 1207 S1	PAPA 1207	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAPA 1208 S1	PAPA 1208	Ovarian		I	Pap brush sample	
Positive		Negative	Positive			
PAPA 1209 S1	PAPA 1209	Endometrial		I	Pap brush sample	
Positive		Positive	Positive			
PAPA 1210 S1	PAPA 1210	Ovarian		III	Pap brush sample	
Positive		Negative	Positive			
PAPA 1211 S1	PAPA 1211	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAPA 1213 S1	PAPA 1213	Ovarian		III	Pap brush sample	
Positive		Negative	Positive			
PAPA 1214 S1	PAPA 1214	Endometrial		III	Pap brush sample	
Positive		Negative	Positive			
PAPA 1215 S1	PAPA 1215	Ovarian		III	Pap brush sample	

Table14.txt

Negative		Negative	Negative			
PAPA 1217 S1	PAPA 1217	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1218 S1	PAPA 1218	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1221 S1	PAPA 1221	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1222 S1	PAPA 1222	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1223 S1	PAPA 1223	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1224 S1	PAPA 1224	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1225 S1	PAPA 1225	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1226 S1	PAPA 1226	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1230 S1	PAPA 1230	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1232 S1	PAPA 1232	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1233 S1	PAPA 1233	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1235 S1	PAPA 1235	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1237 S1	PAPA 1237	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1239 S1	PAPA 1239	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1240 S1	PAPA 1240	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1242 S1	PAPA 1242	Endometrial		I		Pap brush sample
Positive		Positive	Positive			
PAPA 1243 S1	PAPA 1243	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1246 S1	PAPA 1246	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1247 S1	PAPA 1247	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1249 S1	PAPA 1249	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1249 S2	PAPA 1249	Endometrial		I		Tao brush sample
Negative		Positive	Positive			
PAPA 1253 S1	PAPA 1253	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1253 S2	PAPA 1253	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1254 S1	PAPA 1254	Endometrial		I		Pap brush sample

Table14.txt

Negative		Negative	Negative			
PAPA 1254 S2	PAPA 1254	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1255 S1	PAPA 1255	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1256 S1	PAPA 1256	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1256 S2	PAPA 1256	Endometrial		I		Tao brush sample
Negative		Negative	Negative			
PAPA 1257 S1	PAPA 1257	Ovarian		III		Pap brush sample
Negative		Positive	Positive			
PAPA 1257 S2	PAPA 1257	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1258 S1	PAPA 1258	Ovarian		IV		Pap brush sample
Negative		Negative	Negative			
PAPA 1258 S2	PAPA 1258	Ovarian		IV		Tao brush sample
Positive		Negative	Positive			
PAPA 1259 S1	PAPA 1259	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1259 S2	PAPA 1259	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1260 S1	PAPA 1260	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1260 S2	PAPA 1260	Ovarian		I		Tao brush sample
Negative		Negative	Negative			
PAPA 1262 S1	PAPA 1262	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1263 S1	PAPA 1263	Ovarian		IV		Pap brush sample
Negative		Negative	Negative			
PAPA 1263 S2	PAPA 1263	Ovarian		IV		Tao brush sample
Positive		Negative	Positive			
PAPA 1264 S1	PAPA 1264	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1264 S2	PAPA 1264	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1284 S1	PAPA 1284	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1286 S1	PAPA 1286	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1292 S1	PAPA 1292	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1293 S1	PAPA 1293	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1295 S1	PAPA 1295	Endometrial		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1296 S1	PAPA 1296	Ovarian		III		Pap brush sample
Positive		Positive	Positive			
PAPA 1297 S1	PAPA 1297	Ovarian		III		Pap brush sample

Table14.txt

Positive		Negative	Positive				
PAPA 1298 S1	PAPA 1298	Ovarian		III	Pap brush sample		
Positive		Positive	Positive				
PAPA 1300 S1	PAPA 1300	Endometrial		I	Pap brush sample		
Positive		Positive	Positive				
PAPA 1301 S1	PAPA 1301	Ovarian		I	Pap brush sample		
Negative		Negative	Negative				
PAPA 1302 S1	PAPA 1302	Ovarian		I	Pap brush sample		
Negative		Positive	Positive				
PAPA 1303 S1	PAPA 1303	Endometrial		IV	Pap brush sample		
Positive		Positive	Positive				
PAPA 1307 S1	PAPA 1307	Endometrial		IV	Pap brush sample		
Negative		Negative	Negative				
PAPA 1308 S1	PAPA 1308	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1309 S1	PAPA 1309	Endometrial		I	Pap brush sample		
Positive		Negative	Positive				
PAPA 1315 S1	PAPA 1315	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1320 S1	PAPA 1320	Ovarian		IV	Pap brush sample		
Negative		Negative	Negative				
PAPA 1321 S1	PAPA 1321	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1322 S1	PAPA 1322	Ovarian		II	Pap brush sample		
Positive		Negative	Positive				
PAPA 1323 S1	PAPA 1323	Ovarian		II	Pap brush sample		
Negative		Negative	Negative				
PAPA 1325 S1	PAPA 1325	Ovarian		III	Pap brush sample		
Negative		Negative	Negative				
PAPA 1326 S1	PAPA 1326	Ovarian		I	Pap brush sample		
Positive		Positive	Positive				
PAPA 1327 S1	PAPA 1327	Ovarian		I	Pap brush sample		
Negative		Negative	Negative				
PAPA 1328 S1	PAPA 1328	Ovarian		III	Pap brush sample		
Positive		Negative	Positive				
PAPA 1329 S1	PAPA 1329	Endometrial		I	Pap brush sample		
Negative		Negative	Negative				
PAPA 1359 S1	PAPA 1359	Ovarian		IV	Pap brush sample		
Negative		Negative	Negative				
PAPA 1359 S2	PAPA 1359	Ovarian		IV	Tao brush sample		
Negative		Negative	Negative				
PAPA 1361 S1	PAPA 1361	Ovarian		II	Pap brush sample		
Negative		Negative	Negative				
PAPA 1361 S2	PAPA 1361	Ovarian		II	Tao brush sample		
Positive		Negative	Positive				
PAPA 1362 S2	PAPA 1362	Ovarian		II	Tao brush sample		
Negative		Negative	Negative				
PAPA 1363 S1	PAPA 1363	Ovarian		III	Pap brush sample		

Table14.txt

Negative		Negative	Negative			
PAPA 1363 S2	PAPA 1363	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1364 S1	PAPA 1364	Ovarian		II		Pap brush sample
Positive		Negative	Positive			
PAPA 1365 S1	PAPA 1365	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1365 S2	PAPA 1365	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1369 S1	PAPA 1369	Ovarian		II		Pap brush sample
Negative		Negative	Negative			
PAPA 1369 S2	PAPA 1369	Ovarian		II		Tao brush sample
Negative		Negative	Negative			
PAPA 1370 S1	PAPA 1370	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1370 S2	PAPA 1370	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1371 S1	PAPA 1371	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1371 S2	PAPA 1371	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1695 S1	PAPA 1695	Ovarian		IV		Pap brush sample
Positive		Negative	Positive			
PAPA 1696 S1	PAPA 1696	Ovarian		III		Pap brush sample
Positive		Positive	Positive			
PAPA 1697 S1	PAPA 1697	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1698 S1	PAPA 1698	Ovarian		II		Pap brush sample
Negative		Negative	Negative			
PAPA 1699 S1	PAPA 1699	Ovarian		IV		Pap brush sample
Negative		Positive	Positive			
PAPA 1700 S1	PAPA 1700	Ovarian		II		Pap brush sample
Positive		Negative	Positive			
PAPA 1701 S1	PAPA 1701	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1702 S1	PAPA 1702	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1703 S1	PAPA 1703	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1705 S1	PAPA 1705	Ovarian		I		Pap brush sample
Positive		Negative	Positive			
PAPA 1706 S1	PAPA 1706	Ovarian		II		Pap brush sample
Positive		Positive	Positive			
PAPA 1707 S1	PAPA 1707	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1710 S1	PAPA 1710	Ovarian		III		Pap brush sample
Negative		Positive	Positive			
PAPA 1712 S1	PAPA 1712	Ovarian		I		Pap brush sample

Table14.txt

```
Negative            Negative     Negative
PAPA 1713 S1 PAPA 1713    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1714 S1 PAPA 1714    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1715 S1 PAPA 1715    Ovarian           I           Pap brush sample
Negative            Negative     Negative
PAPA 1716 S1 PAPA 1716    Ovarian           II          Pap brush sample
Positive            Negative     Positive
PAPA 1717 S1 PAPA 1717    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1720 S1 PAPA 1720    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1721 S1 PAPA 1721    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1722 S1 PAPA 1722    Ovarian           IV          Pap brush sample
Negative            Negative     Negative
PAPA 1724 S1 PAPA 1724    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1725 S1 PAPA 1725    Ovarian           I           Pap brush sample
Positive            Negative     Positive
PAPA 1727 S1 PAPA 1727    Ovarian           I           Pap brush sample
Negative            Negative     Negative
PAPA 1728 S1 PAPA 1728    Ovarian           I           Pap brush sample
Negative            Negative     Negative
PAPA 1730 S1 PAPA 1730    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1732 S1 PAPA 1732    Ovarian           II          Pap brush sample
Negative            Negative     Negative
PAPA 1734 S1 PAPA 1734    Ovarian           IV          Pap brush sample
Positive            Negative     Positive
PAPA 1735 S1 PAPA 1735    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1736 S1 PAPA 1736    Ovarian           II          Pap brush sample
Positive            Negative     Positive
PAPA 1737 S1 PAPA 1737    Ovarian           II          Pap brush sample
Negative            Negative     Negative
PAPA 1738 S1 PAPA 1738    Ovarian           III         Pap brush sample
Negative            Negative     Negative
PAPA 1739 S1 PAPA 1739    Ovarian           I           Pap brush sample
Negative            Negative     Negative
PAPA 1816 S1 PAPA 1816    Ovarian           I           Tao brush sample
Negative            Negative     Negative
PAPA 1816 S2 PAPA 1816    Ovarian           I           Pap brush sample
Negative            Negative     Negative
PAPA 1817 S1 PAPA 1817    Ovarian           III         Tao brush sample
Negative            Negative     Negative
PAPA 1817 S2 PAPA 1817    Ovarian           III         Pap brush sample
```

Negative		Negative	Negative			
PAPA 1819 S1	PAPA 1819	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1819 S2	PAPA 1819	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1820 S1	PAPA 1820	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1820 S2	PAPA 1820	Endometrial		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1821 S1	PAPA 1821	Ovarian		II		Tao brush sample
Positive		Positive	Positive			
PAPA 1821 S2	PAPA 1821	Ovarian		II		Pap brush sample
Negative		Negative	Negative			
PAPA 1823 S1	PAPA 1823	Ovarian		IV		Tao brush sample
Positive		Negative	Positive			
PAPA 1823 S2	PAPA 1823	Ovarian		IV		Pap brush sample
Negative		Negative	Negative			
PAPA 1826 S1	PAPA 1826	Ovarian		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1826 S2	PAPA 1826	Ovarian		I		Pap brush sample
Negative		Positive	Positive			
PAPA 1828 S1	PAPA 1828	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1828 S2	PAPA 1828	Ovarian		III		Pap brush sample
Positive		Negative	Positive			
PAPA 1829 S1	PAPA 1829	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1829 S2	PAPA 1829	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1832 S1	PAPA 1832	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1833 S1	PAPA 1833	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1833 S2	PAPA 1833	Ovarian		III		Pap brush sample
Negative		Negative	Negative			
PAPA 1834 S1	PAPA 1834	Ovarian		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1834 S2	PAPA 1834	Ovarian		I		Pap brush sample
Negative		Negative	Negative			
PAPA 1836 S1	PAPA 1836	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1837 S1	PAPA 1837	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1838 S1	PAPA 1838	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1839 S1	PAPA 1839	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1840 S1	PAPA 1840	Endometrial		I		Tao brush sample

Table14.txt

Positive		Positive	Positive			
PAPA 1842 S1	PAPA 1842	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1843 S1	PAPA 1843	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1844 S1	PAPA 1844	Ovarian		III		Tao brush sample
Positive		Negative	Positive			
PAPA 1845 S1	PAPA 1845	Ovarian		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1847 S1	PAPA 1847	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1848 S1	PAPA 1848	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1849 S1	PAPA 1849	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1850 S1	PAPA 1850	Ovarian		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1852 S1	PAPA 1852	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1855 S1	PAPA 1855	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1856 S1	PAPA 1856	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1857 S1	PAPA 1857	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1858 S1	PAPA 1858	Endometrial		III		Tao brush sample
Positive		Positive	Positive			
PAPA 1859 S1	PAPA 1859	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1860 S1	PAPA 1860	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1861 S1	PAPA 1861	Endometrial		IV		Tao brush sample
Positive		Positive	Positive			
PAPA 1862 S1	PAPA 1862	Endometrial		I		Tao brush sample
Positive		Negative	Positive			
PAPA 1864 S1	PAPA 1864	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1865 S1	PAPA 1865	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAPA 1866 S1	PAPA 1866	Ovarian		III		Tao brush sample
Negative		Negative	Negative			
PAPA 1867 S1	PAPA 1867	Endometrial		I		Tao brush sample
Positive		Positive	Positive			
PAP 033 S	PAP 033	Endometrial		I		Pap brush sample
Positive		Negative	Positive			
PAP 042 S	PAP 042	Ovarian		III		Pap brush sample
Positive		Positive	Positive			
PAP 261 S	PAP 261	Ovarian		I		Pap brush sample

Table14.txt

Negative		Negative	Negative		
PAP 532 S	PAP 532	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 533 S	PAP 533	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 544 S	PAP 544	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 562 S	PAP 562	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 570 S	PAP 570	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 588 S	PAP 588	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 590 S	PAP 590	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 601 S	PAP 601	Endometrial		II	Pap brush sample
Positive		Positive	Positive		
PAP 645 S1	PAP 645	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 651 S1	PAP 651	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 653 S1	PAP 653	Endometrial		II	Pap brush sample
Negative		Negative	Negative		
PAP 655 S1	PAP 655	Endometrial		II	Pap brush sample
Negative		Negative	Negative		
PAP 027 S	PAP 027	Ovarian		NA	Pap brush sample
Negative		Negative	Negative		
PAP 582 S	PAP 582	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 083 S	PAP 083	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 265 S	PAP 265	Endometrial		II	Pap brush sample
Positive		Negative	Positive		
PAP 555 S	PAP 555	Endometrial		IV	Pap brush sample
Positive		Positive	Positive		
PAP 618 S	PAP 618	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 059 S	PAP 059	Ovarian		NA	Pap brush sample
Positive		Negative	Positive		
PAP 174 S	PAP 174	Ovarian		I	Pap brush sample
Negative		Negative	Negative		
PAP 175 S	PAP 175	Endometrial		IV	Pap brush sample
Positive		Positive	Positive		
PAP 184 S	PAP 184	Ovarian		I	Pap brush sample
Positive		Positive	Positive		
PAP 032 S	PAP 032	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 035 S	PAP 035	Endometrial		IV	Pap brush sample

Table14.txt

Positive		Positive	Positive		
PAP 206 S	PAP 206	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 218 S	PAP 218	Endometrial		IV	Pap brush sample
Positive		Positive	Positive		
PAP 186 S	PAP 186	Ovarian		II	Pap brush sample
Positive		Negative	Positive		
PAP 220 S	PAP 220	Endometrial		III	Pap brush sample
Negative		Positive	Positive		
PAP 173 S	PAP 173	Ovarian		I	Pap brush sample
Positive		Positive	Positive		
PAP 194 S	PAP 194	Ovarian		I	Pap brush sample
Positive		Positive	Positive		
PAP 241 S	PAP 241	Ovarian		NA	Pap brush sample
Negative		Negative	Negative		
PAP 608 S	PAP 608	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAP 616 S	PAP 616	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 627 S	PAP 627	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 275 S	PAP 275	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 708 S1	PAP 708	Ovarian		II	Pap brush sample
Negative		Negative	Negative		
PAP 675 S1	PAP 675	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAPA 1012 S1	PAPA 1012	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 208 S	PAP 208	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 936 S1	PAP 936	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 937 S1	PAP 937	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 753 S1	PAP 753	Endometrial		IV	Pap brush sample
Positive		Positive	Positive		
PAP 757 S1	PAP 757	Endometrial		III	Pap brush sample
Positive		Positive	Positive		
PAP 799 S1	PAP 799	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 800 S1	PAP 800	Endometrial		IV	Pap brush sample
Positive		Positive	Positive		
PAP 866 S1	PAP 866	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAP 865 S1	PAP 865	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAPA 1080 S1	PAPA 1080	Endometrial		I	Pap brush sample

Table14.txt

Positive		Negative	Positive		
PAPA 1086 S1	PAPA 1086	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAPA 1181 S1	PAPA 1181	Endometrial		IV	Pap brush sample
Negative		Negative	Negative		
PAPA 1189 S1	PAPA 1189	Ovarian		III	Pap brush sample
Negative		Negative	Negative		
PAPA 1251 S2	PAPA 1251	Endometrial		I	Tao brush sample
Positive		Positive	Positive		
PAPA 1255 S2	PAPA 1255	Endometrial		I	Tao brush sample
Positive		Positive	Positive		
PAPA 1262 S2	PAPA 1262	Ovarian		I	Tao brush sample
Negative		Negative	Negative		
PAPA 1251 S1	PAPA 1251	Endometrial		I	Pap brush sample
Positive		Negative	Positive		
PAPA 1299 S1	PAPA 1299	Endometrial		I	Pap brush sample
Positive		Positive	Positive		
PAP 030 S	PAP 030	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 591 S	PAP 591	Endometrial		I	Pap brush sample
Negative		Negative	Negative		
PAP 182 PLS	PAP 182	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAP 184 PLS	PAP 184	Ovarian		I	Plasma sample
Positive		Not tested	NA		
PAP 185 PLS	PAP 185	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAP 186 PLS	PAP 186	Ovarian		II	Plasma sample
Positive		Not tested	NA		
PAP 193 PLS	PAP 193	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAP 195 PLS	PAP 195	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAP 196 PLS	PAP 196	Ovarian		I	Plasma sample
Positive		Not tested	NA		
PAP 197 PLS	PAP 197	Ovarian		I	Plasma sample
Positive		Not tested	NA		
PAP 198 PLS	PAP 198	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAP 199 PLS	PAP 199	Ovarian		I	Plasma sample
Positive		Not tested	NA		
PAP 210 PLS	PAP 210	Ovarian		I	Plasma sample
Positive		Not tested	NA		
PAP 230 PLS	PAP 230	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAP 241 PLS	PAP 241	Ovarian		NA	Plasma sample
Negative		Not tested	NA		
PAP 248 PLS	PAP 248	Ovarian		III	Plasma sample

Table14.txt

Negative Not tested NA
PAP 250 PLS PAP 250 Ovarian IV Plasma sample
Positive Not tested NA
PAP 251 PLS PAP 251 Ovarian I Plasma sample
Positive Not tested NA
PAP 252 PLS PAP 252 Ovarian I Plasma sample
Negative Not tested NA
PAP 253 PLS PAP 253 Ovarian III Plasma sample
Negative Not tested NA
PAP 254 PLS PAP 254 Ovarian I Plasma sample
Negative Not tested NA
PAP 255 PLS PAP 255 Ovarian III Plasma sample
Positive Not tested NA
PAP 257 PLS PAP 257 Ovarian I Plasma sample
Negative Not tested NA
PAP 258 PLS PAP 258 Ovarian I Plasma sample
Negative Not tested NA
PAP 259 PLS PAP 259 Ovarian I Plasma sample
Negative Not tested NA
PAP 261 PLS PAP 261 Ovarian I Plasma sample
Positive Not tested NA
PAP 262 PLS PAP 262 Ovarian III Plasma sample
Positive Not tested NA
PAP 263 PLS PAP 263 Ovarian I Plasma sample
Negative Not tested NA
PAP 264 PLS PAP 264 Ovarian I Plasma sample
Negative Not tested NA
PAP 579 PLS PAP 579 Ovarian I Plasma sample
Negative Not tested NA
PAP 641 PLS PAP 641 Ovarian II Plasma sample
Negative Not tested NA
PAP 642 PLS PAP 642 Ovarian I Plasma sample
Positive Not tested NA
PAP 643 PLS PAP 643 Ovarian I Plasma sample
Positive Not tested NA
PAP 644 PLS PAP 644 Ovarian II Plasma sample
Positive Not tested NA
PAP 645 PLS PAP 645 Ovarian I Plasma sample
Positive Not tested NA
PAP 701 PLS PAP 701 Ovarian I Plasma sample
Negative Not tested NA
PAP 704 PLS PAP 704 Ovarian I Plasma sample
Negative Not tested NA
PAP 705 PLS PAP 705 Ovarian I Plasma sample
Negative Not tested NA
PAP 707 PLS PAP 707 Ovarian III Plasma sample
Positive Not tested NA
PAP 708 PLS PAP 708 Ovarian II Plasma sample

Table14.txt

Negative		Not tested	NA		
PAP 709 PLS	PAP 709	Ovarian		II	Plasma sample
Negative		Not tested	NA		
PAP 710 PLS	PAP 710	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAP 711 PLS	PAP 711	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAP 715 PLS	PAP 715	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAP 815 PLS	PAP 815	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAPA 1037 PLS	PAPA 1037	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAPA 1062 PLS	PAPA 1062	Ovarian		IV	Plasma sample
Negative		Not tested	NA		
PAPA 1072 PLS	PAPA 1072	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAPA 1074 PLS	PAPA 1074	Ovarian		III	Plasma sample
Negative		Not tested	NA		
PAPA 1084 PLS	PAPA 1084	Ovarian		II	Plasma sample
Negative		Not tested	NA		
PAPA 1094 PLS	PAPA 1094	Ovarian		IV	Plasma sample
Negative		Not tested	NA		
PAPA 1096 PLS	PAPA 1096	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAPA 1098 PLS	PAPA 1098	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1110 PLS	PAPA 1110	Ovarian		II	Plasma sample
Negative		Not tested	NA		
PAPA 1112 PLS	PAPA 1112	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1113 PLS	PAPA 1113	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAPA 1115 PLS	PAPA 1115	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAPA 1116 PLS	PAPA 1116	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1117 PLS	PAPA 1117	Ovarian		III	Plasma sample
Positive		Not tested	NA		
PAPA 1118 PLS	PAPA 1118	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1119 PLS	PAPA 1119	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1120 PLS	PAPA 1120	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1121 PLS	PAPA 1121	Ovarian		I	Plasma sample
Negative		Not tested	NA		
PAPA 1122 PLS	PAPA 1122	Ovarian		I	Plasma sample

Table14.txt

Positive		Not tested	NA			
PAPA 1208	PLSPAPA 1208	Ovarian		I		Plasma sample
Negative		Not tested	NA			
PAPA 1213	PLSPAPA 1213	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1215	PLSPAPA 1215	Ovarian		III		Plasma sample
Negative		Not tested	NA			
PAPA 1235	PLSPAPA 1235	Ovarian		III		Plasma sample
Negative		Not tested	NA			
PAPA 1237	PLSPAPA 1237	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1240	PLSPAPA 1240	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1246	PLSPAPA 1246	Ovarian		I		Plasma sample
Negative		Not tested	NA			
PAPA 1292	PLSPAPA 1292	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1296	PLSPAPA 1296	Ovarian		III		Plasma sample
Negative		Not tested	NA			
PAPA 1297	PLSPAPA 1297	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1298	PLSPAPA 1298	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1301	PLSPAPA 1301	Ovarian		I		Plasma sample
Negative		Not tested	NA			
PAPA 1315	PLSPAPA 1315	Ovarian		III		Plasma sample
Negative		Not tested	NA			
PAPA 1320	PLSPAPA 1320	Ovarian		IV		Plasma sample
Positive		Not tested	NA			
PAPA 1321	PLSPAPA 1321	Ovarian		III		Plasma sample
Positive		Not tested	NA			
PAPA 1322	PLSPAPA 1322	Ovarian		II		Plasma sample
Positive		Not tested	NA			
PAPA 1323	PLSPAPA 1323	Ovarian		II		Plasma sample
Negative		Not tested	NA			
PAPA 1325	PLSPAPA 1325	Ovarian		III		Plasma sample
Negative		Not tested	NA			
PAPA 1326	PLSPAPA 1326	Ovarian		I		Plasma sample
Positive		Not tested	NA			
PAPA 1327	PLSPAPA 1327	Ovarian		I		Plasma sample
Positive		Not tested	NA			
PAPA 1328	PLSPAPA 1328	Ovarian		III		Plasma sample
Negative		Not tested	NA			

Table15.txt

Table 15. Mutations identified in Pap brush and Tao brush samples from patients from ovarian or endometrial cancer.

Patient ID	Cancer Type	Sample Type	WT Codon	MT Codon	Splice Site	Exon	MAF	Chrom	Position*	MutType	Base	WT Gene	Nucleotide	Total # Supermutants
PAP 001	Endometrial	Pap brush	sample					chr5	67591119	Indel	TAT	PIK3R1	1712	
	571	I	NULL	No	No	0.76	63							
PAP 010	Endometrial	Pap brush	sample					chr5	67589602	Indel	GTTTCAAGA			
PIK3R1	1365	455	Q	NULL	No	No	11.37	671						
PAP 011	Endometrial	Pap brush	sample					chr5	67589619	Indel	GAG	PIK3R1	1382	
	461	R	NULL	No	No	3.56	311							
PAP 034	Endometrial	Pap brush	sample					chr5	67591116	Indel	TTATCC	PIK3R1	1709	
	570	L	NULL	No	No	21.07	2481							
PAP 066	Endometrial	Pap brush	sample					chr17	7578235	SBS	T	TP53	614	
	205	Y	C	No	No	8.35	357							
PAP 066	Endometrial	Pap brush	sample					chr9	21974705	Indel	GGTGCGTTGGGCAGCGCCCC (SEQ ID NO:749)			
CDKN2A	122	41	P	NULL	No	No	0.61	73						
PAP 067	Endometrial	Pap brush	sample					chr5	67589618	SBS	C	PIK3R1	1381	
	461	R	*	No	No	2.41	1187							
PAP 069	Endometrial	Pap brush	sample					chr17	7579359	SBS	G	TP53	328	
	110	R	C	No	No	15.22	2175							
PAP 079	Ovarian	Pap brush	sample					chr17	7579349	Indel	AAG	TP53	338	
	113	F	NULL	No	No	0.11	55							
PAP 084	Endometrial	Pap brush	sample					chr5	112174371	Indel	A	APC	3080	
	1027	Y	NULL	No	No	0.52	217							
PAP 084	Endometrial	Pap brush	sample					chr5	112175973	Indel	AGGA	APC	4682	
	1561	K	NULL	No	No	0.14	71							
PAP 119	Endometrial	Pap brush	sample					chr5	67589590	Indel	ATA	PIK3R1	1353	
	451	E	NULL	No	No	0.42	20							
PAP 120	Endometrial	Pap brush	sample					chr10	89692818	SBS	T	PTEN	302	
	101	I	T	No	No	3.84	437							
PAP 120	Endometrial	Pap brush	sample					chr10	89720693	Indel				

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						TT					PTEN		844
	282	G	NULL	No	No	1.87	483						
PAP	131	Endometrial	Pap brush	sample		chr5	112175856	SBS	T				
						G					APC		4565
	1522	L	*	No	No	0.11	21						
PAP	131	Endometrial	Pap brush	sample		chr5	67589618	SBS	C				
						T					PIK3R1		1381
	461	R	*	No	No	5.21	399						
PAP	131	Endometrial	Pap brush	sample		chr5	67591116	Indel	TTATCC				
											PIK3R1		1709
	570	L	NULL	No	No	0.31	16						
PAP	132	Endometrial	Pap brush	sample		chr5	112175852	SBS	G				
						T					APC		4561
	1521	E	*	No	No	43.29	2057						
PAP	168	Ovarian	Pap brush	sample		chr17	7577536	SBS	T				
						C					TP53		745
	249	R	G	No	No	13.61	1900						
PAP	176	Endometrial	Pap brush	sample		chr5	112175957	Indel					
						A					APC		4666
	1556	T	NULL	No	No	0.57	20						
PAP	180	Endometrial	Pap brush	sample		chr5	67589609	SBS	G				
						T					PIK3R1		1372
	458	E	*	No	No	2.70	137						
PAP	202	Endometrial	Pap brush	sample		chr17	7577534	SBS	C				
						A					TP53		747
	249	R	S	No	No	2.34	182						
PAP	202	Endometrial	Pap brush	sample		chr17	7577565	SBS	T				
						C					TP53		716
	239	N	S	No	No	0.50	39						
PAP	202	Endometrial	Pap brush	sample		chr17	7579419	Indel					
						T					TP53		268
	90	S	NULL	No	No	0.24	28						
PAP	204	Endometrial	Pap brush	sample		chr17	7579419	Indel					
						T					TP53		268
	90	S	NULL	No	No	16.26	1400						
PAP	215	Endometrial	Pap brush	sample		chr17	7577538	SBS	C				
						A					TP53		743
	248	R	L	No	No	73.92	5722						
PAP	216	Endometrial	Pap brush	sample		chr5	67589623	Indel	ATATGA				
											PIK3R1		1386
	462	E	NULL	No	No	0.25	24						
PAP	219	Endometrial	Pap brush	sample		chr3	178952018	SBS	A				
						G					PIK3CA		3073
	1025	T	A	No	No	20.03	578						
PAP	224	Endometrial	Pap brush	sample		chr17	7577094	SBS	G				
						A					TP53		844
	282	R	W	No	No	4.88	470						
PAP	227	Endometrial	Pap brush	sample		chr17	7577568	SBS	C				

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                                    T                                       TP53    713
     238     C       Y       No      No      0.69    53
PAP 228     Endometrial     Pap brush sample     chr10   89720757     Indel
                                    G                                       PTEN    908
     303     I       NULL    No      No      15.89   1514
PAP 230     Ovarian         Pap brush sample     chr17   7579374      SBS     C
                                    G                                       TP53    313
     105     G       R       No      No      0.09    19
PAP 234     Endometrial     Pap brush sample     chr17   7577548      SBS     C
                                    A                                       TP53    733
     245     G       C       No      No      1.52    296
PAP 237     Endometrial     Pap brush sample     chr5    67589589     Indel
                                    TGA                                     PIK3R1  1352
     451     E       NULL    No      No      1.29    66
PAP 246     Endometrial     Pap brush sample     chr10   89717650     SBS     T
                                    G                                       PTEN    675
     225     Y       *       No      No      2.86    112
PAP 246     Endometrial     Pap brush sample     chr5    67589613     Indel   AAA
                                                                            PIK3R1  1376
     459     K       NULL    No      No      1.48    79
PAP 247     Endometrial     Pap brush sample     chr5    112176020    SBS     G
                                    T                                       APC     4729
     1577    E       *       No      No      1.43    68
PAP 254     Ovarian         Pap brush sample     chr9    21971117     Indel
GTCGGGTGAGAGTGGCGGGG (SEQ ID NO:750)
CDKN2A  241     81      P       NULL    No      No      8.25    67
PAP 255     Ovarian         Pap brush sample     chr17   7577102      SBS     C
                                    T                                       TP53    836
     279     G       E       No      No      1.18    243
PAP 255     Ovarian         Pap brush sample     chr5    67589590     Indel   ATA
                                                                            PIK3R1  1353
     451     E       NULL    No      No      0.18    8
PAP 255     Ovarian         Pap brush sample     chr5    67591116     Indel   TTATCC
                                                                            PIK3R1  1709
     570     L       NULL    No      No      0.05    6
PAP 262     Ovarian         Pap brush sample     chr17   7574004      Indel   G
                                                                            TP53    1023
     341     F       NULL    No      No      0.23    41
PAP 264     Ovarian         Pap brush sample     chr17   7578460      SBS     A
                                    T                                       TP53    470
     157     V       D       No      No      14.56   1565
PAP 266     Endometrial     Pap brush sample     chr5    67591121     Indel
                                    C                                       PIK3R1  1714
     572     Q       NULL    No      No      0.62    26
PAP 267     Endometrial     Pap brush sample     chr10   89653808     SBS     G
                                    T                                       PTEN    106
     36      G       *       No      No      29.21   678
PAP 267     Endometrial     Pap brush sample     chr10   89692930     SBS     T
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						G					PTEN		414
	138	Y	*	No	No	2.64	50						
PAP	267	Endometrial	Pap brush	sample		chr12	133250289	SBS	C				
						A					POLE		1231
	411	V	L	No	No	27.16	1216						
PAP	267	Endometrial	Pap brush	sample		chr17	7578212	SBS	G				
						A					TP53		637
	213	R	*	No	No	7.65	191						
PAP	267	Endometrial	Pap brush	sample		chr17	7578550	SBS	G				
						A					TP53		380
	127	S	F	No	No	6.45	147						
PAP	267	Endometrial	Pap brush	sample		chr17	7579312	SBS	C				
						T					TP53		375
	125	T	T	No	Yes	2.11	124						
PAP	267	Endometrial	Pap brush	sample		chr3	178952007	SBS	A				
						G					PIK3CA		3062
	1021	Y	C	No	No	27.59	226						
PAP	267	Endometrial	Pap brush	sample		chr3	41266097	SBS	G				
						A					CTNNB1		94
	32	D	N	No	No	6.08	223						
PAP	267	Endometrial	Pap brush	sample		chr3	41266098	SBS	A				
						G					CTNNB1		95
	32	D	G	No	No	0.41	15						
PAP	267	Endometrial	Pap brush	sample		chr3	41266124	SBS	A				
						G					CTNNB1		121
	41	T	A	No	No	3.25	119						
PAP	268	Endometrial	Pap brush	sample		chr17	7577580	SBS	T				
						C					TP53		701
	234	Y	C	No	No	3.25	499						
PAP	269	Endometrial	Pap brush	sample		chr17	7578275	SBS	G				
						A					TP53		574
	192	Q	*	No	No	6.00	824						
PAP	270	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				
						A					PIK3CA		263
	88	R	Q	No	No	6.87	1218						
PAP	270	Endometrial	Pap brush	sample		chr4	153247289	SBS	G				
						A					FBXW7		1513
	505	R	C	No	No	8.31	1254						
PAP	271	Endometrial	Pap brush	sample		chr5	67590457	SBS	G				
						T					PIK3R1		1519
	507	E	*	No	No	12.06	48						
PAP	273	Endometrial	Pap brush	sample		chr10	89624245	SBS	G				
						T					PTEN		19
	7	E	*	No	No	7.04	126						
PAP	273	Endometrial	Pap brush	sample		chr10	89653803	SBS	C				
						A					PTEN		101
	34	A	D	No	No	9.88	335						
PAP	273	Endometrial	Pap brush	sample		chr10	89720744	SBS	G				

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                                    T                                       PTEN    895
     299     E       *       No      No      3.33    597
PAP 273     Endometrial     Pap brush sample     chr12   133253184     SBS     G
                                    C                                       POLE    857
     286     P       R       No      No      11.95   340
PAP 273     Endometrial     Pap brush sample     chr17   7578212       SBS     G
                                    A                                       TP53    637
     213     R       *       No      No      3.74    105
PAP 273     Endometrial     Pap brush sample     chr17   7578263       SBS     G
                                    A                                       TP53    586
     196     R       *       No      No      3.99    234
PAP 273     Endometrial     Pap brush sample     chr3    178952085     SBS     A
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      11.65   433
PAP 273     Endometrial     Pap brush sample     chr5    112175105     Indel
                                    T                                       APC     3814
     1272    S       NULL    No      No      3.75    61
PAP 273     Endometrial     Pap brush sample     chr5    112175639     SBS     C
                                    T                                       APC     4348
     1450    R       *       No      No      3.64    139
PAP 274     Endometrial     Pap brush sample     chr5    112175190     Indel
ATACCCTGCAAATA (SEQ ID NO:751)                                                  APC
   3899       1300    N       NULL    No      No      12.93   1456
PAP 276     Endometrial     Pap brush sample     chr10   89717613      Indel   C
                                                                        PTEN    638
     213     P       NULL    No      No      39.06   407
PAP 276     Endometrial     Pap brush sample     chr3    178952085     SBS     A
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      16.57   395
PAP 429     Healthy ControPap brush sample     chr5    67589590      Indel   ATA
                                                                        PIK3R1  1353
     451     E       NULL    No      No      0.22    14
PAP 528     Ovarian         Pap brush sample     chr17   7579349       SBS     A
                                    G                                       TP53    338
     113     F       S       No      No      0.08    20
PAP 531     Ovarian         Pap brush sample     chr17   7579443       Indel   G
                                                                        TP53    244
     82      P       NULL    No      No      0.23    52
PAP 556     Endometrial     Pap brush sample     chr5    67591117      Indel
                                    T                                       PIK3R1  1710
     570     L       NULL    No      No      0.48    19
PAP 557     Endometrial     Pap brush sample     chr17   7577094       SBS     G
                                    A                                       TP53    844
     282     R       W       No      No      1.90    140
PAP 560     Endometrial     Pap brush sample     chr17   7577567       Indel
                                    A                                       TP53    714
     238     C       NULL    No      No      0.17    8
PAP 564     Endometrial     Pap brush sample     chr17   7577548       SBS     C
```

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						T				TP53	733	
	245	G	S	No	No	17.13	620					
PAP	569	Ovarian		Pap brush	sample	chr17	7577545	SBS	T			
						C				TP53	736	
	246	M	V	No	No	1.77	67					
PAP	574	Endometrial		Pap brush	sample	chr5	67589618	SBS	C			
						T				PIK3R1	1381	
	461	R	*	No	No	1.74	280					
PAP	576	Ovarian		Pap brush	sample	chr17	7579439	Indel	GC			
										TP53	248	
	83	A	NULL	No	No	0.06	12					
PAP	584	Endometrial		Pap brush	sample	chr5	67589609	Indel	GAA			
										PIK3R1	1372	
	458	E	NULL	No	No	16.92	2302					
PAP	587	Endometrial		Pap brush	sample	chr17	7577536	SBS	T			
						A				TP53	745	
	249	R	W	No	No	2.68	198					
PAP	587	Endometrial		Pap brush	sample	chr5	112175957	Indel				
						A				APC	4666	
	1556	T	NULL	No	No	1.36	359					
PAP	589	Endometrial		Pap brush	sample	chr17	7576851	SBS	A			
						G				TP53	0	
	0	NULL	NULL	1	No	3.30	84					
PAP	589	Endometrial		Pap brush	sample	chr17	7579369	SBS	G			
						C				TP53	318	
	106	S	R	No	No	2.33	485					
PAP	595	Endometrial		Pap brush	sample	chr17	7577533	Indel				
						ATGGG				TP53	748	
	250	P	NULL	No	No	4.31	52					
PAP	595	Endometrial		Pap brush	sample	chr17	7577538	SBS	C			
						T				TP53	743	
	248	R	Q	No	No	4.64	56					
PAP	604	Endometrial		Pap brush	sample	chr17	7577580	SBS	T			
						C				TP53	701	
	234	Y	C	No	No	0.40	39					
PAP	609	Endometrial		Pap brush	sample	chr3	178952018	SBS	A			
						G				PIK3CA	3073	
	1025	T	A	No	No	5.38	395					
PAP	617	Endometrial		Pap brush	sample	chr17	7577539	SBS	G			
						A				TP53	742	
	248	R	W	No	No	1.32	152					
PAP	617	Endometrial		Pap brush	sample	chr17	7578271	SBS	T			
						C				TP53	578	
	193	H	R	No	No	0.24	23					
PAP	619	Endometrial		Pap brush	sample	chr3	178952018	SBS	A			
						G				PIK3CA	3073	
	1025	T	A	No	No	6.41	152					
PAP	621	Endometrial		Pap brush	sample	chr5	67591120	Indel				

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						ACCAGACCTTATC (SEQ ID NO:777)					PIK3R1	1713	
	571	I	NULL	No	No	1.66	43						
PAP	625	Endometrial	Pap brush	sample		chr10	89711983	SBS	G				
						T					PTEN	601	
	201	E	*	No	No	1.97	365						
PAP	632	Endometrial	Pap brush	sample		chr17	7577094	SBS	G				
						A					TP53	844	
	282	R	W	No	No	2.14	400						
PAP	632	Endometrial	Pap brush	sample		chr3	178952018	SBS	A				
						T					PIK3CA	3073	
	1025	T	S	No	No	2.26	214						
PAP	633	Endometrial	Pap brush	sample		chr5	67589617	Indel	TCG				
											PIK3R1	1380	
	460	S	NULL	No	No	1.17	116						
PAP	637	Endometrial	Tao brush	sample		chr17	7577559	SBS	G				
						T					TP53	722	
	241	S	Y	No	No	3.47	76						
PAP	638	Endometrial	Pap brush	sample		chr17	7577556	SBS	C				
						A					TP53	725	
	242	C	F	No	No	3.67	43						
PAP	638	Endometrial	Tao brush	sample		chr17	7577556	SBS	C				
						A					TP53	725	
	242	C	F	No	No	30.79	315						
PAP	646	Endometrial	Pap brush	sample		chr10	89692900	SBS	G				
						T					PTEN	384	
	128	K	N	No	No	1.02	37						
PAP	648	Endometrial	Pap brush	sample		chr17	7577538	SBS	C				
						T					TP53	743	
	248	R	Q	No	No	24.64	924						
PAP	650	Endometrial	Pap brush	sample		chr5	112175957	Indel					
						A					APC	4666	
	1556	T	NULL	No	No	9.68	1188						
PAP	654	Endometrial	Pap brush	sample		chr17	7577548	SBS	C				
						T					TP53	733	
	245	G	S	No	No	2.41	469						
PAP	654	Endometrial	Pap brush	sample		chr4	153247373	SBS	C				
						T					FBXW7	1429	
	477	G	S	No	No	2.33	93						
PAP	654	Endometrial	Pap brush	sample		chr5	112174424	SBS	C				
						T					APC	3133	
	1045	Q	*	No	No	1.79	210						
PAP	654	Endometrial	Pap brush	sample		chr5	112175945	SBS	G				
						T					APC	4654	
	1552	E	*	No	No	2.05	123						
PAP	663	Endometrial	Pap brush	sample		chr3	178952018	SBS	A				
						G					PIK3CA	3073	
	1025	T	A	No	No	1.13	26						
PAP	663	Endometrial	Pap brush	sample		chr5	112176020	SBS	G				

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                                    T                                   APC     4729
     1577    E       *       No      No      6.78    94
PAP 663     Endometrial   Pap brush sample     chr5    67588951      SBS     C
                                    T                                   PIK3R1  1042
     348     R       *       No      No      12.80   219
PAP 667     Endometrial   Pap brush sample     chr10   89690819      Indel   T
                                                                        PTEN    226
     76      Y       NULL    No      No      49.33   962
PAP 669     Endometrial   Pap brush sample     chr17   7577556       SBS     C
                                    G                                   TP53    725
     242     C       S       No      No      0.37    54
PAP 671     Endometrial   Pap brush sample     chr10   89717650      SBS     T
                                    G                                   PTEN    675
     225     Y       *       No      No      0.24    9
PAP 679     Endometrial   Pap brush sample     chr17   7577089       Indel   GCGCCGGT
                                                                        TP53    849
     283     R       NULL    No      No      1.52    36
PAP 681     Endometrial   Pap brush sample     chr5    67589590      Indel   ATA
                                                                        PIK3R1  1353
     451     E       NULL    No      No      2.40    150
PAP 684     Endometrial   Pap brush sample     chr5    67589607      SBS     A
                                    C                                   PIK3R1  1370
     457     Q       P       No      No      0.18    7
PAP 688     Endometrial   Pap brush sample     chr10   89720734      Indel   AT
                                                                        PTEN    885
     295     L       NULL    No      No      1.95    174
PAP 688     Endometrial   Tao brush sample     chr10   89720734      Indel   AT
                                                                        PTEN    885
     295     L       NULL    No      No      10.47   714
PAP 689     Endometrial   Pap brush sample     chr17   7577538       SBS     C
                                    T                                   TP53    743
     248     R       Q       No      No      10.90   326
PAP 689     Endometrial   Tao brush sample     chr17   7577538       SBS     C
                                    T                                   TP53    743
     248     R       Q       No      No      61.68   3016
PAP 691     Endometrial   Pap brush sample     chr3    178952019     SBS     C
                                    A                                   PIK3CA  3074
     1025    T       N       No      No      5.62    337
PAP 691     Endometrial   Tao brush sample     chr3    178952019     SBS     C
                                    A                                   PIK3CA  3074
     1025    T       N       No      No      21.16   1086
PAP 697     Endometrial   Pap brush sample     chr5    112175840     SBS     C
                                    T                                   APC     4549
     1517    Q       *       No      No      8.72    49
PAP 699     Endometrial   Pap brush sample     chr10   89690819      Indel   TAT
                                                                        PTEN    226
     76      Y       NULL    No      No      41.34   592
PAP 699     Endometrial   Pap brush sample     chr5    112175957     Indel
```

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A APC 4666
1556 T NULL No No 28.44 1521
PAP 705 Ovarian Pap brush sample chr17 7577538 SBS C
T TP53 743
248 R Q No No 0.83 180
PAP 711 Ovarian Pap brush sample chr5 67589604 Indel
AACTCAGTT PIK3R1 1367
456 F NULL No No 0.46 19
PAP 719 Endometrial Pap brush sample chr10 89720716 Indel A
PTEN 867
289 K NULL No No 0.58 35
PAP 726 Endometrial Pap brush sample chr5 67589628 Indel ATA
PIK3R1 1391
464 D NULL No No 2.32 358
PAP 726 Endometrial Pap brush sample chr5 67589629 Indel
TAGATTATATGA (SEQ ID NO:752)
PIK3R1 1392 464 D NULL No No 0.11 17
PAP 730 Endometrial Pap brush sample chr10 89690819 Indel TAT
PTEN 226
76 Y NULL No No 1.41 29
PAP 730 Endometrial Pap brush sample chr10 89720749 Indel C
PTEN 900
300 I NULL No No 11.21 1081
PAP 730 Endometrial Pap brush sample chr5 112174742 Indel GAA
APC 3451
1151 E NULL No No 10.97 2039
PAP 730 Endometrial Pap brush sample chr5 67589633 Indel
ATGATAGAT PIK3R1 1396
466 L NULL No No 20.63 3314
PAP 744 Endometrial Pap brush sample chr17 7572968 Indel T
TP53 1141
381 K NULL No No 1.77 347
PAP 754 Endometrial Pap brush sample chr17 7577579 SBS G
T TP53 702
234 Y * No No 0.83 72
PAP 768 Endometrial Pap brush sample chr17 7577094 SBS G
A TP53 844
282 R W No No 1.07 92
PAP 775 Endometrial Pap brush sample chr5 67589590 Indel ATATAA
PIK3R1 1353
451 E NULL No No 3.00 339
PAP 790 Endometrial Pap brush sample chr17 7577534 SBS C
A TP53 747
249 R S No No 9.16 272
PAP 804 Endometrial Pap brush sample chr17 7579366 SBS G
T TP53 321
107 Y * No No 0.68 38
PAP 804 Endometrial Pap brush sample chr5 112173893 SBS G

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						T					APC		2602
	868	E	*		No	No	11.11	1014					
PAP	813	Endometrial	Pap brush		sample	chr10	89717650	SBS	T				
						G					PTEN		675
	225	Y	*		No	No	0.82	49					
PAP	813	Endometrial	Pap brush		sample	chr5	67591116	SBS	T				
						C					PIK3R1		1709
	570	L	P		No	No	1.31	99					
PAP	829	Endometrial	Pap brush		sample	chr5	67589630	Indel	AGAT				
											PIK3R1		1393
	465	R	NULL		No	No	0.17	12					
PAP	831	Endometrial	Pap brush		sample	chr17	7577538	SBS	C				
						T					TP53		743
	248	R	Q		No	No	36.99	2189					
PAP	831	Endometrial	Tao brush		sample	chr17	7577538	SBS	C				
						T					TP53		743
	248	R	Q		No	No	21.27	1191					
PAP	835	Endometrial	Pap brush		sample	chr17	7577539	SBS	G				
						A					TP53		742
	248	R	W		No	No	73.09	3313					
PAP	835	Endometrial	Tao brush		sample	chr17	7577539	SBS	G				
						A					TP53		742
	248	R	W		No	No	72.63	2563					
PAP	836	Endometrial	Tao brush		sample	chr17	7577547	SBS	C				
						T					TP53		734
	245	G	D		No	No	4.20	328					
PAP	841	Endometrial	Pap brush		sample	chr17	7579358	SBS	C				
						A					TP53		329
	110	R	L		No	No	10.00	159					
PAP	841	Endometrial	Tao brush		sample	chr17	7579358	SBS	C				
						A					TP53		329
	110	R	L		No	No	35.42	8229					
PAP	850	Endometrial	Pap brush		sample	chr17	7579469	SBS	A				
						G					TP53		218
	73	V	A		No	No	46.51	1080					
PAP	850	Endometrial	Tao brush		sample	chr17	7579469	SBS	A				
						G					TP53		218
	73	V	A		No	No	31.13	2131					
PAP	851	Endometrial	Tao brush		sample	chr17	7577538	SBS	C				
						T					TP53		743
	248	R	Q		No	No	35.62	1900					
PAP	860	Endometrial	Pap brush		sample	chr17	7577538	SBS	C				
						T					TP53		743
	248	R	Q		No	No	1.91	310					
PAP	879	Endometrial	Pap brush		sample	chr5	67589607	SBS	A				
						C					PIK3R1		1370
	457	Q	P		No	No	0.12	13					
PAP	884	Endometrial	Pap brush		sample	chr17	7577094	SBS	G				

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						A					TP53	844	
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PAP	884	Endometrial	Tao	brush	sample	chr17	7577094	SBS	G				
						A					TP53	844	
	282	R	W	No	No	22.28	1727						
PAP	884	Endometrial	Tao	brush	sample	chr17	7577548	SBS	C				
						T					TP53	733	
	245	G	S	No	No	5.91	357						
PAP	901	Endometrial	Tao	brush	sample	chr17	7579550	Indel	G				
											TP53	137	
	46	S	NULL	No	No	0.56	38						
PAP	904	Endometrial	Pap	brush	sample	chr3	178952018	SBS	A				
						G					PIK3CA	3073	
	1025	T	A	No	No	17.38	380						
PAP	904	Endometrial	Tao	brush	sample	chr3	178952018	SBS	A				
						G					PIK3CA	3073	
	1025	T	A	No	No	36.93	942						
PAP	910	Endometrial	Pap	brush	sample	chr10	89692847	SBS	T				
						C					PTEN	331	
	111	W	R	No	No	1.74	98						
PAP	910	Endometrial	Tao	brush	sample	chr10	89692847	SBS	T				
						C					PTEN	331	
	111	W	R	No	No	29.71	773						
PAP	922	Endometrial	Pap	brush	sample	chr5	67589613	Indel	AAA				
											PIK3R1	1376	
	459	K	NULL	No	No	2.16	64						
PAP	922	Endometrial	Tao	brush	sample	chr5	67589613	Indel	AAA				
											PIK3R1	1376	
	459	K	NULL	No	No	23.50	553						
PAP	925	Ovarian	Tao	brush	sample	chr17	7577548	SBS	C				
						A					TP53	733	
	245	G	C	No	No	2.30	218						
PAP	931	Endometrial	Pap	brush	sample	chr10	89711973	Indel	G				
											PTEN	591	
	197	K	NULL	No	No	3.58	86						
PAP	931	Endometrial	Tao	brush	sample	chr10	89711973	Indel	G				
											PTEN	591	
	197	K	NULL	No	No	23.35	1939						
PAP	993	Ovarian	Pap	brush	sample	chr17	7577556	SBS	C				
						T					TP53	725	
	242	C	Y	No	No	1.33	108						
PAP	993	Ovarian	Pap	brush	sample	chr5	67588968	Indel					
						G					PIK3R1	1059	
	353	G	NULL	No	No	0.55	51						
PAP	993	Ovarian	Tao	brush	sample	chr17	7577556	SBS	C				
						T					TP53	725	
	242	C	Y	No	No	2.82	423						
PAP	995	Endometrial	Pap	brush	sample	chr17	7577099	SBS	C				

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						G					TP53	839	
	280	R	T	No	No	14.92	1777						
PAP 995	Endometrial	Tao brush		sample		chr17	7577099	SBS	C				
						G					TP53	839	
	280	R	T	No	No	14.92	1340						
PAP 998	Endometrial	Tao brush		sample		chr17	7577552	SBS	C				
						G					TP53	729	
	243	M	I	No	No	0.32	45						
PAPA 1001	Endometrial	Tao brush		sample		chr17	7577565	Indel					
						GGT					TP53	716	
	239	N	NULL	No	No	6.40	348						
PAPA 1011	Endometrial	Tao brush		sample		chr5	112173917	SBS	C				
						T					APC	2626	
	876	R	*	No	No	6.58	327						
PAPA 1013	Endometrial	Pap brush		sample		chr17	7579358	SBS	C				
						G					TP53	329	
	110	R	P	No	No	0.29	51						
PAPA 1013	Endometrial	Tao brush		sample		chr17	7579358	SBS	C				
						G					TP53	329	
	110	R	P	No	No	0.30	27						
PAPA 1035	Endometrial	Pap brush		sample		chr5	67589607	Indel					
						GTTTCA					PIK3R1	1370	
	457	Q	NULL	No	No	7.14	285						
PAPA 1043	Endometrial	Pap brush		sample		chr17	7577090	SBS	C				
						T					TP53	848	
	283	R	H	No	No	44.60	2220						
PAPA 1048	Endometrial	Pap brush		sample		chr17	7577094	SBS	G				
						A					TP53	844	
	282	R	W	No	No	7.97	654						
PAPA 1059	Endometrial	Pap brush		sample		chr10	89692839	SBS	T				
						G					PTEN	323	
	108	L	R	No	No	10.59	656						
PAPA 1069	Endometrial	Pap brush		sample		chr3	178952018	SBS	A				
						G					PIK3CA	3073	
	1025	T	A	No	No	2.16	169						
PAPA 1081	Endometrial	Pap brush		sample		chr17	7579418	SBS	G				
						A					TP53	269	
	90	S	F	No	No	0.83	131						
PAPA 1081	Endometrial	Pap brush		sample		chr5	67589618	SBS	C				
						T					PIK3R1	1381	
	461	R	*	No	No	21.10	1375						
PAPA 1094	Ovarian	Pap brush		sample		chr5	67589590	Indel	ATA				
											PIK3R1	1353	
	451	E	NULL	No	No	0.17	9						
PAPA 1113	Ovarian	Pap brush		sample		chr17	7577568	SBS	C				
						G					TP53	713	
	238	C	S	No	No	1.66	235						
PAPA 1126	Endometrial	Pap brush		sample		chr10	89692904	SBS	C				

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                                    G                                   PTEN    388
     130     R       G       No      No      0.21    15
PAPA 1126  Endometrial   Tao brush sample     chr10   89692904     SBS     C
                                    G                                   PTEN    388
     130     R       G       No      No      26.91   3214
PAPA 1126  Endometrial   Tao brush sample     chr3    41266113     SBS     C
                                    T                                   CTNNB1  110
     37      S       F       No      No      22.67   836
PAPA 1128  Endometrial   Tao brush sample     chr10   89720803     Indel
                                    T                                   PTEN    954
     318     L       NULL    No      No      39.07   586
PAPA 1128  Endometrial   Tao brush sample     chr1    115256536    SBS     C
                                    T                                   NRAS    175
     59      A       T       No      No      18.11   2107
PAPA 1128  Endometrial   Tao brush sample     chr3    178936082    SBS     G
                                    C                                   PIK3CA  1624
     542     E       Q       No      No      17.18   376
PAPA 1128  Endometrial   Tao brush sample     chr3    41266104     SBS     G
                                    A                                   CTNNB1  101
     34      G       E       No      No      6.12    193
PAPA 1129  Endometrial   Tao brush sample     chr17   7577556      SBS     C
                                    T                                   TP53    725
     242     C       Y       No      No      14.89   2919
PAPA 1130  Endometrial   Pap brush sample     chr10   89624245     SBS     G
                                    T                                   PTEN    19
     7       E       *       No      No      0.05    12
PAPA 1130  Endometrial   Pap brush sample     chr10   89685281     SBS     C
                                    A                                   PTEN    176
     59      S       *       No      No      8.20    1881
PAPA 1130  Endometrial   Pap brush sample     chr10   89720870     SBS     T
                                    G                                   PTEN    1021
     341     F       V       No      No      10.66   114
PAPA 1130  Endometrial   Pap brush sample     chr12   133253184    SBS     G
                                    C                                   POLE    857
     286     P       R       No      No      7.56    171
PAPA 1130  Endometrial   Pap brush sample     chr5    112175216    SBS     G
                                    T                                   APC     3925
     1309    E       *       No      No      8.54    677
PAPA 1130  Endometrial   Pap brush sample     chr5    67588951     SBS     C
                                    T                                   PIK3R1  1042
     348     R       *       No      No      7.54    318
PAPA 1130  Endometrial   Pap brush sample     chr5    67589595     Indel   ACA
                                                                        PIK3R1  1358
     453     N       NULL    No      No      0.12    9
PAPA 1130  Endometrial   Pap brush sample     chr5    67589629     Indel
TAGATTATATGA (SEQ ID NO:753)
PIK3R1  1392       464     D       NULL    No      No      0.97    76
PAPA 1130  Endometrial   Tao brush sample     chr10   89685281     SBS     C
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A PTEN 176
59 S * No No 37.81 11182
PAPA 1130 Endometrial Tao brush sample chr10 89720870 SBS T
G PTEN 1021
341 F V No No 46.86 812
PAPA 1130 Endometrial Tao brush sample chr12 133253184 SBS G
C POLE 857
286 P R No No 40.16 1026
PAPA 1130 Endometrial Tao brush sample chr5 112175216 SBS G
T APC 3925
1309 E * No No 38.89 5084
PAPA 1130 Endometrial Tao brush sample chr5 67588951 SBS C
T PIK3R1 1042
348 R * No No 38.75 2023
PAPA 1131 Endometrial Pap brush sample chr10 123279677 SBS G
C FGFR2 755
252 S W No No 0.82 100
PAPA 1131 Endometrial Pap brush sample chr10 89725042 SBS A
G PTEN 0
0 NULL NULL 1 No 4.92 156
PAPA 1131 Endometrial Pap brush sample chr3 41266101 SBS C
A CTNNB1 98
33 S Y No No 1.89 78
PAPA 1131 Endometrial Pap brush sample chr5 67591106 SBS A
G PIK3R1 1699
567 K E No No 2.13 132
PAPA 1131 Endometrial Tao brush sample chr10 123279677 SBS G
C FGFR2 755
252 S W No No 11.53 1186
PAPA 1131 Endometrial Tao brush sample chr10 89725042 SBS A
G PTEN 0
0 NULL NULL 1 No 64.10 2537
PAPA 1131 Endometrial Tao brush sample chr3 41266101 SBS C
A CTNNB1 98
33 S Y No No 30.45 1382
PAPA 1131 Endometrial Tao brush sample chr5 67591106 SBS A
G PIK3R1 1699
567 K E No No 30.40 2938
PAPA 1132 Endometrial Pap brush sample chr10 89624296 SBS G
C PTEN 70
24 D H No No 0.54 86
PAPA 1132 Endometrial Pap brush sample chr3 41266137 SBS C
T CTNNB1 134
45 S F No No 0.23 5
PAPA 1132 Endometrial Pap brush sample chr5 67591092 Indel
GTATGAACAGCATTAAAC (SEQ ID NO:754)
PIK3R1 1685 562 R NULL No No 0.19 11
PAPA 1132 Endometrial Tao brush sample chr10 123279677 SBS G

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```
                                    C                                   FGFR2   755
     252     S       W       No      No      7.01    570
PAPA 1132  Endometrial   Tao brush sample     chr10   89624296     SBS     G
                                    C                                   PTEN    70
     24      D       H       No      No      42.81   10046
PAPA 1132  Endometrial   Tao brush sample     chr17   7578406      SBS     C
                                    T                                   TP53    524
     175     R       H       No      No      3.21    201
PAPA 1132  Endometrial   Tao brush sample     chr5    67591092     Indel
GTATGAACAGCATTAAAC (SEQ ID NO:755)
PIK3R1  1685       562     R       NULL    No      No      26.45   1141
PAPA 1133  Endometrial   Pap brush sample     chr10   89712017     SBS     G
                                    C                                   PTEN    0
     0       NULL    NULL    1       No      0.41    31
PAPA 1133  Endometrial   Pap brush sample     chr10   89717775     Indel   A
                                                                        PTEN    800
     267     K       NULL    No      No      1.32    106
PAPA 1133  Endometrial   Pap brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      1.32    68
PAPA 1133  Endometrial   Pap brush sample     chr5    67591106     SBS     A
                                    G                                   PIK3R1  1699
     567     K       E       No      No      0.60    39
PAPA 1133  Endometrial   Tao brush sample     chr10   89712017     SBS     G
                                    C                                   PTEN    0
     0       NULL    NULL    1       No      6.60    351
PAPA 1133  Endometrial   Tao brush sample     chr10   89717775     Indel   A
                                                                        PTEN    800
     267     K       NULL    No      No      19.11   1244
PAPA 1133  Endometrial   Tao brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      9.01    363
PAPA 1133  Endometrial   Tao brush sample     chr5    67591106     SBS     A
                                    G                                   PIK3R1  1699
     567     K       E       No      No      11.58   696
PAPA 1134  Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    T                                   KRAS    35
     12      G       D       No      No      5.34    465
PAPA 1134  Endometrial   Pap brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      7.56    296
PAPA 1134  Endometrial   Pap brush sample     chr3    178936091    SBS     G
                                    A                                   PIK3CA  1633
     545     E       K       No      No      5.24    101
PAPA 1134  Endometrial   Pap brush sample     chr3    41266125     SBS     C
                                    T                                   CTNNB1  122
     41      T       I       No      No      0.93    29
PAPA 1134  Endometrial   Tao brush sample     chr12   25398284     SBS     C
```

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						T					KRAS	35	
	12	G	D	No	No	30.32	2699						
PAPA	1134	Endometrial	Tao	brush	sample	chr17	56435167	Indel	C				
											RNF43	1970	
	657	R	NULL	No	No	29.06	1162						
PAPA	1134	Endometrial	Tao	brush	sample	chr3	178936091	SBS	G				
						A					PIK3CA	1633	
	545	E	K	No	No	32.26	590						
PAPA	1134	Endometrial	Tao	brush	sample	chr9	21970966	SBS	C				
						T					CDKN2A	392	
	131	R	H	No	No	9.12	461						
PAPA	1135	Endometrial	Pap	brush	sample	chr17	7577120	SBS	C				
						T					TP53	818	
	273	R	H	No	No	4.18	467						
PAPA	1135	Endometrial	Pap	brush	sample	chr17	7577556	SBS	C				
						T					TP53	725	
	242	C	Y	No	No	2.23	376						
PAPA	1135	Endometrial	Tao	brush	sample	chr17	7577120	SBS	C				
						T					TP53	818	
	273	R	H	No	No	26.76	2342						
PAPA	1135	Endometrial	Tao	brush	sample	chr17	7577556	SBS	C				
						T					TP53	725	
	242	C	Y	No	No	16.04	1968						
PAPA	1135	Endometrial	Tao	brush	sample	chr17	7577565	SBS	T				
						C					TP53	716	
	239	N	S	No	No	2.10	346						
PAPA	1136	Ovarian	Pap	brush	sample	chr10	123279677	SBS	G				
						C					FGFR2	755	
	252	S	W	No	No	0.22	29						
PAPA	1136	Ovarian	Pap	brush	sample	chr3	178952077	SBS	T				
						G					PIK3CA	3132	
	1044	N	K	No	No	0.18	15						
PAPA	1136	Ovarian	Pap	brush	sample	chr5	67589613	Indel	AAA				
											PIK3R1	1376	
	459	K	NULL	No	No	0.17	21						
PAPA	1136	Ovarian	Pap	brush	sample	chr5	67591134	Indel	C				
											PIK3R1	1727	
	576	T	NULL	No	No	0.45	31						
PAPA	1137	Endometrial	Pap	brush	sample	chr10	89624245	SBS	G				
						T					PTEN	19	
	7	E	*	No	No	9.63	1679						
PAPA	1137	Endometrial	Pap	brush	sample	chr10	89692905	SBS	G				
						A					PTEN	389	
	130	R	Q	No	No	3.99	262						
PAPA	1137	Endometrial	Pap	brush	sample	chr12	133250289	SBS	C				
						A					POLE	1231	
	411	V	L	No	No	12.28	700						
PAPA	1137	Endometrial	Pap	brush	sample	chr4	153247367	SBS	G				

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						A						FBXW7	1435	
	479	R	*	No	No	9.07	194							
PAPA	1137	Endometrial	Pap brush	sample		chr5	112176051	SBS	C					
						A						APC	4760	
	1587	S	*	No	No	11.06	346							
PAPA	1137	Endometrial	Tao brush	sample		chr10	89624245	SBS	G					
						T						PTEN	19	
	7	E	*	No	No	33.26	8803							
PAPA	1137	Endometrial	Tao brush	sample		chr10	89692905	SBS	G					
						A						PTEN	389	
	130	R	Q	No	No	15.98	1226							
PAPA	1137	Endometrial	Tao brush	sample		chr12	133250289	SBS	C					
						A						POLE	1231	
	411	V	L	No	No	26.72	1178							
PAPA	1137	Endometrial	Tao brush	sample		chr4	153247367	SBS	G					
						A						FBXW7	1435	
	479	R	*	No	No	28.42	661							
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						A						APC	4760	
	1587	S	*	No	No	26.86	896							
PAPA	1140	Endometrial	Pap brush	sample		chr10	123247516	SBS	T					
						C						FGFR2	1975	
	659	K	E	No	No	10.89	823							
PAPA	1140	Endometrial	Pap brush	sample		chr10	123258034	SBS	A					
						T						FGFR2	1647	
	549	N	K	No	No	15.06	481							
PAPA	1140	Endometrial	Pap brush	sample		chr10	89624285	SBS	G					
						A						PTEN	59	
	20	G	E	No	No	0.07	18							
PAPA	1140	Endometrial	Pap brush	sample		chr10	89717695	SBS	C					
						A						PTEN	720	
	240	Y	*	No	No	37.17	11022							
PAPA	1140	Endometrial	Pap brush	sample		chr17	7577121	SBS	G					
						A						TP53	817	
	273	R	C	No	No	4.20	342							
PAPA	1140	Endometrial	Pap brush	sample		chr17	7578500	SBS	G					
						A						TP53	430	
	144	Q	*	No	No	1.63	112							
PAPA	1140	Endometrial	Tao brush	sample		chr10	89717695	SBS	C					
						A						PTEN	720	
	240	Y	*	No	No	34.63	7142							
PAPA	1140	Endometrial	Tao brush	sample		chr17	7577121	SBS	G					
						A						TP53	817	
	273	R	C	No	No	2.27	220							
PAPA	1140	Endometrial	Tao brush	sample		chr17	7577551	SBS	C					
						A						TP53	730	
	244	G	C	No	No	24.42	3007							
PAPA	1141	Endometrial	Pap brush	sample		chr17	7574007	Indel						

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TTCC TP53 1020
340 M NULL No No 76.40 4650
PAPA 1141 Endometrial Tao brush sample chr17 7574007 Indel
TTCC TP53 1020
340 M NULL No No 59.39 1952
PAPA 1142 Endometrial Pap brush sample chr3 178952085 SBS A
G PIK3CA 3140
1047 H R No No 4.21 489
PAPA 1142 Endometrial Pap brush sample chr3 41266098 SBS A
G CTNNB1 95
32 D G No No 3.33 242
PAPA 1142 Endometrial Tao brush sample chr3 178952085 SBS A
G PIK3CA 3140
1047 H R No No 10.39 927
PAPA 1142 Endometrial Tao brush sample chr3 41266098 SBS A
G CTNNB1 95
32 D G No No 7.84 308
PAPA 1143 Endometrial Pap brush sample chr10 89692904 SBS C
G PTEN 388
130 R G No No 0.69 95
PAPA 1143 Endometrial Pap brush sample chr10 89692905 SBS G
T PTEN 389
130 R L No No 0.39 54
PAPA 1143 Endometrial Pap brush sample chr5 67591067 Indel
GCTGAGTATCGAGAAATTGAC (SEQ ID NO:756)
PIK3R1 1660 554 A NULL No No 0.24 25
PAPA 1143 Endometrial Tao brush sample chr10 89692904 SBS C
G PTEN 388
130 R G No No 14.02 1038
PAPA 1143 Endometrial Tao brush sample chr10 89692905 SBS G
T PTEN 389
130 R L No No 7.14 529
PAPA 1143 Endometrial Tao brush sample chr12 25398284 SBS C
T KRAS 35
12 G D No No 22.09 2200
PAPA 1143 Endometrial Tao brush sample chr3 178952074 SBS G
T PIK3CA 3129
1043 M I No No 19.17 1790
PAPA 1143 Endometrial Tao brush sample chr5 67591067 Indel
GCTGAGTATCGAGAAATTGAC (SEQ ID NO:757)
PIK3R1 1660 554 A NULL No No 12.89 1004
PAPA 1145 Endometrial Pap brush sample chr17 7577565 SBS T
C TP53 716
239 N S No No 2.39 299
PAPA 1145 Endometrial Tao brush sample chr12 133253184 SBS G
C POLE 857
286 P R No No 25.69 552
PAPA 1145 Endometrial Tao brush sample chr17 7577064 SBS T

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						G					TP53		874
	292	K	Q	No	No	0.55	46						
PAPA	1145	Endometrial	Tao	brush	sample	chr17	7577565	SBS	T				
						C					TP53		716
	239	N	S	No	No	24.65	3384						
PAPA	1145	Endometrial	Tao	brush	sample	chr17	7578212	SBS	G				
						A					TP53		637
	213	R	*	No	No	22.14	636						
PAPA	1145	Endometrial	Tao	brush	sample	chr19	52715982	SBS	C				
						T					PPP2R1A		547
	183	R	W	No	No	27.09	1255						
PAPA	1145	Endometrial	Tao	brush	sample	chr3	178952074	SBS	G				
						T					PIK3CA		3129
	1043	M	I	No	No	12.17	1045						
PAPA	1146	Endometrial	Tao	brush	sample	chr10	89717615	SBS	C				
						T					PTEN		640
	214	Q	*	No	No	11.22	226						
PAPA	1146	Endometrial	Tao	brush	sample	chr12	25398284	SBS	C				
						T					KRAS		35
	12	G	D	No	No	14.60	1827						
PAPA	1146	Endometrial	Tao	brush	sample	chr3	178952072	SBS	A				
						G					PIK3CA		3127
	1043	M	V	No	No	8.67	878						
PAPA	1147	Endometrial	Pap	brush	sample	chr10	123247516	SBS	T				
						C					FGFR2		1975
	659	K	E	No	No	0.42	27						
PAPA	1147	Endometrial	Pap	brush	sample	chr10	89692905	SBS	G				
						A					PTEN		389
	130	R	Q	No	No	1.28	121						
PAPA	1147	Endometrial	Pap	brush	sample	chr10	89692935	SBS	T				
						G					PTEN		419
	140	L	*	No	No	1.06	101						
PAPA	1147	Endometrial	Pap	brush	sample	chr12	133250289	SBS	C				
						A					POLE		1231
	411	V	L	No	No	2.79	267						
PAPA	1147	Endometrial	Pap	brush	sample	chr3	178952007	SBS	A				
						G					PIK3CA		3062
	1021	Y	C	No	No	3.74	50						
PAPA	1147	Endometrial	Pap	brush	sample	chr3	41266097	SBS	G				
						A					CTNNB1		94
	32	D	N	No	No	0.31	15						
PAPA	1147	Endometrial	Pap	brush	sample	chr3	41266098	SBS	A				
						C					CTNNB1		95
	32	D	A	No	No	0.16	8						
PAPA	1147	Endometrial	Pap	brush	sample	chr3	41266113	SBS	C				
						T					CTNNB1		110
	37	S	F	No	No	0.49	24						
PAPA	1147	Endometrial	Pap	brush	sample	chr4	153249385	SBS	G				

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						A					FBXW7	1393	
	465	R	C	No	No	2.22	149						
PAPA	1147	Endometrial	Tao	brush	sample	chr10	123247516	SBS	T				
						C					FGFR2	1975	
	659	K	E	No	No	26.03	1780						
PAPA	1147	Endometrial	Tao	brush	sample	chr10	89692905	SBS	G				
						A					PTEN	389	
	130	R	Q	No	No	15.40	1332						
PAPA	1147	Endometrial	Tao	brush	sample	chr10	89693007	Indel					
						A					PTEN	491	
	164	K	NULL	No	No	16.48	609						
PAPA	1147	Endometrial	Tao	brush	sample	chr12	133250289	SBS	C				
						A					POLE	1231	
	411	V	L	No	No	24.74	2194						
PAPA	1147	Endometrial	Tao	brush	sample	chr3	178952007	SBS	A				
						G					PIK3CA	3062	
	1021	Y	C	No	No	24.27	281						
PAPA	1148	Endometrial	Pap	brush	sample	chr10	89692839	SBS	T				
						G					PTEN	323	
	108	L	R	No	No	62.86	4865						
PAPA	1148	Endometrial	Pap	brush	sample	chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	29.35	3059						
PAPA	1148	Endometrial	Pap	brush	sample	chr17	7577538	SBS	C				
						T					TP53	743	
	248	R	Q	No	No	9.00	1538						
PAPA	1148	Endometrial	Pap	brush	sample	chr3	41266124	SBS	A				
						G					CTNNB1	121	
	41	T	A	No	No	40.95	1882						
PAPA	1148	Endometrial	Tao	brush	sample	chr10	89692839	SBS	T				
						G					PTEN	323	
	108	L	R	No	No	75.36	5762						
PAPA	1148	Endometrial	Tao	brush	sample	chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	33.00	3198						
PAPA	1148	Endometrial	Tao	brush	sample	chr17	7577538	SBS	C				
						T					TP53	743	
	248	R	Q	No	No	1.24	256						
PAPA	1148	Endometrial	Tao	brush	sample	chr3	41266124	SBS	A				
						G					CTNNB1	121	
	41	T	A	No	No	43.24	1806						
PAPA	1149	Endometrial	Pap	brush	sample	chr10	123258034	SBS	A				
						T					FGFR2	1647	
	549	N	K	No	No	24.43	713						
PAPA	1149	Endometrial	Pap	brush	sample	chr14	105246551	SBS	C				
						T					AKT1	49	
	17	E	K	No	No	44.41	2856						
PAPA	1149	Endometrial	Tao	brush	sample	chr14	105246551	SBS	C				

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						T					AKT1		49
	17	E	K		No	No	5.30	324					
PAPA	1150	Endometrial		Pap brush		sample	chr17	7577120	SBS	C			
						T					TP53		818
	273	R	H		No	No	3.89	294					
PAPA	1150	Endometrial		Tao brush		sample	chr17	7577120	SBS	C			
						T					TP53		818
	273	R	H		No	No	61.75	5936					
PAPA	1150	Endometrial		Tao brush		sample	chr17	7578541	SBS	A			
						C					TP53		389
	130	L	R		No	No	0.11	8					
PAPA	1150	Endometrial		Tao brush		sample	chr19	52716323	SBS	C			
						T					PPP2R1A		767
	256	S	F		No	No	52.82	7492					
PAPA	1150	Endometrial		Tao brush		sample	chr5	67590490	SBS	G			
						T					PIK3R1		1552
	518	E	*		No	No	8.96	1348					
PAPA	1152	Endometrial		Pap brush		sample	chr5	112175957	Indel				
						A					APC		4666
	1556	T	NULL		No	No	0.36	59					
PAPA	1152	Endometrial		Tao brush		sample	chr5	112175957	Indel				
						A					APC		4666
	1556	T	NULL		No	No	37.41	709					
PAPA	1154	Endometrial		Tao brush		sample	chr5	67589588	SBS	G			
						T					PIK3R1		1351
	451	E	*		No	No	7.12	242					
PAPA	1155	Endometrial		Pap brush		sample	chr17	7577094	SBS	G			
						C					TP53		844
	282	R	G		No	No	8.04	431					
PAPA	1155	Endometrial		Tao brush		sample	chr17	7577094	SBS	G			
						C					TP53		844
	282	R	G		No	No	65.08	2708					
PAPA	1157	Endometrial		Pap brush		sample	chr17	7577538	SBS	C			
						T					TP53		743
	248	R	Q		No	No	38.55	3299					
PAPA	1157	Endometrial		Tao brush		sample	chr17	7577538	SBS	C			
						T					TP53		743
	248	R	Q		No	No	47.96	4353					
PAPA	1159	Ovarian		Tao brush		sample	chr17	7577539	SBS	G			
						A					TP53		742
	248	R	W		No	No	0.80	92					
PAPA	1160	Endometrial		Pap brush		sample	chr10	89692905	SBS	G			
						A					PTEN		389
	130	R	Q		No	No	1.36	167					
PAPA	1160	Endometrial		Pap brush		sample	chr10	89711899	SBS	C			
						T					PTEN		517
	173	R	C		No	No	2.02	96					
PAPA	1160	Endometrial		Pap brush		sample	chr12	133250289	SBS	C			

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						A					POLE	1231	
	411	V	L	No	No	1.78	225						
PAPA	1160	Endometrial	Pap brush	sample		chr4	153247366	SBS	C				
						T					FBXW7	1436	
	479	R	Q	No	No	1.65	60						
PAPA	1160	Endometrial	Pap brush	sample		chr5	67591106	SBS	A				
						G					PIK3R1	1699	
	567	K	E	No	No	2.02	195						
PAPA	1161	Endometrial	Pap brush	sample		chr10	89685293	Indel	A				
											PTEN	188	
	63	N	NULL	No	No	0.65	241						
PAPA	1161	Endometrial	Pap brush	sample		chr5	67591115	Indel	CTT				
											PIK3R1	1708	
	570	L	NULL	No	No	0.39	33						
PAPA	1161	Endometrial	Tao brush	sample		chr10	89685293	Indel	A				
											PTEN	188	
	63	N	NULL	No	No	3.08	889						
PAPA	1162	Endometrial	Pap brush	sample		chr10	89685315	Indel	GT				
											PTEN	0	
	0	NULL	NULL	1	No	1.71	633						
PAPA	1162	Endometrial	Pap brush	sample		chr10	89720804	Indel	ACTT				
											PTEN	955	
	319	T	NULL	No	No	1.62	51						
PAPA	1162	Endometrial	Tao brush	sample		chr10	89685315	Indel	GT				
											PTEN	0	
	0	NULL	NULL	1	No	32.87	9502						
PAPA	1162	Endometrial	Tao brush	sample		chr10	89720804	Indel	ACTT				
											PTEN	955	
	319	T	NULL	No	No	33.25	656						
PAPA	1162	Endometrial	Tao brush	sample		chr12	25398284	SBS	C				
						T					KRAS	35	
	12	G	D	No	No	31.02	3984						
PAPA	1164	Endometrial	Tao brush	sample		chr10	89711926	Indel					
TTAAAGAATCATCTGG (SEQ ID NO:758)												PTEN	
	544	182	L	NULL	No	No	0.68	191					
PAPA	1172	Ovarian	Pap brush	sample		chr17	7577539	SBS	G				
						C					TP53	742	
	248	R	G	No	No	0.12	9						
PAPA	1189	Ovarian	Tao brush	sample		chr17	7577097	SBS	C				
						G					TP53	841	
	281	D	H	No	No	0.91	75						
PAPA	1193	Endometrial	Pap brush	sample		chr10	89692844	SBS	C				
						T					PTEN	328	
	110	Q	*	No	No	7.67	561						
PAPA	1194	Endometrial	Pap brush	sample		chr10	89717650	SBS	T				
						G					PTEN	675	
	225	Y	*	No	No	0.15	54						
PAPA	1202	Endometrial	Pap brush	sample		chr17	7579414	SBS	C				

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						T					TP53	273	
	91	W	*	No	No	0.58	89						
PAPA	1209	Endometrial	Pap	brush	sample	chr10	89717732	Indel	AT				
											PTEN	757	
	253	I	NULL	No	No	6.42	2265						
PAPA	1213	Ovarian	Pap	brush	sample	chr17	7577090	SBS	C				
						G					TP53	848	
	283	R	P	No	No	0.39	27						
PAPA	1213	Ovarian	Pap	brush	sample	chr17	7579368	Indel	A				
											TP53	319	
	107	Y	NULL	No	No	0.39	58						
PAPA	1217	Ovarian	Pap	brush	sample	chr17	7577583	Indel					
						TGTAGT					TP53	698	
	233	H	NULL	No	No	0.13	17						
PAPA	1223	Endometrial	Pap	brush	sample	chr5	67589593	Indel	TAA				
											PIK3R1	1356	
	452	Y	NULL	No	No	0.34	9						
PAPA	1239	Endometrial	Pap	brush	sample	chr17	7577548	SBS	C				
						T					TP53	733	
	245	G	S	No	No	4.63	461						
PAPA	1242	Endometrial	Pap	brush	sample	chr17	7577550	SBS	C				
						T					TP53	731	
	244	G	D	No	No	16.98	1743						
PAPA	1256	Endometrial	Pap	brush	sample	chr5	67589613	Indel	AAA				
											PIK3R1	1376	
	459	K	NULL	No	No	0.96	21						
PAPA	1263	Ovarian	Tao	brush	sample	chr19	52715971	SBS	C				
						G					PPP2R1A	536	
	179	P	R	No	No	0.61	230						
PAPA	1292	Ovarian	Pap	brush	sample	chr5	67589559	Indel	A				
											PIK3R1	1322	
	441	N	NULL	No	No	0.53	15						
PAPA	1297	Ovarian	Pap	brush	sample	chr17	7577556	SBS	C				
						G					TP53	725	
	242	C	S	No	No	0.35	34						
PAPA	1308	Endometrial	Pap	brush	sample	chr17	7577539	SBS	G				
						A					TP53	742	
	248	R	W	No	No	29.43	3588						
PAPA	1322	Ovarian	Pap	brush	sample	chr17	7578271	SBS	T				
						C					TP53	578	
	193	H	R	No	No	0.46	28						
PAPA	1705	Ovarian	Pap	brush	sample	chr5	67589596	Indel	C				
											PIK3R1	1359	
	453	N	NULL	No	No	0.46	34						
PAPA	1736	Ovarian	Pap	brush	sample	chr17	7579368	SBS	A				
						T					TP53	319	
	107	Y	N	No	No	0.10	35						
PAPA	1821	Ovarian	Tao	brush	sample	chr17	7577534	SBS	C				

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					A					TP53	747	
	249	R	S	No	No	8.62	2791					
PAPA	1834	Ovarian	Tao	brush	sample	chr17	7577097	SBS	C			
					T					TP53	841	
	281	D	N	No	No	0.36	61					
PAPA	1850	Ovarian	Tao	brush	sample	chr17	7579424	Indel	G			
										TP53	263	
	88	A	NULL	No	No	14.74	3276					
PAPA	1859	Endometrial	Tao	brush	sample	chr17	7577538	SBS	C			
					T					TP53	743	
	248	R	Q	No	No	26.26	8779					
PAPA	1865	Endometrial	Tao	brush	sample	chr17	7577538	SBS	C			
					T					TP53	743	
	248	R	Q	No	No	4.23	1224					
PAPA	1865	Endometrial	Tao	brush	sample	chr5	67589590	Indel	ATA			
										PIK3R1	1353	
	451	E	NULL	No	No	21.36	642					
PAP	010	Endometrial	Pap	brush	sample	chr4	153247367	SBS	G			
					A					FBXW7	1435	
	479	R	*	No	No	10.43	39					
PAP	010	Endometrial	Pap	brush	sample	chr10	123279677	SBS	G			
					C					FGFR2	755	
	252	S	W	No	No	10.08	67					
PAP	010	Endometrial	Pap	brush	sample	chr10	89653791	Indel	C			
										PTEN	89	
	30	P	NULL	No	No	13.23	254					
PAP	010	Endometrial	Pap	brush	sample	chr10	89692904	SBS	C			
					G					PTEN	388	
	130	R	G	No	No	12.37	123					
PAP	010	Endometrial	Pap	brush	sample	chr17	7579713	Indel	T			
										TP53	83	
	28	E	NULL	No	No	1.56	28					
PAP	033	Endometrial	Pap	brush	sample	chr10	89717656	Indel				
					C					PTEN	681	
	227	S	NULL	No	No	1.22	14					
PAP	037	Endometrial	Pap	brush	sample	chr5	112174631	SBS	C			
					T					APC	3340	
	1114	R	*	No	No	13.88	232					
PAP	037	Endometrial	Pap	brush	sample	chr5	112175897	SBS	G			
					T					APC	4606	
	1536	E	*	No	No	10.02	57					
PAP	037	Endometrial	Pap	brush	sample	chr12	133253151	SBS	G			
					A					POLE	890	
	297	S	F	No	No	13.65	74					
PAP	037	Endometrial	Pap	brush	sample	chr10	89711913	SBS	T			
					G					PTEN	531	
	177	Y	*	No	No	16.94	173					
PAP	042	Ovarian	Pap	brush	sample	chr17	7579350	Indel				

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A TP53 337
113 F NULL No No 3.44 26
PAP 562 Endometrial Pap brush sample chr10 89653800 SBS T
G PTEN 98
33 I S No No 4.71 146
PAP 570 Endometrial Pap brush sample chr17 7574021 SBS C
A TP53 1006
336 E * No No 30.83 967
PAP 583 Endometrial Pap brush sample chr3 41266137 SBS C
G CTNNB1 134
45 S C No No 1.40 16
PAP 583 Endometrial Pap brush sample chr3 178916876 SBS G
A PIK3CA 263
88 R Q No No 8.66 35
PAP 583 Endometrial Pap brush sample chr5 67591135 Indel
GAGAGACCA
PIK3R1 1728 576 T NULL No No 9.02 144
PAP 583 Endometrial Pap brush sample chr5 67591144 Indel
CAA PIK3R1 1737
579 Q NULL No No 0.63 10
PAP 583 Endometrial Pap brush sample chr10 89692919 SBS A
G PTEN 403
135 I V No No 3.82 95
PAP 583 Endometrial Pap brush sample chr10 89720817 Indel
A PTEN 968
323 N NULL No No 12.10 107
PAP 583 Endometrial Pap brush sample chr17 7577530 SBS T
A TP53 751
251 I F No No 4.07 33
PAP 584 Endometrial Pap brush sample chr3 41266104 SBS G
A CTNNB1 101
34 G E No No 23.03 401
PAP 584 Endometrial Pap brush sample chr10 89717703 Indel T
PTEN 728
243 F NULL No No 11.06 182
PAP 584 Endometrial Pap brush sample chr17 7578397 Indel
TGGGGGCAGC (SEQ ID NO:759) TP53
533 178 H NULL No No 1.97 23
PAP 588 Endometrial Pap brush sample chr5 67591085 SBS G
C PIK3R1 1678
560 D H No No 1.76 53
PAP 588 Endometrial Pap brush sample chr10 89717725 Indel TG
PTEN 750
250 C NULL No No 4.68 39
PAP 590 Endometrial Pap brush sample chr9 21974819 Indel
GGCTCCATGCTGCTCCCCGCCGCC (SEQ ID NO:760)
CDKN2A 8 3 P NULL No No 54.66 938
PAP 594 Endometrial Pap brush sample chr14 105246551 SBS C

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                                        T                                       AKT1    49
     17      E       K       No      No      18.22   356
PAP 594    Endometrial   Pap brush sample     chr3    41266104     SBS     G
                                        T                                       CTNNB1  101
     34      G       V       No      No      7.50    71
PAP 595    Endometrial   Pap brush sample     chr10   89692905     SBS     G
                                        T                                       PTEN    389
     130     R       L       No      No      3.90    24
PAP 601    Endometrial   Pap brush sample     chr3    178952090    SBS     G
                                        C                                       PIK3CA  3145
     1049    G       R       No      No      60.22   2346
PAP 619    Endometrial   Pap brush sample     chr5    112175639    SBS     C
                                        T                                       APC     4348
     1450    R       *       No      No      3.73    82
PAP 619    Endometrial   Pap brush sample     chr3    178916876    SBS     G
                                        A                                       PIK3CA  263
     88      R       Q       No      No      3.86    8
PAP 619    Endometrial   Pap brush sample     chr12   133253151    SBS     G
                                        A                                       POLE    890
     297     S       F       No      No      7.22    62
PAP 637    Endometrial   Tao brush sample     chr17   7579327      SBS     C
                                        G                                       TP53    360
     120     K       N       No      No      0.34    4
PAP 650    Endometrial   Pap brush sample     chr5    67591147     Indel
CTTGATGTA
PIK3R1  1740       580     Y       NULL    No      No      15.62   157
PAP 650    Endometrial   Pap brush sample     chr10   89720804     Indel   ACTT
                                                                        PTEN    955
     319     T       NULL    No      No      22.43   155
PAP 001    Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                        G                                       KRAS    35
     12      G       A       No      No      13.64   1255
PAP 001    Endometrial   Pap brush sample     chr3    178952085    SBS     A
                                        G                                       PIK3CA  3140
     1047    H       R       No      No      5.43    514
PAP 001    Endometrial   Pap brush sample     chr10   89692904     SBS     C
                                        G                                       PTEN    388
     130     R       G       No      No      1.75    79
PAP 084    Endometrial   Pap brush sample     chr5    112175682    Indel   AGAG
                                                                        APC     4391
     1464    E       NULL    No      No      0.07    25
PAP 084    Endometrial   Pap brush sample     chr5    112175752    Indel   TTTATTAC
                                                                        APC     4461
     1487    T       NULL    No      No      0.12    10
PAP 084    Endometrial   Pap brush sample     chr10   89720702     SBS     G
                                        T                                       PTEN    853
     285     E       *       No      No      8.52    1570
PAP 084    Endometrial   Pap brush sample     chr17   7576915      Indel
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					CTGGTGTG					TP53	931
	311	N	NULL	No	No	34.37	5812				
PAP	524	Ovarian	Pap	brush	sample	chr3	178952085	SBS	A		
					T					PIK3CA	3140
	1047	H	L	No	No	0.32	12				
PAP	530	Ovarian	Pap	brush	sample	chr12	25398282	SBS	C		
					T					KRAS	37
	13	G	S	No	No	0.03	2				
PAP	541	Ovarian	Pap	brush	sample	chr17	7578486	Indel	A		
										TP53	444
	148	D	NULL	No	No	0.22	15				
PAP	549	Endometrial	Pap	brush	sample	chr10	89624268	Indel			
					GG					PTEN	42
	14	R	NULL	No	No	0.40	52				
PAP	549	Endometrial	Pap	brush	sample	chr17	7579589	Indel			
					G					TP53	98
	33	S	NULL	No	No	0.25	41				
PAP	554	Endometrial	Pap	brush	sample	chr3	178952090	SBS	G		
					C					PIK3CA	3145
	1049	G	R	No	No	1.60	114				
PAP	565	Endometrial	Pap	brush	sample	chr10	89692904	SBS	C		
					G					PTEN	388
	130	R	G	No	No	0.47	17				
PAP	565	Endometrial	Pap	brush	sample	chr10	89720805	Indel	CTTT		
										PTEN	956
	319	T	NULL	No	No	1.92	27				
PAP	572	Endometrial	Pap	brush	sample	chr12	25398284	SBS	C		
					A					KRAS	35
	12	G	V	No	No	13.41	1857				
PAP	572	Endometrial	Pap	brush	sample	chr3	178952084	SBS	C		
					T					PIK3CA	3139
	1047	H	Y	No	No	12.24	1463				
PAP	572	Endometrial	Pap	brush	sample	chr17	7578542	SBS	G		
					A					TP53	388
	130	L	F	No	No	11.51	2352				
PAP	574	Endometrial	Pap	brush	sample	chr3	41266113	SBS	C		
					A					CTNNB1	110
	37	S	Y	No	No	1.95	74				
PAP	574	Endometrial	Pap	brush	sample	chr10	89653786	SBS	T		
					G					PTEN	84
	28	I	M	No	No	1.69	177				
PAP	574	Endometrial	Pap	brush	sample	chr17	7578212	SBS	G		
					A					TP53	637
	213	R	*	No	No	2.40	130				
PAP	582	Endometrial	Pap	brush	sample	chr5	67588951	SBS	C		
					T					PIK3R1	1042
	348	R	*	No	No	3.29	14				
PAP	582	Endometrial	Pap	brush	sample	chr12	133253184	SBS	G		

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						C						POLE	857
	286	P	R		No	No	3.01	107					
PAP	582	Endometrial		Pap brush		sample	chr10	89720744	SBS	G			
						T						PTEN	895
	299	E	*		No	No	1.40	90					
PAP	582	Endometrial		Pap brush		sample	chr17	7578212	SBS	G			
						A						TP53	637
	213	R	*		No	No	3.51	162					
PAP	585	Endometrial		Pap brush		sample	chr3	41266097	SBS	G			
						A						CTNNB1	94
	32	D	N		No	No	4.86	328					
PAP	585	Endometrial		Pap brush		sample	chr3	41266124	SBS	A			
						G						CTNNB1	121
	41	T	A		No	No	2.07	140					
PAP	585	Endometrial		Pap brush		sample	chr10	123279674	SBS	G			
						C						FGFR2	758
	253	P	R		No	No	31.98	1799					
PAP	585	Endometrial		Pap brush		sample	chr5	67591135	Indel	G			
												PIK3R1	1728
	576	T	NULL		No	No	4.15	159					
PAP	585	Endometrial		Pap brush		sample	chr10	89653789	SBS	T			
						G						PTEN	87
	29	Y	*		No	No	24.16	1809					
PAP	585	Endometrial		Pap brush		sample	chr10	89685293	Indel	A			
												PTEN	188
	63	N	NULL		No	No	12.71	99					
PAP	587	Endometrial		Pap brush		sample	chr3	41266100	SBS	T			
						C						CTNNB1	97
	33	S	P		No	No	1.50	78					
PAP	587	Endometrial		Pap brush		sample	chr3	41266125	SBS	C			
						T						CTNNB1	122
	41	T	I		No	No	3.32	173					
PAP	587	Endometrial		Pap brush		sample	chr4	153247373	SBS	C			
						T						FBXW7	1429
	477	G	S		No	No	3.70	178					
PAP	587	Endometrial		Pap brush		sample	chr5	67591106	SBS	A			
						G						PIK3R1	1699
	567	K	E		No	No	9.96	634					
PAP	587	Endometrial		Pap brush		sample	chr10	89720828	SBS	A			
						T						PTEN	979
	327	K	*		No	No	13.71	205					
PAP	646	Endometrial		Pap brush		sample	chr9	21970976	SBS	G			
						A						CDKN2A	382
	128	R	W		No	No	1.25	93					
PAP	646	Endometrial		Pap brush		sample	chr7	55241726	SBS	C			
						T						EGFR	2174
	725	T	M		No	No	22.36	1878					
PAP	646	Endometrial		Pap brush		sample	chr4	153249384	SBS	C			

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T FBXW7 1394
465 R H No No 19.89 1191
PAP 646 Endometrial Pap brush sample chr3 178952074 SBS G
A PIK3CA 3129
1043 M I No No 19.51 1334
PAP 646 Endometrial Pap brush sample chr19 52715982 SBS C
T PPP2R1A 547
183 R W No No 41.12 183
PAP 646 Endometrial Pap brush sample chr10 89624266 SBS A
G PTEN 40
14 R G No No 0.34 51
PAP 646 Endometrial Pap brush sample chr10 89717609 SBS G
T PTEN 0
0 NULL NULL 1 No 4.14 172
PAP 646 Endometrial Pap brush sample chr10 89717712 SBS C
T PTEN 737
246 P L No No 6.12 663
PAP 646 Endometrial Pap brush sample chr17 7577121 SBS G
A TP53 817
273 R C No No 5.45 518
PAP 646 Endometrial Pap brush sample chr17 7577022 SBS G
A TP53 916
306 R * No No 20.03 811
PAP 646 Endometrial Pap brush sample chr17 7574018 SBS G
A TP53 1009
337 R C No No 3.40 301
PAP 647 Endometrial Pap brush sample chr10 123258034 SBS A
C FGFR2 1647
549 N K No No 8.75 470
PAP 647 Endometrial Pap brush sample chr10 89692904 SBS C
T PTEN 388
130 R * No No 1.90 80
PAP 648 Endometrial Pap brush sample chr3 41266113 SBS C
A CTNNB1 110
37 S Y No No 33.87 961
PAP 648 Endometrial Pap brush sample chr10 89692904 SBS C
T PTEN 388
130 R * No No 23.66 767
PAP 649 Endometrial Pap brush sample chr19 52715971 SBS C
G PPP2R1A 536
179 P R No No 9.31 57
PAP 649 Endometrial Pap brush sample chr17 7578383 Indel
AGCAGCGCTCATGGTGGG (SEQ ID NO:761) TP53
547 183 S NULL No No 16.54 552
PAP 176 Endometrial Pap brush sample chr12 25398284 SBS C
T KRAS 35
12 G D No No 4.07 76
PAP 176 Endometrial Pap brush sample chr3 178936094 SBS C

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					A					PIK3CA	1636	
546	Q	K	No	No	37.83	457						
PAP 176	Endometrial	Pap brush	sample		chr10	89720716	Indel	A				
										PTEN	867	
289	K	NULL	No	No	0.46	64						
PAP 177	Endometrial	Pap brush	sample		chr3	41266113	SBS	C				
					T					CTNNB1	110	
37	S	F	No	No	1.14	31						
PAP 177	Endometrial	Pap brush	sample		chr10	89720804	Indel	ACTT				
										PTEN	955	
319	T	NULL	No	No	1.20	47						
PAP 200	Endometrial	Pap brush	sample		chr3	178916854	SBS	G				
					A					PIK3CA	241	
81	E	K	No	No	4.71	496						
PAP 200	Endometrial	Pap brush	sample		chr12	133250289	SBS	C				
					A					POLE	1231	
411	V	L	No	No	4.50	202						
PAP 200	Endometrial	Pap brush	sample		chr10	89720876	SBS	G				
					A					PTEN	0	
0	NULL	NULL	1	No	7.87	27						
PAP 243	Endometrial	Pap brush	sample		chr3	41266101	SBS	C				
					A					CTNNB1	98	
33	S	Y	No	No	22.50	602						
PAP 243	Endometrial	Pap brush	sample		chr3	41266124	SBS	A				
					G					CTNNB1	121	
41	T	A	No	No	13.50	361						
PAP 243	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				
					A					PIK3CA	263	
88	R	Q	No	No	10.25	1305						
PAP 243	Endometrial	Pap brush	sample		chr10	89692905	SBS	G				
					A					PTEN	389	
130	R	Q	No	No	2.35	52						
PAP 250	Ovarian	Pap brush	sample		chr17	7577022	SBS	G				
					A					TP53	916	
306	R	*	No	No	2.04	193						
PAP 265	Endometrial	Pap brush	sample		chr3	41266097	SBS	G				
					T					CTNNB1	94	
32	D	Y	No	No	1.52	64						
PAP 267	Endometrial	Pap brush	sample		chr3	41266112	SBS	T				
					C					CTNNB1	109	
37	S	P	No	No	0.25	9						
PAP 555	Endometrial	Pap brush	sample		chr5	112175639	SBS	C				
					T					APC	4348	
1450	R	*	No	No	25.99	563						
PAP 555	Endometrial	Pap brush	sample		chr5	67591146	Indel	ACT				
										PIK3R1	1739	
580	Y	NULL	No	No	31.09	415						
PAP 555	Endometrial	Pap brush	sample		chr17	7578263	SBS	G				

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						A					TP53	586	
	196	R	*	No	No	27.89	1063						
PAP	556	Endometrial	Pap brush	sample		chr10	89720749	Indel	C				
											PTEN	900	
	300	I	NULL	No	No	0.13	36						
PAP	618	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				
						T					KRAS	35	
	12	G	D	No	No	13.23	592						
PAP	618	Endometrial	Pap brush	sample		chr3	178952085	SBS	A				
						G					PIK3CA	3140	
	1047	H	R	No	No	8.25	170						
PAP	003	Endometrial	Pap brush	sample		chr5	112175639	SBS	C				
						T					APC	4348	
	1450	R	*	No	No	11.56	289						
PAP	003	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				
						A					PIK3CA	263	
	88	R	Q	No	No	7.56	1546						
PAP	003	Endometrial	Pap brush	sample		chr5	67588951	SBS	C				
						T					PIK3R1	1042	
	348	R	*	No	No	5.57	17						
PAP	003	Endometrial	Pap brush	sample		chr12	133250289	SBS	C				
						A					POLE	1231	
	411	V	L	No	No	9.79	525						
PAP	003	Endometrial	Pap brush	sample		chr10	89624245	SBS	G				
						T					PTEN	19	
	7	E	*	No	No	7.91	211						
PAP	003	Endometrial	Pap brush	sample		chr10	89711899	SBS	C				
						T					PTEN	517	
	173	R	C	No	No	2.72	69						
PAP	169	Ovarian	Pap brush	sample		chr14	105246551	SBS	C				
						T					AKT1	49	
	17	E	K	No	No	31.02	2016						
PAP	169	Ovarian	Pap brush	sample		chr10	123258034	SBS	A				
						C					FGFR2	1647	
	549	N	K	No	No	17.29	120						
PAP	169	Ovarian	Pap brush	sample		chr12	133253184	SBS	G				
						C					POLE	857	
	286	P	R	No	No	18.51	238						
PAP	169	Ovarian	Pap brush	sample		chr17	7578212	SBS	G				
						A					TP53	637	
	213	R	*	No	No	22.24	226						
PAP	175	Endometrial	Pap brush	sample		chr10	123258034	SBS	A				
						C					FGFR2	1647	
	549	N	K	No	No	0.42	12						
PAP	175	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				
						T					KRAS	35	
	12	G	D	No	No	3.45	142						
PAP	175	Endometrial	Pap brush	sample		chr3	178952074	SBS	G				

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						T					PIK3CA	3129	
	1043	M	I		No	No	7.60	147					
PAP	175	Endometrial	Pap brush		sample		chr5	67591144	Indel				
						A					PIK3R1	1737	
	579	Q	NULL		No	No	11.95	455					
PAP	175	Endometrial	Pap brush		sample		chr12	133253184	SBS	G			
						C					POLE	857	
	286	P	R		No	No	0.60	30					
PAP	175	Endometrial	Pap brush		sample		chr10	89692904	SBS	C			
						G					PTEN	388	
	130	R	G		No	No	3.11	104					
PAP	175	Endometrial	Pap brush		sample		chr10	89720741	SBS	C			
						T					PTEN	892	
	298	Q	*		No	No	4.04	522					
PAP	184	Ovarian	Pap brush		sample		chr3	41266113	SBS	C			
						T					CTNNB1	110	
	37	S	F		No	No	11.83	227					
PAP	184	Ovarian	Pap brush		sample		chr3	178952085	SBS	A			
						G					PIK3CA	3140	
	1047	H	R		No	No	12.27	208					
PAP	184	Ovarian	Pap brush		sample		chr10	89720716	Indel	A			
											PTEN	867	
	289	K	NULL		No	No	14.97	1549					
PAP	201	Endometrial	Pap brush		sample		chr10	123279677	SBS	G			
						C					FGFR2	755	
	252	S	W		No	No	0.31	13					
PAP	201	Endometrial	Pap brush		sample		chr10	89711928	Indel				
						A					PTEN	546	
	182	L	NULL		No	No	1.88	30					
PAP	201	Endometrial	Pap brush		sample		chr10	89711930	Indel				
						A					PTEN	548	
	183	K	NULL		No	No	0.87	64					
PAP	205	Endometrial	Pap brush		sample		chr3	178916876	SBS	G			
						A					PIK3CA	263	
	88	R	Q		No	No	1.29	142					
PAP	235	Endometrial	Pap brush		sample		chr1	115258747	SBS	C			
						T					NRAS	35	
	12	G	D		No	No	1.34	44					
PAP	235	Endometrial	Pap brush		sample		chr1	115256528	SBS	T			
						G					NRAS	183	
	61	Q	H		No	No	0.36	12					
PAP	235	Endometrial	Pap brush		sample		chr1	115256530	SBS	G			
						T					NRAS	181	
	61	Q	K		No	No	3.58	120					
PAP	235	Endometrial	Pap brush		sample		chr3	178936091	SBS	G			
						A					PIK3CA	1633	
	545	E	K		No	No	41.95	1001					
PAP	235	Endometrial	Pap brush		sample		chr17	7579312	SBS	C			

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                                    T                                   TP53    375
     125     T       T       No      Yes     25.57   1504
PAP 238     Endometrial   Pap brush sample     chr12   25398281      SBS     C
                                    T                                   KRAS    38
     13      G       D       No      No      6.31    155
PAP 238     Endometrial   Pap brush sample     chr5    67591106      SBS     A
                                    G                                   PIK3R1  1699
     567     K       E       No      No      0.53    16
PAP 245     Endometrial   Pap brush sample     chr12   25398284      SBS     C
                                    T                                   KRAS    35
     12      G       D       No      No      9.26    263
PAP 245     Endometrial   Pap brush sample     chr3    178952085     SBS     A
                                    G                                   PIK3CA  3140
     1047    H       R       No      No      8.06    173
PAP 245     Endometrial   Pap brush sample     chr10   89653829      SBS     G
                                    T                                   PTEN    127
     43      E       *       No      No      7.37    159
PAP 011     Endometrial   Pap brush sample     chr12   25398284      SBS     C
                                    G                                   KRAS    35
     12      G       A       No      No      3.53    93
PAP 011     Endometrial   Pap brush sample     chr5    67588976      Indel
                                    T                                   PIK3R1  1067
     356     L       NULL    No      No      4.15    10
PAP 011     Endometrial   Pap brush sample     chr10   89692893      Indel   C
                                                                        PTEN    377
     126     A       NULL    No      No      4.66    23
PAP 066     Endometrial   Pap brush sample     chr12   25398285      SBS     C
                                    A                                   KRAS    34
     12      G       C       No      No      5.21    149
PAP 225     Endometrial   Pap brush sample     chr3    178936091     SBS     G
                                    A                                   PIK3CA  1633
     545     E       K       No      No      1.17    22
PAP 225     Endometrial   Pap brush sample     chr10   89720817      Indel
                                    A                                   PTEN    968
     323     N       NULL    No      No      1.02    81
PAP 034     Endometrial   Pap brush sample     chr3    41266103      SBS     G
                                    A                                   CTNNB1  100
     34      G       R       No      No      20.13   2734
PAP 034     Endometrial   Pap brush sample     chr5    67591040      Indel
TTGGAAGAAGA (SEQ ID NO:762)
PIK3R1  1633        545     L       NULL    No      No      0.50    35
PAP 034     Endometrial   Pap brush sample     chr5    67591110      Indel   CAGACC
                                                                        PIK3R1  1703
     568     P       NULL    No      No      0.16    19
PAP 034     Endometrial   Pap brush sample     chr10   89692904      SBS     C
                                    G                                   PTEN    388
     130     R       G       No      No      4.83    441
PAP 039     Ovarian       Pap brush sample     chr17   7577519       Indel   G
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						T					PTEN	892	
	298	Q	*	No	No	13.14	3286						
PAP	234	Endometrial	Pap brush	sample		chr12	25398281	SBS	C				
						T					KRAS	38	
	13	G	D	No	No	1.64	45						
PAP	234	Endometrial	Pap brush	sample		chr5	67589581	Indel	ATTACA				
											PIK3R1	1344	
	448	K	NULL	No	No	1.06	35						
PAP	234	Endometrial	Pap brush	sample		chr5	67589582	Indel	TTACAT				
											PIK3R1	1345	
	449	L	NULL	No	No	0.23	28						
PAP	234	Endometrial	Pap brush	sample		chr10	89717678	Indel	G				
											PTEN	703	
	235	E	NULL	No	No	0.18	8						
PAP	236	Endometrial	Pap brush	sample		chr10	89653799	Indel	ATT				
											PTEN	97	
	33	I	NULL	No	No	0.72	49						
PAP	236	Endometrial	Pap brush	sample		chr10	89692975	Indel	T				
											PTEN	459	
	153	D	NULL	No	No	0.56	31						
PAP	242	Endometrial	Pap brush	sample		chr4	153249384	SBS	C				
						T					FBXW7	1394	
	465	R	H	No	No	5.29	269						
PAP	242	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	4.11	150						
PAP	652	Endometrial	Pap brush	sample		chr5	112174093	Indel	TTAC				
											APC	2802	
	934	T	NULL	No	No	0.70	32						
PAP	652	Endometrial	Pap brush	sample		chr5	112175639	SBS	C				
						T					APC	4348	
	1450	R	*	No	No	8.22	458						
PAP	652	Endometrial	Pap brush	sample		chr3	178952085	SBS	A				
						G					PIK3CA	3140	
	1047	H	R	No	No	8.28	502						
PAP	652	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	7.48	337						
PAP	652	Endometrial	Pap brush	sample		chr17	7578406	SBS	C				
						T					TP53	524	
	175	R	H	No	No	7.69	419						
PAP	002	Ovarian	Pap brush	sample		chr17	7578490	SBS	A				
						T					TP53	440	
	147	V	D	No	No	0.26	14						
PAP	025	Endometrial	Pap brush	sample		chr17	7579395	Indel	GG				
											TP53	292	
	98	P	NULL	No	No	10.13	245						
PAP	035	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				

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                                    T                                       KRAS    35
     12      G       D       No      No      4.18    21
PAP 035    Endometrial   Pap brush sample     chr3    178916854    SBS     G
                                    A                                       PIK3CA  241
     81      E       K       No      No      3.92    155
PAP 119    Endometrial   Pap brush sample     chr5    67589651     Indel
                                    GCACATCCCAGGCCC (SEQ ID NO:778)    PIK3R1  1414
     472     R       NULL    No      No      0.27    13
PAP 119    Endometrial   Pap brush sample     chr10   89692932     SBS     T
                                    A                                       PTEN    416
     139     L       *       No      No      0.37    9
PAP 121    Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    A                                       KRAS    35
     12      G       V       No      No      2.92    61
PAP 121    Endometrial   Pap brush sample     chr10   89692904     SBS     C
                                    G                                       PTEN    388
     130     R       G       No      No      1.48    27
PAP 178    Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    T                                       KRAS    35
     12      G       D       No      No      4.60    97
PAP 178    Endometrial   Pap brush sample     chr3    178952052    SBS     T
                                    C                                       PIK3CA  3107
     1036    L       S       No      No      4.39    108
PAP 178    Endometrial   Pap brush sample     chr10   89692905     SBS     G
                                    C                                       PTEN    389
     130     R       P       No      No      1.52    55
PAP 179    Endometrial   Pap brush sample     chr5    67589568     Indel
CTGTAGGGAAAAAATTACATGAAT (SEQ ID NO:763)
PIK3R1  1331       444     A       NULL    No      No      3.57    51
PAP 179    Endometrial   Pap brush sample     chr17   7578265      SBS     A
                                    G                                       TP53    584
     195     I       T       No      No      6.16    227
PAP 180    Endometrial   Pap brush sample     chr12   133253184    SBS     G
                                    C                                       POLE    857
     286     P       R       No      No      2.78    90
PAP 180    Endometrial   Pap brush sample     chr10   89711899     SBS     C
                                    T                                       PTEN    517
     173     R       C       No      No      1.84    31
PAP 199    Ovarian       Pap brush sample     chr17   7578265      SBS     A
                                    G                                       TP53    584
     195     I       T       No      No      5.68    473
PAP 202    Endometrial   Pap brush sample     chr3    178936083    SBS     A
                                    C                                       PIK3CA  1625
     542     E       A       No      No      1.16    29
PAP 202    Endometrial   Pap brush sample     chr3    178952090    SBS     G
                                    A                                       PIK3CA  3145
     1049    G       S       No      No      1.16    56
PAP 202    Endometrial   Pap brush sample     chr10   89720716     Indel
```

Table15.txt

```
                                    A                                   PTEN    867
     289     K       NULL    No      No      4.53    846
PAP 202     Endometrial     Pap brush sample     chr10   89720817     Indel
                                    A                                   PTEN    968
     323     N       NULL    No      No      15.49   1405
PAP 202     Endometrial     Pap brush sample     chr17   7578553      SBS     T
                                    C                                   TP53    377
     126     Y       C       No      No      1.26    31
PAP 202     Endometrial     Pap brush sample     chr17   7577524      SBS     T
                                    G                                   TP53    757
     253     T       P       No      No      13.92   1083
PAP 206     Endometrial     Pap brush sample     chr10   123258034    SBS     A
                                    T                                   FGFR2   1647
     549     N       K       No      No      2.23    38
PAP 206     Endometrial     Pap brush sample     chr5    67591130     Indel
AAGACGAGA
PIK3R1  1723        575     K       NULL    No      No      0.26    7
PAP 209     Endometrial     Pap brush sample     chr9    21971099     SBS     G
                                    A                                   CDKN2A  259
     87      R       W       No      No      6.04    62
PAP 209     Endometrial     Pap brush sample     chr3    41266100     SBS     T
                                    G                                   CTNNB1  97
     33      S       A       No      No      22.72   556
PAP 209     Endometrial     Pap brush sample     chr3    41266104     SBS     G
                                    A                                   CTNNB1  101
     34      G       E       No      No      0.82    20
PAP 209     Endometrial     Pap brush sample     chr5    67592091     Indel
                                    A                                   PIK3R1  1907
     636     N       NULL    No      No      0.62    14
PAP 209     Endometrial     Pap brush sample     chr10   89690805     SBS     G
                                    A                                   PTEN    212
     71      C       Y       No      No      8.58    23
PAP 209     Endometrial     Pap brush sample     chr10   89692905     SBS     G
                                    A                                   PTEN    389
     130     R       Q       No      No      7.82    88
PAP 209     Endometrial     Pap brush sample     chr10   89692911     SBS     G
                                    A                                   PTEN    395
     132     G       D       No      No      6.48    73
PAP 218     Endometrial     Pap brush sample     chr3    178952085    SBS     A
                                    G                                   PIK3CA  3140
     1047    H       R       No      No      51.44   946
PAP 218     Endometrial     Pap brush sample     chr19   52715971     SBS     C
                                    G                                   PPP2R1A 536
     179     P       R       No      No      27.54   76
PAP 218     Endometrial     Pap brush sample     chr17   7578427      SBS     T
                                    C                                   TP53    503
     168     H       R       No      No      72.66   760
PAP 229     Endometrial     Pap brush sample     chr3    41266125     SBS     C
```

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						T					CTNNB1	122	
41	T	I	No	No	2.54	148							
PAP 229	Endometrial	Pap brush	sample		chr4	153247289	SBS	G					
						A					FBXW7	1513	
505	R	C	No	No	2.69	311							
PAP 229	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A					PIK3CA	263	
88	R	Q	No	No	3.10	622							
PAP 240	Endometrial	Pap brush	sample		chr19	52715971	SBS	C					
						G					PPP2R1A	536	
179	P	R	No	No	17.07	164							
PAP 240	Endometrial	Pap brush	sample		chr17	7578290	SBS	C					
						T					TP53	0	
0	NULL	NULL	1	No	22.31	1283							
PAP 240	Endometrial	Pap brush	sample		chr17	7577141	SBS	C					
						T					TP53	797	
266	G	E	No	No	23.71	468							
PAP 247	Endometrial	Pap brush	sample		chr3	41266104	SBS	G					
						A					CTNNB1	101	
34	G	E	No	No	0.47	17							
PAP 247	Endometrial	Pap brush	sample		chr5	67591147	SBS	C					
						A					PIK3R1	1740	
580	Y	*	No	No	1.50	43							
PAP 247	Endometrial	Pap brush	sample		chr12	133253184	SBS	G					
						C					POLE	857	
286	P	R	No	No	2.39	79							
PAP 247	Endometrial	Pap brush	sample		chr10	89720870	SBS	T					
						G					PTEN	1021	
341	F	V	No	No	5.08	30							
PAP 070	Endometrial	Pap brush	sample		chr10	123258034	SBS	A					
						T					FGFR2	1647	
549	N	K	No	No	0.31	6							
PAP 070	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A					PIK3CA	263	
88	R	Q	No	No	23.62	3349							
PAP 070	Endometrial	Pap brush	sample		chr17	7578556	SBS	T					
						C					TP53	0	
0	NULL	NULL	1	No	7.08	148							
PAP 131	Endometrial	Pap brush	sample		chr4	153249385	SBS	G					
						A					FBXW7	1393	
465	R	C	No	No	2.55	144							
PAP 131	Endometrial	Pap brush	sample		chr12	25378562	SBS	C					
						T					KRAS	436	
146	A	T	No	No	34.03	1433							
PAP 131	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A					PIK3CA	263	
88	R	Q	No	No	33.88	6544							
PAP 131	Endometrial	Pap brush	sample		chr10	89685308	SBS	A					

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						G					PTEN	203	
68	Y	C	No	No	43.57	122							
PAP 186	Ovarian	Pap brush	sample		chr17	7579589	Indel	G					
											TP53	98	
33	S	NULL	No	No	0.49	34							
PAP 195	Ovarian	Pap brush	sample		chr3	178916854	SBS	G					
						A					PIK3CA	241	
81	E	K	No	No	0.27	30							
PAP 195	Ovarian	Pap brush	sample		chr12	133250289	SBS	C					
						A					POLE	1231	
411	V	L	No	No	0.33	25							
PAP 195	Ovarian	Pap brush	sample		chr17	7578486	Indel	A					
											TP53	444	
148	D	NULL	No	No	3.39	221							
PAP 219	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A					PIK3CA	263	
88	R	Q	No	No	17.52	2099							
PAP 219	Endometrial	Pap brush	sample		chr10	89624245	SBS	G					
						T					PTEN	19	
7	E	*	No	No	22.28	123							
PAP 219	Endometrial	Pap brush	sample		chr10	89624270	SBS	G					
						A					PTEN	44	
15	R	K	No	No	19.75	109							
PAP 222	Endometrial	Pap brush	sample		chr3	41266097	SBS	G					
						A					CTNNB1	94	
32	D	N	No	No	0.56	16							
PAP 222	Endometrial	Pap brush	sample		chr3	41266112	SBS	T					
						C					CTNNB1	109	
37	S	P	No	No	2.06	59							
PAP 222	Endometrial	Pap brush	sample		chr4	153249385	SBS	G					
						A					FBXW7	1393	
465	R	C	No	No	13.32	325							
PAP 222	Endometrial	Pap brush	sample		chr10	123247516	SBS	T					
						C					FGFR2	1975	
659	K	E	No	No	0.78	17							
PAP 222	Endometrial	Pap brush	sample		chr12	25378562	SBS	C					
						T					KRAS	436	
146	A	T	No	No	6.94	128							
PAP 222	Endometrial	Pap brush	sample		chr3	178952085	SBS	A					
						G					PIK3CA	3140	
1047	H	R	No	No	22.33	527							
PAP 222	Endometrial	Pap brush	sample		chr5	67591150	Indel						
GATGTAAGTATT (SEQ ID NO:764)													
PIK3R1 1743	581	L	NULL	No	No	0.29	6						
PAP 222	Endometrial	Pap brush	sample		chr10	89692904	SBS	C					
						G					PTEN	388	
130	R	G	No	No	3.25	46							
PAP 233	Endometrial	Pap brush	sample		chr3	178952085	SBS	A					

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```
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      20.39   1011
PAP 233     Endometrial   Pap brush sample     chr10   89692904     SBS     C
                                    G                                       PTEN    388
     130     R       G       No      No      8.62    369
PAP 233     Endometrial   Pap brush sample     chr10   89720817     Indel
                                    A                                       PTEN    968
     323     N       NULL    No      No      18.54   1973
PAP 237     Endometrial   Pap brush sample     chr3    41266097     SBS     G
                                    A                                       CTNNB1  94
     32      D       N       No      No      0.59    22
PAP 237     Endometrial   Pap brush sample     chr10   89624249     Indel   T
                                                                            PTEN    23
     8       I       NULL    No      No      4.00    50
PAP 237     Endometrial   Pap brush sample     chr10   89720781     Indel   A
                                                                            PTEN    932
     311     N       NULL    No      No      1.29    98
PAP 239     Endometrial   Pap brush sample     chr17   7577108      SBS     C
                                    A                                       TP53    830
     277     C       F       No      No      80.44   1197
PAP 244     Endometrial   Pap brush sample     chr4    153249393    SBS     G
                                    A                                       FBXW7   1385
     462     S       F       No      No      4.07    205
PAP 244     Endometrial   Pap brush sample     chr17   7578413      SBS     C
                                    T                                       TP53    517
     173     V       M       No      No      5.90    315
PAP 244     Endometrial   Pap brush sample     chr17   7576911      Indel
GTGTTGTTGGGCAG (SEQ ID NO:765)                                                      TP53
   935      312     T       NULL    No      No      4.10    389
PAP 062     Ovarian       Pap brush sample     chr17   7577120      SBS     C
                                    T                                       TP53    818
     273     R       H       No      No      4.16    79
PAP 204     Endometrial   Pap brush sample     chr5    112174631    SBS     C
                                    T                                       APC     3340
     1114    R       *       No      No      4.39    199
PAP 204     Endometrial   Pap brush sample     chr3    41266113     SBS     C
                                    A                                       CTNNB1  110
     37      S       Y       No      No      16.06   624
PAP 204     Endometrial   Pap brush sample     chr12   25380272     SBS     C
                                    A                                       KRAS    186
     62      E       D       No      No      0.52    31
PAP 204     Endometrial   Pap brush sample     chr3    178916876    SBS     G
                                    A                                       PIK3CA  263
     88      R       Q       No      No      11.96   1811
PAP 204     Endometrial   Pap brush sample     chr10   89692905     SBS     G
                                    A                                       PTEN    389
     130     R       Q       No      No      3.29    93
PAP 204     Endometrial   Pap brush sample     chr10   89720744     SBS     G
```

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						T					PTEN		895
	299	E	*	No	No	0.11	12						
PAP	204	Endometrial	Pap brush	sample		chr17	7579702	SBS	G				
						T					TP53		94
	32	L	M	No	No	6.87	296						
PAP	204	Endometrial	Pap brush	sample		chr17	7579348	SBS	G				
						T					TP53		339
	113	F	L	No	No	1.52	139						
PAP	204	Endometrial	Pap brush	sample		chr17	7578463	SBS	C				
						T					TP53		467
	156	R	H	No	No	15.39	862						
PAP	213	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				
						A					KRAS		35
	12	G	V	No	No	10.46	266						
PAP	213	Endometrial	Pap brush	sample		chr3	178936091	SBS	G				
						A					PIK3CA		1633
	545	E	K	No	No	20.94	422						
PAP	213	Endometrial	Pap brush	sample		chr10	89720817	Indel					
						A					PTEN		968
	323	N	NULL	No	No	18.36	1483						
PAP	216	Endometrial	Pap brush	sample		chr10	123258034	SBS	A				
						C					FGFR2		1647
	549	N	K	No	No	1.72	47						
PAP	216	Endometrial	Pap brush	sample		chr10	89653809	Indel	G				
											PTEN		107
	36	G	NULL	No	No	1.24	48						
PAP	227	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				
						G					KRAS		35
	12	G	A	No	No	15.76	410						
PAP	227	Endometrial	Pap brush	sample		chr3	178952088	SBS	A				
						G					PIK3CA		3143
	1048	H	R	No	No	3.31	129						
PAP	228	Endometrial	Pap brush	sample		chr3	41266097	SBS	G				
						A					CTNNB1		94
	32	D	N	No	No	23.44	546						
PAP	228	Endometrial	Pap brush	sample		chr5	67591097	SBS	A				
						G					PIK3R1		1690
	564	N	D	No	No	25.65	1646						
PAP	231	Endometrial	Pap brush	sample		chr17	7578268	SBS	A				
						C					TP53		581
	194	L	R	No	No	0.82	67						
PAP	122	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						G					PTEN		388
	130	R	G	No	No	0.15	7						
PAP	132	Endometrial	Pap brush	sample		chr5	112174631	SBS	C				
						T					APC		3340
	1114	R	*	No	No	41.74	3872						
PAP	132	Endometrial	Pap brush	sample		chr3	178952074	SBS	G				

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						T					PIK3CA	3129
	1043	M	I	No	No	25.70	1627					
PAP	132	Endometrial	Pap brush	sample		chr5	67588951	SBS	C			
						T					PIK3R1	1042
	348	R	*	No	No	18.08	113					
PAP	132	Endometrial	Pap brush	sample		chr5	67589562	SBS	T			
						G					PIK3R1	1325
	442	I	S	No	No	0.23	12					
PAP	132	Endometrial	Pap brush	sample		chr10	89624245	SBS	G			
						T					PTEN	19
	7	E	*	No	No	50.74	4886					
PAP	132	Endometrial	Pap brush	sample		chr10	89624270	SBS	G			
						T					PTEN	44
	15	R	I	No	No	23.30	2244					
PAP	132	Endometrial	Pap brush	sample		chr10	89711900	SBS	G			
						A					PTEN	518
	173	R	H	No	No	3.17	393					
PAP	132	Endometrial	Pap brush	sample		chr10	89720744	SBS	G			
						T					PTEN	895
	299	E	*	No	No	3.67	1282					
PAP	132	Endometrial	Pap brush	sample		chr17	7578211	SBS	C			
						T					TP53	638
	213	R	Q	No	No	0.99	124					
PAP	132	Endometrial	Pap brush	sample		chr17	7577138	SBS	C			
						T					TP53	800
	267	R	Q	No	No	12.60	1032					
PAP	173	Ovarian	Pap brush	sample		chr3	41266101	SBS	C			
						G					CTNNB1	98
	33	S	C	No	No	0.72	24					
PAP	173	Ovarian	Pap brush	sample		chr3	178936091	SBS	G			
						A					PIK3CA	1633
	545	E	K	No	No	2.47	47					
PAP	181	Endometrial	Pap brush	sample		chr19	52716323	SBS	C			
						T					PPP2R1A	767
	256	S	F	No	No	68.96	6377					
PAP	181	Endometrial	Pap brush	sample		chr17	7578190	SBS	T			
						C					TP53	659
	220	Y	C	No	No	62.45	1791					
PAP	194	Ovarian	Pap brush	sample		chr17	7578484	Indel	G			
											TP53	446
	149	S	NULL	No	No	5.75	338					
PAP	203	Endometrial	Pap brush	sample		chr3	178952077	SBS	T			
						A					PIK3CA	3132
	1044	N	K	No	No	9.45	387					
PAP	203	Endometrial	Pap brush	sample		chr5	67589579	Indel	AAA			
											PIK3R1	1342
	448	K	NULL	No	No	2.47	78					
PAP	203	Endometrial	Pap brush	sample		chr10	89712018	SBS	T			

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```
                                    C                                       PTEN    0
     0       NULL    NULL    1       No      15.58   1111
PAP 203     Endometrial   Pap brush sample     chr10   89720716     Indel   A
                                                                            PTEN    867
     289     K       NULL    No      No      0.57    57
PAP 203     Endometrial   Pap brush sample     chr10   89720761     SBS     C
                                    A                                       PTEN    912
     304     C       *       No      No      8.20    373
PAP 207     Endometrial   Pap brush sample     chr12   25378561     SBS     G
                                    A                                       KRAS    437
     146     A       V       No      No      26.74   878
PAP 207     Endometrial   Pap brush sample     chr5    67592099     SBS     C
                                    T                                       PIK3R1  1915
     639     R       *       No      No      32.58   1518
PAP 214     Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    T                                       KRAS    35
     12      G       D       No      No      4.94    198
PAP 214     Endometrial   Pap brush sample     chr10   89692904     SBS     C
                                    G                                       PTEN    388
     130     R       G       No      No      0.44    22
PAP 214     Endometrial   Pap brush sample     chr17   7578212      SBS     G
                                    A                                       TP53    637
     213     R       *       No      No      2.96    166
PAP 221     Endometrial   Pap brush sample     chr3    178936092    SBS     A
                                    C                                       PIK3CA  1634
     545     E       A       No      No      2.28    42
PAP 609     Endometrial   Pap brush sample     chr12   133250289    SBS     C
                                    G                                       POLE    1231
     411     V       L       No      No      6.28    951
PAP 609     Endometrial   Pap brush sample     chr17   7577102      Indel   C
                                                                            TP53    836
     279     G       NULL    No      No      0.16    30
PAP 616     Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    A                                       KRAS    35
     12      G       V       No      No      6.49    149
PAP 616     Endometrial   Pap brush sample     chr3    178916876    SBS     G
                                    A                                       PIK3CA  263
     88      R       Q       No      No      1.09    153
PAP 616     Endometrial   Pap brush sample     chr5    67591135     Indel   G
                                                                            PIK3R1  1728
     576     T       NULL    No      No      1.96    29
PAP 616     Endometrial   Pap brush sample     chr10   89692905     SBS     G
                                    A                                       PTEN    389
     130     R       Q       No      No      2.31    31
PAP 621     Endometrial   Pap brush sample     chr1    115258747    SBS     C
                                    G                                       NRAS    35
     12      G       A       No      No      2.29    70
PAP 629     Endometrial   Pap brush sample     chr5    67591098     Indel
```

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					ACGTATGAA						PIK3R1	1691	
	564	N	NULL	No	No	0.30	25						
PAP	596	Endometrial	Pap brush	sample		chr10	89720767	Indel					
					A						PTEN	918	
	306	I	NULL	No	No	0.19	15						
PAP	633	Endometrial	Pap brush	sample		chr3	41266098	SBS	A				
					T						CTNNB1	95	
	32	D	V	No	No	0.63	52						
PAP	633	Endometrial	Pap brush	sample		chr12	25398282	SBS	C				
					A						KRAS	37	
	13	G	C	No	No	1.89	100						
PAP	633	Endometrial	Pap brush	sample		chr5	67591106	SBS	A				
					G						PIK3R1	1699	
	567	K	E	No	No	2.12	197						
PAP	633	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
					G						PTEN	388	
	130	R	G	No	No	0.60	61						
PAP	272	Endometrial	Pap brush	sample		chr4	153247288	SBS	C				
					T						FBXW7	1514	
	505	R	H	No	No	61.62	12245						
PAP	272	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
					C						FGFR2	755	
	252	S	W	No	No	12.52	879						
PAP	272	Endometrial	Pap brush	sample		chr3	178916854	SBS	G				
					A						PIK3CA	241	
	81	E	K	No	No	57.20	10210						
PAP	272	Endometrial	Pap brush	sample		chr12	133250289	SBS	C				
					A						POLE	1231	
	411	V	L	No	No	30.12	4672						
PAP	272	Endometrial	Pap brush	sample		chr10	89624245	SBS	G				
					T						PTEN	19	
	7	E	*	No	No	46.63	788						
PAP	272	Endometrial	Pap brush	sample		chr10	89692905	SBS	G				
					A						PTEN	389	
	130	R	Q	No	No	7.08	151						
PAP	272	Endometrial	Pap brush	sample		chr17	7577117	SBS	A				
					G						TP53	821	
	274	V	A	No	No	83.83	1835						
PAP	274	Endometrial	Pap brush	sample		chr14	105246551	SBS	C				
					T						AKT1	49	
	17	E	K	No	No	20.36	2957						
PAP	274	Endometrial	Pap brush	sample		chr5	112175681	Indel	GA				
											APC	4390	
	1464	E	NULL	No	No	10.22	992						
PAP	274	Endometrial	Pap brush	sample		chr5	112175684	Indel	AG				
											APC	4393	
	1465	S	NULL	No	No	11.13	1652						
PAP	274	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				

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						T					KRAS	35	
	12	G	D	No	No	10.16	463						
PAP	277	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
						C					FGFR2	755	
	252	S	W	No	No	1.21	254						
PAP	552	Ovarian	Pap brush	sample		chr17	7578556	SBS	T				
						C					TP53	0	
	0	NULL	NULL	1	No	3.12	87						
PAP	581	Endometrial	Pap brush	sample		chr5	67591123	Indel	GCTGAG				
											PIK3R1	1716	
	572	Q	NULL	No	No	8.14	262						
PAP	581	Endometrial	Pap brush	sample		chr10	89692920	SBS	T				
						A					PTEN	404	
	135	I	K	No	No	1.74	82						
PAP	593	Endometrial	Pap brush	sample		chr3	41266113	SBS	C				
						G					CTNNB1	110	
	37	S	C	No	No	0.60	26						
PAP	593	Endometrial	Pap brush	sample		chr3	41266113	SBS	C				
						T					CTNNB1	110	
	37	S	F	No	No	0.21	9						
PAP	593	Endometrial	Pap brush	sample		chr10	89692893	SBS	C				
						T					PTEN	377	
	126	A	V	No	No	16.18	296						
PAP	599	Endometrial	Pap brush	sample		chr10	89653799	Indel	ATT				
											PTEN	97	
	33	I	NULL	No	No	0.98	68						
PAP	625	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				
						A					PIK3CA	263	
	88	R	Q	No	No	2.62	830						
PAP	625	Endometrial	Pap brush	sample		chr3	178952007	SBS	A				
						G					PIK3CA	3062	
	1021	Y	C	No	No	5.57	78						
PAP	625	Endometrial	Pap brush	sample		chr12	133253184	SBS	G				
						C					POLE	857	
	286	P	R	No	No	4.91	297						
PAP	625	Endometrial	Pap brush	sample		chr17	7578212	SBS	G				
						A					TP53	637	
	213	R	*	No	No	5.91	260						
PAP	632	Endometrial	Pap brush	sample		chr4	153247366	SBS	C				
						T					FBXW7	1436	
	479	R	Q	No	No	1.81	82						
PAP	632	Endometrial	Pap brush	sample		chr19	52716327	SBS	G				
						T					PPP2R1A	771	
	257	W	C	No	No	3.76	301						
PAP	271	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				
						A					PIK3CA	263	
	88	R	Q	No	No	7.85	68						
PAP	271	Endometrial	Pap brush	sample		chr12	133253151	SBS	G				

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						A					POLE		890
	297	S	F		No	No	11.88	41					
PAP	271	Endometrial	Pap brush		sample		chr10	89720744	SBS	G			
						T					PTEN		895
	299	E	*		No	No	13.89	75					
PAP	275	Endometrial	Pap brush		sample		chr3	41266104	SBS	G			
						T					CTNNB1		101
	34	G	V		No	No	9.50	32					
PAP	686	Endometrial	Tao brush		sample		chr10	89692905	SBS	G			
						C					PTEN		389
	130	R	P		No	No	1.43	330					
PAP	686	Endometrial	Tao brush		sample		chr10	89717610	Indel	A			
											PTEN		635
	212	N	NULL		No	No	5.15	152					
PAP	687	Endometrial	Pap brush		sample		chr17	7578397	SBS	T			
						G					TP53		533
	178	H	P		No	No	0.41	20					
PAP	691	Endometrial	Pap brush		sample		chr5	112174631	SBS	C			
						T					APC		3340
	1114	R	*		No	No	8.23	352					
PAP	691	Endometrial	Pap brush		sample		chr10	123258036	SBS	T			
						G					FGFR2		1645
	549	N	H		No	No	8.51	233					
PAP	691	Endometrial	Pap brush		sample		chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	4.17	35					
PAP	691	Endometrial	Pap brush		sample		chr12	133253184	SBS	G			
						C					POLE		857
	286	P	R		No	No	9.13	240					
PAP	691	Endometrial	Pap brush		sample		chr10	89624245	SBS	G			
						T					PTEN		19
	7	E	*		No	No	7.13	1671					
PAP	691	Endometrial	Pap brush		sample		chr10	89692905	SBS	G			
						A					PTEN		389
	130	R	Q		No	No	2.87	343					
PAP	691	Endometrial	Pap brush		sample		chr17	7577027	SBS	G			
						T					TP53		911
	304	T	N		No	No	0.33	32					
PAP	691	Endometrial	Tao brush		sample		chr5	112174631	SBS	C			
						T					APC		3340
	1114	R	*		No	No	25.90	967					
PAP	691	Endometrial	Tao brush		sample		chr10	123258036	SBS	T			
						G					FGFR2		1645
	549	N	H		No	No	28.73	507					
PAP	691	Endometrial	Tao brush		sample		chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	12.80	54					
PAP	691	Endometrial	Tao brush		sample		chr12	133253184	SBS	G			

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						C					POLE		857
	286	P	R		No	No	26.11	377					
PAP	691	Endometrial		Tao brush		sample	chr10	89624245	SBS	G			
						T					PTEN		19
	7	E	*		No	No	25.51	4937					
PAP	691	Endometrial		Tao brush		sample	chr10	89692905	SBS	G			
						A					PTEN		389
	130	R	Q		No	No	10.03	838					
PAP	707	Ovarian		Pap brush		sample	chr17	7578271	SBS	T			
						C					TP53		578
	193	H	R		No	No	1.05	79					
PAP	824	Endometrial		Pap brush		sample	chr10	89692904	SBS	C			
						G					PTEN		388
	130	R	G		No	No	0.12	26					
PAP	829	Endometrial		Pap brush		sample	chr3	178916854	SBS	G			
						A					PIK3CA		241
	81	E	K		No	No	2.83	31					
PAP	829	Endometrial		Pap brush		sample	chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	2.47	27					
PAP	829	Endometrial		Pap brush		sample	chr5	67590993	Indel	A			
											PIK3R1		1586
	529	D	NULL		No	No	0.52	11					
PAP	829	Endometrial		Pap brush		sample	chr12	133253184	SBS	G			
						C					POLE		857
	286	P	R		No	No	6.29	167					
PAP	829	Endometrial		Pap brush		sample	chr10	89692995	SBS	C			
						T					PTEN		479
	160	T	I		No	No	5.65	157					
PAP	829	Endometrial		Pap brush		sample	chr10	89711891	SBS	G			
						A					PTEN		509
	170	S	N		No	No	5.05	103					
PAP	832	Endometrial		Tao brush		sample	chr17	7578539	Indel	T			
											TP53		391
	131	N	NULL		No	No	1.73	108					
PAP	839	Endometrial		Tao brush		sample	chr5	67591097	SBS	A			
						G					PIK3R1		1690
	564	N	D		No	No	37.48	1366					
PAP	841	Endometrial		Pap brush		sample	chr17	7577022	SBS	G			
						A					TP53		916
	306	R	*		No	No	12.47	244					
PAP	690	Endometrial		Pap brush		sample	chr3	41266113	SBS	C			
						T					CTNNB1		110
	37	S	F		No	No	0.30	14					
PAP	690	Endometrial		Pap brush		sample	chr12	25398284	SBS	C			
						A					KRAS		35
	12	G	V		No	No	14.68	1083					
PAP	690	Endometrial		Pap brush		sample	chr3	178952085	SBS	A			

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						G						PIK3CA	3140
	1047	H	R		No	No	7.55	317					
PAP	831	Endometrial	Pap brush		sample		chr19	52716323	SBS	C			
						T						PPP2R1A	767
	256	S	F		No	No	39.91	1462					
PAP	831	Endometrial	Tao brush		sample		chr19	52716323	SBS	C			
						T						PPP2R1A	767
	256	S	F		No	No	32.93	753					
PAP	836	Endometrial	Tao brush		sample		chr10	89692905	SBS	G			
						C						PTEN	389
	130	R	P		No	No	4.54	433					
PAP	839	Endometrial	Pap brush		sample		chr5	67591097	SBS	A			
						G						PIK3R1	1690
	564	N	D		No	No	1.85	59					
PAP	842	Endometrial	Tao brush		sample		chr10	89720817	Indel	A			
												PTEN	968
	323	N	NULL		No	No	9.41	149					
PAP	688	Endometrial	Pap brush		sample		chr12	25398285	SBS	C			
						A						KRAS	34
	12	G	C		No	No	2.40	201					
PAP	688	Endometrial	Tao brush		sample		chr12	25398285	SBS	C			
						A						KRAS	34
	12	G	C		No	No	15.45	1018					
PAP	688	Endometrial	Tao brush		sample		chr5	67591128	SBS	G			
						T						PIK3R1	1721
	574	R	I		No	No	10.50	90					
PAP	690	Endometrial	Tao brush		sample		chr12	25398284	SBS	C			
						A						KRAS	35
	12	G	V		No	No	28.98	3154					
PAP	690	Endometrial	Tao brush		sample		chr3	178952085	SBS	A			
						G						PIK3CA	3140
	1047	H	R		No	No	16.15	1457					
PAP	696	Endometrial	Pap brush		sample		chr3	41266101	SBS	C			
						G						CTNNB1	98
	33	S	C		No	No	0.80	52					
PAP	696	Endometrial	Pap brush		sample		chr12	25398284	SBS	C			
						T						KRAS	35
	12	G	D		No	No	48.69	5000					
PAP	696	Endometrial	Pap brush		sample		chr10	89653829	SBS	G			
						T						PTEN	127
	43	E	*		No	No	74.40	5874					
PAP	824	Endometrial	Tao brush		sample		chr3	178952085	SBS	A			
						G						PIK3CA	3140
	1047	H	R		No	No	38.71	2444					
PAP	824	Endometrial	Tao brush		sample		chr10	89692790	SBS	G			
						T						PTEN	274
	92	D	Y		No	No	22.52	93					
PAP	824	Endometrial	Tao brush		sample		chr10	89692904	SBS	C			

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                                    G                                       PTEN    388
     130     R       G       No      No      12.46   1807
PAP 835     Endometrial   Pap brush sample     chr3    178936082    SBS     G
                                    A                                       PIK3CA  1624
     542     E       K       No      No      42.89   1216
PAP 835     Endometrial   Tao brush sample     chr3    178936082    SBS     G
                                    A                                       PIK3CA  1624
     542     E       K       No      No      46.57   1268
PAP 841     Endometrial   Tao brush sample     chr17   7577022      SBS     G
                                    A                                       TP53    916
     306     R       *       No      No      35.37   5336
PAP 685     Endometrial   Pap brush sample     chr10   89692845     Indel   AATGGC
                                                                            PTEN    329
     110     Q       NULL    No      No      0.15    11
PAP 685     Endometrial   Tao brush sample     chr10   123247516    SBS     T
                                    C                                       FGFR2   1975
     659     K       E       No      No      17.49   832
PAP 685     Endometrial   Tao brush sample     chr10   89692845     Indel   AATGGC
                                                                            PTEN    329
     110     Q       NULL    No      No      16.92   1274
PAP 685     Endometrial   Tao brush sample     chr10   89692904     SBS     C
                                    T                                       PTEN    388
     130     R       *       No      No      7.16    1137
PAP 687     Endometrial   Tao brush sample     chr3    178952085    SBS     A
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      29.65   1645
PAP 687     Endometrial   Tao brush sample     chr17   7578403      SBS     C
                                    T                                       TP53    527
     176     C       Y       No      No      68.66   1512
PAP 695     Endometrial   Pap brush sample     chr3    178952085    SBS     A
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      15.67   954
PAP 695     Endometrial   Pap brush sample     chr17   7577120      SBS     C
                                    T                                       TP53    818
     273     R       H       No      No      17.66   1090
PAP 697     Endometrial   Pap brush sample     chr5    112174257    Indel
ATGATGAAAG (SEQ ID NO:766)                                                  APC
   2966       989     D       NULL    No      No      6.79    154
PAP 697     Endometrial   Pap brush sample     chr10   89692918     Indel   GAT
                                                                            PTEN    402
     134     M       NULL    No      No      6.34    413
PAP 699     Endometrial   Pap brush sample     chr5    112173791    Indel
                                    T                                       APC     2500
     834     S       NULL    No      No      25.20   1214
PAP 699     Endometrial   Pap brush sample     chr4    153247303    SBS     T
                                    C                                       FBXW7   1499
     500     H       R       No      No      11.56   743
PAP 699     Endometrial   Pap brush sample     chr10   89711899     SBS     C
```

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T PTEN 517
173 R C No No 28.54 774
PAP 699 Endometrial Pap brush sample chr10 89717775 Indel
A PTEN 800
267 K NULL No No 29.15 1123
PAP 711 Ovarian Pap brush sample chr5 67589596 Indel
CACTCAGTTTCAAGAAAAAAG (SEQ ID NO:767)
PIK3R1 1359 453 N NULL No No 0.24 10
PAP 711 Ovarian Pap brush sample chr19 52716327 SBS G
T PPP2R1A 771
257 W C No No 3.34 52
PAP 711 Ovarian Pap brush sample chr17 7578429 Indel C
TP53 501
167 Q NULL No No 0.46 18
PAP 837 Endometrial Tao brush sample chr10 89692904 SBS C
G PTEN 388
130 R G No No 1.28 291
PAP 837 Endometrial Tao brush sample chr17 7577120 SBS C
G TP53 818
273 R P No No 0.27 31
PAP 842 Endometrial Pap brush sample chr12 25380275 SBS T
G KRAS 183
61 Q H No No 1.32 91
PAP 842 Endometrial Pap brush sample chr5 67590478 SBS C
T PIK3R1 1540
514 R C No No 1.25 77
PAP 842 Endometrial Pap brush sample chr10 89720817 Indel A
PTEN 968
323 N NULL No No 2.82 65
PAP 845 Ovarian Tao brush sample chr17 7577120 SBS C
T TP53 818
273 R H No No 24.65 1480
PAP 675 Endometrial Pap brush sample chr5 112175684 Indel AG
APC 4393
1465 S NULL No No 0.56 49
PAP 675 Endometrial Pap brush sample chr3 178952084 SBS C
T PIK3CA 3139
1047 H Y No No 10.14 262
PAP 675 Endometrial Pap brush sample chr10 89720867 Indel AATT
PTEN 1018
340 N NULL No No 3.03 8
PAP 675 Endometrial Pap brush sample chr17 56435083 Indel G
RNF43 2054
685 T NULL No No 1.39 34
PAP 675 Endometrial Pap brush sample chr17 7577114 SBS C
A TP53 824
275 C F No No 24.95 1142
PAP 850 Endometrial Pap brush sample chr3 41266113 SBS C

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						T					CTNNB1	110	
37	S	F	No	No	43.61	1310							
PAP 850	Endometrial	Pap brush	sample		chr10	123279677	SBS	G					
						C					FGFR2	755	
252	S	W	No	No	13.37	226							
PAP 850	Endometrial	Pap brush	sample		chr3	178936091	SBS	G					
						A					PIK3CA	1633	
545	E	K	No	No	45.49	2906							
PAP 850	Endometrial	Pap brush	sample		chr10	89720852	SBS	C					
						T					PTEN	1003	
335	R	*	No	No	91.18	2109							
PAP 850	Endometrial	Tao brush	sample		chr10	123279677	SBS	G					
						C					FGFR2	755	
252	S	W	No	No	17.12	839							
PAP 850	Endometrial	Tao brush	sample		chr3	178936091	SBS	G					
						A					PIK3CA	1633	
545	E	K	No	No	46.00	3229							
PAP 850	Endometrial	Tao brush	sample		chr10	89720852	SBS	C					
						T					PTEN	1003	
335	R	*	No	No	92.59	3871							
PAP 850	Endometrial	Tao brush	sample		chr17	56435167	Indel	C					
											RNF43	1970	
657	R	NULL	No	No	10.13	211							
PAP 850	Endometrial	Tao brush	sample		chr17	7578421	SBS	G					
						A					TP53	509	
170	T	M	No	No	0.49	17							
PAPA 1010	Endometrial	Tao brush	sample		chr12	25398284	SBS	C					
						A					KRAS	35	
12	G	V	No	No	32.34	1389							
PAPA 1010	Endometrial	Tao brush	sample		chr10	89692893	SBS	C					
						A					PTEN	377	
126	A	D	No	No	29.37	1775							
PAPA 1010	Endometrial	Tao brush	sample		chr17	7577124	SBS	C					
						T					TP53	814	
272	V	M	No	No	21.10	882							
PAPA 1011	Endometrial	Tao brush	sample		chr10	123258036	SBS	T					
						G					FGFR2	1645	
549	N	H	No	No	7.60	65							
PAPA 1012	Endometrial	Tao brush	sample		chr12	25398281	SBS	C					
						T					KRAS	38	
13	G	D	No	No	28.11	610							
PAPA 1012	Endometrial	Tao brush	sample		chr3	178916876	SBS	G					
						A					PIK3CA	263	
88	R	Q	No	No	20.13	62							
PAPA 1012	Endometrial	Tao brush	sample		chr10	89717775	Indel						
						A					PTEN	800	
267	K	NULL	No	No	23.69	258							
PAPA 1012	Endometrial	Tao brush	sample		chr10	89717775	Indel	A					

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											PTEN	800
	267	K	NULL	No	No	27.09	295					
PAPA	1013	Endometrial	Pap brush	sample		chr17	7577141	SBS	C			
					T						TP53	797
	266	G	E	No	No	22.35	1500					
PAPA	1016	Endometrial	Pap brush	sample		chr10	123279677	SBS	G			
					C						FGFR2	755
	252	S	W	No	No	9.62	282					
PAPA	1016	Endometrial	Pap brush	sample		chr3	178916836	SBS	C			
					G						PIK3CA	223
	75	Q	E	No	No	20.03	152					
PAPA	1016	Endometrial	Pap brush	sample		chr5	67591152	Indel	TGT			
											PIK3R1	1745
	582	M	NULL	No	Yes	1.32	17					
PAPA	1016	Endometrial	Pap brush	sample		chr5	67592052	Indel	CA			
											PIK3R1	1868
	623	T	NULL	No	No	9.18	187					
PAPA	1016	Endometrial	Pap brush	sample		chr10	89692904	SBS	C			
					G						PTEN	388
	130	R	G	No	No	8.80	923					
PAPA	1016	Endometrial	Tao brush	sample		chr10	123279677	SBS	G			
					C						FGFR2	755
	252	S	W	No	No	37.50	309					
PAPA	1016	Endometrial	Tao brush	sample		chr3	178916836	SBS	C			
					G						PIK3CA	223
	75	Q	E	No	No	55.86	224					
PAPA	1016	Endometrial	Tao brush	sample		chr5	67591152	Indel	TGT			
											PIK3R1	1745
	582	M	NULL	No	Yes	6.39	68					
PAPA	1016	Endometrial	Tao brush	sample		chr5	67592052	Indel	CA			
											PIK3R1	1868
	623	T	NULL	No	No	33.15	648					
PAPA	1016	Endometrial	Tao brush	sample		chr10	89692904	SBS	C			
					G						PTEN	388
	130	R	G	No	No	27.11	2378					
PAP	120	Endometrial	Pap brush	sample		chr3	41266101	SBS	C			
					G						CTNNB1	98
	33	S	C	No	No	3.86	378					
PAP	120	Endometrial	Pap brush	sample		chr3	178952085	SBS	A			
					G						PIK3CA	3140
	1047	H	R	No	No	6.76	700					
PAP	853	Endometrial	Tao brush	sample		chr3	41266101	SBS	C			
					G						CTNNB1	98
	33	S	C	No	No	39.42	2871					
PAP	853	Endometrial	Tao brush	sample		chr3	178952085	SBS	A			
					G						PIK3CA	3140
	1047	H	R	No	No	37.18	5264					
PAP	853	Endometrial	Tao brush	sample		chr10	89711899	SBS	C			

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						T					PTEN		517
	173	R	C	No	No	39.25	3020						
PAP	860	Endometrial	Pap brush	sample		chr3	41266101	SBS	C				
						T					CTNNB1		98
	33	S	F	No	No	1.04	159						
PAP	860	Endometrial	Pap brush	sample		chr3	178936091	SBS	G				
						A					PIK3CA		1633
	545	E	K	No	No	0.92	294						
PAPA	1010	Endometrial	Pap brush	sample		chr17	7577124	SBS	C				
						T					TP53		814
	272	V	M	No	No	1.26	84						
PAPA	1013	Endometrial	Tao brush	sample		chr17	7577141	SBS	C				
						T					TP53		797
	266	G	E	No	No	20.53	1279						
PAPA	1019	Endometrial	Pap brush	sample		chr10	89692961	SBS	C				
						T					PTEN		445
	149	Q	*	No	No	0.13	25						
PAPA	1019	Endometrial	Tao brush	sample		chr4	153247366	SBS	C				
						T					FBXW7		1436
	479	R	Q	No	No	21.45	118						
PAPA	1019	Endometrial	Tao brush	sample		chr5	67591139	Indel	GA				
											PIK3R1		1732
	578	D	NULL	No	No	28.79	152						
PAPA	1019	Endometrial	Tao brush	sample		chr10	89692961	SBS	C				
						T					PTEN		445
	149	Q	*	No	No	13.07	556						
PAPA	1019	Endometrial	Tao brush	sample		chr10	89717672	SBS	C				
						T					PTEN		697
	233	R	*	No	No	9.33	358						
PAPA	1019	Endometrial	Tao brush	sample		chr17	7578388	SBS	C				
						T					TP53		542
	181	R	H	No	No	30.55	172						
PAP	671	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
						C					FGFR2		755
	252	S	W	No	No	0.75	17						
PAP	671	Endometrial	Pap brush	sample		chr10	123258034	SBS	A				
						T					FGFR2		1647
	549	N	K	No	No	3.97	86						
PAP	671	Endometrial	Pap brush	sample		chr10	89692922	SBS	T				
						C					PTEN		406
	136	C	R	No	No	1.63	149						
PAP	681	Endometrial	Pap brush	sample		chr10	89692902	SBS	G				
						T					PTEN		386
	129	G	V	No	No	2.02	405						
PAP	684	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						G					PTEN		388
	130	R	G	No	No	2.89	201						
PAP	684	Endometrial	Pap brush	sample		chr10	89720808	SBS	T				

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						A					PTEN	959	
320	L	*	No	No	6.48	49							
PAP 851	Endometrial	Tao	brush	sample		chr3	41266124	SBS	A				
						G					CTNNB1	121	
41	T	A	No	No	36.57	918							
PAP 851	Endometrial	Tao	brush	sample		chr4	153247367	SBS	G				
						C					FBXW7	1435	
479	R	G	No	No	34.66	670							
PAP 851	Endometrial	Tao	brush	sample		chr10	89653834	Indel	C				
											PTEN	132	
44	G	NULL	No	No	9.75	46							
PAP 851	Endometrial	Tao	brush	sample		chr17	7578525	SBS	G				
						T					TP53	405	
135	C	*	No	No	35.95	1141							
PAP 860	Endometrial	Tao	brush	sample		chr3	178936091	SBS	G				
						A					PIK3CA	1633	
545	E	K	No	No	11.82	612							
PAP 860	Endometrial	Tao	brush	sample		chr17	56435167	Indel	C				
											RNF43	1970	
657	R	NULL	No	No	6.32	151							
PAPA 1012	Endometrial	Pap	brush	sample		chr12	25398281	SBS	C				
						T					KRAS	38	
13	G	D	No	No	17.35	369							
PAPA 1012	Endometrial	Pap	brush	sample		chr3	178916876	SBS	G				
						A					PIK3CA	263	
88	R	Q	No	No	9.79	32							
PAPA 1012	Endometrial	Pap	brush	sample		chr10	89717775	Indel					
						A					PTEN	800	
267	K	NULL	No	No	18.01	515							
PAPA 1012	Endometrial	Pap	brush	sample		chr10	89717775	Indel	A				
											PTEN	800	
267	K	NULL	No	No	16.47	471							
PAP 667	Endometrial	Pap	brush	sample		chr12	25398284	SBS	C				
						T					KRAS	35	
12	G	D	No	No	49.63	2526							
PAP 668	Endometrial	Pap	brush	sample		chr19	52715971	SBS	C				
						G					PPP2R1A	536	
179	P	R	No	No	0.23	27							
PAP 669	Endometrial	Pap	brush	sample		chr5	67591112	Indel					
						G					PIK3R1	1705	
569	D	NULL	No	No	0.22	19							
PAP 669	Endometrial	Pap	brush	sample		chr10	89692904	SBS	C				
						G					PTEN	388	
130	R	G	No	No	0.17	22							
PAP 851	Endometrial	Pap	brush	sample		chr3	41266124	SBS	A				
						G					CTNNB1	121	
41	T	A	No	No	0.83	51							
PAP 851	Endometrial	Pap	brush	sample		chr4	153247367	SBS	G				

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						C					FBXW7	1435	
	479	R	G		No	No	0.97	49					
PAP	851	Endometrial	Pap brush		sample		chr10	89653834	Indel	C			
											PTEN	132	
	44	G	NULL		No	No	0.60	14					
PAP	858	Endometrial	Tao brush		sample		chr3	178952072	SBS	A			
						G					PIK3CA	3127	
	1043	M	V		No	No	38.59	3862					
PAP	858	Endometrial	Tao brush		sample		chr17	7578175	SBS	A			
						C					TP53	0	
	0	NULL	NULL		1	No	74.82	3917					
PAP	862	Endometrial	Tao brush		sample		chr17	7578212	SBS	G			
						A					TP53	637	
	213	R	*		No	No	85.71	1662					
PAP	128	Endometrial	Pap brush		sample		chr10	123258034	SBS	A			
						T					FGFR2	1647	
	549	N	K		No	No	41.03	1931					
PAP	128	Endometrial	Pap brush		sample		chr3	178952090	SBS	G			
						A					PIK3CA	3145	
	1049	G	S		No	No	28.74	1070					
PAP	128	Endometrial	Pap brush		sample		chr5	67591128	SBS	G			
						C					PIK3R1	1721	
	574	R	T		No	No	21.02	641					
PAP	663	Endometrial	Pap brush		sample		chr4	153247367	SBS	G			
						A					FBXW7	1435	
	479	R	*		No	No	11.58	130					
PAP	663	Endometrial	Pap brush		sample		chr3	178916854	SBS	G			
						A					PIK3CA	241	
	81	E	K		No	No	15.92	124					
PAP	663	Endometrial	Pap brush		sample		chr12	133253184	SBS	G			
						C					POLE	857	
	286	P	R		No	No	16.28	142					
PAP	663	Endometrial	Pap brush		sample		chr10	89690835	SBS	T			
						G					PTEN	242	
	81	F	C		No	No	2.01	34					
PAP	663	Endometrial	Pap brush		sample		chr10	89624245	SBS	G			
						T					PTEN	19	
	7	E	*		No	No	16.69	426					
PAP	663	Endometrial	Pap brush		sample		chr10	89692905	SBS	G			
						A					PTEN	389	
	130	R	Q		No	No	1.71	93					
PAP	663	Endometrial	Pap brush		sample		chr17	7578212	SBS	G			
						A					TP53	637	
	213	R	*		No	No	17.73	269					
PAP	989	Endometrial	Pap brush		sample		chr3	178936091	SBS	G			
						A					PIK3CA	1633	
	545	E	K		No	No	29.40	2667					
PAP	989	Endometrial	Pap brush		sample		chr17	7577121	SBS	G			

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```
                                    A                                       TP53    817
     273     R       C       No      No      13.85   1103
PAP 990     Endometrial   Tao brush sample     chr1    115258744     SBS     C
                                    A                                       NRAS    38
     13      G       V       No      No      40.79   2113
PAP 990     Endometrial   Tao brush sample     chr10   89692904      SBS     C
                                    T                                       PTEN    388
     130     R       *       No      No      54.79   9533
PAP 990     Endometrial   Tao brush sample     chr17   56448310      SBS     G
                                    A                                       RNF43   337
     113     R       *       No      No      18.34   350
PAP 990     Endometrial   Tao brush sample     chr17   56435167      Indel   C
                                                                            RNF43   1970
     657     R       NULL    No      No      35.49   368
PAP 994     Endometrial   Pap brush sample     chr10   89692921      Indel
                                    A                                       PTEN    405
     135     I       NULL    No      No      0.27    62
PAP 994     Endometrial   Pap brush sample     chr10   89720804      Indel   ACTT
                                                                            PTEN    955
     319     T       NULL    No      No      1.23    34
PAP 996     Endometrial   Pap brush sample     chr3    41266113      SBS     C
                                    T                                       CTNNB1  110
     37      S       F       No      No      7.97    421
PAP 996     Endometrial   Pap brush sample     chr10   123279677     SBS     G
                                    C                                       FGFR2   755
     252     S       W       No      No      2.82    136
PAP 996     Endometrial   Pap brush sample     chr3    178936095     SBS     A
                                    G                                       PIK3CA  1637
     546     Q       R       No      No      8.12    411
PAP 996     Endometrial   Pap brush sample     chr10   89693009      Indel   G
                                                                            PTEN    0
     0       NULL    NULL    1       No      6.68    146
PAP 996     Endometrial   Pap brush sample     chr10   89725042      SBS     A
                                    G                                       PTEN    0
     0       NULL    NULL    1       No      8.64    408
PAP 998     Endometrial   Pap brush sample     chr9    21971186      Indel
GGGCGCTGCCCATC (SEQ ID NO:768)
CDKN2A  172         58      R       NULL    No      No      1.78    40
PAP 998     Endometrial   Pap brush sample     chr12   25380275      SBS     T
                                    A                                       KRAS    183
     61      Q       H       No      No      2.20    134
PAP 998     Endometrial   Pap brush sample     chr10   89720804      Indel
                                    A                                       PTEN    955
     319     T       NULL    No      No      2.44    90
PAP 999     Endometrial   Pap brush sample     chr12   25398281      SBS     C
                                    T                                       KRAS    38
     13      G       D       No      No      42.44   7827
PAP 999     Endometrial   Pap brush sample     chr19   52715971      SBS     C
```

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						G						PPP2R1A	536	
	179	P	R	No	No	18.27	1666							
PAP	999	Endometrial	Pap brush	sample		chr17	7578406	SBS	C					
						T						TP53	524	
	175	R	H	No	No	32.61	2038							
PAP	999	Endometrial	Tao brush	sample		chr12	25398281	SBS	C					
						T						KRAS	38	
	13	G	D	No	No	63.85	15888							
PAP	999	Endometrial	Tao brush	sample		chr19	52715971	SBS	C					
						G						PPP2R1A	536	
	179	P	R	No	No	34.43	3006							
PAP	999	Endometrial	Tao brush	sample		chr17	7578406	SBS	C					
						T						TP53	524	
	175	R	H	No	No	72.46	5025							
PAPA	1001	Endometrial	Pap brush	sample		chr10	89624305	SBS	T					
						G						PTEN	79	
	27	Y	D	No	Yes	0.14	36							
PAPA	1001	Endometrial	Tao brush	sample		chr12	25398284	SBS	C					
						A						KRAS	35	
	12	G	V	No	No	27.73	2467							
PAPA	1001	Endometrial	Tao brush	sample		chr5	67591094	Indel						
						AACGTA						PIK3R1	1687	
	563	M	NULL	No	No	36.12	1215							
PAPA	1001	Endometrial	Tao brush	sample		chr10	89624305	SBS	T					
						G						PTEN	79	
	27	Y	D	No	Yes	61.28	15665							
PAPA	1002	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A						PIK3CA	263	
	88	R	Q	No	No	3.30	56							
PAPA	1002	Endometrial	Pap brush	sample		chr3	178952077	SBS	T					
						G						PIK3CA	3132	
	1044	N	K	No	No	5.56	419							
PAPA	1002	Endometrial	Pap brush	sample		chr10	89624297	SBS	A					
						G						PTEN	71	
	24	D	G	No	No	0.25	61							
PAPA	1002	Endometrial	Pap brush	sample		chr10	89692905	SBS	G					
						A						PTEN	389	
	130	R	Q	No	No	1.80	444							
PAPA	1003	Endometrial	Tao brush	sample		chr14	105246551	SBS	C					
						T						AKT1	49	
	17	E	K	No	No	68.94	1884							
PAPA	1003	Endometrial	Tao brush	sample		chr3	41266098	SBS	A					
						G						CTNNB1	95	
	32	D	G	No	No	34.85	2859							
PAP	926	Endometrial	Pap brush	sample		chr3	41266104	SBS	G					
						A						CTNNB1	101	
	34	G	E	No	No	0.71	62							
PAP	926	Endometrial	Pap brush	sample		chr12	133250289	SBS	C					

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```
                                    G                                   POLE    1231
     411     V       L       No      No      2.23    309
PAP 926     Endometrial     Pap brush sample     chr10   89692905    SBS     G
                                    A                                   PTEN    389
     130     R       Q       No      No      1.19    280
PAP 926     Endometrial     Pap brush sample     chr10   89717672    SBS     C
                                    T                                   PTEN    697
     233     R       *       No      No      0.92    145
PAP 934     Endometrial     Tao brush sample     chr3    41266101    SBS     C
                                    A                                   CTNNB1  98
     33      S       Y       No      No      31.73   2632
PAP 934     Endometrial     Tao brush sample     chr3    178952085   SBS     A
                                    G                                   PIK3CA  3140
     1047    H       R       No      No      31.20   1862
PAP 990     Endometrial     Pap brush sample     chr1    115258744   SBS     C
                                    A                                   NRAS    38
     13      G       V       No      No      4.08    326
PAP 990     Endometrial     Pap brush sample     chr10   89692904    SBS     C
                                    T                                   PTEN    388
     130     R       *       No      No      4.94    782
PAP 990     Endometrial     Pap brush sample     chr17   56448303    Indel
                                    G                                   RNF43   344
     115     A       NULL    No      No      7.03    37
PAP 991     Endometrial     Tao brush sample     chr5    67591134    Indel   CGA
                                                                        PIK3R1  1727
     576     T       NULL    No      No      32.66   763
PAP 991     Endometrial     Tao brush sample     chr10   89692896    SBS     G
                                    T                                   PTEN    380
     127     G       V       No      No      33.50   3167
PAP 991     Endometrial     Tao brush sample     chr10   89692985    Indel
                                    G                                   PTEN    469
     157     E       NULL    No      No      31.94   842
PAP 991     Endometrial     Tao brush sample     chr17   7578279     Indel   AGG
                                                                        TP53    570
     190     P       NULL    No      No      0.54    88
PAP 996     Endometrial     Tao brush sample     chr3    41266113    SBS     C
                                    T                                   CTNNB1  110
     37      S       F       No      No      8.63    921
PAP 996     Endometrial     Tao brush sample     chr10   123279677   SBS     G
                                    C                                   FGFR2   755
     252     S       W       No      No      11.37   581
PAP 996     Endometrial     Tao brush sample     chr3    178936095   SBS     A
                                    G                                   PIK3CA  1637
     546     Q       R       No      No      25.71   2157
PAP 996     Endometrial     Tao brush sample     chr10   89693009    Indel   G
                                                                        PTEN    0
     0       NULL    NULL    1       No      27.21   590
PAP 996     Endometrial     Tao brush sample     chr10   89725042    SBS     A
```

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```
                                    G                                   PTEN    0
     0       NULL    NULL    1       No      31.25   3517
PAP 998     Endometrial   Tao brush sample     chr10   89720804     Indel
                                    A                                   PTEN    955
     319     T       NULL    No      No      5.39    180
PAPA 1002   Endometrial   Tao brush sample     chr3    178916876    SBS     G
                                    A                                   PIK3CA  263
     88      R       Q       No      No      15.45   306
PAPA 1002   Endometrial   Tao brush sample     chr3    178952077    SBS     T
                                    G                                   PIK3CA  3132
     1044    N       K       No      No      26.93   3461
PAPA 1002   Endometrial   Tao brush sample     chr10   89692905     SBS     G
                                    A                                   PTEN    389
     130     R       Q       No      No      11.09   3351
PAPA 1003   Endometrial   Pap brush sample     chr14   105246551    SBS     C
                                    T                                   AKT1    49
     17      E       K       No      No      3.93    192
PAPA 1003   Endometrial   Pap brush sample     chr3    41266098     SBS     A
                                    G                                   CTNNB1  95
     32      D       G       No      No      1.47    160
PAPA 1005   Endometrial   Pap brush sample     chr4    153249384    SBS     C
                                    T                                   FBXW7   1394
     465     R       H       No      No      4.00    268
PAPA 1005   Endometrial   Pap brush sample     chr12   25398284     SBS     C
                                    T                                   KRAS    35
     12      G       D       No      No      4.87    513
PAPA 1005   Endometrial   Pap brush sample     chr5    67591130     Indel
AAGACGAGA
PIK3R1  1723        575     K       NULL    No      No      2.82    55
PAPA 1005   Endometrial   Pap brush sample     chr17   7578413      SBS     C
                                    A                                   TP53    517
     173     V       L       No      No      4.74    433
PAP 922     Endometrial   Pap brush sample     chr3    41266097     SBS     G
                                    T                                   CTNNB1  94
     32      D       Y       No      No      1.66    121
PAP 922     Endometrial   Tao brush sample     chr3    41266097     SBS     G
                                    T                                   CTNNB1  94
     32      D       Y       No      No      17.44   1686
PAP 926     Endometrial   Tao brush sample     chr12   133250289    SBS     C
                                    G                                   POLE    1231
     411     V       L       No      No      7.76    895
PAP 927     Endometrial   Tao brush sample     chr10   89692883     SBS     C
                                    G                                   PTEN    367
     123     H       D       No      No      51.94   4503
PAP 928     Ovarian       Tao brush sample     chr17   7577127      SBS     C
                                    T                                   TP53    811
     271     E       K       No      No      0.70    100
PAP 931     Endometrial   Tao brush sample     chr3    41266113     SBS     C
```

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					T					CTNNB1	110	
	37	S	F	No	No	44.11	3924					
PAP	934	Endometrial	Pap brush	sample	chr3	41266101	SBS	C				
					A					CTNNB1	98	
	33	S	Y	No	No	0.26	22					
PAP	936	Endometrial	Tao brush	sample	chr4	153249384	SBS	C				
					T					FBXW7	1394	
	465	R	H	No	No	30.77	2312					
PAP	936	Endometrial	Tao brush	sample	chr3	178936082	SBS	G				
					A					PIK3CA	1624	
	542	E	K	No	No	28.74	2211					
PAP	936	Endometrial	Tao brush	sample	chr10	89692769	SBS	G				
					C					PTEN	0	
	0	NULL	NULL	1	No	34.13	443					
PAP	936	Endometrial	Tao brush	sample	chr10	89717775	Indel	A				
										PTEN	800	
	267	K	NULL	No	No	27.45	342					
PAP	936	Endometrial	Tao brush	sample	chr17	56435167	Indel	C				
										RNF43	1970	
	657	R	NULL	No	No	51.72	301					
PAP	989	Endometrial	Tao brush	sample	chr3	178936091	SBS	G				
					A					PIK3CA	1633	
	545	E	K	No	No	30.99	2697					
PAP	989	Endometrial	Tao brush	sample	chr17	7577121	SBS	G				
					A					TP53	817	
	273	R	C	No	No	12.99	1720					
PAP	991	Endometrial	Pap brush	sample	chr3	178936096	SBS	G				
					T					PIK3CA	1638	
	546	Q	H	No	No	3.89	428					
PAP	991	Endometrial	Pap brush	sample	chr3	178952085	SBS	A				
					G					PIK3CA	3140	
	1047	H	R	No	No	3.30	345					
PAP	991	Endometrial	Pap brush	sample	chr5	67591134	Indel	CGA				
										PIK3R1	1727	
	576	T	NULL	No	No	6.06	285					
PAP	991	Endometrial	Pap brush	sample	chr10	89692896	SBS	G				
					T					PTEN	380	
	127	G	V	No	No	12.78	1618					
PAP	991	Endometrial	Pap brush	sample	chr10	89692985	Indel					
					G					PTEN	469	
	157	E	NULL	No	No	12.36	616					
PAP	208	Endometrial	Pap brush	sample	chr3	41266101	SBS	C				
					A					CTNNB1	98	
	33	S	Y	No	No	0.40	19					
PAP	208	Endometrial	Pap brush	sample	chr1	115256530	SBS	G				
					T					NRAS	181	
	61	Q	K	No	No	6.38	306					
PAP	208	Endometrial	Pap brush	sample	chr3	178952085	SBS	A				

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```
                                    G                                       PIK3CA  3140
     1047    H       R       No      No      8.21    308
PAP 208     Endometrial   Pap brush sample     chr10   89717775      Indel
                                    A                                       PTEN    800
     267     K       NULL    No      No      2.48    6
PAP 208     Endometrial   Pap brush sample     chr10   89717775      Indel   A
                                                                            PTEN    800
     267     K       NULL    No      No      5.37    13
PAP 208     Endometrial   Pap brush sample     chr17   7578479       Indel   G
                                                                            TP53    451
     151     P       NULL    No      No      13.97   276
PAP 208     Endometrial   Pap brush sample     chr17   7578407       SBS     G
                                    A                                       TP53    523
     175     R       C       No      No      1.91    61
PAP 927     Endometrial   Pap brush sample     chr10   89692883      SBS     C
                                    G                                       PTEN    367
     123     H       D       No      No      0.72    30
PAP 928     Ovarian       Pap brush sample     chr17   7577498       SBS     C
                                    T                                       TP53    0
     0       NULL    NULL    1       No      0.66    52
PAP 931     Endometrial   Pap brush sample     chr3    41266113      SBS     C
                                    T                                       CTNNB1  110
     37      S       F       No      No      6.22    137
PAP 936     Endometrial   Pap brush sample     chr4    153249384     SBS     C
                                    T                                       FBXW7   1394
     465     R       H       No      No      2.98    62
PAP 936     Endometrial   Pap brush sample     chr10   89692769      SBS     G
                                    C                                       PTEN    0
     0       NULL    NULL    1       No      2.55    12
PAP 936     Endometrial   Pap brush sample     chr10   89717775      Indel   A
                                                                            PTEN    800
     267     K       NULL    No      No      2.84    16
PAP 936     Endometrial   Pap brush sample     chr17   56435167      Indel   C
                                                                            RNF43   1970
     657     R       NULL    No      No      6.85    51
PAPA 1005   Endometrial   Tao brush sample     chr17   7578413       SBS     C
                                    A                                       TP53    517
     173     V       L       No      No      3.44    83
PAP 728     Endometrial   Pap brush sample     chr10   89624272      Indel
TATCAAGAGG (SEQ ID NO:769)                                                                  PTEN
   46        16      Y       NULL    No      No      4.30    1067
PAP 728     Endometrial   Pap brush sample     chr10   89711893      SBS     C
                                    T                                       PTEN    511
     171     Q       *       No      No      5.61    307
PAP 728     Endometrial   Pap brush sample     chr10   89711899      SBS     C
                                    T                                       PTEN    517
     173     R       C       No      No      50.41   2760
PAP 728     Endometrial   Pap brush sample     chr17   7578402       Indel
```

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						G					TP53	528	
	176	C	NULL	No	No	5.57	332						
PAP	728	Endometrial	Pap brush	sample		chr17	7577105	SBS	G				
						C					TP53	833	
	278	P	R	No	No	5.09	524						
PAP	730	Endometrial	Pap brush	sample		chr3	41266118	SBS	G				
						A					CTNNB1	115	
	39	A	T	No	No	0.48	89						
PAP	730	Endometrial	Pap brush	sample		chr3	41266124	SBS	A				
						G					CTNNB1	121	
	41	T	A	No	No	1.05	196						
PAP	730	Endometrial	Pap brush	sample		chr3	41266136	SBS	T				
						C					CTNNB1	133	
	45	S	P	No	No	0.17	31						
PAP	730	Endometrial	Pap brush	sample		chr12	25398281	SBS	C				
						T					KRAS	38	
	13	G	D	No	No	5.71	1936						
PAP	730	Endometrial	Pap brush	sample		chr12	25398284	SBS	C				
						T					KRAS	35	
	12	G	D	No	No	3.14	1064						
PAP	730	Endometrial	Pap brush	sample		chr12	25398285	SBS	C				
						A					KRAS	34	
	12	G	C	No	No	5.65	1913						
PAP	730	Endometrial	Pap brush	sample		chr10	89624236	Indel	A				
											PTEN	10	
	4	I	NULL	No	No	66.14	26888						
PAP	730	Endometrial	Pap brush	sample		chr10	89725042	SBS	A				
						G					PTEN	0	
	0	NULL	NULL	1	No	1.34	180						
PAP	730	Endometrial	Pap brush	sample		chr17	56435167	Indel	C				
											RNF43	1970	
	657	R	NULL	No	No	23.41	1488						
PAP	730	Endometrial	Pap brush	sample		chr17	7579716	SBS	G				
						A					TP53	80	
	27	P	L	No	No	0.62	128						
PAP	735	Endometrial	Pap brush	sample		chr5	67591125	SBS	T				
						C					PIK3R1	1718	
	573	L	P	No	No	3.95	53						
PAP	735	Endometrial	Pap brush	sample		chr5	67591145	SBS	T				
						G					PIK3R1	1738	
	580	Y	D	No	No	1.79	24						
PAP	735	Endometrial	Pap brush	sample		chr10	89711916	SBS	T				
						G					PTEN	534	
	178	Y	*	No	No	7.31	253						
PAP	736	Endometrial	Pap brush	sample		chr3	41266137	SBS	C				
						G					CTNNB1	134	
	45	S	C	No	No	0.19	11						
PAP	736	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				

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						G					PTEN		388
	130	R	G		No	No	0.35	49					
PAP	789	Endometrial	Pap brush		sample	chr3	41266113	SBS	C				
						G					CTNNB1		110
	37	S	C		No	No	15.39	570					
PAP	789	Endometrial	Pap brush		sample	chr3	178952085	SBS	A				
						G					PIK3CA		3140
	1047	H	R		No	No	14.09	514					
PAP	789	Endometrial	Pap brush		sample	chr10	89692904	SBS	C				
						T					PTEN		388
	130	R	*		No	No	2.61	298					
PAP	790	Endometrial	Pap brush		sample	chr4	153249384	SBS	C				
						T					FBXW7		1394
	465	R	H		No	No	15.13	77					
PAP	790	Endometrial	Pap brush		sample	chr17	7578206	SBS	T				
						C					TP53		643
	215	S	G		No	No	20.33	669					
PAP	791	Endometrial	Pap brush		sample	chr12	25398282	SBS	C				
						A					KRAS		37
	13	G	C		No	No	16.36	1113					
PAP	791	Endometrial	Pap brush		sample	chr17	56435167	Indel	C				
											RNF43		1970
	657	R	NULL		No	No	16.61	771					
PAP	791	Endometrial	Pap brush		sample	chr17	7579554	SBS	G				
						C					TP53		133
	45	L	V		No	No	0.37	58					
PAP	802	Endometrial	Pap brush		sample	chr3	41266098	SBS	A				
						T					CTNNB1		95
	32	D	V		No	No	13.89	548					
PAP	802	Endometrial	Pap brush		sample	chr3	178916854	SBS	G				
						A					PIK3CA		241
	81	E	K		No	No	12.26	103					
PAP	802	Endometrial	Pap brush		sample	chr10	89711899	SBS	C				
						T					PTEN		517
	173	R	C		No	No	15.52	382					
PAP	802	Endometrial	Pap brush		sample	chr10	89717778	SBS	T				
						G					PTEN		0
	0	NULL	NULL		1	No	14.77	682					
PAP	802	Endometrial	Pap brush		sample	chr17	7573948	SBS	C				
						G					TP53		1079
	360	G	A		No	No	52.85	2114					
PAP	717	Endometrial	Pap brush		sample	chr3	178952085	SBS	A				
						G					PIK3CA		3140
	1047	H	R		No	No	4.79	114					
PAP	717	Endometrial	Pap brush		sample	chr10	89692944	Indel	G				
											PTEN		428
	143	G	NULL		No	No	0.43	85					
PAP	717	Endometrial	Pap brush		sample	chr17	7578271	SBS	T				

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						C					TP53		578
	193	H	R		No	No	14.78	457					
PAP	719	Endometrial		Pap brush		sample	chr3	41266137	SBS	C			
						T					CTNNB1		134
	45	S	F		No	No	0.17	18					
PAP	749	Ovarian		Pap brush		sample	chr1	115258747	SBS	C			
						T					NRAS		35
	12	G	D		No	No	0.81	47					
PAP	753	Endometrial		Pap brush		sample	chr19	52715971	SBS	C			
						G					PPP2R1A		536
	179	P	R		No	No	19.16	465					
PAP	753	Endometrial		Pap brush		sample	chr17	7577121	SBS	G			
						A					TP53		817
	273	R	C		No	No	50.52	3183					
PAP	763	Ovarian		Pap brush		sample	chr17	7578263	SBS	G			
						A					TP53		586
	196	R	*		No	No	2.19	120					
PAP	775	Endometrial		Pap brush		sample	chr12	25398284	SBS	C			
						G					KRAS		35
	12	G	A		No	No	4.48	321					
PAP	775	Endometrial		Pap brush		sample	chr10	89711917	Indel	AG			
											PTEN		535
	179	S	NULL		No	No	3.98	132					
PAP	744	Endometrial		Pap brush		sample	chr12	25378562	SBS	C			
						T					KRAS		436
	146	A	T		No	No	11.42	1223					
PAP	744	Endometrial		Pap brush		sample	chr3	178952085	SBS	A			
						G					PIK3CA		3140
	1047	H	R		No	No	13.32	838					
PAP	744	Endometrial		Pap brush		sample	chr10	89720817	Indel				
						A					PTEN		968
	323	N	NULL		No	No	11.62	620					
PAP	748	Endometrial		Pap brush		sample	chr17	7579350	SBS	A			
						C					TP53		337
	113	F	V		No	No	39.12	947					
PAP	757	Endometrial		Pap brush		sample	chr3	41266101	SBS	C			
						G					CTNNB1		98
	33	S	C		No	No	10.28	985					
PAP	757	Endometrial		Pap brush		sample	chr12	25398285	SBS	C			
						G					KRAS		34
	12	G	R		No	No	8.59	1059					
PAP	757	Endometrial		Pap brush		sample	chr5	67591134	Indel	CGA			
											PIK3R1		1727
	576	T	NULL		No	No	8.78	165					
PAP	757	Endometrial		Pap brush		sample	chr10	89692904	SBS	C			
						G					PTEN		388
	130	R	G		No	No	13.51	3149					
PAP	761	Endometrial		Pap brush		sample	chr3	178936091	SBS	G			

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					A						PIK3CA	1633	
	545	E	K	No	No	17.38	1089						
PAP	761	Endometrial	Pap brush	sample		chr17	7578413	SBS	C				
					G						TP53	517	
	173	V	L	No	No	36.22	1122						
PAP	770	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
					C						FGFR2	755	
	252	S	W	No	No	0.24	13						
PAP	770	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
					G						PTEN	388	
	130	R	G	No	No	0.65	63						
PAP	805	Endometrial	Pap brush	sample		chr3	178936074	SBS	C				
					G						PIK3CA	1616	
	539	P	R	No	No	4.89	300						
PAP	805	Endometrial	Pap brush	sample		chr17	7578403	SBS	C				
					T						TP53	527	
	176	C	Y	No	No	2.16	190						
PAP	721	Ovarian	Pap brush	sample		chr10	89717749	Indel	CC				
											PTEN	774	
	258	F	NULL	No	No	0.71	60						
PAP	742	Ovarian	Pap brush	sample		chr3	178952074	SBS	G				
					C						PIK3CA	3129	
	1043	M	I	No	No	1.54	74						
PAP	742	Ovarian	Pap brush	sample		chr17	7577509	Indel					
					TC						TP53	772	
	258	E	NULL	No	No	0.12	11						
PAP	754	Endometrial	Pap brush	sample		chr10	89653819	Indel	A				
											PTEN	117	
	39	A	NULL	No	No	8.00	353						
PAP	754	Endometrial	Pap brush	sample		chr10	89720817	Indel					
					A						PTEN	968	
	323	N	NULL	No	No	16.80	697						
PAP	768	Endometrial	Pap brush	sample		chr17	7577082	SBS	C				
					T						TP53	856	
	286	E	K	No	No	21.17	1825						
PAP	800	Endometrial	Pap brush	sample		chr3	41266097	SBS	G				
					T						CTNNB1	94	
	32	D	Y	No	No	2.61	145						
PAP	800	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
					G						PTEN	388	
	130	R	G	No	No	1.29	118						
PAP	800	Endometrial	Pap brush	sample		chr10	89692905	Indel	G				
											PTEN	389	
	130	R	NULL	No	No	2.79	255						
PAP	804	Endometrial	Pap brush	sample		chr5	112174631	SBS	C				
					T						APC	3340	
	1114	R	*	No	No	11.26	208						
PAP	804	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				

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						C					FGFR2	755	
	252	S	W	No	No	2.71	67						
PAP	804	Endometrial	Pap brush	sample		chr3	178952074	SBS	G				
						T					PIK3CA	3129	
	1043	M	I	No	No	12.59	272						
PAP	804	Endometrial	Pap brush	sample		chr12	133253184	SBS	G				
						C					POLE	857	
	286	P	R	No	No	11.86	686						
PAP	804	Endometrial	Pap brush	sample		chr10	89692905	SBS	G				
						A					PTEN	389	
	130	R	Q	No	No	5.08	1132						
PAP	804	Endometrial	Pap brush	sample		chr10	89692964	SBS	G				
						T					PTEN	448	
	150	E	*	No	No	7.81	1740						
PAP	804	Endometrial	Pap brush	sample		chr10	89692973	SBS	G				
						T					PTEN	457	
	153	D	Y	No	No	0.46	103						
PAP	807	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	0.15	19						
PAP	812	Endometrial	Pap brush	sample		chr12	25398281	SBS	C				
						T					KRAS	38	
	13	G	D	No	No	2.85	159						
PAP	812	Endometrial	Pap brush	sample		chr5	67590991	SBS	T				
						A					PIK3R1	1584	
	528	Y	*	No	No	1.68	32						
PAP	812	Endometrial	Pap brush	sample		chr5	67591080	Indel	AAA				
											PIK3R1	1673	
	558	E	NULL	No	No	2.72	84						
PAP	812	Endometrial	Pap brush	sample		chr10	89692905	Indel	G				
											PTEN	389	
	130	R	NULL	No	No	3.71	439						
PAP	866	Endometrial	Pap brush	sample		chr17	7578280	SBS	G				
						A					TP53	569	
	190	P	L	No	No	5.64	503						
PAP	877	Endometrial	Pap brush	sample		chr10	89692920	SBS	T				
						A					PTEN	404	
	135	I	K	No	No	0.16	16						
PAP	884	Endometrial	Pap brush	sample		chr3	41266104	SBS	G				
						T					CTNNB1	101	
	34	G	V	No	No	2.61	84						
PAP	884	Endometrial	Pap brush	sample		chr4	153249366	Indel	T				
											FBXW7	1412	
	471	E	NULL	No	No	2.60	125						
PAP	884	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
						C					FGFR2	755	
	252	S	W	No	No	3.77	179						
PAP	884	Endometrial	Pap brush	sample		chr5	67589138	SBS	G				

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                                    A                                   PIK3R1  1126
     376     G       R       No      No      2.63    20
PAP 884     Endometrial   Pap brush sample     chr12   133250289     SBS     C
                                    A                                   POLE    1231
     411     V       L       No      No      3.16    130
PAP 884     Endometrial   Pap brush sample     chr10   89692905      SBS     G
                                    A                                   PTEN    389
     130     R       Q       No      No      2.80    260
PAP 884     Endometrial   Pap brush sample     chr10   89692976      SBS     T
                                    G                                   PTEN    460
     154     F       V       No      No      2.76    208
PAP 884     Endometrial   Pap brush sample     chr17   7578475       SBS     G
                                    A                                   TP53    455
     152     P       L       No      No      4.74    181
PAP 892     Endometrial   Pap brush sample     chr5    67589639      Indel
GAAGAATAT
PIK3R1  1402       468     E       NULL    No      No      4.30    130
PAP 892     Endometrial   Pap brush sample     chr10   89720771      Indel
                                    C                                   PTEN    922
     308     R       NULL    No      No      1.39    21
PAP 892     Endometrial   Tao brush sample     chr5    67589639      Indel
GAAGAATAT
PIK3R1  1402       468     E       NULL    No      No      7.93    220
PAP 892     Endometrial   Tao brush sample     chr10   89720771      Indel
                                    C                                   PTEN    922
     308     R       NULL    No      No      5.41    85
PAP 897     Endometrial   Pap brush sample     chr12   25398284      SBS     C
                                    T                                   KRAS    35
     12      G       D       No      No      4.04    225
PAP 897     Endometrial   Pap brush sample     chr3    178952007     SBS     A
                                    G                                   PIK3CA  3062
     1021    Y       C       No      No      5.12    28
PAP 897     Endometrial   Pap brush sample     chr10   89717775      Indel   A
                                                                        PTEN    800
     267     K       NULL    No      No      4.80    156
PAP 897     Endometrial   Pap brush sample     chr17   56435167      Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      8.44    216
PAP 897     Endometrial   Tao brush sample     chr12   25398284      SBS     C
                                    T                                   KRAS    35
     12      G       D       No      No      20.69   952
PAP 897     Endometrial   Tao brush sample     chr3    178952007     SBS     A
                                    G                                   PIK3CA  3062
     1021    Y       C       No      No      15.62   77
PAP 897     Endometrial   Tao brush sample     chr10   89717775      Indel   A
                                                                        PTEN    800
     267     K       NULL    No      No      25.53   1287
PAP 897     Endometrial   Tao brush sample     chr17   56435167      Indel   C
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											RNF43	1970
	657	R	NULL	No	No	44.94	2136					
PAP	901	Endometrial	Pap brush	sample		chr12	25398284	SBS	C			
					T						KRAS	35
	12	G	D	No	No	31.90	1359					
PAP	901	Endometrial	Pap brush	sample		chr5	67591130	Indel	AA			
											PIK3R1	1723
	575	K	NULL	No	No	32.98	187					
PAP	901	Endometrial	Pap brush	sample		chr17	56435167	Indel	C			
											RNF43	1970
	657	R	NULL	No	No	59.29	1445					
PAP	901	Endometrial	Tao brush	sample		chr12	25398284	SBS	C			
					T						KRAS	35
	12	G	D	No	No	44.57	3934					
PAP	901	Endometrial	Tao brush	sample		chr5	67589581	Indel	A			
											PIK3R1	1344
	448	K	NULL	No	No	12.36	860					
PAP	901	Endometrial	Tao brush	sample		chr5	67591130	Indel	AA			
											PIK3R1	1723
	575	K	NULL	No	No	39.56	731					
PAP	901	Endometrial	Tao brush	sample		chr17	56435167	Indel	C			
											RNF43	1970
	657	R	NULL	No	No	83.28	1564					
PAP	904	Endometrial	Pap brush	sample		chr10	89624305	SBS	T			
					A						PTEN	79
	27	Y	N	No	Yes	16.66	2343					
PAP	904	Endometrial	Pap brush	sample		chr17	7578519	Indel	C			
											TP53	411
	137	L	NULL	No	No	40.70	2119					
PAP	904	Endometrial	Pap brush	sample		chr17	7578518	Indel	C			
											TP53	412
	138	A	NULL	No	No	45.35	795					
PAP	904	Endometrial	Tao brush	sample		chr10	89624305	SBS	T			
					A						PTEN	79
	27	Y	N	No	Yes	21.03	5169					
PAP	904	Endometrial	Tao brush	sample		chr17	7578519	Indel	C			
											TP53	411
	137	L	NULL	No	No	63.57	4506					
PAP	904	Endometrial	Tao brush	sample		chr17	7578518	Indel	C			
											TP53	412
	138	A	NULL	No	No	64.24	1202					
PAP	910	Endometrial	Tao brush	sample		chr10	123279677	SBS	G			
					C						FGFR2	755
	252	S	W	No	No	15.79	422					
PAP	910	Endometrial	Tao brush	sample		chr3	178952085	SBS	A			
					G						PIK3CA	3140
	1047	H	R	No	No	24.27	647					
PAP	813	Endometrial	Pap brush	sample		chr10	123279677	SBS	G			

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						C					FGFR2	755	
	252	S	W	No	No	1.27	119						
PAP	813	Endometrial	Pap brush	sample		chr12	25398285	SBS	C				
						A					KRAS	34	
	12	G	C	No	No	1.21	73						
PAP	813	Endometrial	Pap brush	sample		chr17	56435167	Indel	C				
											RNF43	1970	
	657	R	NULL	No	No	7.49	382						
PAP	867	Endometrial	Pap brush	sample		chr12	25380275	SBS	T				
						G					KRAS	183	
	61	Q	H	No	No	7.55	447						
PAP	867	Endometrial	Pap brush	sample		chr10	89692904	SBS	C				
						T					PTEN	388	
	130	R	*	No	No	2.93	415						
PAP	867	Endometrial	Pap brush	sample		chr17	56435167	Indel	C				
											RNF43	1970	
	657	R	NULL	No	No	0.87	93						
PAP	868	Endometrial	Pap brush	sample		chr10	89717684	SBS	A				
						T					PTEN	709	
	237	K	*	No	No	0.78	58						
PAP	868	Endometrial	Pap brush	sample		chr10	89720804	Indel	ACTT				
											PTEN	955	
	319	T	NULL	No	No	5.06	69						
PAP	869	Endometrial	Pap brush	sample		chr3	178952085	SBS	A				
						T					PIK3CA	3140	
	1047	H	L	No	No	44.98	4729						
PAP	869	Endometrial	Pap brush	sample		chr17	7578448	Indel					
						GGATGG					TP53	482	
	161	A	NULL	No	No	17.27	1196						
PAP	869	Endometrial	Pap brush	sample		chr17	7578204	SBS	A				
						C					TP53	645	
	215	S	R	No	No	19.74	696						
PAP	878	Endometrial	Pap brush	sample		chr10	123279677	SBS	G				
						C					FGFR2	755	
	252	S	W	No	No	0.45	26						
PAP	878	Endometrial	Pap brush	sample		chr5	67589642	Indel					
						AATATGAAG					PIK3R1	1405	
	469	E	NULL	No	No	0.57	27						
PAP	878	Endometrial	Pap brush	sample		chr5	67589647	Indel					
						GAAGAATAT					PIK3R1	1410	
	470	Y	NULL	No	No	0.34	22						
PAP	879	Endometrial	Pap brush	sample		chr10	89690847	SBS	G				
						C					PTEN	0	
	0	NULL	NULL	1	No	5.45	105						
PAP	881	Endometrial	Pap brush	sample		chr3	178936082	SBS	G				
						A					PIK3CA	1624	
	542	E	K	No	No	18.88	602						
PAP	881	Endometrial	Pap brush	sample		chr19	52716323	SBS	C				

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						A						PPP2R1A	767	
	256	S	Y	No	No	21.32	397							
PAP	881	Endometrial	Pap brush	sample		chr17	7578268	SBS	A					
						C						TP53	581	
	194	L	R	No	No	15.58	1616							
PAP	910	Endometrial	Pap brush	sample		chr10	123279677	SBS	G					
						C						FGFR2	755	
	252	S	W	No	No	1.34	88							
PAP	865	Endometrial	Pap brush	sample		chr17	7577121	SBS	G					
						A						TP53	817	
	273	R	C	No	No	8.02	363							
PAP	870	Endometrial	Pap brush	sample		chr10	123258034	SBS	A					
						T						FGFR2	1647	
	549	N	K	No	No	1.06	49							
PAP	870	Endometrial	Pap brush	sample		chr10	123247516	SBS	T					
						C						FGFR2	1975	
	659	K	E	No	No	1.77	62							
PAP	870	Endometrial	Pap brush	sample		chr5	67588989	Indel						
						CG						PIK3R1	1080	
	360	A	NULL	No	No	6.62	70							
PAP	870	Endometrial	Pap brush	sample		chr10	89692904	SBS	C					
						T						PTEN	388	
	130	R	*	No	No	2.27	418							
PAP	871	Endometrial	Pap brush	sample		chr3	41266100	SBS	T					
						G						CTNNB1	97	
	33	S	A	No	No	0.51	28							
PAP	871	Endometrial	Pap brush	sample		chr3	41266112	SBS	T					
						C						CTNNB1	109	
	37	S	P	No	No	0.27	15							
PAP	871	Endometrial	Pap brush	sample		chr3	178916876	SBS	G					
						A						PIK3CA	263	
	88	R	Q	No	No	27.06	266							
PAP	871	Endometrial	Pap brush	sample		chr10	89717672	SBS	C					
						T						PTEN	697	
	233	R	*	No	No	8.50	480							
PAP	871	Endometrial	Pap brush	sample		chr10	89725065	Indel	A					
												PTEN	1048	
	350	T	NULL	No	No	3.85	86							
PAP	871	Endometrial	Pap brush	sample		chr17	56435168	Indel	G					
												RNF43	1969	
	657	R	NULL	No	No	17.29	1289							
PAP	871	Endometrial	Pap brush	sample		chr17	56435168	Indel	GC					
												RNF43	1969	
	657	R	NULL	No	No	1.42	106							
PAP	874	Endometrial	Pap brush	sample		chr10	89690847	SBS	G					
						T						PTEN	0	
	0	NULL	NULL	1	No	31.21	437							
PAP	874	Endometrial	Pap brush	sample		chr10	89692905	Indel	G					

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											PTEN	389
	130	R	NULL	No	No	15.68	1520					
PAP	884	Endometrial	Tao brush	sample		chr3	41266104	SBS	G			
									T		CTNNB1	101
	34	G	V	No	No	21.72	1089					
PAP	884	Endometrial	Tao brush	sample		chr4	153249366	Indel	T			
											FBXW7	1412
	471	E	NULL	No	No	20.00	1195					
PAP	884	Endometrial	Tao brush	sample		chr10	123279677	SBS	G			
									C		FGFR2	755
	252	S	W	No	No	14.98	834					
PAP	884	Endometrial	Tao brush	sample		chr12	133250289	SBS	C			
									A		POLE	1231
	411	V	L	No	No	27.17	1521					
PAP	884	Endometrial	Tao brush	sample		chr10	89692905	SBS	G			
									A		PTEN	389
	130	R	Q	No	No	15.99	1820					
PAP	884	Endometrial	Tao brush	sample		chr10	89692976	SBS	T			
									G		PTEN	460
	154	F	V	No	No	26.62	1801					
PAP	884	Endometrial	Tao brush	sample		chr17	7578475	SBS	G			
									A		TP53	455
	152	P	L	No	No	37.28	2010					
PAP	894	Endometrial	Tao brush	sample		chr3	178936082	SBS	G			
									A		PIK3CA	1624
	542	E	K	No	No	18.89	512					
PAP	894	Endometrial	Tao brush	sample		chr10	89720817	Indel				
									A		PTEN	968
	323	N	NULL	No	No	39.93	825					
PAP	914	Ovarian	Tao brush	sample		chr17	7577139	SBS	G			
									A		TP53	799
	267	R	W	No	No	4.65	361					
PAP	816	Endometrial	Pap brush	sample		chr14	105246551	SBS	C			
									T		AKT1	49
	17	E	K	No	No	6.04	346					
PAP	816	Endometrial	Pap brush	sample		chr3	41266101	SBS	C			
									G		CTNNB1	98
	33	S	C	No	No	3.13	239					
PAP	875	Endometrial	Pap brush	sample		chr3	41266124	SBS	A			
									G		CTNNB1	121
	41	T	A	No	No	0.55	49					
PAP	875	Endometrial	Pap brush	sample		chr10	89692855	Indel	TGAAG			
											PTEN	339
	113	S	NULL	No	No	86.54	4610					
PAP	875	Endometrial	Pap brush	sample		chr17	56435167	Indel	C			
											RNF43	1970
	657	R	NULL	No	No	41.31	3390					
PAP	876	Endometrial	Pap brush	sample		chr12	25398285	SBS	C			

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                                    A                                   KRAS    34
     12      G       C       No      No      6.98    669
PAP 876     Endometrial   Pap brush sample     chr5    67591030     Indel   TAG
                                                                        PIK3R1  1623
     541     S       NULL    No      No      1.25    36
PAP 876     Endometrial   Pap brush sample     chr10   89692980     SBS     A
                                    G                                   PTEN    464
     155     Y       C       No      No      14.81   899
PAP 876     Endometrial   Pap brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      5.76    483
PAP 894     Endometrial   Pap brush sample     chr10   89720817     Indel
                                    A                                   PTEN    968
     323     N       NULL    No      No      1.07    188
PAP 902     Endometrial   Pap brush sample     chr19   52715982     SBS     C
                                    T                                   PPP2R1A 547
     183     R       W       No      No      39.23   3035
PAP 902     Endometrial   Pap brush sample     chr10   89692904     SBS     C
                                    G                                   PTEN    388
     130     R       G       No      No      14.81   1441
PAP 902     Endometrial   Pap brush sample     chr10   89720804     Indel   ACTT
                                                                        PTEN    955
     319     T       NULL    No      No      53.03   815
PAP 902     Endometrial   Pap brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      3.96    159
PAP 902     Endometrial   Tao brush sample     chr19   52715982     SBS     C
                                    T                                   PPP2R1A 547
     183     R       W       No      No      36.92   2698
PAP 902     Endometrial   Tao brush sample     chr10   89692904     SBS     C
                                    G                                   PTEN    388
     130     R       G       No      No      15.26   2711
PAP 902     Endometrial   Tao brush sample     chr10   89720804     Indel   ACTT
                                                                        PTEN    955
     319     T       NULL    No      No      52.33   1753
PAP 907     Endometrial   Pap brush sample     chr10   89653832     Indel
                                    GAAG                                PTEN    130
     44      G       NULL    No      No      4.89    514
PAP 907     Endometrial   Pap brush sample     chr10   89653833     Indel
                                    AAGG                                PTEN    131
     44      G       NULL    No      No      3.93    37
PAP 907     Endometrial   Pap brush sample     chr17   56435167     Indel   C
                                                                        RNF43   1970
     657     R       NULL    No      No      2.26    133
PAP 907     Endometrial   Tao brush sample     chr12   25398282     SBS     C
                                    T                                   KRAS    37
     13      G       S       No      No      0.03    2
PAP 907     Endometrial   Tao brush sample     chr10   89653832     Indel
```

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					GAAG					PTEN		130
	44	G	NULL	No	No	6.67	341					
PAP	907	Endometrial	Tao	brush	sample	chr10	89653833	Indel				
					AAGG					PTEN		131
	44	G	NULL	No	No	7.87	98					
PAPA	1135	Endometrial	Pap	brush	sample	chr12	25398282	SBS	C			
					T					KRAS		37
	13	G	S	No	No	0.02	2					
PAPA	1145	Endometrial	Pap	brush	sample	chr12	133253184	SBS	G			
					C					POLE		857
	286	P	R	No	No	1.97	68					
PAPA	1145	Endometrial	Pap	brush	sample	chr17	7578212	SBS	G			
					A					TP53		637
	213	R	*	No	No	2.50	97					
PAPA	1160	Endometrial	Tao	brush	sample	chr4	153247366	SBS	C			
					T					FBXW7		1436
	479	R	Q	No	No	24.54	766					
PAPA	1160	Endometrial	Tao	brush	sample	chr5	67591106	SBS	A			
					G					PIK3R1		1699
	567	K	E	No	No	30.60	4501					
PAPA	1160	Endometrial	Tao	brush	sample	chr12	133250289	SBS	C			
					A					POLE		1231
	411	V	L	No	No	25.39	2932					
PAPA	1160	Endometrial	Tao	brush	sample	chr10	89692905	SBS	G			
					A					PTEN		389
	130	R	Q	No	No	27.56	2991					
PAPA	1160	Endometrial	Tao	brush	sample	chr10	89711899	SBS	C			
					T					PTEN		517
	173	R	C	No	No	28.80	1407					
PAPA	1160	Endometrial	Tao	brush	sample	chr17	7578212	SBS	G			
					A					TP53		637
	213	R	*	No	No	9.82	491					
PAPA	1136	Ovarian	Pap	brush	sample	chr5	67590390	Indel				
					T					PIK3R1		1452
	484	I	NULL	No	No	0.22	10					
PAPA	1129	Endometrial	Tao	brush	sample	chr17	7577120	SBS	C			
					T					TP53		818
	273	R	H	No	No	26.46	1658					
PAPA	1135	Endometrial	Tao	brush	sample	chr17	7578212	SBS	G			
					A					TP53		637
	213	R	*	No	No	2.20	41					
PAPA	1035	Endometrial	Pap	brush	sample	chr19	52715971	SBS	C			
					G					PPP2R1A		536
	179	P	R	No	No	4.90	149					
PAPA	1035	Endometrial	Pap	brush	sample	chr17	7577046	SBS	C			
					A					TP53		892
	298	E	*	No	No	7.34	423					
PAPA	1037	Ovarian	Pap	brush	sample	chr17	7577117	SBS	A			

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						C					TP53		821
	274	V	G		No	No	69.69	1750					
PAPA	1048	Endometrial		Pap brush	sample		chr10	89692905	Indel	G			
											PTEN		389
	130	R	NULL		No	No	0.90	46					
PAPA	1048	Endometrial		Pap brush	sample		chr10	89692905	SBS	G			
						A					PTEN		389
	130	R	Q		No	No	1.35	69					
PAPA	1080	Endometrial		Pap brush	sample		chr10	89720724	Indel	A			
											PTEN		875
	292	N	NULL		No	No	2.53	13					
PAPA	1086	Endometrial		Pap brush	sample		chr10	89692791	SBS	A			
						C					PTEN		275
	92	D	A		No	No	2.80	108					
PAPA	1092	Endometrial		Pap brush	sample		chr3	41266104	SBS	G			
						T					CTNNB1		101
	34	G	V		No	No	31.49	1031					
PAPA	1092	Endometrial		Pap brush	sample		chr19	52715983	SBS	G			
						A					PPP2R1A		548
	183	R	Q		No	No	30.51	1114					
PAPA	1095	Endometrial		Pap brush	sample		chr10	89692904	SBS	C			
						G					PTEN		388
	130	R	G		No	No	0.19	12					
PAPA	1059	Endometrial		Pap brush	sample		chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	7.91	792					
PAPA	1081	Endometrial		Pap brush	sample		chr3	41266124	SBS	A			
						G					CTNNB1		121
	41	T	A		No	No	19.73	540					
PAPA	1081	Endometrial		Pap brush	sample		chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	11.41	1170					
PAPA	1081	Endometrial		Pap brush	sample		chr3	178952074	SBS	G			
						T					PIK3CA		3129
	1043	M	I		No	No	17.28	1627					
PAPA	1081	Endometrial		Pap brush	sample		chr10	89624245	SBS	G			
						T					PTEN		19
	7	E	*		No	No	21.44	4758					
PAPA	1081	Endometrial		Pap brush	sample		chr10	89692973	SBS	G			
						T					PTEN		457
	153	D	Y		No	No	0.24	19					
PAPA	1081	Endometrial		Pap brush	sample		chr10	89711900	SBS	G			
						A					PTEN		518
	173	R	H		No	No	18.38	506					
PAPA	1098	Ovarian		Pap brush	sample		chr10	123258034	SBS	A			
						T					FGFR2		1647
	549	N	K		No	No	1.12	30					
PAPA	1098	Ovarian		Pap brush	sample		chr10	89624270	Indel	GA			

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											PTEN	521	
	174	Y	NULL	No	No	1.17	44						
PAPA	1077	Endometrial	Pap brush	sample		chr10	89717775	Indel		A			
											PTEN	800	
	267	K	NULL	No	No	7.60	318						
PAPA	1077	Endometrial	Pap brush	sample		chr10	89720804	Indel	ACTT				
											PTEN	955	
	319	T	NULL	No	No	0.95	24						
PAPA	1097	Endometrial	Pap brush	sample		chr3	178952085	SBS	A	G			
											PIK3CA	3140	
	1047	H	R	No	No	15.86	1507						
PAPA	1097	Endometrial	Pap brush	sample		chr10	89690810	SBS	G	T			
											PTEN	217	
	73	E	*	No	No	37.79	947						
PAPA	1097	Endometrial	Pap brush	sample		chr10	89692953	Indel	T				
											PTEN	437	
	146	L	NULL	No	No	9.86	978						
PAPA	1097	Endometrial	Pap brush	sample		chr17	7579314	SBS	T	C			
											TP53	373	
	125	T	A	No	No	11.72	461						
PAPA	1100	Endometrial	Pap brush	sample		chr14	105246551	SBS	C	T			
											AKT1	49	
	17	E	K	No	No	0.72	40						
PAPA	1100	Endometrial	Pap brush	sample		chr3	41266125	SBS	C	T			
											CTNNB1	122	
	41	T	I	No	No	0.46	21						
PAPA	1110	Ovarian	Pap brush	sample		chr17	7578490	SBS	A	C			
											TP53	440	
	147	V	G	No	No	0.71	59						
PAPA	1115	Ovarian	Pap brush	sample		chr5	67589583	SBS	T	G			
											PIK3R1	1346	
	449	L	*	No	No	0.28	12						
PAPA	1115	Ovarian	Pap brush	sample		chr17	7578263	SBS	G	A			
											TP53	586	
	196	R	*	No	No	1.56	78						
PAPA	1057	Endometrial	Pap brush	sample		chr1	115258747	SBS	C	T			
											NRAS	35	
	12	G	D	No	No	38.24	4736						
PAPA	1057	Endometrial	Pap brush	sample		chr3	178936082	SBS	G	A			
											PIK3CA	1624	
	542	E	K	No	No	26.78	1638						
PAPA	1057	Endometrial	Pap brush	sample		chr17	7578406	SBS	C	T			
											TP53	524	
	175	R	H	No	No	4.59	369						
PAPA	1057	Endometrial	Pap brush	sample		chr17	7577141	SBS	C	T			
											TP53	797	
	266	G	E	No	No	37.91	1877						
PAPA	1069	Endometrial	Pap brush	sample		chr3	178916876	SBS	G				

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						A						PIK3CA	263	
	88	R	Q		No	No	0.90	131						
PAPA	1069	Endometrial		Pap brush		sample	chr10	89690835	SBS	T				
						G						PTEN	242	
	81	F	C		No	No	0.63	18						
PAPA	1069	Endometrial		Pap brush		sample	chr10	89624245	SBS	G				
						T						PTEN	19	
	7	E	*		No	No	1.18	248						
PAPA	1069	Endometrial		Pap brush		sample	chr10	89624270	SBS	G				
						T						PTEN	44	
	15	R	I		No	No	1.70	356						
PAPA	1076	Endometrial		Pap brush		sample	chr3	178952084	SBS	C				
						T						PIK3CA	3139	
	1047	H	Y		No	No	3.36	245						
PAPA	1112	Ovarian		Pap brush		sample	chr3	41266137	SBS	C				
						G						CTNNB1	134	
	45	S	C		No	No	0.31	12						
PAPA	1152	Endometrial		Tao brush		sample	chr4	153249384	SBS	C				
						T						FBXW7	1394	
	465	R	H		No	No	33.80	576						
PAPA	1152	Endometrial		Tao brush		sample	chr5	67591106	SBS	A				
						G						PIK3R1	1699	
	567	K	E		No	No	43.61	3021						
PAPA	1153	Endometrial		Pap brush		sample	chr3	41266100	SBS	T				
						G						CTNNB1	97	
	33	S	A		No	No	2.33	100						
PAPA	1153	Endometrial		Pap brush		sample	chr3	178952085	SBS	A				
						G						PIK3CA	3140	
	1047	H	R		No	No	3.89	208						
PAPA	1153	Endometrial		Pap brush		sample	chr10	89692811	SBS	G				
						T						PTEN	295	
	99	E	*		No	No	7.16	29						
PAPA	1153	Endometrial		Pap brush		sample	chr17	56435167	Indel	C				
												RNF43	1970	
	657	R	NULL		No	No	2.38	69						
PAPA	1153	Endometrial		Pap brush		sample	chr17	7578229	SBS	T				
						C						TP53	620	
	207	D	G		No	No	1.42	7						
PAPA	1154	Endometrial		Pap brush		sample	chr5	67591103	Indel					
						AACGTATGAACAGCA (SEQ ID NO:779)						PIK3R1	1696	
	566	I	NULL		No	No	0.44	19						
PAPA	1154	Endometrial		Tao brush		sample	chr10	123279677	SBS	G				
						C						FGFR2	755	
	252	S	W		No	No	7.65	507						
PAPA	1154	Endometrial		Tao brush		sample	chr5	67591103	Indel					
						AACGTATGAACAGCA (SEQ ID NO:780)						PIK3R1	1696	
	566	I	NULL		No	No	35.33	2309						
PAPA	1155	Endometrial		Pap brush		sample	chr10	123279677	SBS	G				

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						C					FGFR2	755	
	252	S	W	No	No	1.74	139						
PAPA	1155	Endometrial	Pap	brush	sample	chr3	178952085	SBS	A				
						G					PIK3CA	3140	
	1047	H	R	No	No	8.61	557						
PAPA	1155	Endometrial	Pap	brush	sample	chr10	89692886	SBS	T				
						A					PTEN	370	
	124	C	S	No	No	7.39	313						
PAPA	1155	Endometrial	Tao	brush	sample	chr10	123279677	SBS	G				
						C					FGFR2	755	
	252	S	W	No	No	12.90	769						
PAPA	1155	Endometrial	Tao	brush	sample	chr3	178952085	SBS	A				
						G					PIK3CA	3140	
	1047	H	R	No	No	35.08	2025						
PAPA	1155	Endometrial	Tao	brush	sample	chr10	89692886	SBS	T				
						A					PTEN	370	
	124	C	S	No	No	65.68	2019						
PAPA	1185	Endometrial	Pap	brush	sample	chr10	89717698	Indel					
						T					PTEN	723	
	241	F	NULL	No	No	0.61	351						
PAPA	1153	Endometrial	Tao	brush	sample	chr3	178952085	SBS	A				
						G					PIK3CA	3140	
	1047	H	R	No	No	28.28	1338						
PAPA	1153	Endometrial	Tao	brush	sample	chr10	89692811	SBS	G				
						T					PTEN	295	
	99	E	*	No	No	56.97	139						
PAPA	1157	Endometrial	Pap	brush	sample	chr3	178952085	SBS	A				
						T					PIK3CA	3140	
	1047	H	L	No	No	34.61	1891						
PAPA	1177	Endometrial	Tao	brush	sample	chr10	123247516	SBS	T				
						C					FGFR2	1975	
	659	K	E	No	No	49.21	17781						
PAPA	1177	Endometrial	Tao	brush	sample	chr3	178952085	SBS	A				
						T					PIK3CA	3140	
	1047	H	L	No	No	26.68	1388						
PAPA	1177	Endometrial	Tao	brush	sample	chr10	89692904	SBS	C				
						G					PTEN	388	
	130	R	G	No	No	20.77	97						
PAPA	1188	Endometrial	Pap	brush	sample	chr17	7578406	SBS	C				
						T					TP53	524	
	175	R	H	No	No	24.02	541						
PAPA	1254	Endometrial	Tao	brush	sample	chr12	25398284	SBS	C				
						T					KRAS	35	
	12	G	D	No	No	12.44	100						
PAPA	1254	Endometrial	Tao	brush	sample	chr3	178952077	SBS	T				
						A					PIK3CA	3132	
	1044	N	K	No	No	13.99	735						
PAPA	1254	Endometrial	Tao	brush	sample	chr10	89692904	SBS	C				

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						G					PTEN	388
	130	R	G	No	No	9.68	24					
PAPA	1157	Endometrial	Tao	brush	sample	chr3	178952085	SBS	A			
						T					PIK3CA	3140
	1047	H	L	No	No	32.88	1959					
PAPA	1184	Endometrial	Tao	brush	sample	chr12	25398284	SBS	C			
						G					KRAS	35
	12	G	A	No	No	15.54	174					
PAPA	1184	Endometrial	Tao	brush	sample	chr10	89692904	SBS	C			
						G					PTEN	388
	130	R	G	No	No	11.97	31					
PAPA	1184	Endometrial	Tao	brush	sample	chr10	89692905	Indel	G			
											PTEN	389
	130	R	NULL	No	No	8.88	23					
PAPA	1185	Endometrial	Tao	brush	sample	chr10	89717698	Indel				
						T					PTEN	723
	241	F	NULL	No	No	0.61	380					
PAPA	1188	Endometrial	Tao	brush	sample	chr17	7578406	SBS	C			
						T					TP53	524
	175	R	H	No	No	64.47	1724					
PAPA	1258	Ovarian	Tao	brush	sample	chr17	7578442	SBS	T			
						C					TP53	488
	163	Y	C	No	No	4.32	188					
PAPA	1258	Ovarian	Tao	brush	sample	chr17	7574010	SBS	C			
						G					TP53	1017
	339	E	D	No	No	0.89	29					
PAPA	1264	Endometrial	Pap	brush	sample	chr3	41266113	SBS	C			
						T					CTNNB1	110
	37	S	F	No	No	0.29	12					
PAPA	1264	Endometrial	Pap	brush	sample	chr10	123279677	SBS	G			
						C					FGFR2	755
	252	S	W	No	No	0.56	47					
PAPA	1264	Endometrial	Pap	brush	sample	chr5	67591135	Indel				
						G					PIK3R1	1728
	576	T	NULL	No	No	3.06	17					
PAPA	1264	Endometrial	Pap	brush	sample	chr10	89692904	SBS	C			
						G					PTEN	388
	130	R	G	No	No	0.40	10					
PAPA	1264	Endometrial	Tao	brush	sample	chr3	41266113	SBS	C			
						T					CTNNB1	110
	37	S	F	No	No	7.75	360					
PAPA	1264	Endometrial	Tao	brush	sample	chr10	123279677	SBS	G			
						C					FGFR2	755
	252	S	W	No	No	10.13	668					
PAPA	1264	Endometrial	Tao	brush	sample	chr3	178952085	SBS	A			
						G					PIK3CA	3140
	1047	H	R	No	No	10.89	576					
PAPA	1264	Endometrial	Tao	brush	sample	chr5	67588989	Indel				

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					CG						PIK3R1	1080	
	360	A	NULL	No	No	10.82	102						
PAPA	1264	Endometrial	Tao	brush	sample	chr5	67591135	Indel					
					G						PIK3R1	1728	
	576	T	NULL	No	No	36.43	161						
PAPA	1264	Endometrial	Tao	brush	sample	chr10	89692904	SBS	C				
					G						PTEN	388	
	130	R	G	No	No	7.02	134						
PAPA	1251	Endometrial	Tao	brush	sample	chr10	89624242	SBS	A				
					T						PTEN	16	
	6	K	*	No	No	70.28	3192						
PAPA	1251	Endometrial	Tao	brush	sample	chr17	7577115	SBS	A				
					G						TP53	823	
	275	C	R	No	No	34.08	122						
PAPA	1253	Ovarian	Tao	brush	sample	chr17	7578190	SBS	T				
					C						TP53	659	
	220	Y	C	No	No	0.88	5						
PAPA	1255	Endometrial	Pap	brush	sample	chr10	89624285	Indel	GA				
											PTEN	59	
	20	G	NULL	No	No	0.45	26						
PAPA	1255	Endometrial	Tao	brush	sample	chr10	89624285	Indel	GA				
											PTEN	59	
	20	G	NULL	No	No	48.11	1664						
PAPA	1256	Endometrial	Pap	brush	sample	chr17	7578394	SBS	T				
					C						TP53	536	
	179	H	R	No	No	7.77	122						
PAPA	1152	Endometrial	Pap	brush	sample	chr5	67591106	SBS	A				
					G						PIK3R1	1699	
	567	K	E	No	No	0.43	46						
PAPA	1158	Endometrial	Pap	brush	sample	chr10	89624245	SBS	G				
					T						PTEN	19	
	7	E	*	No	No	0.14	37						
PAPA	1177	Endometrial	Pap	brush	sample	chr10	123247516	SBS	T				
					C						FGFR2	1975	
	659	K	E	No	No	3.21	699						
PAPA	1177	Endometrial	Pap	brush	sample	chr3	178952085	SBS	A				
					T						PIK3CA	3140	
	1047	H	L	No	No	1.53	99						
PAPA	1177	Endometrial	Pap	brush	sample	chr10	89692904	SBS	C				
					G						PTEN	388	
	130	R	G	No	No	1.16	201						
PAPA	1251	Endometrial	Pap	brush	sample	chr10	89624242	SBS	A				
					T						PTEN	16	
	6	K	*	No	No	5.77	548						
PAPA	1251	Endometrial	Pap	brush	sample	chr17	7577115	SBS	A				
					G						TP53	823	
	275	C	R	No	No	2.28	35						
PAPA	1259	Ovarian	Tao	brush	sample	chr19	52716327	SBS	G				

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						T							PPP2R1A	771
	257	W	C		No	No	6.14	184						
PAPA	1259	Ovarian		Tao brush	sample		chr17	7578201	Indel	CAC				
													TP53	648
	216	V	NULL		No	No	0.32	3						
PAPA	1198	Endometrial		Pap brush	sample		chr17	7577114	SBS	C				
						T							TP53	824
	275	C	Y		No	No	59.37	2559						
PAPA	1209	Endometrial		Pap brush	sample		chr10	89690810	SBS	G				
						T							PTEN	217
	73	E	*		No	No	12.49	289						
PAPA	1209	Endometrial		Pap brush	sample		chr17	56435167	Indel	C				
													RNF43	1970
	657	R	NULL		No	No	0.85	86						
PAPA	1209	Endometrial		Pap brush	sample		chr17	7577022	SBS	G				
						A							TP53	916
	306	R	*		No	No	14.76	851						
PAPA	1211	Endometrial		Pap brush	sample		chr10	89692908	Indel					
CTGGTGTAA														PTEN
	392	131	T		NULL	No	No	0.28	10					
PAPA	1214	Endometrial		Pap brush	sample		chr1	115258744	SBS	C				
						T							NRAS	38
	13	G	D		No	No	2.59	436						
PAPA	1214	Endometrial		Pap brush	sample		chr3	178952085	SBS	A				
						G							PIK3CA	3140
	1047	H	R		No	No	4.04	170						
PAPA	1214	Endometrial		Pap brush	sample		chr10	89717775	Indel					
						A							PTEN	800
	267	K	NULL		No	No	1.34	27						
PAPA	1226	Endometrial		Pap brush	sample		chr10	89693007	Indel					
						A							PTEN	491
	164	K	NULL		No	No	2.95	24						
PAPA	1235	Ovarian		Pap brush	sample		chr9	21971080	SBS	G				
						A							CDKN2A	278
	93	T	M		No	No	1.22	3						
PAPA	1239	Endometrial		Pap brush	sample		chr3	41266101	SBS	C				
						A							CTNNB1	98
	33	S	Y		No	No	0.47	66						
PAPA	1239	Endometrial		Pap brush	sample		chr3	41266113	SBS	C				
						T							CTNNB1	110
	37	S	F		No	No	4.15	580						
PAPA	1239	Endometrial		Pap brush	sample		chr3	41266137	SBS	C				
						T							CTNNB1	134
	45	S	F		No	No	0.09	12						
PAPA	1239	Endometrial		Pap brush	sample		chr1	115258747	SBS	C				
						T							NRAS	35
	12	G	D		No	No	0.44	72						
PAPA	1239	Endometrial		Pap brush	sample		chr3	178936092	SBS	A				

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```
                                    G                                   PIK3CA  1634
     545     E       G       No      No      21.19   275
PAPA 1239  Endometrial   Pap brush sample     chr10   89717615     SBS     C
                                    T                                   PTEN    640
     214     Q       *       No      No      18.23   1134
PAPA 1239  Endometrial   Pap brush sample     chr10   89720804     Indel
                                    A                                   PTEN    955
     319     T       NULL    No      No      9.58    82
PAPA 1239  Endometrial   Pap brush sample     chr17   7579312      SBS     C
                                    T                                   TP53    375
     125     T       T       No      Yes     14.35   1498
PAPA 1293  Endometrial   Pap brush sample     chr3    41266125     SBS     C
                                    T                                   CTNNB1  122
     41      T       I       No      No      0.35    34
PAPA 1299  Endometrial   Pap brush sample     chr3    41266104     SBS     G
                                    A                                   CTNNB1  101
     34      G       E       No      No      19.53   2476
PAPA 1299  Endometrial   Pap brush sample     chr10   89624243     Indel   AA
                                                                        PTEN    17
     6       K       NULL    No      No      22.56   3980
PAPA 1299  Endometrial   Pap brush sample     chr10   89711914     Indel   T
                                                                        PTEN    532
     178     Y       NULL    No      No      21.83   429
PAPA 1300  Endometrial   Pap brush sample     chr5    67589634     Indel
TATATGAAGAAT (SEQ ID NO:772)
PIK3R1  1397       466     L       NULL    No      No      9.56    256
PAPA 1300  Endometrial   Pap brush sample     chr10   89692802     SBS     C
                                    G                                   PTEN    286
     96      P       A       No      No      16.06   128
PAPA 1300  Endometrial   Pap brush sample     chr10   89717750     Indel   C
                                                                        PTEN    775
     259     H       NULL    No      No      13.47   277
PAPA 1300  Endometrial   Pap brush sample     chr10   89720741     SBS     C
                                    T                                   PTEN    892
     298     Q       *       No      No      12.66   71
PAPA 1300  Endometrial   Pap brush sample     chr17   7578206      SBS     T
                                    C                                   TP53    643
     215     S       G       No      No      19.48   493
PAPA 1303  Endometrial   Pap brush sample     chr17   7577022      SBS     G
                                    A                                   TP53    916
     306     R       *       No      No      4.89    390
PAPA 1308  Endometrial   Pap brush sample     chr3    41266097     SBS     G
                                    A                                   CTNNB1  94
     32      D       N       No      No      0.56    72
PAPA 1308  Endometrial   Pap brush sample     chr10   123258035    SBS     T
                                    C                                   FGFR2   1646
     549     N       S       No      No      1.23    21
PAPA 1308  Endometrial   Pap brush sample     chr10   89624297     Indel   AC
```

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											PTEN	71
	24	D	NULL	No	No	0.14	29					
PAPA	1192	Endometrial	Pap brush	sample		chr5	67591134	Indel	CGAGAG			
											PIK3R1	1727
	576	T	NULL	No	No	34.94	647					
PAPA	1192	Endometrial	Pap brush	sample		chr10	89692904	SBS	C			
					T						PTEN	388
	130	R	*	No	No	8.96	306					
PAPA	1192	Endometrial	Pap brush	sample		chr10	89720669	Indel	T			
											PTEN	820
	274	W	NULL	No	No	34.16	221					
PAPA	1192	Endometrial	Pap brush	sample		chr17	7577114	SBS	C			
					T						TP53	824
	275	C	Y	No	No	19.06	710					
PAPA	1192	Endometrial	Pap brush	sample		chr17	7574017	SBS	C			
					A						TP53	1010
	337	R	L	No	No	19.45	399					
PAPA	1207	Endometrial	Pap brush	sample		chr12	25398284	SBS	C			
					T						KRAS	35
	12	G	D	No	No	11.90	1210					
PAPA	1207	Endometrial	Pap brush	sample		chr10	89717672	SBS	C			
					T						PTEN	697
	233	R	*	No	No	5.49	2001					
PAPA	1207	Endometrial	Pap brush	sample		chr10	89717775	Indel	A			
											PTEN	800
	267	K	NULL	No	No	11.87	225					
PAPA	1218	Endometrial	Pap brush	sample		chr10	89720804	Indel	ACTT			
											PTEN	955
	319	T	NULL	No	No	3.63	30					
PAPA	1218	Endometrial	Pap brush	sample		chr10	89725042	SBS	A			
					C						PTEN	0
	0	NULL	NULL	1	No	9.98	169					
PAPA	1218	Endometrial	Pap brush	sample		chr17	56435167	Indel	C			
											RNF43	1970
	657	R	NULL	No	No	11.25	1105					
PAPA	1223	Endometrial	Pap brush	sample		chr10	89624284	SBS	G			
					T						PTEN	58
	20	G	*	No	No	1.83	328					
PAPA	1242	Endometrial	Pap brush	sample		chr12	25398284	SBS	C			
					T						KRAS	35
	12	G	D	No	No	12.30	1580					
PAPA	1298	Ovarian	Pap brush	sample		chr17	7578413	SBS	C			
					A						TP53	517
	173	V	L	No	No	7.52	576					
PAPA	1326	Ovarian	Pap brush	sample		chr5	112175639	SBS	C			
					T						APC	4348
	1450	R	*	No	No	4.37	572					
PAPA	1326	Ovarian	Pap brush	sample		chr12	25398281	SBS	C			

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						T					KRAS	38
	13	G	D		No	No	12.18	1118				
PAPA	1326	Ovarian		Pap brush	sample		chr3	178916854	SBS	G		
						A					PIK3CA	241
	81	E	K		No	No	1.16	42				
PAPA	1326	Ovarian		Pap brush	sample		chr3	178952085	SBS	A		
						T					PIK3CA	3140
	1047	H	L		No	No	0.25	14				
PAPA	1326	Ovarian		Pap brush	sample		chr17	7576900	Indel			
						GGGG					TP53	946
	316	P	NULL		No	No	5.72	216				
PAPA	1204	Endometrial		Pap brush	sample		chr12	25398284	SBS	C		
						A					KRAS	35
	12	G	V		No	No	12.53	1730				
PAPA	1204	Endometrial		Pap brush	sample		chr3	178916876	SBS	G		
						A					PIK3CA	263
	88	R	Q		No	No	7.15	272				
PAPA	1204	Endometrial		Pap brush	sample		chr10	89717762	SBS	A		
						T					PTEN	787
	263	K	*		No	No	13.98	284				
PAPA	1204	Endometrial		Pap brush	sample		chr10	89720804	Indel	ACTT		
											PTEN	955
	319	T	NULL		No	No	13.26	159				
PAPA	1204	Endometrial		Pap brush	sample		chr17	56435167	Indel	C		
											RNF43	1970
	657	R	NULL		No	No	28.52	2933				
PAPA	1224	Endometrial		Pap brush	sample		chr12	133250289	SBS	C		
						G					POLE	1231
	411	V	L		No	No	0.21	22				
PAPA	1233	Endometrial		Pap brush	sample		chr3	41266097	SBS	G		
						T					CTNNB1	94
	32	D	Y		No	No	0.45	63				
PAPA	1233	Endometrial		Pap brush	sample		chr10	89653784	Indel			
						A					PTEN	82
	28	I	NULL		No	No	0.74	26				
PAPA	1309	Endometrial		Pap brush	sample		chr17	7579909	SBS	C		
						T					TP53	4
	2	E	K		No	No	48.42	4775				
PAPA	1328	Ovarian		Pap brush	sample		chr12	133253184	SBS	G		
						C					POLE	857
	286	P	R		No	No	0.77	74				
PAPA	1191	Endometrial		Pap brush	sample		chr10	89685269	SBS	G		
						A					PTEN	0
	0	NULL	NULL		1	No	0.18	44				
PAPA	1193	Endometrial		Pap brush	sample		chr3	41266097	SBS	G		
						T					CTNNB1	94
	32	D	Y		No	No	8.42	984				
PAPA	1193	Endometrial		Pap brush	sample		chr10	89692852	Indel			

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AAGTGAAGATGACAAT (SEQ ID NO:773) PTEN
336 112 L NULL No No 4.91 359
PAPA 1221 Endometrial Pap brush sample chr10 123279677 SBS G
C FGFR2 755
252 S W No No 2.04 213
PAPA 1221 Endometrial Pap brush sample chr10 89711875 SBS G
A PTEN 493
165 G R No No 5.73 291
PAPA 1221 Endometrial Pap brush sample chr10 89717736 Indel AAGTA
PTEN 761
254 K NULL No No 1.87 85
PAPA 1232 Endometrial Pap brush sample chr17 7578263 SBS G
A TP53 586
196 R * No No 1.32 75
PAPA 1292 Ovarian Pap brush sample chr17 7578397 SBS T
G TP53 533
178 H P No No 0.29 22
PAPA 1296 Ovarian Pap brush sample chr17 7579312 Indel
CGTGCAAGTCACAGAC (SEQ ID NO:774) TP53
375 125 T NULL No Yes 0.13 18
PAPA 1361 Ovarian Tao brush sample chr3 41266137 SBS C
T CTNNB1 134
45 S F No No 0.85 107
PAPA 1364 Ovarian Pap brush sample chr10 123279677 SBS G
C FGFR2 755
252 S W No No 0.14 32
PAP 536 Ovarian Pap brush sample chr10 123279677 SBS G
C FGFR2 755
252 S W No No 0.10 28
PAP 536 Ovarian Pap brush sample chr3 178936091 SBS G
A PIK3CA 1633
545 E K No No 4.57 159
PAP 536 Ovarian Pap brush sample chr5 67590427 Indel C
PIK3R1 1489
497 Q NULL No No 0.16 10
PAP 536 Ovarian Pap brush sample chr10 89692904 SBS C
G PTEN 388
130 R G No No 2.16 229
PAP 536 Ovarian Pap brush sample chr10 89717672 SBS C
T PTEN 697
233 R * No No 4.52 1724
PAP 536 Ovarian Pap brush sample chr17 7578406 SBS C
T TP53 524
175 R H No No 5.17 779
PAPA 1696 Ovarian Pap brush sample chr17 7577532 SBS G
A TP53 749
250 P L No No 22.77 3899
PAPA 1697 Ovarian Pap brush sample chr17 7578370 SBS C

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						T					TP53	0	
	0	NULL	NULL	1	No	0.92	171						
PAPA	1700	Ovarian	Pap	brush	sample	chr5	67589567	Indel					
						AAG					PIK3R1	1330	
	444	A	NULL	No	No	0.71	158						
PAPA	1700	Ovarian	Pap	brush	sample	chr17	7578394	SBS	T				
						A					TP53	536	
	179	H	L	No	No	0.11	12						
PAPA	1705	Ovarian	Pap	brush	sample	chr10	123258034	SBS	A				
						T					FGFR2	1647	
	549	N	K	No	No	0.35	22						
PAPA	1706	Ovarian	Pap	brush	sample	chr17	7578555	SBS	C				
						T					TP53	0	
	0	NULL	NULL	1	No	5.00	952						
PAPA	1716	Ovarian	Pap	brush	sample	chr17	7578203	SBS	C				
						T					TP53	646	
	216	V	M	No	No	0.48	46						
PAPA	1716	Ovarian	Pap	brush	sample	chr17	7577130	SBS	A				
						T					TP53	808	
	270	F	I	No	No	0.41	38						
PAPA	1725	Ovarian	Pap	brush	sample	chr3	41266113	SBS	C				
						T					CTNNB1	110	
	37	S	F	No	No	3.82	430						
PAPA	1734	Ovarian	Pap	brush	sample	chr17	7577560	SBS	A				
						C					TP53	721	
	241	S	A	No	No	0.08	17						
PAPA	1819	Ovarian	Tao	brush	sample	chr17	7577527	Indel	GGA				
											TP53	754	
	252	L	NULL	No	No	0.16	62						
PAPA	1819	Ovarian	Pap	brush	sample	chr10	123258035	SBS	T				
						C					FGFR2	1646	
	549	N	S	No	No	0.16	22						
PAPA	1819	Ovarian	Pap	brush	sample	chr17	7577527	Indel	GGA				
											TP53	754	
	252	L	NULL	No	No	0.13	43						
PAPA	1819	Ovarian	Pap	brush	sample	chr17	7577124	SBS	C				
						A					TP53	814	
	272	V	L	No	No	1.23	262						
PAPA	1820	Endometrial	Tao	brush	sample	chr12	25398284	SBS	C				
						A					KRAS	35	
	12	G	V	No	No	58.32	13079						
PAPA	1820	Endometrial	Tao	brush	sample	chr17	7578271	SBS	T				
						A					TP53	578	
	193	H	L	No	No	35.34	4849						
PAPA	1820	Endometrial	Pap	brush	sample	chr12	25398284	SBS	C				
						A					KRAS	35	
	12	G	V	No	No	1.76	258						
PAPA	1820	Endometrial	Pap	brush	sample	chr17	7578271	SBS	T				

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						A					TP53	578	
	193	H	L		No	No	0.35	57					
PAPA	1823	Ovarian		Tao	brush	sample	chr17	7578265	SBS	A			
						G					TP53	584	
	195	I	T		No	No	0.35	58					
PAPA	1826	Ovarian		Tao	brush	sample	chr5	67591134	Indel	CGA			
											PIK3R1	1727	
	576	T	NULL		No	No	6.59	82					
PAPA	1828	Ovarian		Pap	brush	sample	chr17	7577106	SBS	G			
						A					TP53	832	
	278	P	S		No	No	0.23	32					
PAPA	1832	Ovarian		Tao	brush	sample	chr17	7577502	Indel	G			
											TP53	779	
	260	S	NULL		No	No	0.19	49					
PAPA	1836	Endometrial		Tao	brush	sample	chr3	41266101	SBS	C			
						T					CTNNB1	98	
	33	S	F		No	No	38.22	2700					
PAPA	1836	Endometrial		Tao	brush	sample	chr3	178952085	SBS	A			
						T					PIK3CA	3140	
	1047	H	L		No	No	38.11	3542					
PAPA	1836	Endometrial		Tao	brush	sample	chr10	89692794	SBS	A			
						G					PTEN	278	
	93	H	R		No	No	40.00	110					
PAPA	1837	Endometrial		Tao	brush	sample	chr3	178952085	SBS	A			
						G					PIK3CA	3140	
	1047	H	R		No	No	21.00	1502					
PAPA	1837	Endometrial		Tao	brush	sample	chr17	56435167	Indel	C			
											RNF43	1970	
	657	R	NULL		No	No	37.86	4648					
PAPA	1839	Endometrial		Tao	brush	sample	chr10	123279677	SBS	G			
						C					FGFR2	755	
	252	S	W		No	No	26.83	2427					
PAPA	1839	Endometrial		Tao	brush	sample	chr5	67592055	Indel				
						TG					PIK3R1	1871	
	624	W	NULL		No	No	29.78	411					
PAPA	1839	Endometrial		Tao	brush	sample	chr10	89692961	SBS	C			
						T					PTEN	445	
	149	Q	*		No	No	16.40	2986					
PAPA	1839	Endometrial		Tao	brush	sample	chr17	56435167	Indel	C			
											RNF43	1970	
	657	R	NULL		No	No	24.46	5736					
PAPA	1840	Endometrial		Tao	brush	sample	chr10	89717708	SBS	C			
						T					PTEN	733	
	245	Q	*		No	No	9.98	609					
PAPA	1840	Endometrial		Tao	brush	sample	chr17	56435167	Indel	C			
											RNF43	1970	
	657	R	NULL		No	No	8.36	1514					
PAPA	1840	Endometrial		Tao	brush	sample	chr17	7576903	Indel	AG			

Table15.txt

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Table15.txt

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PAPA	1852	Endometrial	Tao brush	sample	chr10	89692904	SBS	C					
					G						PTEN	388	
	130	R	G	No	No	29.60	8206						
PAPA	1855	Endometrial	Tao brush	sample	chr12	25398284	SBS	C					
					A						KRAS	35	
	12	G	V	No	No	31.60	4143						
PAPA	1855	Endometrial	Tao brush	sample	chr10	89692904	SBS	C					
					G						PTEN	388	
	130	R	G	No	No	21.51	5163						
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PAPA	1857	Endometrial	Tao brush	sample	chr19	52715971	SBS	C					
					G						PPP2R1A	536	
	179	P	R	No	No	21.34	1762						
PAPA	1857	Endometrial	Tao brush	sample	chr17	7578551	SBS	A					
					G						TP53	379	
	127	S	P	No	No	58.32	11338						
PAPA	1858	Endometrial	Tao brush	sample	chr3	178952085	SBS	A					
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PAPA	1858	Endometrial	Tao brush	sample	chr10	89692803	SBS	C					
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PAPA	1858	Endometrial	Tao brush	sample	chr10	89692929	SBS	A					
					G						PTEN	413	
	138	Y	C	No	No	20.75	5651						
PAPA	1859	Endometrial	Tao brush	sample	chr10	123258034	SBS	A					
					T						FGFR2	1647	
	549	N	K	No	No	65.86	5734						
PAPA	1859	Endometrial	Tao brush	sample	chr3	178916876	SBS	G					
					A						PIK3CA	263	
	88	R	Q	No	No	33.91	352						
PAPA	1859	Endometrial	Tao brush	sample	chr10	89720737	SBS	T					
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PAPA	1860	Endometrial	Tao brush	sample	chr3	41266113	SBS	C					
					T						CTNNB1	110	
	37	S	F	No	No	8.40	516						
PAPA	1860	Endometrial	Tao brush	sample	chr5	67591086	SBS	A					
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	560	D	G	No	No	7.77	521						
PAPA	1861	Endometrial	Tao brush	sample	chr3	178916876	SBS	G					
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	88	R	Q	No	No	6.22	58						
PAPA	1862	Endometrial	Tao brush	sample	chr10	89720817	Indel						

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	332	K	NULL	No	No	6.46	97						
PAPA	1865	Endometrial	Tao	brush	sample	chr10	89692935	SBS	T				
						G					PTEN		419
	140	L	*	No	No	6.18	2564						
PAPA	1865	Endometrial	Tao	brush	sample	chr17	7578419	SBS	C				
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	171	E	*	No	No	2.00	339						
PAPA	1865	Endometrial	Tao	brush	sample	chr17	7577120	SBS	C				
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	273	R	H	No	No	45.33	7911						
PAPA	1867	Endometrial	Tao	brush	sample	chr12	25398284	SBS	C				
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	12	G	V	No	No	53.24	12357						
PAP	266	Endometrial	Pap	brush	sample	chr10	89720733	Indel					
						T					PTEN		884
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PAP	059	Ovarian	Pap	brush	sample	chr12	25398282	SBS	C				
						T					KRAS		37
	13	G	S	No	No	0.10	6						
PAP	581	Endometrial	Pap	brush	sample	chr5	67590364	SBS	G				
						A					PIK3R1		1426
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PAP	208	Endometrial	Pap	brush	sample	chr10	89720716	Indel	A				
											PTEN		867
	289	K	NULL	No	No	0.22	16						
PAPA	1153	Endometrial	Tao	brush	sample	chr17	7578229	SBS	T				
						C					TP53		620
	207	D	G	No	No	0.70	3						
PAPA	1256	Endometrial	Pap	brush	sample	chr10	89685307	SBS	T				
						C					PTEN		202
	68	Y	H	No	No	0.28	14						
PAPA	1208	Ovarian	Pap	brush	sample	chr9	21971082	Indel	G				
											CDKN2A		276
	92	D	NULL	No	No	2.85	7						
PAPA	1210	Ovarian	Pap	brush	sample	chr9	21971080	SBS	G				
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	93	T	M	No	No	1.36	3						
PAPA	1695	Ovarian	Pap	brush	sample	chr17	7578535	SBS	T				
						C					TP53		395
	132	K	R	No	No	0.05	10						
PAPA	1697	Ovarian	Pap	brush	sample	chr17	7579541	SBS	T				
						C					TP53		146
	49	D	G	No	No	0.09	23						
PAPA	1140	Endometrial	Pap	brush	sample	chr17	7577551	SBS	C				

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						A					TP53	730	
	244	G	C	No	No	0.64	117						
PAP	378	Healthy	ControPap	brush	sample		chr3	178936082	SBS	G			
						A					PIK3CA	1624	
	542	E	K	No	No	3.55	127						
PAP	433	Healthy	ControPap	brush	sample		chr5	67591134	Indel	CGA			
											PIK3R1	1727	
	576	T	NULL	No	No	0.60	10						
PAP	829	Endometrial	Pap	brush	sample		chr5	67591134	Indel	CGA			
											PIK3R1	1727	
	576	T	NULL	No	No	0.55	10						
PAP	663	Endometrial	Pap	brush	sample		chr4	153247288	SBS	C			
						T					FBXW7	1514	
	505	R	H	No	No	1.51	41						
PAP	922	Endometrial	Pap	brush	sample		chr10	89717672	SBS	C			
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	233	R	*	No	No	0.72	115						
PAP	739	Healthy	ControPap	brush	sample		chr17	7577509	SBS	C			
						A					TP53	772	
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PAP	901	Endometrial	Pap	brush	sample		chr5	67589581	Indel	A			
											PIK3R1	1344	
	448	K	NULL	No	No	1.38	63						
PAPA	1094	Ovarian	Pap	brush	sample		chr7	140453154	SBS	T			
						C					BRAF	1781	
	594	D	G	No	No	0.19	6						
PAPA	1152	Endometrial	Pap	brush	sample		chr4	153249384	SBS	C			
						T					FBXW7	1394	
	465	R	H	No	No	1.05	81						
PAPA	1259	Ovarian	Tao	brush	sample		chr19	52715971	SBS	C			
						G					PPP2R1A	536	
	179	P	R	No	No	1.89	271						
PAPA	1328	Ovarian	Pap	brush	sample		chr10	89653809	SBS	G			
						A					PTEN	107	
	36	G	E	No	No	0.63	24						
PAP	238	Endometrial	Pap	brush	sample		chr5	67589615	Indel	A			
											PIK3R1	1378	
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PAPA	1145	Endometrial	Tao	brush	sample		chr10	89685303	SBS	G			
						T					PTEN	198	
	66	K	N	No	No	1.71	415						
PAP	671	Endometrial	Pap	brush	sample		chr17	7578271	SBS	T			
						G					TP53	578	
	193	H	P	No	No	0.17	10						
PAPA	1145	Endometrial	Pap	brush	sample		chr10	89685303	SBS	G			
						T					PTEN	198	
	66	K	N	No	No	0.34	148						
PAPA	1077	Endometrial	Pap	brush	sample		chr10	89692793	SBS	C			

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						T						PTEN	277	
93	H	Y	No	No	0.07	4								
PAPA 1328	Ovarian	Pap brush	sample		chr3	178916854	SBS	G						
						A						PIK3CA	241	
81	E	K	No	No	0.39	12								
PAP 142	Healthy Contro	Pap brush	sample		chr17	7577518	Indel	TGATGGTGA						
												TP53		
763	255	I	NULL	No	No	0.48	22							
PAP 255	Ovarian	Pap brush	sample		chr19	52716325	SBS	T						
						G						PPP2R1A	769	
257	W	G	No	No	0.11	9								
PAP 583	Endometrial	Pap brush	sample		chr3	178952019	SBS	C						
						A						PIK3CA	3074	
1025	T	N	No	No	0.46	22								
PAPA 1217	Ovarian	Pap brush	sample		chr5	67591106	SBS	A						
						G						PIK3R1	1699	
567	K	E	No	No	0.26	13								
PAP 386	Healthy Contro	Pap brush	sample		chr10	89692981	SBS	T						
						G						PTEN	465	
155	Y	*	No	No	0.51	9								
PAP 242	Endometrial	Pap brush	sample		chr3	41266097	SBS	G						
						A						CTNNB1	94	
32	D	N	No	No	0.21	14								
PAP 277	Endometrial	Pap brush	sample		chr5	112175684	Indel	AG						
												APC	4393	
1465	S	NULL	No	No	0.44	38								
PAPA 1043	Endometrial	Pap brush	sample		chr12	25398284	SBS	C						
						A						KRAS	35	
12	G	V	No	No	2.44	82								
PAPA 1218	Endometrial	Pap brush	sample		chr17	7577105	SBS	G						
						T						TP53	833	
278	P	H	No	No	0.67	21								
PAP 277	Endometrial	Pap brush	sample		chr5	67589588	Indel	GAATAT						
												PIK3R1	1351	
451	E	NULL	No	No	0.31	18								
PAPA 1145	Endometrial	Tao brush	sample		chr10	89624245	SBS	G						
						T						PTEN	19	
7	E	*	No	No	0.35	83								
PAP 235	Endometrial	Pap brush	sample		chr10	123247516	SBS	T						
						C						FGFR2	1975	
659	K	E	No	No	0.65	13								
PAP 034	Endometrial	Pap brush	sample		chr17	7578253	SBS	C						
						T						TP53	596	
199	G	E	No	No	0.16	19								
PAP 685	Endometrial	Pap brush	sample		chr10	123247516	SBS	T						
						C						FGFR2	1975	
659	K	E	No	No	0.21	8								
PAP 208	Endometrial	Pap brush	sample		chr12	25398284	SBS	C						

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```
                                    G                                       KRAS    35
     12      G       A       No      No      1.91    71
PAP 869     Endometrial   Pap brush sample     chr10   89720670      SBS     G
                                    A                                       PTEN    821
     274     W       *       No      No      0.76    20
PAPA 1160   Endometrial   Tao brush sample     chr17   7578412       SBS     A
                                    G                                       TP53    518
     173     V       A       No      No      0.18    19
PAPA 1110   Ovarian       Pap brush sample     chr12   25398284      SBS     C
                                    G                                       KRAS    35
     12      G       A       No      No      1.13    82
PAPA 1239   Endometrial   Pap brush sample     chr17   7577115       SBS     A
                                    C                                       TP53    823
     275     C       G       No      No      0.14    6
PAPA 1328   Ovarian       Pap brush sample     chr10   89624245      SBS     G
                                    T                                       PTEN    19
     7       E       *       No      No      0.07    7
PAPA 1705   Ovarian       Pap brush sample     chr3    178936074     SBS     C
                                    G                                       PIK3CA  1616
     539     P       R       No      No      0.51    27
PAP 204     Endometrial   Pap brush sample     chr17   7577099       SBS     C
                                    A                                       TP53    839
     280     R       I       No      No      0.15    12
PAP 280     Healthy ControPap brush sample     chr5    67589598      Indel
                                    ACACAC                                  PIK3R1  1361
     454     T       NULL    No      No      0.11    13
PAP 569     Ovarian       Pap brush sample     chr17   7578235       SBS     T
                                    C                                       TP53    614
     205     Y       C       No      No      0.21    8
PAPA 1832   Ovarian       Tao brush sample     chr17   7577099       SBS     C
                                    A                                       TP53    839
     280     R       I       No      No      0.27    31
PAP 280     Healthy ControPap brush sample     chr5    67589596      Indel   CAC
                                                                            PIK3R1  1359
     453     N       NULL    No      No      0.10    12
PAP 177     Endometrial   Pap brush sample     chr10   89717620      Indel   T
                                                                            PTEN    645
     215     F       NULL    No      No      1.72    22
PAP 557     Endometrial   Pap brush sample     chr17   7577018       SBS     C
                                    A                                       TP53    0
     0       NULL    NULL    1       No      0.34    25
PAP 236     Endometrial   Pap brush sample     chr10   89692977      Indel   T
                                                                            PTEN    461
     154     F       NULL    No      No      0.22    7
PAP 998     Endometrial   Tao brush sample     chr9    21971186      Indel
GGGCGCTGCCCATC (SEQ ID NO:776)
CDKN2A  172         58      R       NULL    No      No      2.77    162
PAPA 1218   Endometrial   Pap brush sample     chr17   7579312       SBS     C
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						T					TP53		438
	146	W	*		No	No	0.17	67					
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	1047	H	L		No	No	1.03	99					
PAP	003	Endometrial		Pap	brush	sample	chr10	89692905	SBS	G			
						A					PTEN		389
	130	R	Q		No	No	1.32	56					
PAP	069	Endometrial		Pap	brush	sample	chr5	67589609	SBS	G			
						T					PIK3R1		1372
	458	E	*		No	No	0.28	19					
PAPA	1140	Endometrial		Pap	brush	sample	chr17	7577557	SBS	A			
						C					TP53		724
	242	C	G		No	No	0.07	13					
PAP	270	Endometrial		Pap	brush	sample	chr3	178936095	SBS	A			
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	546	Q	R		No	No	1.10	19					
PAP	654	Endometrial		Pap	brush	sample	chr3	178952085	SBS	A			
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	1047	H	R		No	No	2.10	212					
PAP	998	Endometrial		Tao	brush	sample	chr17	7577100	SBS	T			
						C					TP53		838
	280	R	G		No	No	0.64	66					
PAPA	1162	Endometrial		Pap	brush	sample	chr12	25398284	SBS	C			
						T					KRAS		35
	12	G	D		No	No	1.63	243					
PAP	378	Healthy Contro		Pap	brush	sample	chr4	153247247	SBS	A			
						C					FBXW7		1555
	519	Y	D		No	No	3.13	110					
PAP	574	Endometrial		Pap	brush	sample	chr3	178916876	SBS	G			
						A					PIK3CA		263
	88	R	Q		No	No	1.95	17					
PAP	320	Healthy Contro		Pap	brush	sample	chr10	123279674	SBS	G			
						C					FGFR2		758
	253	P	R		No	No	0.86	20					
PAP	320	Healthy Contro		Pap	brush	sample	chr17	7578529	SBS	A			
						C					TP53		401
	134	F	C		No	No	0.36	17					
PAP	145	Healthy Contro		Pap	brush	sample	chr17	7578182	SBS	G			
						A					TP53		667
	223	P	S		No	No	1.46	38					
PAP	145	Healthy Contro		Pap	brush	sample	chr17	7577105	SBS	G			
						C					TP53		833
	278	P	R		No	No	1.37	23					
PAP	229	Endometrial		Pap	brush	sample	chr12	25398284	SBS	C			

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					T					KRAS		35
	12	G	D	No	No	3.27	108					
PAP	936	Endometrial	Pap brush	sample	chr3	178936082	SBS	G				
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	542	E	K	No	No	2.89	88					
PAP	726	Endometrial	Pap brush	sample	chr12	25398284	SBS	C				
					T					KRAS		35
	12	G	D	No	No	2.94	168					
PAP	879	Endometrial	Pap brush	sample	chr12	25398284	SBS	C				
					T					KRAS		35
	12	G	D	No	No	3.36	156					
PAPA	1043	Endometrial	Pap brush	sample	chr3	178936082	SBS	G				
					A					PIK3CA		1624
	542	E	K	No	No	2.44	75					
PAPA	1066	Endometrial	Pap brush	sample	chr12	25398284	SBS	C				
					T					KRAS		35
	12	G	D	No	No	2.56	279					
PAPA	1155	Endometrial	Tao brush	sample	chr17	7577120	SBS	C				
					T					TP53		818
	273	R	H	No	No	0.65	2					
PAPA	1189	Ovarian	Tao brush	sample	chr17	7577120	SBS	C				
					T					TP53		818
	273	R	H	No	No	0.76	6					
PAPA	1264	Endometrial	Pap brush	sample	chr5	67588989	Indel					
					CG					PIK3R1		1080
	360	A	NULL	No	No	1.08	10					
PAPA	1191	Endometrial	Pap brush	sample	chr3	178936095	SBS	A				
					G					PIK3CA		1637
	546	Q	R	No	No	0.49	15					
PAPA	1202	Endometrial	Pap brush	sample	chr17	7577120	SBS	C				
					T					TP53		818
	273	R	H	No	No	1.23	96					

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

Total # UIDs	Mutation in Primary Tumor
8,317	Tumor tissue unavailable
5,900	Tumor tissue unavailable
8,737	Tumor tissue unavailable
11,773	Tumor tissue unavailable
4,278	Tumor tissue unavailable
12,038	Tumor tissue unavailable
49,208	Tumor tissue unavailable
14,290	Tumor tissue unavailable
48,916	Tumor tissue unavailable
41,873	Not present
51,075	Not present

4,771	Not present
11,369	Present
25,810	Present
19,946	Not present
7,658	Not present
5,146	Not present
4,752	Present
13,958	Present
3,535	Not present
5,072	Present
7,780	Not present
7,780	Not present
11,553	Not present
8,610	Present
7,741	Present
9,561	Not present
2,885	Present
9,629	Present
7,643	Not present
9,527	Present
21,539	Insufficient neoplastic
19,529	Present
5,132	Present
3,917	Present
5,338	Present
4,753	Present
812	Insufficient neoplastic
20,529	Present
4,494	Not present
11,168	Not present
17,497	Present
10,746	Insufficient sequence co
4,194	Present
2,321	Present
1,891	Insufficient sequence co
4,477	Present
2,498	Not present
2,278	Not present
5,889	Not present
819	Present
3,667	Not present
3,667	Not present
3,667	Not present
15,370	Present
13,737	Present
17,720	Insufficient sequence co
15,094	Not present
398	Insufficient sequence co

Table15.txt

1,791	Present
3,389	Present
17,945	Insufficient sequence co
2,844	Present
2,805	Insufficient sequence co
5,862	Insufficient sequence co
3,716	Present
1,626	Insufficient sequence co
3,821	Insufficient sequence co
11,263	Present
1,042	Present
2,384	Present
6,479	Tumor tissue unavailable
23,572	Insufficient sequence co
22,984	Present
3,959	Present
7,385	Present
4,692	Not present
3,619	Present
3,792	Present
16,046	Present
19,257	Insufficient sequence co
13,605	Present
7,379	Present
26,387	Present
2,544	Present
20,833	Present
1,207	Present
1,207	Present
9,865	Not present
7,343	Present
11,511	Present
9,699	Not present
2,373	Present
2,593	Present
18,514	Present
18,654	Present
9,489	Present
9,903	Present
2,192	Present
1,172	Present
1,023	Present
3,618	Present
3,750	Not present
12,276	Present
19,446	Present
3,987	Present
11,708	Present

Table15.txt

5,995	Present
2,302	Not present
1,387	Present
1,711	Present
1,950	Present
14,566	Not present
3,780	Present
2,365	Not present
6,238	Present
3,916	Not present
8,913	Present
6,820	Present
2,992	Present
4,890	Present
5,999	Tumor tissue unavailable
5,133	Tumor tissue unavailable
562	Present
1,432	Present
5,348	Present
21,758	Not present
4,101	Not present
6,071	Present
15,454	Present
15,454	Present
2,051	Tumor tissue unavailable
9,646	Tumor tissue unavailable
18,593	Tumor tissue unavailable
16,061	Tumor tissue unavailable
19,559	Not present
8,662	Not present
8,619	Present
11,312	Present
2,971	Tumor tissue unavailable
5,599	Present
9,130	Present
5,994	Tumor tissue unavailable
7,542	Tumor tissue unavailable
6,957	Not present
5,918	Present
5,600	Present
4,533	Present
3,529	Present
7,813	Present
1,590	Present
23,232	Present
2,322	Tumor tissue unavailable
6,846	Tumor tissue unavailable
5,334	Present

16,264	Not present
11,271	Not present
3,024	Tumor tissue unavailable
7,753	Tumor tissue unavailable
6,038	Tumor tissue unavailable
6,771	Not present
2,186	Present
2,551	Present
5,646	Present
2,602	Present
2,960	Present
2,353	Present
9,493	Present
2,405	Present
8,303	Present
8,141	Present
9,275	Not present
14,975	Present
11,907	Present
8,981	Present
14,065	Not present
5,435	Not present
4,968	Present
17,348	Not present
9,141	Not present
3,992	Present
4,978	Tumor tissue unavailable
8,204	Present
6,192	Not present
7,841	Tumor tissue unavailable
15,827	Not present
6,516	Present
5,280	Insufficient neoplastic
14,141	Present
7,117	Present
11,943	Present
3,687	Not present
1,500	Present
11,634	Present
2,189	Present
3,153	Present
19,601	Insufficient neoplastic
24,630	Not present
22,950	Present
1,069	Present
2,262	Present
7,926	Present
4,217	Present

Table15.txt

7,825	Not present
7,825	Not present
29,578	Present
1,733	Present
2,555	Present
13,074	Present
5,220	Present
12,181	Present
3,168	Present
4,125	Present
6,183	Present
10,284	Present
3,958	Present
4,538	Present
9,664	Present
15,861	Present
2,161	Not present
5,677	Present
8,132	Present
23,467	Present
6,266	Not present
4,314	Present
7,532	Present
8,020	Present
5,160	Present
6,540	Present
5,317	Present
6,509	Present
4,030	Present
6,010	Present
8,701	Not present
3,913	Not present
1,928	Present
3,117	Present
8,902	Not present
3,999	Not present
1,829	Present
5,053	Not present
11,163	Present
16,883	Present
8,751	Present
12,268	Present
16,479	Not present
13,209	Insufficient neoplastic
8,423	Insufficient neoplastic
12,688	Insufficient neoplastic
6,881	Insufficient neoplastic
17,440	Present

Table15.txt

6,569	Present
5,699	Present
2,139	Present
3,127	Present
26,469	Present
7,674	Present
4,409	Present
2,326	Present
3,336	Present
7,559	Not present
3,193	Not present
24,646	Not present
29,656	Present
8,152	Present
6,881	Not present
20,626	Present
9,707	Present
12,315	Not present
6,086	Present
3,287	Present
11,627	Present
7,278	Present
8,918	Present
3,929	Present
13,811	Present
13,811	Present
10,597	Present
7,406	Present
7,406	Present
9,961	Present
9,337	Present
7,789	Present
12,490	Present
2,149	Present
8,384	Not present
13,727	Present
2,873	Present
4,633	Present
8,588	Not present
2,015	Tumor tissue unavailable
12,513	Tumor tissue unavailable
10,127	Tumor tissue unavailable
6,419	Present
9,484	Present
9,484	Not present
9,570	Present
1,336	Present
4,851	Not present

Table15.txt

4,851	Not present
4,851	Not present
6,709	Present
6,839	Present
8,649	Present
3,695	Present
8,869	Present
1,158	Present
7,739	Present
10,421	Present
17,090	Present
4,596	Present
7,646	Present
9,691	Present
20,690	Present
4,177	Present
2,919	Present
6,431	Present
6,117	Present
7,559	Tumor tissue unavailable
9,613	Tumor tissue unavailable
7,196	Tumor tissue unavailable
14,183	Tumor tissue unavailable
15,043	Tumor tissue unavailable
16,619	Present
1,895	Present
3,398	Present
5,364	Present
4,161	Present
8,557	Present
9,076	Present
11,571	Not present
12,288	Present
4,754	Present
12,662	Present
3,643	Present
9,676	Present
37,116	Present
8,409	Present
28,861	Present
37,034	Present
3,148	Present
28,906	Present
1,973	Present
12,845	Present
28,286	Insufficient neoplastic
7,379	Not present
8,213	Insufficient neoplastic

Table15.txt

7,317	Present
35,552	Present
15,426	Not present
35,305	Present
6,920	Present
15,051	Not present
13,204	Tumor tissue unavailable
2,626	Present
9,950	Present
10,262	Present
2,187	Not present
38,012	Not present
2,830	Not present
9,800	Present
12,192	Present
6,117	Present
7,383	Insufficient sequence co
34,241	Not present
32,383	Present
16,824	Not present
22,218	Present
33,427	Present
28,914	Not present
3,006	Present
374	Tumor tissue unavailable
665	Tumor tissue unavailable
1,920	Tumor tissue unavailable
994	Tumor tissue unavailable
1,795	Tumor tissue unavailable
1,150	Tumor tissue unavailable
1,671	Tumor tissue unavailable
569	Tumor tissue unavailable
542	Tumor tissue unavailable
1,021	Tumor tissue unavailable
755	Tumor tissue unavailable
3,098	Present
3,137	Present
1,144	Insufficient neoplastic
404	Present
1,597	Present
1,597	Insufficient neoplastic
2,490	Present
884	Present
810	Insufficient neoplastic
1,741	Present
1,646	Present
1,165	Insufficient sequence co
3,017	Present

Table15.txt

834	Present
1,716	Present
1,954	Present
947	Present
616	Present
3,896	Present
2,198	Present
207	Present
859	Present
1,174	Not present
1,005	Present
691	Present
9,202	Tumor tissue unavailable
9,468	Tumor tissue unavailable
4,511	Tumor tissue unavailable
35,417	Not present
8,176	Not present
18,418	Present
16,911	Present
3,754	Not present
7,957	Insufficient sequence co
6,867	Present
12,871	Present
16,594	Present
7,122	Present
3,649	Present
1,408	Present
13,843	Present
11,957	Present
20,434	Present
3,793	Present
10,476	Present
5,426	Present
426	Present
3,560	Present
6,439	Present
4,614	Present
6,752	Present
6,752	Not present
5,626	Present
3,828	Present
7,488	Present
779	Present
5,214	Present
5,214	Not present
4,807	Not present
6,365	Present
1,495	Present

7,425	Present
8,400	Present
5,989	Present
6,839	Present
445	Present
14,934	Not present
4,157	Present
10,833	Present
9,507	Present
4,048	Present
8,865	Not present
5,370	Present
4,204	Present
2,837	Present
3,242	Present
612	Present
3,337	Present
1,868	Not present
1,208	Present
14,050	Not present
2,730	Present
3,906	Insufficient sequence co
10,527	Present
4,484	Present
343	Present
2,675	Not present
2,675	Present
12,736	Present
2,216	Present
9,479	Present
4,218	Present
3,667	Not present
2,166	Present
1,335	Present
3,811	Present
27,573	Present
4,474	Tumor tissue unavailable
2,060	Tumor tissue unavailable
2,499	Tumor tissue unavailable
20,438	Tumor tissue unavailable
305	Tumor tissue unavailable
5,362	Tumor tissue unavailable
2,667	Tumor tissue unavailable
2,534	Tumor tissue unavailable
6,499	Present
694	Present
1,286	Present
1,016	Present

2,825	Not present
4,117	Present
1,935	Present
3,807	Present
5,005	Not present
3,345	Present
12,921	Present
1,919	Present
1,695	Present
10,347	Present
4,229	Present
1,598	Present
7,358	Present
11,004	Present
3,284	Present
3,356	Not present
3,356	Not present
2,386	Present
5,883	Present
2,456	Present
3,000	Not present
2,841	Present
2,147	Present
2,157	Present
2,635	Tumor tissue unavailable
241	Tumor tissue unavailable
494	Tumor tissue unavailable
2,859	Tumor tissue unavailable
1,881	Present
7,926	Present
13,583	Tumor tissue unavailable
7,020	Tumor tissue unavailable
11,773	Tumor tissue unavailable
9,132	Tumor tissue unavailable
7,359	Tumor tissue unavailable
14,259	Tumor tissue unavailable
10,181	Tumor tissue unavailable
16,382	Tumor tissue unavailable
5,363	Tumor tissue unavailable
8,615	Tumor tissue unavailable
8,749	Tumor tissue unavailable
4,569	Tumor tissue unavailable
1,255	Tumor tissue unavailable
2,735	Tumor tissue unavailable
2,735	Tumor tissue unavailable
9,408	Tumor tissue unavailable
516	Tumor tissue unavailable
7,119	Tumor tissue unavailable

Table15.txt

14,373	Tumor tissue unavailable
8,113	Not present
25,013	Present
2,749	Present
3,316	Present
12,296	Present
4,533	Present
6,761	Present
5,570	Present
5,085	Present
3,649	Present
4,571	Not present
5,571	Not present
6,064	Present
4,505	Present
5,449	Present
5,299	Tumor tissue unavailable
2,418	Tumor tissue unavailable
502	Tumor tissue unavailable
3,958	Tumor tissue unavailable
4,771	Not present
2,461	Present
2,090	Present
1,819	Present
2,107	Present
2,461	Present
3,614	Present
1,429	Present
3,686	Present
3,238	Present
1,681	Present
8,326	Present
2,503	Not present
4,846	Not present
18,667	Present
9,069	Present
2,454	Not present
7,780	Present
1,704	Present
2,714	Present
1,027	Not present
2,447	Not present
2,447	Not present
2,270	Present
268	Not present
1,126	Present
1,126	Present
1,839	Present

276	Present
1,046	Present
5,827	Present
11,574	Present
20,042	Present
961	Present
5,750	Present
1,974	Present
3,652	Not present
2,866	Present
3,311	Present
591	Present
1,924	Tumor tissue unavailable
14,177	Tumor tissue unavailable
2,090	Tumor tissue unavailable
5,656	Not present
4,211	Present
19,318	Present
280	Present
6,872	Present
11,106	Insufficient sequence co
7,494	Insufficient sequence co
6,521	Present
11,980	Present
552	Present
552	Present
2,862	Not present
2,862	Present
2,440	Present
2,191	Not present
1,845	Not present
2,360	Present
2,047	Not present
1,416	Present
4,958	Present
4,279	Present
10,639	Present
3,701	Present
1,249	Present
7,609	Present
1,488	Present
5,035	Present
5,340	Present
9,488	Present
1,900	Tumor tissue unavailable
4,537	Present
3,886	Present
6,016	Not present

Table15.txt

15,140	Present
2,830	Present
11,051	Not present
4,310	Present
9,116	Not present
5,601	Present
2,544	Insufficient sequence co
2,015	Insufficient sequence co
8,076	Insufficient sequence co
2,736	Present
3,886	Present
2,601	Present
3,898	Not present
2,329	Present
6,417	Present
8,167	Present
4,762	Present
9,276	Present
6,331	Present
625	Present
5,113	Insufficient sequence co
9,630	Present
9,630	Present
12,378	Insufficient sequence co
34,978	Not present
12,515	Insufficient sequence co
8,188	Not present
3,339	Not present
1,901	Present
9,247	Present
2,868	Present
5,874	Present
4,094	Present
3,155	Not present
7,133	Present
10,021	Not present
4,550	Present
3,283	Present
4,660	Present
4,007	Present
4,983	Present
5,601	Present
1,844	Present
15,152	Present
19,302	Not present
2,296	Present
13,991	Present
1,482	Present

Table15.txt

1,341	Present
3,059	Present
8,451	Present
7,881	Present
8,199	Not present
5,290	Present
9,303	Present
10,192	Present
19,873	Present
7,022	Present
17,849	Present
15,510	Present
1,690	Present
2,134	Present
2,189	Present
14,521	Present
9,704	Present
14,840	Present
4,556	Present
20,977	Present
2,787	Present
3,218	Present
4,706	Present
4,358	Not present
4,358	Not present
1,829	Present
6,944	Present
31,671	Present
1,401	Present
6,045	Present
4,403	Present
4,541	Present
7,998	Present
866	Insufficient sequence co
345	Insufficient sequence co
540	Insufficient sequence co
337	Present
23,046	Present
2,951	Present
4,921	Not present
4,279	Tumor tissue unavailable
2,739	Tumor tissue unavailable
839	Tumor tissue unavailable
2,628	Tumor tissue unavailable
23,422	Tumor tissue unavailable
11,970	Tumor tissue unavailable
9,807	Tumor tissue unavailable
3,733	Tumor tissue unavailable

Table15.txt

1,765	Tumor tissue unavailable
422	Tumor tissue unavailable
1,444	Tumor tissue unavailable
19,353	Tumor tissue unavailable
8,357	Tumor tissue unavailable
7,498	Present
22,367	Present
1,095	Present
1,095	Present
2,098	Not present
2,657	Present
2,780	Present
2,041	Present
6,227	Present
3,645	Present
1,957	Present
4,680	Tumor tissue unavailable
7,378	Tumor tissue unavailable
4,199	Tumor tissue unavailable
3,663	Present
2,287	Present
9,536	Present
3,192	Present
1,583	Present
8,387	Present
6,587	Present
857	Present
10,885	Tumor tissue unavailable
9,021	Tumor tissue unavailable
6,512	Not present
10,270	Present
7,895	Present
6,314	Present
413	Present
14,504	Present
2,835	Present
2,723	Present
15,086	Present
7,157	Present
4,756	Present
7,529	Present
15,888	Present
5,548	Present
2,202	Present
6,087	Present
6,173	Present
2,269	Present
6,516	Present

Table15.txt

4,817	Present
6,425	Not present
2,712	Present
3,852	Present
4,101	Not present
1,556	Not present
3,902	Present
22,750	Present
11,284	Not present
6,887	Present
6,166	Present
2,302	Present
6,004	Tumor tissue unavailable
8,697	Not present
2,583	Not present
264	Present
2,447	Not present
4,578	Present
3,004	Tumor tissue unavailable
1,690	Tumor tissue unavailable
6,388	Tumor tissue unavailable
2,313	Tumor tissue unavailable
4,901	Tumor tissue unavailable
7,019	Tumor tissue unavailable
4,181	Tumor tissue unavailable
2,082	Tumor tissue unavailable
3,456	Tumor tissue unavailable
4,295	Tumor tissue unavailable
6,044	Tumor tissue unavailable
4,180	Tumor tissue unavailable
855	Present
2,170	Present
308	Present
1,089	Present
1,089	Present
6,711	Present
2,931	Not present
759	Not present
1,289	Not present
2,036	Not present
10,485	Not present
824	Not present
401	Not present
1,064	Not present
1,955	Not present
8,772	Not present
9,797	Present
10,352	Present

7,284	Present
14,160	Present
7,694	Present
15,332	Present
31,946	Present
6,666	Tumor tissue unavailable
6,229	Present
18,726	Not present
550	Not present
528	Not present
4,255	Not present
3,836	Not present
563	Not present
2,260	Present
2,168	Present
9,128	Present
20,083	Present
6,957	Present
756	Present
2,510	Present
1,933	Present
472	Present
3,174	Present
5,176	Present
2,390	Present
2,127	Present
327	Present
2,860	Present
2,860	Present
5,090	Present
11,711	Present
8,771	Present
13,160	Present
6,142	Present
5,038	Present
2,318	Present
10,007	Present
5,235	Present
1,939	Present
4,706	Present
3,723	Insufficient sequence co
3,050	Present
1,123	Present
779	Present
872	Present
1,693	Not present
2,552	Present
5,440	Not present

Table15.txt

1,517	Present
9,072	Present
7,965	Present
5,180	Present
17,398	Present
1,908	Present
1,037	Present
23,235	Present
2,774	Present
5,285	Present
4,818	Present
5,060	Present
2,187	Present
4,722	Present
2,242	Present
6,082	Present
3,690	Present
18,443	Present
9,118	Present
6,250	Present
24,884	Present
8,730	Present
6,935	Present
25,927	Present
8,896	Present
3,364	Present
25,565	Present
1,696	Present
7,536	Present
24,374	Not present
24,659	Present
2,733	Present
8,204	Present
8,716	Not present
13,839	Present
23,498	Present
15,726	Present
8,296	Tumor tissue unavailable
5,967	Tumor tissue unavailable
7,987	Present
15,845	Present
526	Present
2,336	Present
9,454	Present
2,636	Present
16,290	Not present
10,671	Present
5,109	Present

Table15.txt

8,391	Present
2,168	Present
11,254	Present
3,342	Present
1,981	Present
12,854	Present
30,223	Present
4,880	Present
10,854	Present
6,700	Present
10,535	Present
1,951	Present
9,142	Present
7,276	Present
9,670	Present
11,530	Present
8,670	Present
14,356	Not present
8,895	Present
8,367	Tumor tissue unavailable
7,514	Tumor tissue unavailable
7,692	Tumor tissue unavailable
1,298	Tumor tissue unavailable
1,246	Tumor tissue unavailable
582	Tumor tissue unavailable
8,702	Present
13,240	Present
10,993	Not present
10,445	Not present
4,704	Present
12,657	Present
4,982	Present
4,764	Not present
4,793	Present
3,751	Present
242	Insufficient sequence co
242	Insufficient sequence co
1,976	Present
3,195	Not present
4,172	Present
7,918	Present
2,204	Present
2,084	Tumor tissue unavailable
470	Tumor tissue unavailable
564	Tumor tissue unavailable
745	Tumor tissue unavailable
2,411	Present
24,841	Present

Table15.txt

5,475	Present
5,475	Present
5,959	Present
10,293	Present
18,630	Tumor tissue unavailable
18,630	Tumor tissue unavailable
18,630	Tumor tissue unavailable
33,883	Tumor tissue unavailable
33,883	Tumor tissue unavailable
33,883	Tumor tissue unavailable
40,654	Tumor tissue unavailable
13,464	Tumor tissue unavailable
6,355	Tumor tissue unavailable
20,668	Tumor tissue unavailable
1,341	Present
1,341	Insufficient sequence co
3,459	Present
5,856	Tumor tissue unavailable
13,884	Tumor tissue unavailable
3,703	Present
3,647	Present
11,420	Not present
509	Tumor tissue unavailable
3,290	Tumor tissue unavailable
6,805	Present
4,643	Present
15,680	Not present
3,946	Present
840	Present
2,462	Present
4,618	Present
4,000	Present
2,382	Present
19,568	Not present
3,092	Present
10,405	Present
5,781	Not present
2,427	Present
6,301	Present
5,476	Present
7,164	Present
3,314	Present
10,706	Insufficient sequence co
6,293	Insufficient sequence co
5,337	Insufficient sequence co
2,421	Tumor tissue unavailable
9,586	Present
12,331	Not present

Table15.txt

1,879	Present
23,317	Present
6,267	Present
3,098	Present
5,382	Present
9,692	Present
6,133	Present
8,812	Present
8,423	Not present
4,790	Tumor tissue unavailable
8,848	Tumor tissue unavailable
4,411	Present
4,150	Present
8,619	Not present
5,565	Present
9,144	Present
9,144	Present
1,848	Present
2,475	Present
2,160	Present
5,783	Present
22,293	Present
22,293	Present
22,293	Not present
12,285	Present
5,588	Present
1,906	Present
3,084	Present
11,836	Present
8,916	Present
10,244	Present
3,216	Tumor tissue unavailable
4,811	Tumor tissue unavailable
4,747	Tumor tissue unavailable
760	Tumor tissue unavailable
4,116	Tumor tissue unavailable
9,274	Tumor tissue unavailable
7,530	Tumor tissue unavailable
3,816	Tumor tissue unavailable
3,026	Present
1,510	Present
2,776	Present
1,570	Present
5,576	Present
547	Present
3,253	Present
2,559	Present
4,602	Present

493	Present
5,042	Present
4,753	Present
4,260	Present
567	Present
2,437	Present
8,826	Present
6,959	Insufficient sequence co
1,848	Present
1,878	Present
14,063	Present
5,207	Present
1,753	Present
24,577	Present
7,088	Present
1,871	Present
2,672	Present
2,666	Present
9,364	Tumor tissue unavailable
6,047	Tumor tissue unavailable
5,098	Tumor tissue unavailable
5,920	Present
14,143	Present
10,726	Present
7,392	Present
1,364	Present
10,513	Present
6,926	Present
3,525	Present
5,819	Present
4,758	Present
6,458	Present
1,925	Present
3,188	Present
1,862	Present
10,372	Present
6,581	Present
4,529	Present
4,636	Present
3,504	Insufficient sequence co
1,057	Present
18,401	Present
5,489	Insufficient sequence co
5,489	Insufficient sequence co
983	Insufficient sequence co
5,645	Insufficient sequence co
2,231	Insufficient sequence co
7,456	Present

Table15.txt

7,456	Insufficient sequence co
1,400	Present
9,696	Present
5,014	Tumor tissue unavailable
5,976	Tumor tissue unavailable
5,567	Tumor tissue unavailable
5,598	Tumor tissue unavailable
11,384	Tumor tissue unavailable
6,766	Tumor tissue unavailable
5,391	Tumor tissue unavailable
2,711	Present
2,066	Present
7,765	Insufficient sequence co
5,728	Present
7,625	Present
8,858	Not present
5,327	Present
8,207	Present
9,588	Present
2,885	Not present
6,070	Present
8,385	Present
17,604	Present
7,737	Present
9,733	Present
1,537	Present
4,014	Present
7,308	Present
17,769	Present
3,350	Present
10,513	Present
942	Present
5,884	Present
6,551	Not present
5,112	Present
1,245	Present
12,470	Not present
3,451	Present
3,879	Present
3,121	Present
14,707	Present
11,548	Present
10,854	Present
4,886	Present
5,000	Present
4,556	Insufficient sequence co
6,266	Insufficient neoplastic
1,860	Not present

3,042	Present
5,760	Present
2,511	Present
5,095	Not present
5,095	Not present
514	Tumor tissue unavailable
3,851	Tumor tissue unavailable
3,274	Present
3,651	Present
6,251	Present
10,016	Present
2,737	Present
10,250	Present
9,418	Present
22,197	Present
7,784	Not present
2,753	Present
2,686	Tumor tissue unavailable
21,180	Tumor tissue unavailable
5,015	Tumor tissue unavailable
658	Present
6,531	Present
15,835	Tumor tissue unavailable
3,359	Tumor tissue unavailable
32,843	Tumor tissue unavailable
19,934	Tumor tissue unavailable
845	Tumor tissue unavailable
5,526	Present
13,283	Present
9,515	Present
9,515	Not present
4,475	Present
16,770	Present
1,993	Present
3,745	Not present
4,184	Present
2,535	Not present
9,504	Not present
2,506	Present
9,919	Present
3,934	Present
5,577	Present
4,535	Present
8,293	Present
4,342	Insufficient sequence co
4,991	Present
12,386	Present
6,117	Present

Table15.txt

8,036	Present
4,951	Not present
14,534	Tumor tissue unavailable
2,856	Tumor tissue unavailable
20,954	Tumor tissue unavailable
20,954	Tumor tissue unavailable
7,286	Tumor tissue unavailable
3,835	Not present
1,704	Present
6,927	Present
4,288	Present
5,350	Present
405	Present
2,905	Present
494	Not present
4,355	Present
6,626	Present
6,536	Present
7,971	Present
6,468	Present
4,238	Present
5,959	Present
5,772	Present
3,074	Present
57,557	Insufficient neoplastic
4,731	Present
244	Present
5,464	Present
36,136	Present
5,202	Present
467	Present
2,252	Present
804	Present
5,253	Present
248	Present
5,958	Present
1,120	Tumor tissue unavailable
259	Tumor tissue unavailable
259	Tumor tissue unavailable
62,500	Insufficient neoplastic
2,674	Present
4,350	Present
3,272	Not present
4,100	Not present
8,393	Present
556	Present
2,475	Present
4,643	Not present

Table15.txt

6,592	Present
5,287	Present
943	Not present
442	Present
1,909	Present
4,542	Present
358	Present
568	Insufficient sequence co
5,754	Present
3,459	Present
1,571	Present
10,717	Present
25,716	Present
21,781	Present
6,478	Present
17,332	Present
9,490	Present
1,534	Present
2,997	Not present
930	Not present
4,310	Present
2,313	Present
10,161	Present
5,764	Present
3,562	Present
16,865	Present
4,209	Present
2,010	Present
813	Tumor tissue unavailable
246	Insufficient neoplastic
13,966	Not present
13,966	Not present
13,966	Present
16,249	Not present
1,298	Present
6,222	Present
856	Present
10,437	Present
9,685	Present
12,680	Tumor tissue unavailable
17,642	Tumor tissue unavailable
1,965	Tumor tissue unavailable
2,677	Present
797	Present
2,057	Present
561	Present
2,531	Present
7,974	Present

Table15.txt

12,872	Present
1,703	Present
20,795	Present
1,852	Present
3,417	Present
647	Present
3,725	Present
2,051	Present
10,171	Present
36,476	Present
1,896	Present
827	Present
1,693	Present
9,823	Present
17,894	Present
12,841	Present
7,655	Present
13,084	Present
9,180	Present
3,619	Not present
5,625	Not present
3,773	Present
13,809	Tumor tissue unavailable
3,803	Tumor tissue unavailable
2,031	Tumor tissue unavailable
1,199	Tumor tissue unavailable
10,283	Tumor tissue unavailable
10,552	Present
13,871	Tumor tissue unavailable
3,500	Tumor tissue unavailable
9,862	Present
9,576	Present
24,321	Present
11,682	Present
7,317	Present
10,433	Present
5,082	Present
4,553	Present
5,685	Not present
7,539	Not present
14,203	Present
12,604	Tumor tissue unavailable
22,843	Not present
27,310	Not present
3,481	Not present
6,264	Insufficient sequence co
10,601	Not present
38,170	Not present

Table15.txt

15,079	Not present
17,123	Present
18,673	Present
22,221	Insufficient sequence co
11,142	Not present
6,303	Insufficient sequence co
19,033	Present
9,586	Insufficient sequence co
9,262	Insufficient sequence co
11,271	Insufficient sequence co
20,746	Present
39,747	Present
13,592	Not present
34,328	Present
21,276	Not present
22,426	Present
13,720	Present
14,645	Present
16,155	Present
16,808	Not present
1,245	Present
13,829	Not present
25,774	Insufficient neoplastic
7,064	Present
9,294	Present
275	Present
7,152	Present
12,277	Present
9,045	Present
1,380	Present
18,207	Present
23,452	Present
6,105	Present
18,118	Not present
1,489	Not present
5,001	Present
924	Present
8,599	Present
833	Present
39,293	Present
39,293	Present
34,473	Not present
6,048	Present
13,125	Present
15,310	Present
4,948	Present
12,047	Present
29,365	Present

Table15.txt

6,913	Present
7,558	Present
6,713	Present
27,724	Present
13,110	Present
24,002	Present
9,039	Present
8,255	Present
19,441	Present
8,911	Present
352	Present
27,235	Present
8,706	Present
1,038	Present
3,842	Present
6,140	Present
6,705	Not present
932	Not present
3,348	Insufficient neoplastic
1,502	Present
41,477	Present
16,944	Not present
17,453	Present
23,211	Present
5,532	Present
5,905	Tumor tissue unavailable
1,217	Insufficient sequence co
7,428	Not present
429	Not present
4,993	Not present
246	Tumor tissue unavailable
220	Insufficient sequence co
19,279	Not present
24,629	Insufficient sequence co
18,347	Not present
3,576	Tumor tissue unavailable
1,667	Tumor tissue unavailable
1,822	Insufficient sequence co
2,724	Not present
16,025	Present
6,221	Tumor tissue unavailable
4,560	Insufficient sequence co
3,082	Insufficient neoplastic
7,702	Present
14,354	Not present
3,810	Present
10,704	Present
24,261	Present

Table15.txt

6,048	Not present
43,375	Present
5,730	Not present
3,075	Present
4,575	Tumor tissue unavailable
8,223	Not present
4,808	Insufficient neoplastic
4,999	Tumor tissue unavailable
1,750	Tumor tissue unavailable
6,650	Not present
8,654	Insufficient neoplastic
3,362	Tumor tissue unavailable
3,118	Not present
5,843	Insufficient neoplastic
23,388	Not present
1,992	Not present
11,931	Tumor tissue unavailable
3,750	Present
3,715	Not present
2,632	Not present
10,547	Not present
7,225	Not present
4,308	Not present
9,824	Present
5,252	Insufficient sequence co
8,123	Not present
11,517	Tumor tissue unavailable
3,847	Insufficient sequence co
11,544	Insufficient neoplastic
11,517	Tumor tissue unavailable
1,278	Present
7,385	Not present
3,139	Present
5,851	Present
9,539	Present
40,072	Not present
9,597	Not present
4,253	Tumor tissue unavailable
6,772	Tumor tissue unavailable
18,347	Not present
1,728	Not present
10,077	Present
10,332	Not present
14,902	Present
3,509	Tumor tissue unavailable
871	Insufficient sequence co
2,336	Tumor tissue unavailable
4,734	Tumor tissue unavailable

Table15.txt

2,600	Tumor tissue unavailable
1,683	Tumor tissue unavailable
3,306	Present
3,043	Tumor tissue unavailable
5,720	Present
4,644	Present
3,073	Tumor tissue unavailable
10,890	Present
310	Not present
793	Insufficient neoplastic
922	Not present
3,031	Present
7,799	Present

Table16.txt

Table 16. Mutations identified in the primary tumors.

Cancer Patient ID	Mutant Type	Splice Site	Exon #	Chrom	Position*	Gene	WT Base	MT Base	MAF %	WT Nucleotide #	WT Codon #	WT Codon	Mutant Codon
PAP 084	#REF!			chr10	89720702	PTEN	G	T	61	853	285	E	*
	No	No	552	907									
PAP 084	#REF!			chr17	7576915	TP53		CTGGTGTG	84	931	311	N	
NULL	No	No	3211	3826									
PAP 119	#REF!			chr10	89692932	PTEN	T	A	13	416	139	L	*
	No	No	10	79									
PAP 119	#REF!			chr10	89717706	PTEN	C			731	244	P	
NULL	No	No	42	360					12				
PAP 119	#REF!			chr5	112175887	APC	C			4596	1532	D	
NULL	No	No	61	147					41				
PAP 120	#REF!			chr10	89692818	PTEN	T	C	31	302	101	I	T
	No	No	512	1626									
PAP 120	#REF!			chr10	89720693	PTEN		TT		844	282	G	
NULL	No	No	117	1643					7				
PAP 120	#REF!			chr3	178952085	PIK3CA	A	G	45	3140	1047	H	R
	No	No	711	1587									
PAP 120	#REF!			chr3	41266101	CTNNB1	C	G	31	98	33	S	C
	No	No	167	542									
PAP 121	#REF!			chr10	89692904	PTEN	C	G	12	388	130	R	G
	No	No	15	128									
PAP 121	#REF!			chr10	89720833	PTEN	AAAT			984	328	A	
NULL	No	No	14	109					13				
PAP 121	#REF!			chr12	25398284	KRAS	C	A	26	35	12	G	V
	No	No	145	558									
PAP 122	#REF!			chr10	89692904	PTEN	C	G	22	388	130	R	G
	No	No	42	193									
PAP 122	#REF!			chr12	25398284	KRAS	C	G		35	12	G	A

Table16.txt

```
      No      No      83      269     31
PAP 123    #REF!          chr3    41266113 CTNNB1  C
                  G                                  110           37      S       C
      No      No      215     1063    20
PAP 123    #REF!          chr5    67591154 PIK3R1
                  TC                                 0             0       NULL
NULL    Yes     No      102     508     20
PAP 123    #REF!          chr5    67591154 PIK3R1  T
                  A                                  0             0       NULL
NULL    Yes     No      102     508     20
PAP 125    #REF!          chr1    115256529NRAS    T
                  C                                  182           61      Q       R
      No      No      69      238     29
PAP 126    #REF!          chr14   105246551AKT1    C
                  T                                  49            17      E       K
      No      No      79      117     68
PAP 126    #REF!          chr3    41266103 CTNNB1  G
                  A                                  100           34      G       R
      No      No      44      146     30
PAP 128    #REF!          chr10   123258034FGFR2   A
                  T                                  1647          549     N       K
      No      No      227     311     73
PAP 128    #REF!          chr5    67591128 PIK3R1  G
                  C                                  1721          574     R       T
      No      No      47      115     41
PAP 129    #REF!          chr10   89720870 PTEN    T
                  G                                  1021          341     F       V
      No      No      3       28      11
PAP 129    #REF!          chr12   133253184POLE    G
                  C                                  857           286     P       R
      No      No      9       59      15
PAP 129    #REF!          chr3    41266112 CTNNB1  T
                  G                                  109           37      S       A
      No      No      4       63      6
PAP 131    #REF!          chr10   89685308 PTEN    A
                  G                                  203           68      Y       C
      No      No      27      59      46
PAP 131    #REF!          chr12   25378562 KRAS    C
                  T                                  436           146     A       T
      No      No      153     428     36
PAP 131    #REF!          chr3    178916876PIK3CA  G
                  A                                  263           88      R       Q
      No      No      12      59      20
PAP 132    #REF!          chr10   89624245 PTEN    G
                  T                                  19            7       E       *
      No      No      170     712     24
PAP 132    #REF!          chr10   89624270 PTEN    G
                  T                                  44            15      R       I
```

Table16.txt

	No	No	162	712	23										
PAP	132	#REF!		chr3	178952074	PIK3CA	G								
			T							3129	1043	M	I		
	No	No	102	462	22										
PAP	132	#REF!		chr5	112174631	APC	C								
			T							3340	1114	R	*		
	No	No	116	554	21										
PAP	132	#REF!		chr5	112175852	APC	G								
			T							4561	1521	E	*		
	No	No	21	106	20										
PAP	132	#REF!		chr5	67588951	PIK3R1	C								
			T							1042	348	R	*		
	No	No	5	18	28										
PAP	168	#REF!		chr17	7577536	TP53	T								
			C							745	249	R	G		
	No	No	78	83	94										
PAP	169	#REF!		chr10	123258034	FGFR2	A								
			C							1647	549	N	K		
	No	No	134	422	32										
PAP	169	#REF!		chr12	133253184	POLE	G								
			C							857	286	P	R		
	No	No	91	323	28										
PAP	169	#REF!		chr14	105246551	AKT1	C								
			T							49	17	E	K		
	No	No	1019	2082	49										
PAP	169	#REF!		chr17	7578212	TP53	G								
			A							637	213	R	*		
	No	No	122	304	40										
PAP	172	#REF!		chr17	7578524	TP53	G								
			A							406	136	Q	*		
	No	No	632	854	74										
PAP	173	#REF!		chr3	178936091	PIK3CA	G								
			A							1633	545	E	K		
	No	No	41	224	18										
PAP	174	#REF!		chr10	89720804	PTEN	ACTT								
										955	319	T			
NULL	No	No	239	789	30										
PAP	174	#REF!		chr12	25398284	KRAS	C								
			A							35	12	G	V		
	No	No	711	4272	17										
PAP	174	#REF!		chr3	41266113	CTNNB1	C								
			T							110	37	S	F		
	No	No	506	2767	18										
PAP	175	#REF!		chr10	89692904	PTEN	C								
			G							388	130	R	G		
	No	No	40	382	10										
PAP	175	#REF!		chr10	89720741	PTEN	C								
			T							892	298	Q	*		

Table16.txt

```
      No      No      32      464     7
PAP 175    #REF!          chr12   25398284 KRAS    C
                   T                                  35          12      G       D
      No      No      24      671     4
PAP 175    #REF!          chr3    178952074PIK3CA  G
                   T                                  3129        1043    M       I
      No      No      107     348     31
PAP 175    #REF!          chr5    67591144 PIK3R1
                   A                                  1737        579     Q
NULL    No      No      72      251     29
PAP 176    #REF!          chr12   25378562 KRAS    C
                   T                                  436         146     A       T
      No      No      10      94      11
PAP 176    #REF!          chr3    178936094PIK3CA  C
                   A                                  1636        546     Q       K
      No      No      42      84      50
PAP 177    #REF!          chr10   89717620 PTEN    T
                                                      645         215     F
NULL    No      No      20      91      22
PAP 177    #REF!          chr3    41266113 CTNNB1  C
                   T                                  110         37      S       F
      No      No      13      93      14
PAP 178    #REF!          chr10   89692880 PTEN    ATTCA
                                                      364         122     I
NULL    No      No      127     630     20
PAP 178    #REF!          chr10   89692905 PTEN    G
                   C                                  389         130     R       P
      No      No      22      473     5
PAP 178    #REF!          chr12   25398284 KRAS    C
                   T                                  35          12      G       D
      No      No      127     1034    12
PAP 178    #REF!          chr3    178952052PIK3CA  T
                   C                                  3107        1036    L       S
      No      No      65      758     9
PAP 179    #REF!          chr17   7578265  TP53    A
                   G                                  584         195     I       T
      No      No      159     256     62
PAP 179    #REF!          chr5    67589568 PIK3R1  CTGTAGGGAAAAAATTACATGAAT (SEQ ID
NO:781)                                               1331        444     A
NULL    No      No      17      46      37
PAP 180    #REF!          chr10   89711899 PTEN    C
                   T                                  517         173     R       C
      No      No      72      266     27
PAP 180    #REF!          chr12   133253184POLE    G
                   C                                  857         286     P       R
      No      No      52      178     29
PAP 180    #REF!          chr5    67589609 PIK3R1  G
                   T                                  1372        458     E       *
```

Table16.txt

```
      No      No      103     405     25
PAP 180    #REF!          chr5    67591076 PIK3R1  C
                   T                                  1669          557     R       *
      No      No      232     952     24
PAP 181    #REF!          chr17   7578190  TP53    T
                   C                                  659           220     Y       C
      No      No      117     140     84
PAP 181    #REF!          chr19   52716323 PPP2R1A C
                   T                                  767           256     S       F
      No      No      565     662     85
PAP 182    #REF!          chr17   7577124  TP53    C
                   A                                  814           272     V       L
      No      No      195     525     37
PAP 183    #REF!          chr17   7578265  TP53    A
                   G                                  584           195     I       T
      No      No      482     744     65
PAP 184    #REF!          chr10   89685313 PTEN    C
                                                      208           70      L
NULL    No      No      9       28      32
PAP 184    #REF!          chr10   89720716 PTEN    A
                                                      867           289     K
NULL    No      No      100     360     28
PAP 184    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140          1047    H       R
      No      No      55      256     21
PAP 184    #REF!          chr3    41266113 CTNNB1  C
                   T                                  110           37      S       F
      No      No      37      175     21
PAP 185    #REF!          chr17   7577538  TP53    C
                   T                                  743           248     R       Q
      No      No      475     867     55
PAP 186    #REF!          chr17   7579589  TP53    G
                                                      98            33      S
NULL    No      No      1170    2193    53
PAP 193    #REF!          chr17   7577550  TP53    C
                   T                                  731           244     G       D
      No      No      88      183     48
PAP 194    #REF!          chr17   7578484  TP53    G
                                                      446           149     S
NULL    No      No      1878    2088    90
PAP 195    #REF!          chr17   7578486  TP53    A
                                                      444           148     D
NULL    No      No      263     351     75
PAP 196    #REF!          chr17   7578290  TP53    C
                   A                                  0             0       NULL
NULL    Yes     No      224     390     57
PAP 197    #REF!          chr17   7578190  TP53    T
                   C                                  659           220     Y       C
```

Table16.txt

```
      No      No      270     378     71
PAP 198    #REF!          chr17   7574027  TP53
                  C                                  1000          334     G
NULL    No      No      2082    4733    44
PAP 199    #REF!          chr17   7578265  TP53    A
                  G                                  584           195     I       T
      No      No      421     552     76
PAP 200    #REF!          chr10   89720876 PTEN    G
                  A                                  0             0       NULL
NULL    Yes     No      4       29      14
PAP 200    #REF!          chr12   133250289POLE    C
                  A                                  1231          411     V       L
      No      No      22      245     9
PAP 200    #REF!          chr3    178916854PIK3CA  G
                  A                                  241           81      E       K
      No      No      2       21      10
PAP 201    #REF!          chr10   123279677FGFR2   G
                  C                                  755           252     S       W
      No      No      34      269     13
PAP 201    #REF!          chr10   89711928 PTEN
                  A                                  546           182     L
NULL    No      No      519     753     69
PAP 201    #REF!          chr10   89711930 PTEN
                  A                                  548           183     K
NULL    No      No      162     356     46
PAP 201    #REF!          chr3    41266097 CTNNB1  G
                  A                                  94            32      D       N
      No      No      36      472     8
PAP 201    #REF!          chr3    41266136 CTNNB1  T
                  C                                  133           45      S       P
      No      No      111     472     24
PAP 202    #REF!          chr10   89720716 PTEN
                  A                                  867           289     K
NULL    No      No      222     3188    7
PAP 202    #REF!          chr10   89720817 PTEN
                  A                                  968           323     N
NULL    No      No      63      220     29
PAP 202    #REF!          chr17   7577524  TP53    T
                  G                                  757           253     T       P
      No      No      334     1251    27
PAP 203    #REF!          chr10   89712018 PTEN    T
                  C                                  0             0       NULL
NULL    Yes     No      3311    6149    54
PAP 203    #REF!          chr10   89720761 PTEN    C
                  A                                  912           304     C       *
      No      No      121     376     32
PAP 203    #REF!          chr3    178952077PIK3CA  T
                  A                                  3132          1044    N       K
```

Table16.txt

```
      No      No      175     2692    7
PAP 204    #REF!          chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
      No      No      561     2723    21
PAP 204    #REF!          chr17   7578463  TP53    C
                   T                                  467          156     R       H
      No      No      1760    5179    34
PAP 204    #REF!          chr17   7579419  TP53
                   T                                  268          90      S
NULL    No      No      2039    5513    37
PAP 204    #REF!          chr17   7579702  TP53    G
                   T                                  94           32      L       M
      No      No      527     3607    15
PAP 204    #REF!          chr3    178916876PIK3CA  G
                   A                                  263          88      R       Q
      No      No      77      486     16
PAP 204    #REF!          chr3    41266113 CTNNB1  C
                   A                                  110          37      S       Y
      No      No      736     2720    27
PAP 204    #REF!          chr5    112174631APC     C
                   T                                  3340         1114    R       *
      No      No      1212    6693    18
PAP 204    #REF!          chr5    112175216APC     G
                   T                                  3925         1309    E       *
      No      No      393     3252    12
PAP 205    #REF!          chr10   89692829 PTEN    T
                                                      313          105     C
NULL    No      No      88      197     45
PAP 205    #REF!          chr3    178916876PIK3CA  G
                   A                                  263          88      R       Q
      No      No      5       11      45
PAP 206    #REF!          chr10   123258034FGFR2   A
                   T                                  1647         549     N       K
      No      No      625     1127    55
PAP 206    #REF!          chr5    67591130 PIK3R1  AAGACGAGA
                                                      1723         575     K
NULL    No      No      133     554     24
PAP 207    #REF!          chr12   25378561 KRAS    G
                   A                                  437          146     A       V
      No      No      296     956     31
PAP 207    #REF!          chr5    67592099 PIK3R1  C
                   T                                  1915         639     R       *
      No      No      159     600     27
PAP 207    #REF!          chr9    21970956 CDKN2A
                   C                                  402          134     A
NULL    No      No      829     4180    20
PAP 208    #REF!          chr1    115256530NRAS    G
                   T                                  181          61      Q       K
```

Table16.txt

```
      No      No      261     625     42
PAP 208    #REF!          chr17   7578479  TP53    G
                                                    451          151     P
NULL    No      No      1131    2526    45
PAP 208    #REF!          chr3    178952085PIK3CA  A
                   G                                3140         1047    H       R
      No      No      946     2035    46
PAP 209    #REF!          chr10   89692905 PTEN    G
                   A                                389          130     R       Q
      No      No      2744    8022    34
PAP 209    #REF!          chr10   89692911 PTEN    G
                   A                                395          132     G       D
      No      No      1419    8022    18
PAP 209    #REF!          chr5    67592091 PIK3R1
                   A                                1907         636     N
NULL    No      No      780     2131    37
PAP 210    #REF!          chr12   25398284 KRAS    C
                   A                                35           12      G       V
      No      No      68      419     16
PAP 213    #REF!          chr5    67589588 PIK3R1  G
                   T                                1351         451     E       *
      No      No      8       44      18
PAP 214    #REF!          chr10   89692904 PTEN    C
                   G                                388          130     R       G
      No      No      34      678     5
PAP 214    #REF!          chr10   89720817 PTEN
                   A                                968          323     N
NULL    No      No      38      323     12
PAP 214    #REF!          chr12   25398284 KRAS    C
                   T                                35           12      G       D
      No      No      135     818     17
PAP 214    #REF!          chr17   7578212  TP53    G
                   A                                637          213     R       *
      No      No      203     1123    18
PAP 214    #REF!          chr3    178936091PIK3CA  G
                   A                                1633         545     E       K
      No      No      101     732     14
PAP 215    #REF!          chr17   7577538  TP53    C
                   A                                743          248     R       L
      No      No      2203    3045    72
PAP 216    #REF!          chr10   123258034FGFR2   A
                   C                                1647         549     N       K
      No      No      80      425     19
PAP 216    #REF!          chr10   89653809 PTEN    G
                                                    107          36      G
NULL    No      No      78      425     18
PAP 216    #REF!          chr10   89692904 PTEN    C
                   T                                388          130     R       *
```

Table16.txt

```
      No      No      23      429     5
PAP 217    #REF!          chr10   89690804 PTEN    T
                                                    211         71      C
NULL    No      No      4       19      21
PAP 217    #REF!          chr10   89692887 PTEN    G
                   C                                371         124     C       S
      No      No      122     435     28
PAP 217    #REF!          chr3    178952074PIK3CA  G
                   A                                3129        1043    M       I
      No      No      99      426     23
PAP 217    #REF!          chr3    41266097 CTNNB1  G
                   T                                94          32      D       Y
      No      No      32      170     19
PAP 218    #REF!          chr17   7578427  TP53    T
                   C                                503         168     H       R
      No      No      2039    2784    73
PAP 218    #REF!          chr19   52715971 PPP2R1A C
                   G                                536         179     P       R
      No      No      4382    13851   32
PAP 218    #REF!          chr3    178952085PIK3CA  A
                   G                                3140        1047    H       R
      No      No      1846    4076    45
PAP 219    #REF!          chr10   89624245 PTEN    G
                   T                                19          7       E       *
      No      No      1693    8658    20
PAP 219    #REF!          chr10   89624270 PTEN    G
                   A                                44          15      R       K
      No      No      1469    8658    17
PAP 219    #REF!          chr3    178916876PIK3CA  G
                   A                                263         88      R       Q
      No      No      111     1084    10
PAP 219    #REF!          chr3    178952018PIK3CA  A
                   G                                3073        1025    T       A
      No      No      1928    10878   18
PAP 221    #REF!          chr10   89692904 PTEN    C
                   T                                388         130     R       *
      No      No      13      129     10
PAP 221    #REF!          chr10   89720727 PTEN    G
                                                    878         293     G
NULL    No      No      71      373     19
PAP 221    #REF!          chr12   25398284 KRAS    C
                   A                                35          12      G       V
      No      No      69      174     40
PAP 221    #REF!          chr3    178936092PIK3CA  A
                   C                                1634        545     E       A
      No      No      63      198     32
PAP 222    #REF!          chr10   89692849 PTEN    G
                   A                                333         111     W       *
```

Table16.txt

```
      No      No      276     714     39
PAP 222    #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      48      300     16
PAP 222    #REF!          chr3    178952085PIK3CA  A
                  G                                  3140         1047    H       R
      No      No      367     1122    33
PAP 222    #REF!          chr3    41266112 CTNNB1  T
                  C                                  109          37      S       P
      No      No      4       287     1
PAP 222    #REF!          chr4    153249385FBXW7   G
                  A                                  1393         465     R       C
      No      No      347     1262    27
PAP 224    #REF!          chr17   7577094  TP53    G
                  A                                  844          282     R       W
      No      No      32      1004    3
PAP 225    #REF!          chr10   89720817 PTEN
                  A                                  968          323     N
NULL    No      No      13      31      42
PAP 225    #REF!          chr3    178936091PIK3CA  G
                  A                                  1633         545     E       K
      No      No      13      94      14
PAP 226    #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      48      241     20
PAP 226    #REF!          chr3    178936091PIK3CA  G
                  A                                  1633         545     E       K
      No      No      56      271     21
PAP 227    #REF!          chr12   25398284 KRAS    C
                  G                                  35           12      G       A
      No      No      134     308     44
PAP 228    #REF!          chr10   89720757 PTEN
                  G                                  908          303     I
NULL    No      No      114     295     39
PAP 228    #REF!          chr3    41266097 CTNNB1  G
                  A                                  94           32      D       N
      No      No      139     376     37
PAP 228    #REF!          chr5    67591097 PIK3R1  A
                  G                                  1690         564     N       D
      No      No      117     320     37
PAP 229    #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      40      115     35
PAP 229    #REF!          chr3    178916876PIK3CA  G
                  A                                  263          88      R       Q
      No      No      5       29      17
PAP 229    #REF!          chr3    41266125 CTNNB1  C
                  T                                  122          41      T       I
```

Table16.txt

```
      No      No      54      128     42
PAP 229    #REF!          chr4    153247289FBXW7   G
                   A                                  1513          505     R       C
      No      No      163     437     37
PAP 231    #REF!          chr17   7578268  TP53    A
                   C                                  581           194     L       R
      No      No      747     1100    68
PAP 231    #REF!          chr19   52716323 PPP2R1A C
                   T                                  767           256     S       F
      No      No      347     643     54
PAP 231    #REF!          chr5    67592075 PIK3R1  C
                   T                                  1891          631     R       *
      No      No      91      197     46
PAP 232    #REF!          chr10   89720741 PTEN    C
                   T                                  892           298     Q       *
      No      No      170     515     33
PAP 233    #REF!          chr10   89692904 PTEN    C
                   G                                  388           130     R       G
      No      No      22      144     15
PAP 233    #REF!          chr10   89720817 PTEN
                   A                                  968           323     N
NULL    No      No      19      72      26
PAP 233    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140          1047    H       R
      No      No      186     529     35
PAP 234    #REF!          chr10   89717678 PTEN    G
                                                      703           235     E
NULL    No      No      93      736     13
PAP 234    #REF!          chr12   25398281 KRAS    C
                   T                                  38            13      G       D
      No      No      119     332     36
PAP 234    #REF!          chr17   7577548  TP53    C
                   A                                  733           245     G       C
      No      No      145     418     35
PAP 234    #REF!          chr5    67589581 PIK3R1  ATTACA
                                                      1344          448     K
NULL    No      No      56      192     29
PAP 234    #REF!          chr5    67589582 PIK3R1  TTACAT
                                                      1345          449     L
NULL    No      No      28      458     6
PAP 235    #REF!          chr1    115258747NRAS    C
                   T                                  35            12      G       D
      No      No      214     5907    4
PAP 235    #REF!          chr17   7579312  TP53    C
                   T                                  375           125     T       T
      No      Yes     1609    3076    52
PAP 235    #REF!          chr3    178936091PIK3CA  G
                   A                                  1633          545     E       K
```

Table16.txt

```
      No      No      3217    4330    74
PAP 236    #REF!          chr10   89653799 PTEN    ATT
                                                    97          33      I
NULL    No      No      1516    4899    31
PAP 236    #REF!          chr10   89692975 PTEN    T
                                                    459         153     D
NULL    No      No      2795    9689    29
PAP 236    #REF!          chr10   89692977 PTEN    T
                                                    461         154     F
NULL    No      No      351     1309    27
PAP 236    #REF!          chr17   56435167 RNF43   C
                                                    1970        657     R
NULL    No      No      216     2016    11
PAP 236    #REF!          chr19   52715982 PPP2R1A C
                   T                                547         183     R       W
      No      No      1537    12726   12
PAP 237    #REF!          chr10   89624249 PTEN    T
                                                    23          8       I
NULL    No      No      1522    4342    35
PAP 237    #REF!          chr10   89720702 PTEN    G
                   T                                853         285     E       *
      No      No      2       13      15
PAP 237    #REF!          chr10   89720781 PTEN    A
                                                    932         311     N
NULL    No      No      142     752     19
PAP 237    #REF!          chr3    178952085PIK3CA  A
                  G                                 3140        1047    H       R
      No      No      820     3651    22
PAP 237    #REF!          chr3    41266097 CTNNB1  G
                  A                                 94          32      D       N
      No      No      572     2630    22
PAP 237    #REF!          chr5    67589589 PIK3R1
                  TGA                               1352        451     E
NULL    No      No      1220    5678    21
PAP 238    #REF!          chr10   89692786 PTEN    T
                                                    270         90      F
NULL    No      No      90      267     34
PAP 238    #REF!          chr10   89693007 PTEN    A
                                                    491         164     K
NULL    No      No      209     945     22
PAP 238    #REF!          chr10   89720716 PTEN
                  A                                 867         289     K
NULL    No      No      115     896     13
PAP 238    #REF!          chr12   25398281 KRAS    C
                   T                                38          13      G       D
      No      No      977     2665    37
PAP 238    #REF!          chr17   56435167 RNF43   C
                                                    1970        657     R
```

Table16.txt

```
NULL    No      No      165     1070    15
PAP 238    #REF!          chr5    67589615 PIK3R1  A
                                                    1378          460     S
NULL    No      No      1273    5173    25
PAP 239    #REF!          chr17   7577108  TP53    C
                  A                                 830           277     C       F
      No      No      1567    2120    74
PAP 240    #REF!          chr17   7577141  TP53    C
                  T                                 797           266     G       E
      No      No      5725    13444   43
PAP 240    #REF!          chr17   7578290  TP53    C
                  T                                 0             0       NULL
NULL    Yes     No      10274   23511   44
PAP 240    #REF!          chr19   52715971 PPP2R1A C
                  G                                 536           179     P       R
      No      No      4966    16116   31
PAP 241    #REF!          chr17   7577545  TP53    T
                  C                                 736           246     M       V
      No      No      4147    7755    53
PAP 242    #REF!          chr10   123279677FGFR2   G
                  A                                 755           252     S       L
      No      No      3236    8999    36
PAP 242    #REF!          chr10   89692904 PTEN    C
                  G                                 388           130     R       G
      No      No      3398    6403    53
PAP 242    #REF!          chr4    153249384FBXW7   C
                  T                                 1394          465     R       H
      No      No      612     1479    41
PAP 243    #REF!          chr10   89692905 PTEN    G
                  A                                 389           130     R       Q
      No      No      714     4902    15
PAP 243    #REF!          chr10   89717716 PTEN
                  A                                 741           247     L
NULL    No      No      1225    2720    45
PAP 243    #REF!          chr3    178916876PIK3CA  G
                  A                                 263           88      R       Q
      No      No      45      186     24
PAP 243    #REF!          chr3    41266124 CTNNB1  A
                  G                                 121           41      T       A
      No      No      864     2052    42
PAP 244    #REF!          chr17   7576911  TP53    GTGTTGTTGGGCAG (SEQ ID NO:782)
                                                    935           312     T
NULL    No      No      200     878     23
PAP 244    #REF!          chr17   7578413  TP53    C
                  T                                 517           173     V       M
      No      No      104     393     26
PAP 244    #REF!          chr4    153249393FBXW7   G
                  A                                 1385          462     S       F
```

Table16.txt

```
      No      No      277     791     35
PAP 245    #REF!          chr10   89653829 PTEN    G
                    T                                 127           43      E       *
      No      No      943     2770    34
PAP 245    #REF!          chr12   25398284 KRAS    C
                    T                                 35            12      G       D
      No      No      1235    3525    35
PAP 245    #REF!          chr3    178952085PIK3CA  A
                    G                                 3140          1047    H       R
      No      No      1394    3748    37
PAP 246    #REF!          chr10   89717650 PTEN    T
                    G                                 675           225     Y       *
      No      No      113     1066    11
PAP 246    #REF!          chr5    67589613 PIK3R1  AAA
                                                      1376          459     K
NULL    No      No      188     912     21
PAP 247    #REF!          chr10   89692905 PTEN    G
                    A                                 389           130     R       Q
      No      No      2333    4366    53
PAP 247    #REF!          chr10   89720870 PTEN    T
                    G                                 1021          341     F       V
      No      No      145     224     65
PAP 247    #REF!          chr12   133253184POLE    G
                    C                                 857           286     P       R
      No      No      473     1045    45
PAP 247    #REF!          chr5    112174631APC     C
                    T                                 3340          1114    R       *
      No      No      1582    3422    46
PAP 247    #REF!          chr5    112176020APC     G
                    T                                 4729          1577    E       *
      No      No      579     1677    35
PAP 247    #REF!          chr5    67591076 PIK3R1  C
                    T                                 1669          557     R       *
      No      No      958     2079    46
PAP 247    #REF!          chr5    67591147 PIK3R1  C
                    A                                 1740          580     Y       *
      No      No      180     376     48
PAP 250    #REF!          chr17   7577022  TP53    G
                    A                                 916           306     R       *
      No      No      39      181     22
PAP 251    #REF!          chr17   7577556  TP53    C
                    T                                 725           242     C       Y
      No      No      91      172     53
PAP 253    #REF!          chr17   7578555  TP53    C
                    T                                 0             0       NULL
NULL    Yes     No      524     1085    48
PAP 255    #REF!          chr17   7577102  TP53    C
                    T                                 836           279     G       E
```

Table16.txt

	No	No	603	809	75										
PAP	257	#REF!		chr1	115256529	NRAS	T								
			C							182	61	Q	R		
	No	No	196	620	32										
PAP	258	#REF!		chr12	25398284	KRAS	C								
			T							35	12	G	D		
	No	No	99	226	44										
PAP	258	#REF!		chr17	7578392	TP53	C								
			A							538	180	E	*		
	No	No	101	131	77										
PAP	258	#REF!		chr9	21971127	CDKN2A	AG								
										231	77	T			
NULL	No	No	546	1238	44										
PAP	258	#REF!		chr9	21974698	CDKN2A	A								
										129	43	S			
NULL	No	No	275	787	35										
PAP	259	#REF!		chr3	178936095	PIK3CA	A								
			T							1637	546	Q	L		
	No	No	28	73	38										
PAP	261	#REF!		chr17	7578530	TP53	A								
			G							400	134	F	L		
	No	No	351	628	56										
PAP	262	#REF!		chr17	7574004	TP53	G								
										1023	341	F			
NULL	No	No	157	286	55										
PAP	265	#REF!		chr3	41266097	CTNNB1	G								
			T							94	32	D	Y		
	No	No	44	207	21										
PAP	266	#REF!		chr10	89720733	PTEN									
			T							884	295	L			
NULL	No	No	34	434	8										
PAP	266	#REF!		chr10	89720804	PTEN	ACTT								
										955	319	T			
NULL	No	No	20	55	36										
PAP	266	#REF!		chr12	25398284	KRAS	C								
			A							35	12	G	V		
	No	No	458	898	51										
PAP	266	#REF!		chr5	67591121	PIK3R1									
			C							1714	572	Q			
NULL	No	No	97	408	24										
PAP	267	#REF!		chr10	89653808	PTEN	G								
			T							106	36	G	*		
	No	No	108	421	26										
PAP	267	#REF!		chr10	89692791	PTEN	A								
			G							275	92	D	G		
	No	No	14	45	31										
PAP	267	#REF!		chr12	133250289	POLE	C								
			A							1231	411	V	L		

Table16.txt

	No	No	130	458	28										
PAP	267	#REF!		chr3	178952007	PIK3CA	A								
			G							3062		1021	Y	C	
	No	No	17	54	31										
PAP	268	#REF!		chr17	7577580	TP53	T								
			C							701		234	Y	C	
	No	No	189	261	72										
PAP	269	#REF!		chr17	7578275	TP53	G								
			A							574		192	Q	*	
	No	No	145	216	67										
PAP	270	#REF!		chr3	178936082	PIK3CA	G								
			A							1624		542	E	K	
	No	No	59	344	17										
PAP	272	#REF!		chr10	123279677	FGFR2	G								
			C							755		252	S	W	
	No	No	12	143	8										
PAP	272	#REF!		chr10	89624245	PTEN	G								
			T							19		7	E	*	
	No	No	202	496	41										
PAP	272	#REF!		chr10	89692905	PTEN	G								
			A							389		130	R	Q	
	No	No	9	49	18										
PAP	272	#REF!		chr12	133250289	POLE	C								
			A							1231		411	V	L	
	No	No	205	352	58										
PAP	272	#REF!		chr17	7577117	TP53	A								
			G							821		274	V	A	
	No	No	273	343	80										
PAP	272	#REF!		chr3	178916854	PIK3CA	G								
			A							241		81	E	K	
	No	No	8	15	53										
PAP	272	#REF!		chr4	153247288	FBXW7	C								
			T							1514		505	R	H	
	No	No	206	365	56										
PAP	273	#REF!		chr10	89624245	PTEN	G								
			T							19		7	E	*	
	No	No	181	577	31										
PAP	273	#REF!		chr10	89653803	PTEN	C								
			A							101		34	A	D	
	No	No	12	49	24										
PAP	273	#REF!		chr12	133253184	POLE	G								
			C							857		286	P	R	
	No	No	6	21	29										
PAP	273	#REF!		chr3	178952085	PIK3CA	A								
			G							3140		1047	H	R	
	No	No	32	115	28										
PAP	274	#REF!		chr12	25398284	KRAS	C								
			T							35		12	G	D	

Table16.txt

```
      No      No      88      423     21
PAP 274    #REF!          chr14   105246551AKT1    C
                   T                                  49          17      E       K
      No      No      334     705     47
PAP 274    #REF!          chr5    112175190APC     ATACCCTGCAAATA (SEQ ID NO:783)
                                                     3899        1300    N
NULL    No      No      136     582     23
PAP 274    #REF!          chr5    112175681APC     GA
                                                     4390        1464    E
NULL    No      No      74      417     18
PAP 274    #REF!          chr5    112175684APC     AG
                                                     4393        1465    S
NULL    No      No      140     632     22
PAP 275    #REF!          chr10   89692921 PTEN
                   A                                 405         135     I
NULL    No      No      18      139     13
PAP 275    #REF!          chr19   52715983 PPP2R1A G
                   A                                 548         183     R       Q
      No      No      148     487     30
PAP 275    #REF!          chr3    41266104 CTNNB1  G
                   T                                 101         34      G       V
      No      No      70      215     33
PAP 276    #REF!          chr10   89717613 PTEN    C
                                                     638         213     P
NULL    No      No      230     459     50
PAP 276    #REF!          chr3    178952085PIK3CA  A
                   G                                 3140        1047    H       R
      No      No      106     590     18
PAP 277    #REF!          chr10   123279677FGFR2   G
                   C                                 755         252     S       W
      No      No      26      590     4
PAP 524    #REF!          chr17   7578406  TP53    C
                   T                                 524         175     R       H
      No      No      532     829     64
PAP 526    #REF!          chr17   7578406  TP53    C
                   T                                 524         175     R       H
      No      No      55      303     18
PAP 527    #REF!          chr17   7577513  TP53    TGTGATGATGGTGAG (SEQ ID NO:784)
                                                     768         256     T
NULL    No      No      181     206     88
PAP 528    #REF!          chr17   7578535  TP53    T
                   C                                 395         132     K       R
      No      No      252     385     65
PAP 529    #REF!          chr17   7577094  TP53    G
                   A                                 844         282     R       W
      No      No      470     793     59
PAP 530    #REF!          chr17   7577144  TP53    A
                   G                                 794         265     L       P
```

Table16.txt

```
      No      No      36      109     33
PAP 531    #REF!          chr17   7579443  TP53    G
                                                    244          82      P
NULL    No      No      267     327     82
PAP 532    #REF!          chr17   7578208  TP53    T
                   C                                641          214     H       R
      No      No      87      175     50
PAP 533    #REF!          chr17   7578268  TP53    A
                   C                                581          194     L       R
      No      No      495     547     90
PAP 535    #REF!          chr17   7577121  TP53    G
                   A                                817          273     R       C
      No      No      313     363     86
PAP 536    #REF!          chr17   7578529  TP53    A
                   G                                401          134     F       S
      No      No      184     665     28
PAP 537    #REF!          chr17   7579480  TP53    A
                                                    207          69      A
NULL    No      No      405     551     74
PAP 540    #REF!          chr17   7578190  TP53    T
                   C                                659          220     Y       C
      No      No      87      145     60
PAP 541    #REF!          chr17   7578486  TP53    A
                                                    444          148     D
NULL    No      No      316     494     64
PAP 542    #REF!          chr17   7578190  TP53    T
                   C                                659          220     Y       C
      No      No      33      181     18
PAP 544    #REF!          chr10   89693009 PTEN    G
                   A                                0            0       NULL
NULL    Yes     No      9       16      56
PAP 544    #REF!          chr3    41266113 CTNNB1  C
                   G                                110          37      S       C
      No      No      24      71      34
PAP 549    #REF!          chr10   89624268 PTEN
                   GG                               42           14      R
NULL    No      No      206     489     42
PAP 549    #REF!          chr17   7577094  TP53    G
                   A                                844          282     R       W
      No      No      52      188     28
PAP 549    #REF!          chr17   7579589  TP53
                   G                                98           33      S
NULL    No      No      71      334     21
PAP 550    #REF!          chr12   25398284 KRAS    C
                   A                                35           12      G       V
      No      No      183     415     44
PAP 552    #REF!          chr17   7578556  TP53    T
                   C                                0            0       NULL
```

Table16.txt

```
NULL    Yes     No      269     459     59
PAP 554    #REF!          chr3    178952090PIK3CA  G
                   C                                  3145          1049    G       R
      No      No      38      176     22
PAP 555    #REF!          chr10   89690802 PTEN    G
                   A                                  0             0       NULL
NULL    Yes     No      4       4       100
PAP 555    #REF!          chr17   7578263  TP53    G
                   A                                  586           196     R       *
      No      No      143     162     88
PAP 555    #REF!          chr5    112175639APC     C
                   T                                  4348          1450    R       *
      No      No      149     172     87
PAP 555    #REF!          chr5    67591146 PIK3R1  ACT
                                                      1739          580     Y
NULL    No      No      19      22      86
PAP 556    #REF!          chr10   89692905 PTEN    G
                   A                                  389           130     R       Q
      No      No      9       169     5
PAP 556    #REF!          chr10   89720749 PTEN    C
                                                      900           300     I
NULL    No      No      29      628     5
PAP 556    #REF!          chr12   25398285 KRAS    C
                   A                                  34            12      G       C
      No      No      160     521     31
PAP 556    #REF!          chr5    67591117 PIK3R1
                   T                                  1710          570     L
NULL    No      No      88      543     16
PAP 557    #REF!          chr10   89720761 PTEN    C
                   A                                  912           304     C       *
      No      No      3       51      6
PAP 557    #REF!          chr17   7577094  TP53    G
                   A                                  844           282     R       W
      No      No      372     558     67
PAP 558    #REF!          chr17   7578433  TP53    G
                                                      497           166     S
NULL    No      No      142     255     56
PAP 560    #REF!          chr10   89653806 PTEN    T
                   G                                  104           35      M       R
      No      No      175     235     74
PAP 560    #REF!          chr3    41266097 CTNNB1  G
                   T                                  94            32      D       Y
      No      No      55      153     36
PAP 561    #REF!          chr10   89720804 PTEN
                   A                                  955           319     T
NULL    No      No      12      14      86
PAP 561    #REF!          chr3    178936095PIK3CA  A
                   G                                  1637          546     Q       R
```

Table16.txt

```
      No      No      21      51      41
PAP 562    #REF!          chr10   89653800 PTEN    T
                   G                                  98          33      I       S
      No      No      76      87      87
PAP 562    #REF!          chr12   25398284 KRAS    C
                   T                                  35          12      G       D
      No      No      17      271     6
PAP 562    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140        1047    H       R
      No      No      90      215     42
PAP 564    #REF!          chr17   7577548  TP53    C
                   T                                  733         245     G       S
      No      No      61      312     20
PAP 565    #REF!          chr10   89692904 PTEN    C
                   G                                  388         130     R       G
      No      No      6       165     4
PAP 565    #REF!          chr10   89720805 PTEN    CTTT
                                                      956         319     T
NULL    No      No      11      45      24
PAP 566    #REF!          chr17   7577578  TP53    T
                                                      703         235     N
NULL    No      No      41      127     32
PAP 568    #REF!          chr17   7577580  TP53    T
                   C                                  701         234     Y       C
      No      No      125     184     68
PAP 569    #REF!          chr17   7577545  TP53    T
                   C                                  736         246     M       V
      No      No      29      54      54
PAP 570    #REF!          chr17   7574021  TP53    C
                   A                                  1006        336     E       *
      No      No      822     894     92
PAP 572    #REF!          chr12   25398284 KRAS    C
                   A                                  35          12      G       V
      No      No      27      49      55
PAP 572    #REF!          chr17   7578542  TP53    G
                   A                                  388         130     L       F
      No      No      36      44      82
PAP 572    #REF!          chr3    178952084PIK3CA  C
                   T                                  3139        1047    H       Y
      No      No      102     184     55
PAP 573    #REF!          chr17   7577550  TP53    C
                   T                                  731         244     G       D
      No      No      44      145     30
PAP 574    #REF!          chr10   89653786 PTEN    T
                   G                                  84          28      I       M
      No      No      12      38      32
PAP 574    #REF!          chr17   7577506  TP53    C
                   A                                  775         259     D       Y
```

Table16.txt

```
      No      No      12      191     6
PAP 574    #REF!          chr17   7578212  TP53    G
                   A                                637          213     R       *
      No      No      14      72      19
PAP 574    #REF!          chr3    41266113 CTNNB1  C
                   A                                110          37      S       Y
      No      No      22      71      31
PAP 574    #REF!          chr5    67589618 PIK3R1  C
                   T                                1381         461     R       *
      No      No      31      124     25
PAP 575    #REF!          chr17   7577539  TP53    G
                   A                                742          248     R       W
      No      No      7       14      50
PAP 576    #REF!          chr17   7578266  TP53    TAAGATGCTGAGGAGGGGCCAGACCTAAGA
(SEQ ID NO:785)                                     583          195     I
NULL    No      No      3       6       50
PAP 576    #REF!          chr17   7578428  TP53    G
                   T                                502          168     H       N
      No      No      2       21      10
PAP 579    #REF!          chr17   7577120  TP53    C
                   T                                818          273     R       H
      No      No      690     1142    60
PAP 581    #REF!          chr10   89685287 PTEN    A
                   G                                182          61      H       R
      No      No      6       23      26
PAP 581    #REF!          chr10   89692920 PTEN    T
                   A                                404          135     I       K
      No      No      3       117     3
PAP 581    #REF!          chr5    67591123 PIK3R1  GCTGAG
                                                    1716         572     Q
NULL    No      No      11      67      16
PAP 582    #REF!          chr10   89720744 PTEN    G
                   T                                895          299     E       *
      No      No      55      573     10
PAP 582    #REF!          chr12   133253184POLE    G
                   C                                857          286     P       R
      No      No      66      236     28
PAP 582    #REF!          chr17   7578212  TP53    G
                   A                                637          213     R       *
      No      No      94      322     29
PAP 582    #REF!          chr5    67588951 PIK3R1  C
                   T                                1042         348     R       *
      No      No      5       32      16
PAP 583    #REF!          chr10   89692919 PTEN    A
                   G                                403          135     I       V
      No      No      8       373     2
PAP 583    #REF!          chr10   89720817 PTEN
                   A                                968          323     N
```

Table16.txt

```
NULL    No      No      9       126     7
PAP 583    #REF!          chr3    178916876PIK3CA  G
                   A                                263          88      R       Q
      No      No      2       60      3
PAP 583    #REF!          chr5    67591135 PIK3R1  GAGAGACCA
                                                    1728         576     T
NULL    No      No      12      209     6
PAP 584    #REF!          chr10   89717703 PTEN    T
                                                    728          243     F
NULL    No      No      112     576     19
PAP 584    #REF!          chr3    41266104 CTNNB1  G
                   A                                101          34      G       E
      No      No      20      76      26
PAP 584    #REF!          chr5    67589609 PIK3R1  GAA
                                                    1372         458     E
NULL    No      No      164     668     25
PAP 585    #REF!          chr10   123279674FGFR2   G
                   C                                758          253     P       R
      No      No      218     540     40
PAP 585    #REF!          chr10   89653789 PTEN    T
                   G                                87           29      Y       *
      No      No      276     678     41
PAP 585    #REF!          chr10   89685293 PTEN    A
                                                    188          63      N
NULL    No      No      7       33      21
PAP 585    #REF!          chr3    41266097 CTNNB1  G
                   A                                94           32      D       N
      No      No      11      235     5
PAP 585    #REF!          chr5    67591135 PIK3R1  G
                                                    1728         576     T
NULL    No      No      8       187     4
PAP 587    #REF!          chr10   89720828 PTEN    A
                   T                                979          327     K       *
      No      No      59      194     30
PAP 587    #REF!          chr17   7577536  TP53    T
                   A                                745          249     R       W
      No      No      139     501     28
PAP 587    #REF!          chr3    41266100 CTNNB1  T
                   C                                97           33      S       P
      No      No      19      415     5
PAP 587    #REF!          chr5    112173835APC
                   A                                2544         848     K
NULL    No      No      55      710     8
PAP 587    #REF!          chr5    112175883APC
                   A                                4592         1531    N
NULL    No      No      40      320     13
PAP 587    #REF!          chr5    112175957APC
                   A                                4666         1556    T
```

Table16.txt

```
NULL    No      No      49      1835    3
PAP 587    #REF!          chr5    67591106 PIK3R1  A
                   G                                  1699          567     K       E
      No      No      192     770     25
PAP 588    #REF!          chr10   89717725 PTEN    TG
                                                      750           250     C
NULL    No      No      83      1397    6
PAP 588    #REF!          chr5    67591085 PIK3R1  G
                   C                                  1678          560     D       H
      No      No      31      884     4
PAP 589    #REF!          chr17   7576851  TP53    A
                   G                                  0             0       NULL
NULL    Yes     No      72      647     11
PAP 589    #REF!          chr17   7579369  TP53    G
                   C                                  318           106     S       R
      No      No      237     1790    13
PAP 590    #REF!          chr9    21974819 CDKN2A  GGCTCCATGCTGCTCCCCGCCGCC (SEQ ID
NO:786)                                               8             3       P
NULL    No      No      458     1143    40
PAP 591    #REF!          chr10   123279677FGFR2   G
                   C                                  755           252     S       W
      No      No      31      303     10
PAP 591    #REF!          chr10   89692904 PTEN    C
                   G                                  388           130     R       G
      No      No      18      260     7
PAP 591    #REF!          chr3    178936091PIK3CA  G
                   A                                  1633          545     E       K
      No      No      103     241     43
PAP 593    #REF!          chr10   89692893 PTEN    C
                   T                                  377           126     A       V
      No      No      387     689     56
PAP 594    #REF!          chr14   105246551AKT1    C
                   T                                  49            17      E       K
      No      No      246     394     62
PAP 594    #REF!          chr3    41266104 CTNNB1  G
                   T                                  101           34      G       V
      No      No      77      208     37
PAP 595    #REF!          chr10   89692905 PTEN    G
                   T                                  389           130     R       L
      No      No      54      162     33
PAP 595    #REF!          chr17   7577533  TP53
                   ATGGG                              748           250     P
NULL    No      No      97      357     27
PAP 595    #REF!          chr17   7577538  TP53    C
                   T                                  743           248     R       Q
      No      No      88      357     25
PAP 596    #REF!          chr10   123279674FGFR2   G
                   C                                  758           253     P       R
```

Table16.txt

```
      No      No      287     2269    13
PAP 596    #REF!          chr10   89720767 PTEN
                  A                                  918          306     I
NULL    No      No      390     1405    28
PAP 596    #REF!          chr5    67589629 PIK3R1  TAGATTATATGA (SEQ ID NO:787)
                                                     1392         464     D
NULL    No      No      447     4727    9
PAP 599    #REF!          chr10   89653799 PTEN    ATT
                                                     97           33      I
NULL    No      No      326     938     35
PAP 599    #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      337     1566    22
PAP 600    #REF!          chr17   7577550  TP53    C
                  A                                  731          244     G       V
      No      No      1080    2279    47
PAP 601    #REF!          chr17   7578409  TP53    CTCACAACCTCCGTCATGTGC (SEQ ID
NO:788)                                              521          174     R
 NULL    No      No      338     604     56
PAP 601    #REF!          chr3    178952090PIK3CA  G
                  C                                  3145         1049    G       R
      No      No      585     781     75
PAP 604    #REF!          chr10   89720733 PTEN
                  T                                  884          295     L
NULL    No      No      277     395     70
PAP 604    #REF!          chr17   7578406  TP53    C
                  T                                  524          175     R       H
      No      No      223     387     58
PAP 604    #REF!          chr5    67591038 PIK3R1  G
                                                     1631         544     R
NULL    No      No      86      172     50
PAP 606    #REF!          chr17   7577081  TP53    T
                  C                                  857          286     E       G
      No      No      202     326     62
PAP 607    #REF!          chr17   7578223  TP53    CT
                                                     626          209     R
NULL    No      No      168     215     78
PAP 608    #REF!          chr17   7578271  TP53    T
                  C                                  578          193     H       R
      No      No      4878    5743    85
PAP 608    #REF!          chr5    67589613 PIK3R1  AAA
                                                     1376         459     K
NULL    No      No      1771    3356    53
PAP 609    #REF!          chr10   89624245 PTEN    G
                  T                                  19           7       E       *
      No      No      149     2186    7
PAP 609    #REF!          chr10   89717775 PTEN
                  A                                  800          267     K
```

Table16.txt

```
NULL    No      No      176     1582    11
PAP 609    #REF!           chr12   133250289POLE    C
                   G                                 1231          411     V       L
      No      No      248     1123    22
PAP 609    #REF!           chr3    178952018PIK3CA  A
                   G                                 3073          1025    T       A
      No      No      82      680     12
PAP 612    #REF!           chr17   7578492  TP53    C
                   T                                 438           146     W       *
      No      No      362     432     84
PAP 616    #REF!           chr10   89692905 PTEN    G
                   A                                 389           130     R       Q
      No      No      163     1307    12
PAP 616    #REF!           chr12   25398284 KRAS    C
                   A                                 35            12      G       V
      No      No      132     714     18
PAP 616    #REF!           chr3    178916876PIK3CA  G
                   A                                 263           88      R       Q
      No      No      2       110     2
PAP 616    #REF!           chr5    67591135 PIK3R1  G
                                                     1728          576     T
NULL    No      No      4       163     2
PAP 617    #REF!           chr17   7577539  TP53    G
                   A                                 742           248     R       W
      No      No      770     2395    32
PAP 617    #REF!           chr19   52716323 PPP2R1A C
                   A                                 767           256     S       Y
      No      No      193     728     27
PAP 619    #REF!           chr12   133253151POLE    G
                   A                                 890           297     S       F
      No      No      317     1234    26
PAP 619    #REF!           chr3    178916876PIK3CA  G
                   A                                 263           88      R       Q
      No      No      60      346     17
PAP 619    #REF!           chr3    178952018PIK3CA  A
                   G                                 3073          1025    T       A
      No      No      427     1698    25
PAP 619    #REF!           chr5    112175639APC     C
                   T                                 4348          1450    R       *
      No      No      617     4819    13
PAP 621    #REF!           chr1    115258747NRAS    C
                   G                                 35            12      G       A
      No      No      1082    2898    37
PAP 621    #REF!           chr5    67591120 PIK3R1
                   ACCAGACCTTATC (SEQ ID NO:805)     1713          571     I
NULL    No      No      456     2110    22
PAP 622    #REF!           chr7    140453136BRAF    A
                   T                                 1799          600     V       E
```

Table16.txt

```
      No      No      371     546     68
PAP 625    #REF!          chr10   89685303 PTEN    G
                   T                                  198          66      K       N
      No      No      4       20      20
PAP 625    #REF!          chr10   89711983 PTEN    G
                   T                                  601          201     E       *
      No      No      1308    8946    15
PAP 625    #REF!          chr12   133253184POLE    G
                   C                                  857          286     P       R
      No      No      188     1016    19
PAP 625    #REF!          chr17   7578212  TP53    G
                   A                                  637          213     R       *
      No      No      201     1033    19
PAP 625    #REF!          chr3    178916876PIK3CA  G
                   A                                  263          88      R       Q
      No      No      43      349     12
PAP 625    #REF!          chr3    178952007PIK3CA  A
                   G                                  3062         1021    Y       C
      No      No      48      284     17
PAP 627    #REF!          chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
      No      No      177     952     19
PAP 627    #REF!          chr10   89720702 PTEN    G
                   T                                  853          285     E       *
      No      No      7       115     6
PAP 627    #REF!          chr12   25398285 KRAS    C
                   A                                  34           12      G       C
      No      No      85      582     15
PAP 627    #REF!          chr3    178936092PIK3CA  A
                   C                                  1634         545     E       A
      No      No      54      269     20
PAP 627    #REF!          chr5    67590370 PIK3R1  C
                   T                                  1432         478     Q       *
      No      No      14      50      28
PAP 628    #REF!          chr17   7578406  TP53    C
                   T                                  524          175     R       H
      No      No      281     354     79
PAP 629    #REF!          chr10   89692905 PTEN    G
                   C                                  389          130     R       P
      No      No      339     2043    17
PAP 629    #REF!          chr10   89717777 PTEN    G
                                                      0            0       NULL
NULL    Yes     No      761     3027    25
PAP 629    #REF!          chr12   25398284 KRAS    C
                   A                                  35           12      G       V
      No      No      646     1401    46
PAP 629    #REF!          chr5    67591098 PIK3R1
                   ACGTATGAA (SEQ ID NO:806)          1691         564     N
```

Table16.txt

```
NULL    No      No      175     668     26
PAP 632    #REF!           chr17   7577094  TP53    G
                   A                                  844          282     R       W
      No      No      1324    1691    78
PAP 632    #REF!           chr19   52716327 PPP2R1A G
                   T                                  771          257     W       C
      No      No      593     903     66
PAP 632    #REF!           chr3    178952018PIK3CA  A
                   T                                  3073         1025    T       S
      No      No      1134    2241    51
PAP 632    #REF!           chr4    153247366FBXW7   C
                   T                                  1436         479     R       Q
      No      No      321     762     42
PAP 633    #REF!           chr10   89692904 PTEN    C
                   G                                  388          130     R       G
      No      No      103     2079    5
PAP 633    #REF!           chr12   25398282 KRAS    C
                   A                                  37           13      G       C
      No      No      124     985     13
PAP 633    #REF!           chr5    67589617 PIK3R1  TCG
                                                      1380         460     S
NULL    No      No      249     2048    12
PAP 633    #REF!           chr5    67591106 PIK3R1  A
                   G                                  1699         567     K       E
      No      No      136     1132    12
PAP 634    #REF!           chr10   89692904 PTEN    C
                   G                                  388          130     R       G
      No      No      315     2877    11
PAP 634    #REF!           chr10   89717672 PTEN    C
                   T                                  697          233     R       *
      No      No      29      300     10
PAP 634    #REF!           chr12   25398281 KRAS    C
                   T                                  38           13      G       D
      No      No      304     1743    17
PAP 634    #REF!           chr17   7578406  TP53    C
                   T                                  524          175     R       H
      No      No      625     2169    29
PAP 635    #REF!           chr17   7577102  TP53    C
                   T                                  836          279     G       E
      No      No      1487    2038    73
PAP 636    #REF!           chr17   7577064  TP53    T
                                                      874          292     K
NULL    No      No      159     285     56
PAP 637    #REF!           chr17   7577559  TP53    G
                   T                                  722          241     S       Y
      No      No      3730    5018    74
PAP 637    #REF!           chr4    153249384FBXW7   C
                   T                                  1394         465     R       H
```

Table16.txt

No No 525 966 54
PAP 637 #REF! chr5 67589621 PIK3R1 GA
1384 462 E
NULL No No 1023 2400 43
PAP 638 #REF! chr17 7577556 TP53 C
A 725 242 C F
No No 1313 3142 42
PAP 641 #REF! chr14 105246551AKT1 C
T 49 17 E K
No No 192 454 42
PAP 641 #REF! chr19 52715982 PPP2R1A C
T 547 183 R W
No No 272 466 58
PAP 642 #REF! chr19 52715982 PPP2R1A C
T 547 183 R W
No No 73 394 19
PAP 642 #REF! chr3 178936082PIK3CA G
A 1624 542 E K
No No 106 284 37
PAP 643 #REF! chr17 7578212 TP53 G
A 637 213 R *
No No 192 426 45
PAP 643 #REF! chr5 112175639APC C
T 4348 1450 R *
No No 57 174 33
PAP 644 #REF! chr17 7578376 TP53 CTATCTGAGCAGCGCTCATGGTG (SEQ ID NO:789)
554 185 S
NULL No No 38 122 31
PAP 645 #REF! chr12 25398284 KRAS C
A 35 12 G V
No No 1503 3155 48
PAP 645 #REF! chr12 25398285 KRAS C
T 34 12 G S
No No 32 3155 1
PAP 646 #REF! chr10 89692900 PTEN G
T 384 128 K N
No No 156 805 19
PAP 646 #REF! chr10 89717609 PTEN G
T 0 0 NULL
NULL Yes No 142 534 27
PAP 646 #REF! chr10 89717712 PTEN C
T 737 246 P L
No No 127 1079 12
PAP 646 #REF! chr17 7577022 TP53 G
A 916 306 R *
No No 148 364 41
PAP 646 #REF! chr17 7577121 TP53 G
A 817 273 R C

Table16.txt

```
      No      No      322     925     35
PAP 646    #REF!          chr19   52715982 PPP2R1A C
                    T                                   547          183     R       W
      No      No      157     752     21
PAP 646    #REF!          chr22   22127202 MAPK1   G
                    A                                   926          309     A       V
      No      No      177     536     33
PAP 646    #REF!          chr3    178952074PIK3CA  G
                    A                                   3129         1043    M       I
      No      No      285     795     36
PAP 646    #REF!          chr4    153249384FBXW7   C
                    T                                   1394         465     R       H
      No      No      260     778     33
PAP 646    #REF!          chr7    55241726 EGFR    C
                    T                                   2174         725     T       M
      No      No      393     1033    38
PAP 646    #REF!          chr9    21970976 CDKN2A  G
                    A                                   382          128     R       W
      No      No      101     980     10
PAP 647    #REF!          chr10   123258034FGFR2   A
                    C                                   1647         549     N       K
      No      No      124     283     44
PAP 647    #REF!          chr10   89692823 PTEN    CCC
                                                        307          103     P
NULL    No      No      77      275     28
PAP 647    #REF!          chr10   89692904 PTEN    C
                    T                                   388          130     R       *
      No      No      32      230     14
PAP 648    #REF!          chr10   89692904 PTEN    C
                    T                                   388          130     R       *
      No      No      41      235     17
PAP 648    #REF!          chr3    41266113 CTNNB1  C
                    A                                   110          37      S       Y
      No      No      89      241     37
PAP 649    #REF!          chr17   7578383  TP53    AGCAGCGCTCATGGTGGG (SEQ ID
NO:790)                                                 547          183     S
    NULL    No      No      3446    3772    91
PAP 649    #REF!          chr19   52715971 PPP2R1A C
                    G                                   536          179     P       R
      No      No      3610    9539    38
PAP 650    #REF!          chr10   89720804 PTEN    ACTT
                                                        955          319     T
NULL    No      No      53      79      67
PAP 650    #REF!          chr5    112175957APC
                    A                                   4666         1556    T
NULL    No      No      480     716     67
PAP 650    #REF!          chr5    67591147 PIK3R1  CTTGATGTA
                                                        1740         580     Y
```

Table16.txt

```
NULL    No      No      55      94      59
PAP 651    #REF!           chr10   89624270 PTEN    G
                   A                                  44          15      R       K
      No      No      280     1357    21
PAP 651    #REF!           chr10   89711899 PTEN    C
                   T                                  517         173     R       C
      No      No      39      255     15
PAP 651    #REF!           chr12   133253184POLE    G
                   C                                  857         286     P       R
      No      No      45      292     15
PAP 651    #REF!           chr3    178952074PIK3CA  G
                   T                                  3129        1043    M       I
      No      No      106     596     18
PAP 651    #REF!           chr3    41266113 CTNNB1  C
                   T                                  110         37      S       F
      No      No      41      269     15
PAP 651    #REF!           chr5    67588951 PIK3R1  C
                   T                                  1042        348     R       *
      No      No      3       29      10
PAP 652    #REF!           chr10   89692904 PTEN    C
                   G                                  388         130     R       G
      No      No      54      209     26
PAP 652    #REF!           chr17   7578406  TP53    C
                   T                                  524         175     R       H
      No      No      73      112     65
PAP 652    #REF!           chr3    178952085PIK3CA  A
                   G                                  3140        1047    H       R
      No      No      151     358     42
PAP 653    #REF!           chr10   123279677FGFR2   G
                   C                                  755         252     S       W
      No      No      21      239     9
PAP 653    #REF!           chr3    41266097 CTNNB1  G
                   A                                  94          32      D       N
      No      No      61      160     38
PAP 654    #REF!           chr10   89692905 PTEN    G
                   A                                  389         130     R       Q
      No      No      16      64      25
PAP 654    #REF!           chr17   7577548  TP53    C
                   T                                  733         245     G       S
      No      No      79      266     30
PAP 654    #REF!           chr3    178952085PIK3CA  A
                   G                                  3140        1047    H       R
      No      No      102     434     24
PAP 654    #REF!           chr4    153247373FBXW7   C
                   T                                  1429        477     G       S
      No      No      18      58      31
PAP 654    #REF!           chr5    112174424APC     C
                   T                                  3133        1045    Q       *
```

Table16.txt

```
      No      No      97      427     23
PAP 654    #REF!           chr5    112175945APC    G
                   T                                    4654          1552    E       *
      No      No      19      59      32
PAP 655    #REF!           chr10   89692904 PTEN   C
                   T                                    388           130     R       *
      No      No      10      188     5
PAP 655    #REF!           chr12   25398284 KRAS   C
                   A                                    35            12      G       V
      No      No      67      493     14
PAP 655    #REF!           chr3    178936083PIK3CA A
                   C                                    1625          542     E       A
      No      No      39      339     12
PAP 663    #REF!           chr10   89624245 PTEN   G
                   T                                    19            7       E       *
      No      No      3420    8961    38
PAP 663    #REF!           chr12   133253184POLE   G
                   C                                    857           286     P       R
      No      No      579     1516    38
PAP 663    #REF!           chr17   7578212  TP53   G
                   A                                    637           213     R       *
      No      No      694     1583    44
PAP 663    #REF!           chr3    178916854PIK3CA G
                   A                                    241           81      E       K
      No      No      152     417     36
PAP 663    #REF!           chr4    153247367FBXW7  G
                   A                                    1435          479     R       *
      No      No      559     1495    37
PAP 663    #REF!           chr5    112174732APC    C
                   A                                    3441          1147    Y       *
      No      No      115     1795    6
PAP 663    #REF!           chr5    112176020APC    G
                   T                                    4729          1577    E       *
      No      No      478     2944    16
PAP 663    #REF!           chr5    67588951 PIK3R1 C
                   T                                    1042          348     R       *
      No      No      778     2029    38
PAP 665    #REF!           chr12   25398284 KRAS   C
                   A                                    35            12      G       V
      No      No      1054    1875    56
PAP 667    #REF!           chr10   89690819 PTEN   T
                                                        226           76      Y
NULL    No      No      85      164     52
PAP 667    #REF!           chr12   25398284 KRAS   C
                   T                                    35            12      G       D
      No      No      352     618     57
PAP 668    #REF!           chr17   7577120  TP53   C
                   A                                    818           273     R       L
```

Table16.txt

```
      No      No      1803    3774    48
PAP 668    #REF!          chr19   52715971 PPP2R1A C
                  G                                  536          179     P       R
      No      No      1507    8039    19
PAP 669    #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      1862    4944    38
PAP 669    #REF!          chr3    41266125 CTNNB1  C
                  T                                  122          41      T       I
      No      No      774     2360    33
PAP 669    #REF!          chr5    67591112 PIK3R1
                  G                                  1705         569     D
NULL    No      No      675     1879    36
PAP 670    #REF!          chr17   7578203  TP53    C
                  T                                  646          216     V       M
      No      No      455     1048    43
PAP 671    #REF!          chr10   123258034FGFR2   A
                  T                                  1647         549     N       K
      No      No      609     1310    46
PAP 671    #REF!          chr10   123279677FGFR2   G
                  C                                  755          252     S       W
      No      No      637     6617    10
PAP 671    #REF!          chr10   89692922 PTEN    T
                  C                                  406          136     C       R
      No      No      1379    5174    27
PAP 671    #REF!          chr10   89717650 PTEN    T
                  G                                  675          225     Y       *
      No      No      234     2019    12
PAP 671    #REF!          chr17   7572968  TP53    T
                                                     1141         381     K
NULL    No      No      1774    5971    30
PAP 674    #REF!          chr17   7578212  TP53    G
                  A                                  637          213     R       *
      No      No      380     841     45
PAP 675    #REF!          chr10   89720867 PTEN    AATT
                                                     1018         340     N
NULL    No      No      9       48      19
PAP 675    #REF!          chr17   7577114  TP53    C
                  A                                  824          275     C       F
      No      No      1800    4621    39
PAP 676    #REF!          chr17   7578402  TP53    G
                                                     528          176     C
NULL    No      No      498     747     67
PAP 678    #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      1247    2721    46
PAP 679    #REF!          chr10   89692905 PTEN    G
                  A                                  389          130     R       Q
```

Table16.txt

```
      No      No      1172    8530    14
PAP 679    #REF!          chr10   89711899 PTEN    C
                  T                                  517          173     R       C
      No      No      564     1860    30
PAP 679    #REF!          chr12   133250289POLE    C
                  A                                  1231         411     V       L
      No      No      1348    4434    30
PAP 681    #REF!          chr10   89692902 PTEN    G
                  T                                  386          129     G       V
      No      No      1321    19910   7
PAP 681    #REF!          chr5    67589590 PIK3R1  ATA
                                                     1353         451     E
NULL    No      No      283     4724    6
PAP 684    #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      1577    13866   11
PAP 684    #REF!          chr10   89720808 PTEN    T
                  A                                  959          320     L       *
      No      No      381     1697    22
PAP 685    #REF!          chr10   123247516FGFR2   T
                  C                                  1975         659     K       E
      No      No      256     798     32
PAP 685    #REF!          chr10   89692845 PTEN    AATGGC
                                                     329          110     Q
NULL    No      No      294     824     36
PAP 685    #REF!          chr10   89692904 PTEN    C
                  T                                  388          130     R       *
      No      No      108     935     12
PAP 686    #REF!          chr10   89692905 PTEN    G
                  C                                  389          130     R       P
      No      No      85      732     12
PAP 686    #REF!          chr10   89717610 PTEN    A
                                                     635          212     N
NULL    No      No      27      115     23
PAP 686    #REF!          chr3    178952090PIK3CA  G
                  A                                  3145         1049    G       S
      No      No      86      333     26
PAP 687    #REF!          chr10   89685268 PTEN    A
                  T                                  0            0       NULL
NULL    Yes     No      81      97      84
PAP 687    #REF!          chr17   7578403  TP53    C
                  T                                  527          176     C       Y
      No      No      439     632     69
PAP 687    #REF!          chr3    178952085PIK3CA  A
                  G                                  3140         1047    H       R
      No      No      638     1762    36
PAP 688    #REF!          chr10   89720734 PTEN    AT
                                                     885          295     L
```

Table16.txt

```
NULL    No      No      29      284     10
PAP 688    #REF!          chr12   25398285 KRAS    C
                   A                                  34           12      G       C
      No      No      342     1904    18
PAP 688    #REF!          chr5    67591128 PIK3R1  G
                   T                                  1721         574     R       I
      No      No      16      314     5
PAP 689    #REF!          chr17   7577538  TP53    C
                   T                                  743          248     R       Q
      No      No      762     1477    52
PAP 694    #REF!          chr10   123279677FGFR2   G
                   C                                  755          252     S       W
      No      No      249     1846    13
PAP 694    #REF!          chr10   89692905 PTEN    G
                   C                                  389          130     R       P
      No      No      195     841     23
PAP 694    #REF!          chr10   89720810 PTEN    A
                                                      961          321     T
NULL    No      No      52      170     31
PAP 694    #REF!          chr5    67591046 PIK3R1  GA
                                                      1639         547     E
NULL    No      No      22      153     14
PAP 695    #REF!          chr17   7577120  TP53    C
                   T                                  818          273     R       H
      No      No      581     976     60
PAP 695    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140         1047    H       R
      No      No      358     770     46
PAP 696    #REF!          chr10   89653829 PTEN    G
                   T                                  127          43      E       *
      No      No      227     307     74
PAP 696    #REF!          chr12   25398284 KRAS    C
                   T                                  35           12      G       D
      No      No      683     1422    48
PAP 697    #REF!          chr10   89692918 PTEN    GAT
                                                      402          134     M
NULL    No      No      830     2013    41
PAP 697    #REF!          chr5    112174257APC     ATGATGAAAG (SEQ ID NO:791)
                                                      2966         989     D
NULL    No      No      223     741     30
PAP 697    #REF!          chr5    112175840APC     C
                   T                                  4549         1517    Q       *
      No      No      39      103     38
PAP 698    #REF!          chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
      No      No      398     3160    13
PAP 698    #REF!          chr10   89711875 PTEN    G
                   A                                  493          165     G       R
```

Table16.txt

```
      No      No      214     548     39
PAP 698    #REF!          chr12   25398284 KRAS    C
                   A                                  35          12      G       V
      No      No      514     1517    34
PAP 699    #REF!          chr10   89690819 PTEN    TAT
                                                      226         76      Y
NULL    No      No      91      172     53
PAP 699    #REF!          chr10   89711899 PTEN    C
                   T                                  517         173     R       C
      No      No      291     723     40
PAP 699    #REF!          chr10   89717775 PTEN
                   A                                  800         267     K
NULL    No      No      1343    3647    37
PAP 699    #REF!          chr5    112173791APC
                   T                                  2500        834     S
NULL    No      No      490     1393    35
PAP 699    #REF!          chr5    112175957APC
                   A                                  4666        1556    T
NULL    No      No      672     1720    39
PAP 701    #REF!          chr12   25398284 KRAS    C
                   A                                  35          12      G       V
      No      No      424     741     57
PAP 701    #REF!          chr17   7574003  TP53    G
                   A                                  1024        342     R       *
      No      No      323     541     60
PAP 702    #REF!          chr17   7578512  TP53    T
                                                      418         140     T
NULL    No      No      3603    4960    73
PAP 704    #REF!          chr10   123279677FGFR2   G
                   C                                  755         252     S       W
      No      No      970     7529    13
PAP 705    #REF!          chr12   25398285 KRAS    C
                   A                                  34          12      G       C
      No      No      396     1239    32
PAP 707    #REF!          chr17   7578271  TP53    T
                   C                                  578         193     H       R
      No      No      2103    2576    82
PAP 708    #REF!          chr10   89717775 PTEN
                   A                                  800         267     K
NULL    No      No      1070    3577    30
PAP 708    #REF!          chr10   89717775 PTEN    A
                                                      800         267     K
NULL    No      No      463     3577    13
PAP 709    #REF!          chr10   89720771 PTEN
                   A                                  922         308     R
NULL    No      No      53      190     28
PAP 709    #REF!          chr10   89720835 PTEN    A
                                                      986         329     N
```

Table16.txt

```
NULL    No      No      100     190     53
PAP 709    #REF!          chr12   25398284 KRAS    C
                   A                                  35          12      G       V
      No      No      418     841     50
PAP 709    #REF!          chr5    67591134 PIK3R1
                   T                                  1727        576     T
NULL    No      No      53      91      58
PAP 711    #REF!          chr17   7578429  TP53    C
                                                      501         167     Q
NULL    No      No      1875    2463    76
PAP 717    #REF!          chr17   7578271  TP53    T
                   C                                  578         193     H       R
      No      No      873     1059    82
PAP 717    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140        1047    H       R
      No      No      57      218     26
PAP 719    #REF!          chr10   89720716 PTEN    A
                                                      867         289     K
NULL    No      No      65      99      66
PAP 719    #REF!          chr3    178916876PIK3CA  G
                   A                                  263         88      R       Q
      No      No      34      68      50
PAP 719    #REF!          chr3    41266137 CTNNB1  C
                   T                                  134         45      S       F
      No      No      182     449     41
PAP 721    #REF!          chr17   7578265  TP53    A
                   G                                  584         195     I       T
      No      No      384     1657    23
PAP 722    #REF!          chr17   7578442  TP53    T
                   C                                  488         163     Y       C
      No      No      436     482     90
PAP 726    #REF!          chr12   25398284 KRAS    C
                   T                                  35          12      G       D
      No      No      107     682     16
PAP 726    #REF!          chr5    67589628 PIK3R1  ATA
                                                      1391        464     D
NULL    No      No      74      1243    6
PAP 726    #REF!          chr5    67589629 PIK3R1  TAGATTATATGA (SEQ ID NO:792)
                                                      1392        464     D
NULL    No      No      87      1243    7
PAP 728    #REF!          chr10   89624272 PTEN    TATCAAGAGG (SEQ ID NO:793)
                                                      46          16      Y
NULL    No      No      702     11469   6
PAP 728    #REF!          chr10   89711893 PTEN    C
                   T                                  511         171     Q       *
      No      No      74      1464    5
PAP 728    #REF!          chr10   89711899 PTEN    C
                   T                                  517         173     R       C
```

Table16.txt

```
      No      No      847     1464    58
PAP 728    #REF!          chr17   7577105  TP53    G
                    C                                   833           278     P       R
      No      No      342     5307    6
PAP 728    #REF!          chr17   7578402  TP53
                    G                                   528           176     C
NULL    No      No      238     3716    6
PAP 728    #REF!          chr3    178936096PIK3CA  G
                    T                                   1638          546     Q       H
      No      No      148     1462    10
PAP 735    #REF!          chr10   123279677FGFR2   G
                    C                                   755           252     S       W
      No      No      154     2449    6
PAP 735    #REF!          chr10   89711916 PTEN    T
                    G                                   534           178     Y       *
      No      No      171     252     68
PAP 735    #REF!          chr5    67591125 PIK3R1  T
                    C                                   1718          573     L       P
      No      No      27      76      36
PAP 744    #REF!          chr10   89717672 PTEN    C
                    T                                   697           233     R       *
      No      No      6       63      10
PAP 744    #REF!          chr10   89720716 PTEN    A
                                                        867           289     K
NULL    No      No      39      142     27
PAP 744    #REF!          chr5    67591139 PIK3R1  GA
                                                        1732          578     D
NULL    No      No      2       21      10
PAP 749    #REF!          chr7    140453136BRAF    A
                    T                                   1799          600     V       E
      No      No      266     694     38
PAP 751    #REF!          chr17   7577538  TP53    C
                    T                                   743           248     R       Q
      No      No      642     952     67
PAP 753    #REF!          chr17   7577121  TP53    G
                    A                                   817           273     R       C
      No      No      246     409     60
PAP 753    #REF!          chr19   52715971 PPP2R1A C
                    G                                   536           179     P       R
      No      No      343     1243    28
PAP 754    #REF!          chr10   89653819 PTEN    A
                                                        117           39      A
NULL    No      No      107     477     22
PAP 754    #REF!          chr10   89720817 PTEN
                    A                                   968           323     N
NULL    No      No      122     272     45
PAP 757    #REF!          chr10   89692904 PTEN    C
                    G                                   388           130     R       G
```

Table16.txt

```
      No      No      243     907     27
PAP 757    #REF!          chr3    41266101 CTNNB1  C
                    G                                  98          33      S       C
      No      No      161     516     31
PAP 757    #REF!          chr5    67591134 PIK3R1  CGA
                                                       1727        576     T
NULL    No      No      16      63      25
PAP 758    #REF!          chr19   52715982 PPP2R1A C
                    T                                  547         183     R       W
      No      No      562     2482    23
PAP 758    #REF!          chr3    178916854PIK3CA  G
                    A                                  241         81      E       K
      No      No      38      188     20
PAP 758    #REF!          chr5    67588951 PIK3R1  C
                    T                                  1042        348     R       *
      No      No      237     1012    23
PAP 761    #REF!          chr17   7578413  TP53    C
                    G                                  517         173     V       L
      No      No      3202    3523    91
PAP 761    #REF!          chr3    178936091PIK3CA  G
                    A                                  1633        545     E       K
      No      No      506     1045    48
PAP 763    #REF!          chr17   7578263  TP53    G
                    A                                  586         196     R       *
      No      No      14      995     1
PAP 767    #REF!          chr17   7578216  TP53    A
                                                       633         211     T
NULL    No      No      510     771     66
PAP 768    #REF!          chr17   7577094  TP53    G
                    A                                  844         282     R       W
      No      No      412     1409    29
PAP 770    #REF!          chr10   123279677FGFR2   G
                    C                                  755         252     S       W
      No      No      125     880     14
PAP 770    #REF!          chr10   89692904 PTEN    C
                    G                                  388         130     R       G
      No      No      115     457     25
PAP 770    #REF!          chr10   89692905 PTEN    G
                    T                                  389         130     R       L
      No      No      60      457     13
PAP 770    #REF!          chr5    67591119 PIK3R1  TCCAGCTGA
                                                       1712        571     I
NULL    No      No      8       68      12
PAP 775    #REF!          chr10   89711917 PTEN    AG
                                                       535         179     S
NULL    No      No      252     838     30
PAP 775    #REF!          chr12   25398284 KRAS    C
                    G                                  35          12      G       A
```

Table16.txt

```
      No      No      1072    3685    29
PAP 775    #REF!          chr5    67589590 PIK3R1  ATATAA
                                                    1353          451     E
NULL    No      No      189     598     32
PAP 777    #REF!          chr17   7574012  TP53    C
                   A                                1015          339     E       *
      No      No      293     492     60
PAP 789    #REF!          chr3    178952085PIK3CA  A
                   G                                3140          1047    H       R
      No      No      461     1262    37
PAP 789    #REF!          chr3    41266113 CTNNB1  C
                   G                                110           37      S       C
      No      No      1156    3303    35
PAP 791    #REF!          chr12   25398282 KRAS    C
                   A                                37            13      G       C
      No      No      346     1289    27
PAP 791    #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      23      1827    1
PAP 799    #REF!          chr12   25380277 KRAS    G
                   T                                181           61      Q       K
      No      No      262     611     43
PAP 800    #REF!          chr10   89692904 PTEN    C
                   G                                388           130     R       G
      No      No      246     1725    14
PAP 800    #REF!          chr10   89692905 PTEN    G
                                                    389           130     R
NULL    No      No      269     1725    16
PAP 800    #REF!          chr3    41266097 CTNNB1  G
                   T                                94            32      D       Y
      No      No      232     1088    21
PAP 802    #REF!          chr10   89711899 PTEN    C
                   T                                517           173     R       C
      No      No      147     521     28
PAP 802    #REF!          chr10   89717778 PTEN    T
                   G                                0             0       NULL
NULL    Yes     No      528     1350    39
PAP 802    #REF!          chr17   7573948  TP53    C
                   G                                1079          360     G       A
      No      No      1325    2423    55
PAP 802    #REF!          chr3    178916854PIK3CA  G
                   A                                241           81      E       K
      No      No      43      161     27
PAP 802    #REF!          chr3    41266098 CTNNB1  A
                   T                                95            32      D       V
      No      No      300     1248    24
PAP 804    #REF!          chr10   123279677FGFR2   G
                   C                                755           252     S       W
```

Table16.txt

```
      No      No      647     5120    13
PAP 804    #REF!          chr10   89692905 PTEN    G
                   A                                 389           130     R       Q
      No      No      163     1144    14
PAP 804    #REF!          chr10   89692964 PTEN    G
                   T                                 448           150     E       *
      No      No      328     1144    29
PAP 804    #REF!          chr12   133253184POLE    G
                   C                                 857           286     P       R
      No      No      105     373     28
PAP 804    #REF!          chr17   7579366  TP53    G
                   T                                 321           107     Y       *
      No      No      185     2185    8
PAP 804    #REF!          chr3    178952074PIK3CA  G
                   T                                 3129          1043    M       I
      No      No      382     1228    31
PAP 804    #REF!          chr5    112173893APC     G
                   T                                 2602          868     E       *
      No      No      572     1780    32
PAP 804    #REF!          chr5    112174631APC     C
                   T                                 3340          1114    R       *
      No      No      176     623     28
PAP 805    #REF!          chr17   7578403  TP53    C
                   T                                 527           176     C       Y
      No      No      591     900     66
PAP 805    #REF!          chr3    178936074PIK3CA  C
                   G                                 1616          539     P       R
      No      No      172     404     43
PAP 807    #REF!          chr10   89692904 PTEN    C
                   G                                 388           130     R       G
      No      No      208     2268    9
PAP 807    #REF!          chr3    178952085PIK3CA  A
                   G                                 3140          1047    H       R
      No      No      587     860     68
PAP 807    #REF!          chr3    41266113 CTNNB1  C
                   T                                 110           37      S       F
      No      No      280     984     28
PAP 809    #REF!          chr12   25398284 KRAS    C
                   A                                 35            12      G       V
      No      No      1404    3480    40
PAP 809    #REF!          chr3    41266113 CTNNB1  C
                   T                                 110           37      S       F
      No      No      1202    2926    41
PAP 812    #REF!          chr10   89692905 PTEN    G
                                                     389           130     R
NULL    No      No      179     589     30
PAP 812    #REF!          chr12   25398281 KRAS    C
                   T                                 38            13      G       D
```

Table16.txt

```
      No      No      399     1626    25
PAP 812    #REF!          chr5    67590991 PIK3R1  T
                   A                                  1584          528     Y       *
      No      No      48      201     24
PAP 812    #REF!          chr5    67591080 PIK3R1  AAA
                                                      1673          558     E
NULL    No      No      406     2741    15
PAP 816    #REF!          chr14   105246551AKT1    C
                   T                                  49            17      E       K
      No      No      3221    4190    77
PAP 816    #REF!          chr3    41266101 CTNNB1  C
                   G                                  98            33      S       C
      No      No      2053    5274    39
PAP 817    #REF!          chr10   123279677FGFR2   G
                   C                                  755           252     S       W
      No      No      1473    2725    54
PAP 824    #REF!          chr10   89692790 PTEN    G
                   T                                  274           92      D       Y
      No      No      190     620     31
PAP 824    #REF!          chr10   89692904 PTEN    C
                   G                                  388           130     R       G
      No      No      1361    7444    18
PAP 824    #REF!          chr3    178952085PIK3CA  A
                   G                                  3140          1047    H       R
      No      No      1545    2324    66
PAP 829    #REF!          chr10   89692995 PTEN    C
                   T                                  479           160     T       I
      No      No      53      207     26
PAP 829    #REF!          chr10   89711891 PTEN    G
                   A                                  509           170     S       N
      No      No      70      344     20
PAP 829    #REF!          chr12   133253184POLE    G
                   C                                  857           286     P       R
      No      No      115     441     26
PAP 829    #REF!          chr3    178916854PIK3CA  G
                   A                                  241           81      E       K
      No      No      8       65      12
PAP 829    #REF!          chr3    178916876PIK3CA  G
                   A                                  263           88      R       Q
      No      No      8       65      12
PAP 830    #REF!          chr3    41266113 CTNNB1  C
                   T                                  110           37      S       F
      No      No      356     1062    34
PAP 831    #REF!          chr17   7577538  TP53    C
                   T                                  743           248     R       Q
      No      No      687     1569    44
PAP 831    #REF!          chr19   52716323 PPP2R1A C
                   T                                  767           256     S       F
```

Table16.txt

```
      No      No      170     369     46
PAP 832    #REF!          chr17   7578539  TP53    T
                                                    391          131     N
NULL    No      No      1410    2053    69
PAP 835    #REF!          chr17   7577539  TP53    G
                   A                                742          248     R       W
      No      No      530     648     82
PAP 835    #REF!          chr3    178936082PIK3CA  G
                   A                                1624         542     E       K
      No      No      65      138     47
PAP 836    #REF!          chr10   89692905 PTEN    G
                   C                                389          130     R       P
      No      No      2009    4335    46
PAP 836    #REF!          chr17   7577547  TP53    C
                   T                                734          245     G       D
      No      No      801     2474    32
PAP 836    #REF!          chr3    178936091PIK3CA  G
                   A                                1633         545     E       K
      No      No      680     2333    29
PAP 837    #REF!          chr10   89692904 PTEN    C
                   G                                388          130     R       G
      No      No      228     814     28
PAP 837    #REF!          chr17   56435167 RNF43   C
                                                    1970         657     R
NULL    No      No      626     1035    61
PAP 839    #REF!          chr10   89685306 PTEN
                   A                                201          67      I
NULL    No      No      5       6       83
PAP 839    #REF!          chr5    67591097 PIK3R1  A
                   G                                1690         564     N       D
      No      No      252     598     42
PAP 841    #REF!          chr17   7577022  TP53    G
                   A                                916          306     R       *
      No      No      306     606     50
PAP 841    #REF!          chr17   7579358  TP53    C
                   A                                329          110     R       L
      No      No      323     780     41
PAP 842    #REF!          chr10   89720817 PTEN    A
                                                    968          323     N
NULL    No      No      123     241     51
PAP 842    #REF!          chr12   25380275 KRAS    T
                   G                                183          61      Q       H
      No      No      311     1026    30
PAP 842    #REF!          chr5    67590478 PIK3R1  C
                   T                                1540         514     R       C
      No      No      332     1264    26
PAP 851    #REF!          chr10   89653834 PTEN    C
                                                    132          44      G
```

Table16.txt

```
NULL    No      No      40      136     29
PAP 851    #REF!          chr10   89690813 PTEN    A
                                                    220         74      R
NULL    No      No      230     891     26
PAP 851    #REF!          chr17   7577538  TP53    C
                   T                                743         248     R       Q
      No      No      2880    7852    37
PAP 851    #REF!          chr17   7578525  TP53    G
                   T                                405         135     C       *
      No      No      498     1243    40
PAP 851    #REF!          chr3    41266124 CTNNB1  A
                   G                                121         41      T       A
      No      No      3352    8579    39
PAP 851    #REF!          chr4    153247367FBXW7   G
                   C                                1435        479     R       G
      No      No      285     704     41
PAP 853    #REF!          chr10   89711899 PTEN    C
                   T                                517         173     R       C
      No      No      156     435     36
PAP 853    #REF!          chr3    178952085PIK3CA  A
                   G                                3140        1047    H       R
      No      No      405     1104    37
PAP 853    #REF!          chr3    41266101 CTNNB1  C
                   G                                98          33      S       C
      No      No      1287    3292    39
Pap 858    #REF!          chr17   7578175  TP53    A
                   C                                0           0       NULL
NULL    Yes     No      846     1434    59
Pap 858    #REF!          chr3    178952072PIK3CA  A
                   G                                3127        1043    M       V
      No      No      1302    3717    35
PAP 860    #REF!          chr17   56435167 RNF43   C
                                                    1970        657     R
NULL    No      No      36      1654    2
PAP 860    #REF!          chr3    178936091PIK3CA  G
                   A                                1633        545     E       K
      No      No      136     318     43
PAP 860    #REF!          chr3    41266101 CTNNB1  C
                   T                                98          33      S       F
      No      No      224     689     33
PAP 862    #REF!          chr17   7578212  TP53    G
                   A                                637         213     R       *
      No      No      686     776     88
PAP 865    #REF!          chr17   7577121  TP53    G
                   A                                817         273     R       C
      No      No      347     521     67
PAP 866    #REF!          chr17   7578280  TP53    G
                   A                                569         190     P       L
```

Table16.txt

```
      No      No      150     272     55
PAP 867    #REF!          chr10   89692904 PTEN    C
                    T                                  388          130     R       *
      No      No      112     402     28
PAP 867    #REF!          chr12   25380275 KRAS    T
                    G                                  183          61      Q       H
      No      No      226     300     75
PAP 867    #REF!          chr17   56435167 RNF43   C
                                                       1970         657     R
NULL    No      No      218     774     28
PAP 868    #REF!          chr10   89717684 PTEN    A
                    T                                  709          237     K       *
      No      No      29      568     5
PAP 868    #REF!          chr10   89720804 PTEN    ACTT
                                                       955          319     T
NULL    No      No      98      261     38
PAP 868    #REF!          chr12   25398284 KRAS    C
                    A                                  35           12      G       V
      No      No      163     794     21
PAP 868    #REF!          chr5    67591130 PIK3R1  AA
                                                       1723         575     K
NULL    No      No      30      171     18
PAP 869    #REF!          chr17   7578204  TP53    A
                    C                                  645          215     S       R
      No      No      140     356     39
PAP 869    #REF!          chr17   7578448  TP53
                    GGATGG                             482          161     A
NULL    No      No      363     1146    32
PAP 869    #REF!          chr3    178952085PIK3CA  A
                    T                                  3140         1047    H       L
      No      No      278     409     68
PAP 870    #REF!          chr10   123258034FGFR2   A
                    T                                  1647         549     N       K
      No      No      4       128     3
PAP 870    #REF!          chr10   89692904 PTEN    C
                    T                                  388          130     R       *
      No      No      42      338     12
PAP 870    #REF!          chr5    67588989 PIK3R1
                    CG                                 1080         360     A
NULL    No      No      2       9       22
PAP 871    #REF!          chr12   25398284 KRAS    C
                    G                                  35           12      G       A
      No      No      3       7       43
PAP 871    #REF!          chr17   56435168 RNF43   G
                                                       1969         657     R
NULL    No      No      2       4       50
PAP 871    #REF!          chr5    67589588 PIK3R1  G
                    T                                  1351         451     E       *
```

Table16.txt

```
      No      No      61      485     13
PAP 873    #REF!          chr10   89711900 PTEN    G
                   A                                  518          173     R       H
      No      No      28      254     11
PAP 873    #REF!          chr10   89717729 PTEN    G
                   T                                  754          252     D       Y
      No      No      159     1438    11
PAP 873    #REF!          chr12   25398281 KRAS    C
                   T                                  38           13      G       D
      No      No      82      489     17
PAP 873    #REF!          chr5    67591122 PIK3R1
                   GGA                                1715         572     Q
NULL    No      No      73      611     12
PAP 873    #REF!          chr5    67591123 PIK3R1
                   GAG                                1716         572     Q
NULL    No      No      14      125     11
PAP 874    #REF!          chr10   89690847 PTEN    G
                   T                                  0            0       NULL
NULL    Yes     No      2       12      17
PAP 874    #REF!          chr10   89692905 PTEN    G
                                                      389          130     R
NULL    No      No      59      458     13
PAP 875    #REF!          chr10   89692855 PTEN    TGAAG
                                                      339          113     S
NULL    No      No      585     762     77
PAP 875    #REF!          chr17   56435167 RNF43   C
                                                      1970         657     R
NULL    No      No      539     2927    18
PAP 875    #REF!          chr17   7572995  TP53    T
                                                      1114         372     K
NULL    No      No      1452    11237   13
PAP 876    #REF!          chr10   89692980 PTEN    A
                   G                                  464          155     Y       C
      No      No      1636    1955    84
PAP 876    #REF!          chr12   25398285 KRAS    C
                   A                                  34           12      G       C
      No      No      646     1501    43
PAP 876    #REF!          chr17   56435167 RNF43   C
                                                      1970         657     R
NULL    No      No      3435    4114    83
PAP 877    #REF!          chr10   89692920 PTEN    T
                   A                                  404          135     I       K
      No      No      83      484     17
PAP 877    #REF!          chr10   89717775 PTEN    A
                                                      800          267     K
NULL    No      No      139     501     28
PAP 877    #REF!          chr12   25398284 KRAS    C
                   T                                  35           12      G       D
```

Table16.txt

```
      No      No      90      330     27
PAP 877    #REF!          chr3    178936096PIK3CA  G
                  T                                 1638          546     Q       H
      No      No      52      124     42
PAP 878    #REF!          chr10   123279677FGFR2   G
                  C                                 755           252     S       W
      No      No      667     4449    15
PAP 878    #REF!          chr10   89653845 PTEN    A
                                                    143           48      N
NULL    No      No      17      55      31
PAP 878    #REF!          chr10   89692784 PTEN    TTT
                                                    268           90      F
NULL    No      No      21      64      33
PAP 878    #REF!          chr17   7578406  TP53    C
                  T                                 524           175     R       H
      No      No      3254    4056    80
PAP 878    #REF!          chr5    67589642 PIK3R1
                  AATATGAAG                         1405          469     E
NULL    No      No      58      136     43
PAP 878    #REF!          chr5    67589647 PIK3R1
                  GAAGAATAT                         1410          470     Y
NULL    No      No      278     727     38
PAP 879    #REF!          chr10   89690847 PTEN    G
                  C                                 0             0       NULL
NULL    Yes     No      30      101     30
PAP 879    #REF!          chr12   25398284 KRAS    C
                  T                                 35            12      G       D
      No      No      291     1537    19
PAP 879    #REF!          chr5    67589606 PIK3R1  CAAGAAAAA
                                                    1369          457     Q
NULL    No      No      216     1734    12
PAP 881    #REF!          chr17   7578268  TP53    A
                  C                                 581           194     L       R
      No      No      597     799     75
PAP 881    #REF!          chr19   52716323 PPP2R1A C
                  A                                 767           256     S       Y
      No      No      769     1191    65
PAP 881    #REF!          chr3    178936082PIK3CA  G
                  A                                 1624          542     E       K
      No      No      253     481     53
PAP 891    #REF!          chr17   7577142  TP53    C
                  T                                 796           266     G       R
      No      No      1699    1766    96
PAP 892    #REF!          chr10   89720771 PTEN
                  C                                 922           308     R
NULL    No      No      47      239     20
PAP 892    #REF!          chr5    67589639 PIK3R1  GAAGAATAT
                                                    1402          468     E
```

Table16.txt

```
NULL    No      No      544     1090    50
PAP 894    #REF!          chr10   89720817 PTEN
                  A                                  968          323     N
NULL    No      No      262     631     42
PAP 894    #REF!          chr3    178936082PIK3CA  G
                  A                                  1624         542     E       K
      No      No      179     763     23
PAP 897    #REF!          chr10   89717775 PTEN    A
                                                     800          267     K
NULL    No      No      201     707     28
PAP 897    #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      315     1313    24
PAP 897    #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      393     925     42
PAP 897    #REF!          chr3    178952007PIK3CA  A
                  G                                  3062         1021    Y       C
      No      No      26      107     24
PAP 901    #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      288     1138    25
PAP 901    #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      323     623     52
PAP 901    #REF!          chr5    67591130 PIK3R1  AA
                                                     1723         575     K
NULL    No      No      20      102     20
PAP 902    #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      204     1938    11
PAP 902    #REF!          chr10   89720804 PTEN    ACTT
                                                     955          319     T
NULL    No      No      144     282     51
PAP 902    #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      11      841     1
PAP 902    #REF!          chr19   52715982 PPP2R1A C
                  T                                  547          183     R       W
      No      No      556     1618    34
PAP 904    #REF!          chr10   89624305 PTEN    T
                  A                                  79           27      Y       N
      No      Yes     1991    6211    32
PAP 904    #REF!          chr17   7578518  TP53    C
                                                     412          138     A
NULL    No      No      2702    3695    73
PAP 904    #REF!          chr17   7578519  TP53    C
                                                     411          137     L
```

Table16.txt

```
NULL    No      No      3610    4990    72
PAP 904    #REF!          chr3    178952018PIK3CA  A
                   G                                3073          1025    T       A
      No      No      379     1104    34
PAP 907    #REF!          chr1    115258748NRAS    C
                   A                                34            12      G       C
      No      No      41      544     8
PAP 907    #REF!          chr10   89653832 PTEN
                   GAAG                             130           44      G
NULL    No      No      193     288     67
PAP 907    #REF!          chr10   89653833 PTEN
                   AAGG                             131           44      G
NULL    No      No      38      62      61
PAP 907    #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      326     872     37
PAP 907    #REF!          chr17   56448303 RNF43
                   G                                344           115     A
NULL    No      No      107     1965    5
PAP 907    #REF!          chr3    178916876PIK3CA  G
                   A                                263           88      R       Q
      No      No      9       105     9
PAP 910    #REF!          chr10   123279677FGFR2   G
                   C                                755           252     S       W
      No      No      289     1996    14
PAP 910    #REF!          chr10   89692847 PTEN    T
                   C                                331           111     W       R
      No      No      280     741     38
PAP 910    #REF!          chr3    178952085PIK3CA  A
                   G                                3140          1047    H       R
      No      No      299     742     40
PAP 914    #REF!          chr17   7578263  TP53    G
                   A                                586           196     R       *
      No      No      163     250     65
PAP 922    #REF!          chr10   89717672 PTEN    C
                   T                                697           233     R       *
      No      No      132     1228    11
PAP 922    #REF!          chr3    41266097 CTNNB1  G
                   T                                94            32      D       Y
      No      No      385     1040    37
PAP 922    #REF!          chr5    67589613 PIK3R1  AAA
                                                    1376          459     K
NULL    No      No      740     2123    35
PAP 925    #REF!          chr17   7577548  TP53    C
                   A                                733           245     G       C
      No      No      480     1132    42
PAP 926    #REF!          chr10   89692905 PTEN    G
                   A                                389           130     R       Q
```

Table16.txt

```
      No      No      110     1287    9
PAP 926    #REF!          chr10   89717672 PTEN    C
                   T                                  697          233     R       *
      No      No      26      305     9
PAP 926    #REF!          chr12   133250289POLE    C
                   G                                  1231         411     V       L
      No      No      154     647     24
PAP 927    #REF!          chr10   89692883 PTEN    C
                   G                                  367          123     H       D
      No      No      181     284     64
PAP 928    #REF!          chr17   7577498  TP53    C
                   T                                  0            0       NULL
NULL    Yes     No      324     430     75
PAP 931    #REF!          chr10   89711973 PTEN    G
                                                      591          197     K
NULL    No      No      144     497     29
PAP 931    #REF!          chr3    41266113 CTNNB1  C
                   T                                  110          37      S       F
      No      No      49      129     38
PAP 937    #REF!          chr10   89717672 PTEN    C
                   T                                  697          233     R       *
      No      No      35      203     17
PAP 937    #REF!          chr12   25398284 KRAS    C
                   A                                  35           12      G       V
      No      No      186     1111    17
PAP 937    #REF!          chr17   7572971  TP53    G
                   A                                  1138         380     H       Y
      No      No      6       73      8
PAP 937    #REF!          chr3    178936082PIK3CA  G
                   A                                  1624         542     E       K
      No      No      4       30      13
PAP 989    #REF!          chr17   7577121  TP53    G
                   A                                  817          273     R       C
      No      No      373     523     71
PAP 989    #REF!          chr3    178936091PIK3CA  G
                   A                                  1633         545     E       K
      No      No      1103    1245    89
PAP 990    #REF!          chr1    115258744NRAS    C
                   A                                  38           13      G       V
      No      No      1497    3306    45
PAP 990    #REF!          chr10   89692904 PTEN    C
                   T                                  388          130     R       *
      No      No      187     354     53
PAP 990    #REF!          chr17   56435167 RNF43   C
                                                      1970         657     R
NULL    No      No      158     363     44
PAP 990    #REF!          chr17   56448303 RNF43
                   G                                  344          115     A
```

Table16.txt

```
NULL    No      No      42      680     6
PAP 990    #REF!           chr17   56448310 RNF43   G
                   A                                  337          113     R       *
      No      No      248     680     37
PAP 991    #REF!           chr10   89692896 PTEN    G
                   T                                  380          127     G       V
      No      No      553     1791    31
PAP 991    #REF!           chr10   89692985 PTEN
                   G                                  469          157     E
NULL    No      No      162     544     30
PAP 991    #REF!           chr5    67591134 PIK3R1  CGA
                                                      1727         576     T
NULL    No      No      259     991     26
PAP 993    #REF!           chr17   7577556  TP53    C
                   T                                  725          242     C       Y
      No      No      3000    4438    68
PAP 994    #REF!           chr10   123279677FGFR2   G
                   C                                  755          252     S       W
      No      No      181     2105    9
PAP 994    #REF!           chr10   89692921 PTEN
                   A                                  405          135     I
NULL    No      No      214     1833    12
PAP 994    #REF!           chr10   89720804 PTEN    ACTT
                                                      955          319     T
NULL    No      No      68      327     21
PAP 995    #REF!           chr17   7577099  TP53    C
                   G                                  839          280     R       T
      No      No      1455    5088    29
PAP 996    #REF!           chr10   123279677FGFR2   G
                   C                                  755          252     S       W
      No      No      499     5020    10
PAP 996    #REF!           chr10   89693009 PTEN    G
                                                      0            0       NULL
NULL    Yes     No      276     1041    27
PAP 996    #REF!           chr10   89725042 PTEN    A
                   G                                  0            0       NULL
NULL    Yes     No      667     1736    38
PAP 996    #REF!           chr3    178936095PIK3CA  A
                   G                                  1637         546     Q       R
      No      No      412     1393    30
PAP 996    #REF!           chr3    41266113 CTNNB1  C
                   T                                  110          37      S       F
      No      No      1744    6576    27
PAP 998    #REF!           chr10   89720804 PTEN
                   A                                  955          319     T
NULL    No      No      135     199     68
PAP 998    #REF!           chr12   25380275 KRAS    T
                   A                                  183          61      Q       H
```

Table16.txt

```
      No      No      1474    1944    76
PAP 998    #REF!          chr9    21971186 CDKN2A  GGGCGCTGCCCATC (SEQ ID NO:794)
                                                    172           58      R
NULL    No      No      590     983     60
PAP 999    #REF!          chr12   25398281 KRAS    C
                   T                                38            13      G       D
      No      No      4000    6009    67
PAP 999    #REF!          chr17   7578406  TP53    C
                   T                                524           175     R       H
      No      No      1192    1607    74
PAP 999    #REF!          chr19   52715971 PPP2R1A C
                   G                                536           179     P       R
      No      No      6238    14722   42
PAPA 1001  #REF!          chr10   89624305 PTEN    T
                   G                                79            27      Y       D
      No      Yes     2518    8582    29
PAPA 1001  #REF!          chr12   25398284 KRAS    C
                   A                                35            12      G       V
      No      No      467     3927    12
PAPA 1001  #REF!          chr5    67591094 PIK3R1
                   AACGTA                           1687          563     M
NULL    No      No      203     1745    12
PAPA 1002  #REF!          chr10   89692905 PTEN    G
                   A                                389           130     R       Q
      No      No      466     8328    6
PAPA 1002  #REF!          chr3    178916876PIK3CA  G
                   A                                263           88      R       Q
      No      No      241     1282    19
PAPA 1002  #REF!          chr3    178952077PIK3CA  T
                   G                                3132          1044    N       K
      No      No      1093    3099    35
PAPA 1003  #REF!          chr14   105246551AKT1    C
                   T                                49            17      E       K
      No      No      1635    2542    64
PAPA 1003  #REF!          chr3    41266098 CTNNB1  A
                   G                                95            32      D       G
      No      No      2089    7462    28
PAPA 1005  #REF!          chr12   25398284 KRAS    C
                   T                                35            12      G       D
      No      No      3345    6372    53
PAPA 1005  #REF!          chr17   7578413  TP53    C
                   A                                517           173     V       L
      No      No      1303    1887    69
PAPA 1005  #REF!          chr4    153249384FBXW7   C
                   T                                1394          465     R       H
      No      No      573     1144    50
PAPA 1005  #REF!          chr5    67591130 PIK3R1  AAGACGAGA
                                                    1723          575     K
```

Table16.txt

```
NULL    No      No      411     1284    32
PAPA 1011  #REF!          chr10   123258036FGFR2   T
                  G                                 1645          549     N       H
      No      No      200     466     43
PAPA 1011  #REF!          chr10   89692905 PTEN    G
                  A                                 389           130     R       Q
      No      No      113     757     15
PAPA 1011  #REF!          chr3    178916876PIK3CA  G
                  A                                 263           88      R       Q
      No      No      29      221     13
PAPA 1011  #REF!          chr5    112173917APC     C
                  T                                 2626          876     R       *
      No      No      1163    2873    41
PAPA 1011  #REF!          chr5    112175925APC     C
                  A                                 4634          1545    S       *
      No      No      28      61      46
PAPA 1012  #REF!          chr10   89717775 PTEN
                  A                                 800           267     K
NULL    No      No      228     554     41
PAPA 1012  #REF!          chr10   89717775 PTEN    A
                                                    800           267     K
NULL    No      No      285     554     51
PAPA 1012  #REF!          chr12   25398281 KRAS    C
                  T                                 38            13      G       D
      No      No      1150    2551    45
PAPA 1012  #REF!          chr3    178916876PIK3CA  G
                  A                                 263           88      R       Q
      No      No      110     472     23
PAPA 1013  #REF!          chr17   7577141  TP53    C
                  T                                 797           266     G       E
      No      No      1502    3022    50
PAPA 1016  #REF!          chr10   89692961 PTEN    C
                  T                                 445           149     Q       *
      No      No      142     1535    9
PAPA 1016  #REF!          chr10   89717672 PTEN    C
                  T                                 697           233     R       *
      No      No      7151    53025   14
PAPA 1016  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      123     1414    9
PAPA 1016  #REF!          chr17   7578388  TP53    C
                  T                                 542           181     R       H
      No      No      566     2065    27
PAPA 1016  #REF!          chr4    153247366FBXW7   C
                  T                                 1436          479     R       Q
      No      No      167     619     27
PAPA 1016  #REF!          chr5    67591139 PIK3R1  GA
                                                    1732          578     D
```

Table16.txt

```
NULL    No      No      287     1177    24
PAPA 1019  #REF!          chr10   123279677FGFR2   G
                  C                                  755          252     S       W
      No      No      575     1495    39
PAPA 1019  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      377     2526    15
PAPA 1019  #REF!          chr3    178916836PIK3CA  C
                  G                                  223          75      Q       E
      No      No      300     415     72
PAPA 1019  #REF!          chr5    67591149 PIK3R1
                  T                                  1742         581     L
NULL    No      No      95      911     10
PAPA 1019  #REF!          chr5    67592052 PIK3R1  CA
                                                     1868         623     T
NULL    No      No      380     1135    34
PAPA 1028  #REF!          chr12   25398284 KRAS    C
                  A                                  35           12      G       V
      No      No      198     1246    16
PAPA 1028  #REF!          chr3    178952072PIK3CA  A
                  G                                  3127         1043    M       V
      No      No      173     908     19
PAPA 1035  #REF!          chr17   7577046  TP53    C
                  A                                  892          298     E       *
      No      No      811     1808    45
PAPA 1035  #REF!          chr19   52715971 PPP2R1A C
                  G                                  536          179     P       R
      No      No      2371    8246    29
PAPA 1035  #REF!          chr5    67589607 PIK3R1
                  GTTTCA                             1370         457     Q
NULL    No      No      174     405     43
PAPA 1037  #REF!          chr17   7577117  TP53    A
                  C                                  821          274     V       G
      No      No      969     1470    66
PAPA 1048  #REF!          chr17   7577094  TP53    G
                  A                                  844          282     R       W
      No      No      1156    1457    79
PAPA 1057  #REF!          chr1    115258747NRAS    C
                  T                                  35           12      G       D
      No      No      7218    12740   57
PAPA 1057  #REF!          chr17   7578406  TP53    C
                  T                                  524          175     R       H
      No      No      799     1974    40
PAPA 1057  #REF!          chr3    178936082PIK3CA  G
                  A                                  1624         542     E       K
      No      No      775     1379    56
PAPA 1059  #REF!          chr12   133250289POLE    C
                  A                                  1231         411     V       L
```

Table16.txt

```
      No      No      1515    4910    31
PAPA 1059  #REF!          chr3    178916876PIK3CA  G
                  A                                  263          88      R       Q
      No      No      22      199     11
PAPA 1059  #REF!          chr3    41266124 CTNNB1  A
                  G                                  121          41      T       A
      No      No      1175    4487    26
PAPA 1062  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      1644    7965    21
PAPA 1062  #REF!          chr17   7577149  TP53
                  A                                  789          263     N
NULL    No      No      835     3292    25
PAPA 1066  #REF!          chr10   89690810 PTEN    G
                  T                                  217          73      E       *
      No      No      157     765     21
PAPA 1066  #REF!          chr10   89692905 PTEN    G
                  T                                  389          130     R       L
      No      No      148     3192    5
PAPA 1066  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      1027    3897    26
PAPA 1066  #REF!          chr4    153247351FBXW7   C
                                                     1451         484     R
NULL    No      No      35      660     5
PAPA 1066  #REF!          chr5    67590484 PIK3R1  GGCAATGAGAA (SEQ ID NO:795)
                                                     1546         516     G
NULL    No      No      55      853     6
PAPA 1066  #REF!          chr5    67591141 PIK3R1  CCAATACTTGA (SEQ ID NO:796)
                                                     1734         578     D
NULL    No      No      80      1258    6
PAPA 1074  #REF!          chr17   7577609  TP53    C
                  G                                  0            0       NULL
NULL    Yes     No      1085    2363    46
PAPA 1077  #REF!          chr10   89717775 PTEN
                  A                                  800          267     K
NULL    No      No      131     256     51
PAPA 1077  #REF!          chr5    67589560 PIK3R1  TATTGA
                                                     1323         441     N
NULL    No      No      433     951     46
PAPA 1081  #REF!          chr10   123258030FGFR2   G
                  T                                  1651         551     L       I
      No      No      35      438     8
PAPA 1081  #REF!          chr10   89624245 PTEN    G
                  T                                  19           7       E       *
      No      No      1585    4015    39
PAPA 1081  #REF!          chr10   89711900 PTEN    G
                  A                                  518          173     R       H
```

Table16.txt

```
      No      No      131     330     40
PAPA 1081  #REF!          chr3    178916876PIK3CA  G
                  A                                  263          88      R       Q
      No      No      40      199     20
PAPA 1081  #REF!          chr3    178952074PIK3CA  G
                  T                                  3129         1043    M       I
      No      No      58      152     38
PAPA 1081  #REF!          chr3    41266124 CTNNB1  A
                  G                                  121          41      T       A
      No      No      1310    2987    44
PAPA 1081  #REF!          chr5    67589618 PIK3R1  C
                  T                                  1381         461     R       *
      No      No      82      223     37
PAPA 1092  #REF!          chr19   52715983 PPP2R1A G
                  A                                  548          183     R       Q
      No      No      485     1385    35
PAPA 1092  #REF!          chr3    41266104 CTNNB1  G
                  T                                  101          34      G       V
      No      No      1359    4323    31
PAPA 1095  #REF!          chr10   89692904 PTEN    C
                                                     388          130     R
NULL    No      No      273     2915    9
PAPA 1095  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      334     2915    11
PAPA 1096  #REF!          chr17   7577595  TP53    CA
                                                     686          229     C
NULL    No      No      1305    2271    57
PAPA 1097  #REF!          chr10   89690810 PTEN    G
                  T                                  217          73      E       *
      No      No      24      47      51
PAPA 1097  #REF!          chr10   89692953 PTEN    T
                                                     437          146     L
NULL    No      No      50      247     20
PAPA 1097  #REF!          chr17   7579314  TP53    T
                  C                                  373          125     T       A
      No      No      1442    3022    48
PAPA 1097  #REF!          chr4    153249385FBXW7   G
                  A                                  1393         465     R       C
      No      No      39      178     22
PAPA 1099  #REF!          chr10   89653867 PTEN    G
                  C                                  0            0       NULL
NULL    Yes     No      32      94      34
PAPA 1099  #REF!          chr10   89720677 PTEN    T
                                                     828          276     N
NULL    No      No      33      91      36
PAPA 1099  #REF!          chr3    178936094PIK3CA  C
                  G                                  1636         546     Q       E
```

Table16.txt

```
      No      No      328     1055    31
PAPA 1099  #REF!          chr3    41266101 CTNNB1  C
                  G                                  98          33      S       C
      No      No      2084    6467    32
PAPA 1100  #REF!          chr14   105246551AKT1    C
                  T                                  49          17      E       K
      No      No      5123    8529    60
PAPA 1100  #REF!          chr3    41266125 CTNNB1  C
                  T                                  122         41      T       I
      No      No      3491    11829   30
PAPA 1103  #REF!          chr10   89720716 PTEN
                  A                                  867         289     K
NULL    No      No      84      141     60
PAPA 1103  #REF!          chr17   56435167 RNF43   C
                                                     1970        657     R
NULL    No      No      1308    1810    72
PAPA 1103  #REF!          chr3    178952085PIK3CA  A
                  G                                  3140        1047    H       R
      No      No      959     2822    34
PAPA 1110  #REF!          chr17   7578490  TP53    A
                  C                                  440         147     V       G
      No      No      692     1811    38
PAPA 1112  #REF!          chr12   25398284 KRAS    C
                  A                                  35          12      G       V
      No      No      1407    3516    40
PAPA 1112  #REF!          chr17   7578208  TP53    T
                  C                                  641         214     H       R
      No      No      1118    1670    67
PAPA 1112  #REF!          chr9    21971186 CDKN2A  G
                  A                                  172         58      R       *
      No      No      2822    3503    81
PAPA 1113  #REF!          chr17   7577568  TP53    C
                  G                                  713         238     C       S
      No      No      372     440     85
PAPA 1115  #REF!          chr17   7578263  TP53    G
                  A                                  586         196     R       *
      No      No      822     1266    65
PAPA 1116  #REF!          chr12   25398284 KRAS    C
                  G                                  35          12      G       A
      No      No      1507    3907    39
PAPA 1116  #REF!          chr3    178952085PIK3CA  A
                  G                                  3140        1047    H       R
      No      No      1508    1999    75
PAPA 1117  #REF!          chr17   7574003  TP53    G
                  A                                  1024        342     R       *
      No      No      803     891     90
PAPA 1117  #REF!          chr5    112174170APC     C
                  A                                  2879        960     S       *
```

Table16.txt

```
      No      No      2       37      5
PAPA 1118  #REF!          chr17   7579476  TP53
                  G                                  211          71      P
NULL    No      No      1178    1854    64
PAPA 1119  #REF!          chr9    21971127 CDKN2A  AG
                                                     231          77      T
NULL    No      No      192     196     98
PAPA 1120  #REF!          chr17   7578503  TP53    C
                  T                                  427          143     V       M
      No      No      305     603     51
PAPA 1122  #REF!          chr3    178936094PIK3CA  C
                  A                                  1636         546     Q       K
      No      No      273     684     40
PAPA 1126  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      991     6901    14
PAPA 1128  #REF!          chr1    115256536NRAS    C
                  T                                  175          59      A       T
      No      No      3099    17192   18
PAPA 1128  #REF!          chr10   89720803 PTEN
                  T                                  954          318     L
NULL    No      No      895     2462    36
PAPA 1128  #REF!          chr3    178936082PIK3CA  G
                  C                                  1624         542     E       Q
      No      No      1018    6448    16
PAPA 1128  #REF!          chr3    41266104 CTNNB1  G
                  A                                  101          34      G       E
      No      No      3235    20855   16
PAPA 1130  #REF!          chr10   89685281 PTEN    C
                  A                                  176          59      S       *
      No      No      210     687     31
PAPA 1130  #REF!          chr10   89720870 PTEN    T
                  G                                  1021         341     F       V
      No      No      151     414     37
PAPA 1130  #REF!          chr12   133253184POLE    G
                  C                                  857          286     P       R
      No      No      858     2721    32
PAPA 1130  #REF!          chr5    112175216APC     G
                  T                                  3925         1309    E       *
      No      No      583     1729    34
PAPA 1130  #REF!          chr5    67588951 PIK3R1  C
                  T                                  1042         348     R       *
      No      No      263     883     30
PAPA 1131  #REF!          chr10   123279677FGFR2   G
                  C                                  755          252     S       W
      No      No      208     1939    11
PAPA 1131  #REF!          chr10   89725042 PTEN    A
                  G                                  0            0       NULL
```

Table16.txt

NULL Yes No 2231 2943 76
PAPA 1131 #REF! chr3 41266101 CTNNB1 C
A 98 33 S Y
No No 3990 11539 35
PAPA 1131 #REF! chr5 67591106 PIK3R1 A
G 1699 567 K E
No No 610 1846 33
PAPA 1132 #REF! chr10 123279677FGFR2 G
C 755 252 S W
No No 300 3632 8
PAPA 1132 #REF! chr10 89624296 PTEN G
C 70 24 D H
No No 6530 12192 54
PAPA 1132 #REF! chr5 67591092 PIK3R1 GTATGAACAGCATTAAAC (SEQ ID NO:797)
1685 562 R
NULL No No 256 2068 12
PAPA 1132 #REF! chr9 21971120 CDKN2A G
A 238 80 R *
No No 2 37 5
PAPA 1133 #REF! chr10 89712017 PTEN G
C 0 0 NULL
NULL Yes No 630 3194 20
PAPA 1133 #REF! chr10 89717775 PTEN A
800 267 K
NULL No No 428 812 53
PAPA 1133 #REF! chr17 56435167 RNF43 C
1970 657 R
NULL No No 482 1108 44
PAPA 1133 #REF! chr5 67591106 PIK3R1 A
G 1699 567 K E
No No 631 1642 38
PAPA 1134 #REF! chr3 178936091PIK3CA G
A 1633 545 E K
No No 448 965 46
PAPA 1134 #REF! chr3 41266125 CTNNB1 C
T 122 41 T I
No No 3466 7397 47
PAPA 1135 #REF! chr17 7577120 TP53 C
T 818 273 R H
No No 809 2376 34
PAPA 1135 #REF! chr17 7577556 TP53 C
T 725 242 C Y
No No 823 3959 21
PAPA 1137 #REF! chr10 89624245 PTEN G
T 19 7 E *
No No 4607 11461 40
PAPA 1137 #REF! chr10 89692905 PTEN G
A 389 130 R Q

Table16.txt

```
      No      No      400     2203    18
PAPA 1137  #REF!          chr12   133250289POLE    C
                  A                                 1231          411     V       L
      No      No      1087    2972    37
PAPA 1137  #REF!          chr4    153247367FBXW7   G
                  A                                 1435          479     R       *
      No      No      341     959     36
PAPA 1137  #REF!          chr5    112176051APC     C
                  A                                 4760          1587    S       *
      No      No      259     711     36
PAPA 1138  #REF!          chr3    178952085PIK3CA  A
                  G                                 3140          1047    H       R
      No      No      3539    5865    60
PAPA 1139  #REF!          chr17   7577120  TP53    C
                  T                                 818           273     R       H
      No      No      1098    2052    54
PAPA 1140  #REF!          chr10   89717695 PTEN    C
                  A                                 720           240     Y       *
      No      No      9042    23316   39
PAPA 1140  #REF!          chr17   7577121  TP53    G
                  A                                 817           273     R       C
      No      No      31      2698    1
PAPA 1140  #REF!          chr17   7578369  TP53    A
                  G                                 0             0       NULL
NULL    Yes     No      384     1475    26
PAPA 1140  #REF!          chr17   7579476  TP53    G
                                                    211           71      P
NULL    No      No      463     1821    25
PAPA 1141  #REF!          chr17   7574007  TP53
                  TTCC                              1020          340     M
NULL    No      No      581     1112    52
PAPA 1142  #REF!          chr3    178952085PIK3CA  A
                  G                                 3140          1047    H       R
      No      No      2711    3389    80
PAPA 1142  #REF!          chr3    41266098 CTNNB1  A
                  G                                 95            32      D       G
      No      No      6563    11051   59
PAPA 1143  #REF!          chr10   89692904 PTEN    C
                  G                                 388           130     R       G
      No      No      458     2130    22
PAPA 1143  #REF!          chr10   89692905 PTEN    G
                  T                                 389           130     R       L
      No      No      214     2130    10
PAPA 1143  #REF!          chr12   25398284 KRAS    C
                  T                                 35            12      G       D
      No      No      1025    4876    21
PAPA 1143  #REF!          chr3    178952074PIK3CA  G
                  T                                 3129          1043    M       I
```

Table16.txt

```
      No      No      440     2107    21
PAPA 1143  #REF!          chr5    67591067 PIK3R1  GCTGAGTATCGAGAAATTGAC (SEQ ID
NO:798)                                      1660         554     A
 NULL    No      No      226     2155    11
PAPA 1145  #REF!          chr10   89685303 PTEN    G
                  T                                  198          66      K       N
      No      No      51      338     15
PAPA 1145  #REF!          chr10   89692905 PTEN    G
                  A                                  389          130     R       Q
      No      No      204     1982    10
PAPA 1145  #REF!          chr12   133253184POLE    G
                  C                                  857          286     P       R
      No      No      978     4165    24
PAPA 1145  #REF!          chr17   7577565  TP53    T
                  C                                  716          239     N       S
      No      No      349     1262    28
PAPA 1145  #REF!          chr17   7578212  TP53    G
                  A                                  637          213     R       *
      No      No      202     1049    19
PAPA 1145  #REF!          chr19   52715982 PPP2R1A C
                  T                                  547          183     R       W
      No      No      540     2350    23
PAPA 1147  #REF!          chr10   123247516FGFR2   T
                  C                                  1975         659     K       E
      No      No      3088    7747    40
PAPA 1147  #REF!          chr10   89692904 PTEN    C
                  T                                  388          130     R       *
      No      No      89      775     12
PAPA 1147  #REF!          chr10   89692905 PTEN    G
                  A                                  389          130     R       Q
      No      No      69      775     9
PAPA 1147  #REF!          chr10   89693007 PTEN
                  A                                  491          164     K
NULL    No      No      269     745     36
PAPA 1147  #REF!          chr12   133250289POLE    C
                  A                                  1231         411     V       L
      No      No      1425    3577    40
PAPA 1147  #REF!          chr17   7578527  TP53    A
                  G                                  403          135     C       R
      No      No      166     1739    10
PAPA 1147  #REF!          chr3    178952007PIK3CA  A
                  G                                  3062         1021    Y       C
      No      No      65      129     50
PAPA 1147  #REF!          chr4    153249385FBXW7   G
                  A                                  1393         465     R       C
      No      No      18      985     2
PAPA 1148  #REF!          chr10   89692839 PTEN    T
                  G                                  323          108     L       R
```

Table16.txt

```
      No      No      816     1075    76
PAPA 1148  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      457     1343    34
PAPA 1148  #REF!          chr17   7577538  TP53    C
                  T                                  743          248     R       Q
      No      No      998     1203    83
PAPA 1148  #REF!          chr3    41266124 CTNNB1  A
                  G                                  121          41      T       A
      No      No      1085    3554    31
PAPA 1149  #REF!          chr10   123258034FGFR2   A
                  T                                  1647         549     N       K
      No      No      239     598     40
PAPA 1149  #REF!          chr14   105246551AKT1    C
                  T                                  49           17      E       K
      No      No      673     860     78
PAPA 1152  #REF!          chr4    153249384FBXW7   C
                  T                                  1394         465     R       H
      No      No      215     536     40
PAPA 1152  #REF!          chr5    112175957APC
                  A                                  4666         1556    T
NULL    No      No      75      189     40
PAPA 1152  #REF!          chr5    67591106 PIK3R1  A
                  G                                  1699         567     K       E
      No      No      413     1056    39
PAPA 1153  #REF!          chr10   89692811 PTEN    G
                  T                                  295          99      E       *
      No      No      475     500     95
PAPA 1153  #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      263     578     46
PAPA 1153  #REF!          chr3    178952085PIK3CA  A
                  G                                  3140         1047    H       R
      No      No      1148    2389    48
PAPA 1153  #REF!          chr3    41266100 CTNNB1  T
                  G                                  97           33      S       A
      No      No      1316    2788    47
PAPA 1154  #REF!          chr10   123279677FGFR2   G
                  C                                  755          252     S       W
      No      No      81      703     12
PAPA 1154  #REF!          chr10   89720817 PTEN
                  A                                  968          323     N
NULL    No      No      20      59      34
PAPA 1154  #REF!          chr5    67589588 PIK3R1  G
                  T                                  1351         451     E       *
      No      No      52      441     12
PAPA 1154  #REF!          chr5    67591103 PIK3R1
                  AACGTATGAACAGCA  (SEQ ID NO:807)  1696         566     I
```

Table16.txt

```
NULL    No      No      485     1186    41
PAPA 1155  #REF!           chr10   123279677FGFR2   G
                   C                                  755          252     S       W
      No      No      165     871     19
PAPA 1155  #REF!           chr10   89692886 PTEN    T
                   A                                  370          124     C       S
      No      No      219     375     58
PAPA 1155  #REF!           chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
      No      No      35      207     17
PAPA 1155  #REF!           chr17   7577094  TP53    G
                   C                                  844          282     R       G
      No      No      237     421     56
PAPA 1155  #REF!           chr3    178952085PIK3CA  A
                   G                                  3140         1047    H       R
      No      No      268     742     36
PAPA 1157  #REF!           chr17   7577538  TP53    C
                   T                                  743          248     R       Q
      No      No      641     800     80
PAPA 1157  #REF!           chr3    178952085PIK3CA  A
                   T                                  3140         1047    H       L
      No      No      535     972     55
PAPA 1158  #REF!           chr10   89624245 PTEN    G
                   T                                  19           7       E       *
      No      No      1798    4455    40
PAPA 1158  #REF!           chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
      No      No      704     2651    27
PAPA 1158  #REF!           chr12   133250289POLE    C
                   A                                  1231         411     V       L
      No      No      812     1824    45
PAPA 1158  #REF!           chr3    178916876PIK3CA  G
                   A                                  263          88      R       Q
      No      No      471     1662    28
PAPA 1158  #REF!           chr3    178952007PIK3CA  A
                   G                                  3062         1021    Y       C
      No      No      326     877     37
PAPA 1158  #REF!           chr4    153247366FBXW7   C
                   T                                  1436         479     R       Q
      No      No      575     1519    38
PAPA 1159  #REF!           chr12   25398284 KRAS    C
                   G                                  35           12      G       A
      No      No      651     708     92
PAPA 1159  #REF!           chr19   52715982 PPP2R1A C
                   T                                  547          183     R       W
      No      No      982     2200    45
PAPA 1160  #REF!           chr10   89692905 PTEN    G
                   A                                  389          130     R       Q
```

Table16.txt

```
      No      No      78      307     25
PAPA 1160  #REF!          chr10   89711899 PTEN    C
                  T                                  517          173     R       C
      No      No      77      245     31
PAPA 1160  #REF!          chr12   133250289POLE    C
                  A                                  1231         411     V       L
      No      No      239     1140    21
PAPA 1160  #REF!          chr17   7578212  TP53    G
                  A                                  637          213     R       *
      No      No      18      212     9
PAPA 1160  #REF!          chr4    153247366FBXW7   C
                  T                                  1436         479     R       Q
      No      No      92      353     26
PAPA 1160  #REF!          chr5    67591106 PIK3R1  A
                  G                                  1699         567     K       E
      No      No      267     1088    25
PAPA 1161  #REF!          chr10   89685293 PTEN    A
                                                     188          63      N
NULL    No      No      94      412     23
PAPA 1161  #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      29      234     12
PAPA 1161  #REF!          chr5    67591115 PIK3R1  CTT
                                                     1708         570     L
NULL    No      No      170     731     23
PAPA 1162  #REF!          chr10   89685315 PTEN    GT
                                                     0            0       NULL
NULL    Yes     No      23      87      26
PAPA 1162  #REF!          chr10   89720804 PTEN    ACTT
                                                     955          319     T
NULL    No      No      1       17      6
PAPA 1162  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      130     372     35
PAPA 1162  #REF!          chr17   7578263  TP53    G
                  A                                  586          196     R       *
      No      No      26      118     22
PAPA 1167  #REF!          chr17   7577575  TP53    A
                  T                                  706          236     Y       N
      No      No      290     1169    25
PAPA 1172  #REF!          chr17   7578413  TP53    C
                  A                                  517          173     V       L
      No      No      199     296     67
PAPA 1176  #REF!          chr17   7579380  TP53    A
                                                     307          103     Y
NULL    No      No      536     615     87
PAPA 1177  #REF!          chr10   123247516FGFR2   T
                  C                                  1975         659     K       E
```

Table16.txt

```
      No      No      3869    8023    48
PAPA 1177  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      293     1371    21
PAPA 1177  #REF!          chr3    178952085PIK3CA  A
                  T                                  3140         1047    H       L
      No      No      572     2389    24
PAPA 1180  #REF!          chr17   7577097  TP53    C
                  G                                  841          281     D       H
      No      No      659     852     77
PAPA 1181  #REF!          chr12   25398284 KRAS    C
                  A                                  35           12      G       V
      No      No      4408    6248    71
PAPA 1181  #REF!          chr17   7577539  TP53    G
                  A                                  742          248     R       W
      No      No      1128    1223    92
PAPA 1188  #REF!          chr17   7578406  TP53    C
                  T                                  524          175     R       H
      No      No      613     864     71
PAPA 1191  #REF!          chr10   89685269 PTEN    G
                  A                                  0            0       NULL
NULL    Yes     No      354     1056    34
PAPA 1191  #REF!          chr3    178936095PIK3CA  A
                  G                                  1637         546     Q       R
      No      No      268     974     28
PAPA 1192  #REF!          chr10   89692904 PTEN    C
                  T                                  388          130     R       *
      No      No      356     2203    16
PAPA 1192  #REF!          chr10   89720669 PTEN    T
                                                     820          274     W
NULL    No      No      238     689     35
PAPA 1192  #REF!          chr17   7574017  TP53    C
                  A                                  1010         337     R       L
      No      No      1775    6097    29
PAPA 1192  #REF!          chr17   7577114  TP53    C
                  T                                  824          275     C       Y
      No      No      849     2926    29
PAPA 1192  #REF!          chr5    67591134 PIK3R1  CGAGAG
                                                     1727         576     T
NULL    No      No      971     1688    58
PAPA 1193  #REF!          chr10   89692844 PTEN    C
                  T                                  328          110     Q       *
      No      No      1769    3393    52
PAPA 1193  #REF!          chr10   89692852 PTEN    AAGTGAAGATGACAAT (SEQ ID NO:799)
                                                     336          112     L
NULL    No      No      1070    3393    32
PAPA 1193  #REF!          chr3    41266097 CTNNB1  G
                  T                                  94           32      D       Y
```

Table16.txt

```
      No      No      1524    3243    47
PAPA 1194  #REF!          chr10   89717650 PTEN    T
                  G                                  675          225     Y       *
      No      No      5170    10244   50
PAPA 1194  #REF!          chr12   25398282 KRAS    C
                  A                                  37           13      G       C
      No      No      5782    30934   19
PAPA 1194  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      4157    30934   13
PAPA 1194  #REF!          chr17   56435167 RNF43   C
                                                     1970         657     R
NULL    No      No      1439    5460    26
PAPA 1194  #REF!          chr3    178952084PIK3CA  C
                  T                                  3139         1047    H       Y
      No      No      256     1891    14
PAPA 1198  #REF!          chr17   7577114  TP53    C
                  T                                  824          275     C       Y
      No      No      257     1843    14
PAPA 1200  #REF!          chr10   89692902 PTEN    G
                  A                                  386          129     G       E
      No      No      133     911     15
PAPA 1200  #REF!          chr10   89720837 PTEN    A
                  T                                  988          330     K       *
      No      No      10      23      43
PAPA 1200  #REF!          chr3    41266103 CTNNB1  G
                  C                                  100          34      G       R
      No      No      735     2164    34
PAPA 1202  #REF!          chr17   7577120  TP53    C
                  T                                  818          273     R       H
      No      No      499     1189    42
PAPA 1202  #REF!          chr19   52715982 PPP2R1A C
                  T                                  547          183     R       W
      No      No      1975    6504    30
PAPA 1202  #REF!          chr19   52715983 PPP2R1A G
                  A                                  548          183     R       Q
      No      No      2051    6504    32
PAPA 1202  #REF!          chr5    112174132APC     T
                  A                                  2841         947     C       *
      No      No      299     1305    23
PAPA 1207  #REF!          chr10   89717672 PTEN    C
                  T                                  697          233     R       *
      No      No      1098    11671   9
PAPA 1207  #REF!          chr10   89717775 PTEN    A
                                                     800          267     K
NULL    No      No      350     1553    23
PAPA 1207  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
```

Table16.txt

```
      No      No      9492    49617   19
PAPA 1209  #REF!          chr10   89690810 PTEN    G
                    T                                 217           73      E       *
      No      No      202     617     33
PAPA 1209  #REF!          chr10   89717732 PTEN    AT
                                                      757           253     I
NULL    No      No      2745    14608   19
PAPA 1209  #REF!          chr17   56435167 RNF43   C
                                                      1970          657     R
NULL    No      No      250     3442    7
PAPA 1209  #REF!          chr17   7577022  TP53    G
                    A                                 916           306     R       *
      No      No      1138    3120    36
PAPA 1210  #REF!          chr17   7578442  TP53    T
                    C                                 488           163     Y       C
      No      No      1458    1599    91
PAPA 1211  #REF!          chr10   89692908 PTEN    CTGGTGTAA
                                                      392           131     T
NULL    No      No      880     4175    21
PAPA 1211  #REF!          chr12   25398284 KRAS    C
                    T                                 35            12      G       D
      No      No      7288    38465   19
PAPA 1211  #REF!          chr4    153247288FBXW7   C
                    T                                 1514          505     R       H
      No      No      1497    7282    21
PAPA 1211  #REF!          chr5    67591134 PIK3R1  CGA
                                                      1727          576     T
NULL    No      No      668     3402    20
PAPA 1213  #REF!          chr17   7577090  TP53    C
                    G                                 848           283     R       P
      No      No      1416    2148    66
PAPA 1214  #REF!          chr1    115258744NRAS    C
                    T                                 38            13      G       D
      No      No      1802    6050    30
PAPA 1214  #REF!          chr10   89717775 PTEN
                    A                                 800           267     K
NULL    No      No      503     1464    34
PAPA 1214  #REF!          chr3    178952085PIK3CA  A
                    G                                 3140          1047    H       R
      No      No      626     1968    32
PAPA 1215  #REF!          chr17   7578553  TP53    T
                    C                                 377           126     Y       C
      No      No      701     966     73
PAPA 1218  #REF!          chr10   89720804 PTEN    ACTT
                                                      955           319     T
NULL    No      No      93      290     32
PAPA 1218  #REF!          chr10   89725042 PTEN    A
                    C                                 0             0       NULL
```

Table16.txt

```
NULL    Yes     No      359     768     47
PAPA 1218  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      2418    3390    71
PAPA 1218  #REF!          chr17   7579312  TP53    C
                A                                   375           125     T       T
      No      Yes     937     6005    16
PAPA 1221  #REF!          chr10   123279677FGFR2   G
                C                                   755           252     S       W
      No      No      1332    4480    30
PAPA 1221  #REF!          chr10   89711875 PTEN    G
                A                                   493           165     G       R
      No      No      150     279     54
PAPA 1221  #REF!          chr10   89717736 PTEN    AAGTA
                                                    761           254     K
NULL    No      No      129     1457    9
PAPA 1223  #REF!          chr10   89624284 PTEN    G
                T                                   58            20      G       *
      No      No      3174    5898    54
PAPA 1223  #REF!          chr5    67589593 PIK3R1  TAA
                                                    1356          452     Y
NULL    No      No      243     1165    21
PAPA 1224  #REF!          chr10   123258036FGFR2   T
                G                                   1645          549     N       H
      No      No      127     426     30
PAPA 1224  #REF!          chr10   89692905 PTEN    G
                A                                   389           130     R       Q
      No      No      88      749     12
PAPA 1224  #REF!          chr12   133250289POLE    C
                G                                   1231          411     V       L
      No      No      1026    3975    26
PAPA 1224  #REF!          chr3    178936094PIK3CA  C
                G                                   1636          546     Q       E
      No      No      76      297     26
PAPA 1225  #REF!          chr3    178952085PIK3CA  A
                G                                   3140          1047    H       R
      No      No      585     1535    38
PAPA 1230  #REF!          chr14   105246551AKT1    C
                T                                   49            17      E       K
      No      No      4201    6411    66
PAPA 1230  #REF!          chr3    41266101 CTNNB1  C
                A                                   98            33      S       Y
      No      No      2146    6454    33
PAPA 1232  #REF!          chr10   89624239 PTEN    ATCAAAGAGATCG (SEQ ID NO:800)
                                                    13            5       I
NULL    No      No      2360    4722    50
PAPA 1232  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
```

Table16.txt

```
NULL    No      No      1165    3283    35
PAPA 1232  #REF!           chr3    178952077PIK3CA  T
                   G                                  3132          1044    N       K
      No      No      286     2083    14
PAPA 1239  #REF!           chr10   89717615 PTEN    C
                   T                                  640           214     Q       *
      No      No      3327    8238    40
PAPA 1239  #REF!           chr10   89720804 PTEN
                   A                                  955           319     T
NULL    No      No      587     2667    22
PAPA 1239  #REF!           chr17   7577548  TP53    C
                   T                                  733           245     G       S
      No      No      53      4813    1
PAPA 1239  #REF!           chr17   7579312  TP53    C
                   T                                  375           125     T       T
      No      Yes     2616    7947    33
PAPA 1239  #REF!           chr3    178936092PIK3CA  A
                   G                                  1634          545     E       G
      No      No      992     1873    53
PAPA 1239  #REF!           chr3    41266137 CTNNB1  C
                   T                                  134           45      S       F
      No      No      169     6313    3
PAPA 1240  #REF!           chr17   7577124  TP53    C
                   A                                  814           272     V       L
      No      No      609     919     66
PAPA 1242  #REF!           chr12   25398284 KRAS    C
                   T                                  35            12      G       D
      No      No      29269   57493   51
PAPA 1242  #REF!           chr17   7577550  TP53    C
                   T                                  731           244     G       D
      No      No      2318    3457    67
PAPA 1243  #REF!           chr12   25398284 KRAS    C
                   A                                  35            12      G       V
      No      No      36813   91553   40
PAPA 1249  #REF!           chr10   89720670 PTEN    G
                   A                                  821           274     W       *
      No      No      27      149     18
PAPA 1249  #REF!           chr10   89720728 PTEN    AA
                                                      879           293     G
NULL    No      No      31      149     21
PAPA 1251  #REF!           chr10   89624242 PTEN    A
                   T                                  16            6       K       *
      No      No      5904    7791    76
PAPA 1251  #REF!           chr17   7577115  TP53    A
                   G                                  823           275     C       R
      No      No      344     1088    32
PAPA 1253  #REF!           chr17   7579349  TP53    A
                   C                                  338           113     F       C
```

Table16.txt

```
      No      No      1043    1068    98
PAPA 1254  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
      No      No      257     2008    13
PAPA 1254  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      512     3877    13
PAPA 1254  #REF!          chr3    178936091PIK3CA  G
                  C                                  1633         545     E       Q
      No      No      108     1142    10
PAPA 1254  #REF!          chr3    178952077PIK3CA  T
                  A                                  3132         1044    N       K
      No      No      476     3695    13
PAPA 1255  #REF!          chr10   89624285 PTEN    GA
                                                     59           20      G
NULL    No      No      2178    4938    44
PAPA 1256  #REF!          chr17   7578394  TP53    T
                  C                                  536          179     H       R
      No      No      944     2279    41
PAPA 1257  #REF!          chr17   7577141  TP53    C
                  T                                  797          266     G       E
      No      No      450     523     86
PAPA 1258  #REF!          chr17   7578442  TP53    T
                  C                                  488          163     Y       C
      No      No      1134    1284    88
PAPA 1259  #REF!          chr17   7577022  TP53    G
                  A                                  916          306     R       *
      No      No      1208    2334    52
PAPA 1260  #REF!          chr12   25398284 KRAS    C
                  A                                  35           12      G       V
      No      No      1292    3439    38
PAPA 1260  #REF!          chr3    178952018PIK3CA  A
                  G                                  3073         1025    T       A
      No      No      1220    3102    39
PAPA 1262  #REF!          chr12   25398284 KRAS    C
                  T                                  35           12      G       D
      No      No      1566    4396    36
PAPA 1262  #REF!          chr17   7578507  TP53    G
                  C                                  423          141     C       W
      No      No      530     1246    43
PAPA 1263  #REF!          chr17   7576885  TP53    T
                                                     961          321     K
NULL    No      No      725     895     81
PAPA 1264  #REF!          chr10   123279677FGFR2   G
                  C                                  755          252     S       W
      No      No      230     2761    8
PAPA 1264  #REF!          chr10   89692904 PTEN    C
                  G                                  388          130     R       G
```

Table16.txt

```
      No      No      154     972     16
PAPA 1264  #REF!          chr3    178952085PIK3CA  A
                  G                                  3140          1047    H       R
      No      No      442     2294    19
PAPA 1264  #REF!          chr5    67591135 PIK3R1
                  G                                  1728          576     T
NULL    No      No      113     481     24
PAPA 1284  #REF!          chr3    41266101 CTNNB1  C
                  G                                  98            33      S       C
      No      No      616     3114    20
PAPA 1292  #REF!          chr12   25398285 KRAS    C
                  A                                  34            12      G       C
      No      No      13503   42875   31
PAPA 1292  #REF!          chr3    178936091PIK3CA  G
                  C                                  1633          545     E       Q
      No      No      238     725     33
PAPA 1292  #REF!          chr3    178952085PIK3CA  A
                  T                                  3140          1047    H       L
      No      No      1407    4442    32
PAPA 1293  #REF!          chr10   89692904 PTEN    C
                  G                                  388           130     R       G
      No      No      232     3519    7
PAPA 1293  #REF!          chr10   89720749 PTEN
                  AAATC                              900           300     I
NULL    No      No      135     576     23
PAPA 1293  #REF!          chr17   56435167 RNF43   C
                                                     1970          657     R
NULL    No      No      2159    9805    22
PAPA 1293  #REF!          chr3    41266125 CTNNB1  C
                  T                                  122           41      T       I
      No      No      318     4018    8
PAPA 1295  #REF!          chr10   89692904 PTEN    C
                  G                                  388           130     R       G
      No      No      1478    4536    33
PAPA 1295  #REF!          chr12   25380275 KRAS    T
                  G                                  183           61      Q       H
      No      No      1451    3298    44
PAPA 1295  #REF!          chr3    178936091PIK3CA  G
                  A                                  1633          545     E       K
      No      No      247     1816    14
PAPA 1296  #REF!          chr17   7579312  TP53    CGTGCAAGTCACAGAC (SEQ ID NO:801)
                                                     375           125     T
NULL    No      Yes     1183    10929   11
PAPA 1297  #REF!          chr17   7577556  TP53    C
                  G                                  725           242     C       S
      No      No      1842    2330    79
PAPA 1298  #REF!          chr17   7578413  TP53    C
                  A                                  517           173     V       L
```

Table16.txt

```
      No      No      946     2030    47
PAPA 1300  #REF!          chr10   89692802 PTEN    C
                    G                                 286           96      P       A
      No      No      118     301     39
PAPA 1300  #REF!          chr10   89717750 PTEN    C
                                                      775           259     H
NULL    No      No      680     1882    36
PAPA 1300  #REF!          chr10   89720741 PTEN    C
                    T                                 892           298     Q       *
      No      No      196     603     33
PAPA 1300  #REF!          chr17   7578206  TP53    T
                    C                                 643           215     S       G
      No      No      307     508     60
PAPA 1300  #REF!          chr5    67589634 PIK3R1  TATATGAAGAAT (SEQ ID NO:802)
                                                      1397          466     L
NULL    No      No      600     2022    30
PAPA 1301  #REF!          chr10   89692904 PTEN    C
                    G                                 388           130     R       G
      No      No      258     927     28
PAPA 1301  #REF!          chr10   89717712 PTEN    C
                    T                                 737           246     P       L
      No      No      2090    14972   14
PAPA 1301  #REF!          chr12   25398284 KRAS    C
                    T                                 35            12      G       D
      No      No      10976   35431   31
PAPA 1302  #REF!          chr3    178952085PIK3CA  A
                    T                                 3140          1047    H       L
      No      No      1399    3539    40
PAPA 1302  #REF!          chr3    41266097 CTNNB1  G
                    T                                 94            32      D       Y
      No      No      928     2382    39
PAPA 1303  #REF!          chr17   7577022  TP53    G
                    A                                 916           306     R       *
      No      No      1813    2149    84
PAPA 1303  #REF!          chr5    112174759APC     AGA
                                                      3468          1156    E
NULL    No      No      399     760     53
PAPA 1308  #REF!          chr10   123258035FGFR2   T
                    C                                 1646          549     N       S
      No      No      73      625     12
PAPA 1308  #REF!          chr10   123279677FGFR2   G
                    C                                 755           252     S       W
      No      No      367     6572    6
PAPA 1308  #REF!          chr10   89624297 PTEN    AC
                                                      71            24      D
NULL    No      No      69      5625    1
PAPA 1308  #REF!          chr10   89720708 PTEN    TC
                                                      859           287     S
```

Table16.txt

```
NULL    No      No      31      394     8
PAPA 1308  #REF!           chr12   25398284 KRAS    C
                   A                                 35          12      G       V
      No      No      5789    79816   7
PAPA 1308  #REF!           chr17   7577120  TP53    C
                   T                                 818         273     R       H
      No      No      145     935     16
PAPA 1308  #REF!           chr17   7577539  TP53    G
                   A                                 742         248     R       W
      No      No      316     5767    5
PAPA 1308  #REF!           chr3    178936094PIK3CA  C
                   A                                 1636        546     Q       K
      No      No      37      447     8
PAPA 1308  #REF!           chr3    41266097 CTNNB1  G
                   A                                 94          32      D       N
      No      No      402     3201    13
PAPA 1309  #REF!           chr10   89624245 PTEN    G
                   T                                 19          7       E       *
      No      No      9201    14423   64
PAPA 1309  #REF!           chr12   133253184POLE    G
                   C                                 857         286     P       R
      No      No      1762    5525    32
PAPA 1309  #REF!           chr17   7579909  TP53    C
                   T                                 4           2       E       K
      No      No      2090    4206    50
PAPA 1321  #REF!           chr17   7579414  TP53    C
                   T                                 273         91      W       *
      No      No      183     282     65
PAPA 1322  #REF!           chr17   7578271  TP53    T
                   C                                 578         193     H       R
      No      No      586     818     72
PAPA 1323  #REF!           chr17   7577539  TP53    G
                   A                                 742         248     R       W
      No      No      83      175     47
PAPA 1325  #REF!           chr17   7577120  TP53    C
                   T                                 818         273     R       H
      No      No      304     391     78
PAPA 1326  #REF!           chr12   25398281 KRAS    C
                   T                                 38          13      G       D
      No      No      3028    4000    76
PAPA 1326  #REF!           chr17   7576900  TP53
                   GGGG                              946         316     P
NULL    No      No      168     302     56
PAPA 1326  #REF!           chr5    112175639APC     C
                   T                                 4348        1450    R       *
      No      No      199     339     59
PAPA 1327  #REF!           chr10   89692905 PTEN    G
                   A                                 389         130     R       Q
```

Table16.txt

	No	No	160	298	54								
PAPA	1327	#REF!		chr17	7579528	TP53	C						
			T						159	53	W	*	
	No	No	1634	1717	95								
PAPA	1327	#REF!		chr3	178916854	PIK3CA	G						
			A						241	81	E	K	
	No	No	174	287	61								
PAPA	1327	#REF!		chr4	153249384	FBXW7	C						
			T						1394	465	R	H	
	No	No	324	714	45								
PAPA	1328	#REF!		chr10	89624245	PTEN	G						
			T						19	7	E	*	
	No	No	103	5275	2								
PAPA	1328	#REF!		chr10	89653809	PTEN	G						
			A						107	36	G	E	
	No	No	642	1441	45								
PAPA	1328	#REF!		chr10	89692905	PTEN	G						
			A						389	130	R	Q	
	No	No	277	742	37								
PAPA	1328	#REF!		chr12	133253184	POLE	G						
			C						857	286	P	R	
	No	No	685	1552	44								
PAPA	1328	#REF!		chr3	178916854	PIK3CA	G						
			A						241	81	E	K	
	No	No	275	577	48								
PAPA	1328	#REF!		chr5	112174857	APC	C						
			A						3566	1189	S	*	
	No	No	125	280	45								
PAPA	1328	#REF!		chr5	67588951	PIK3R1	C						
			T						1042	348	R	*	
	No	No	826	1707	48								
PAPA	1329	#REF!		chr10	89720726	PTEN	G						
			T						877	293	G	*	
	No	No	130	337	39								
PAPA	1329	#REF!		chr3	178936082	PIK3CA	G						
			A						1624	542	E	K	
	No	No	129	257	50								
PAPA	1362	#REF!		chr10	89624245	PTEN	G						
			T						19	7	E	*	
	No	No	154	1548	10								
PAPA	1362	#REF!		chr12	133253184	POLE	G						
			C						857	286	P	R	
	No	No	71	488	15								
PAPA	1362	#REF!		chr12	25398281	KRAS	C						
			T						38	13	G	D	
	No	No	999	6349	16								
PAPA	1362	#REF!		chr17	7578212	TP53	G						
			A						637	213	R	*	

Table16.txt

```
      No      No      9       160     6
PAPA 1364  #REF!          chr17   7577120  TP53    C
                    A                                  818          273     R       L
      No      No      29      47      62
PAPA 1364  #REF!          chr17   7578185  TP53    G
                    T                                  664          222     P       T
      No      No      2       15      13
PAPA 1365  #REF!          chr17   7578406  TP53    C
                    T                                  524          175     R       H
      No      No      20      23      87
PAPA 1369  #REF!          chr12   25398284 KRAS    C
                    A                                  35           12      G       V
      No      No      2970    5049    59
PAPA 1369  #REF!          chr17   7577539  TP53    G
                    A                                  742          248     R       W
      No      No      654     1039    63
PAPA 1370  #REF!          chr17   7577560  TP53    A
                    C                                  721          241     S       A
      No      No      728     972     75
PAPA 1371  #REF!          chr17   7577120  TP53    C
                    T                                  818          273     R       H
      No      No      60      152     39
PAPA 1695  #REF!          chr17   7578529  TP53    A
                    G                                  401          134     F       S
      No      No      237     284     83
PAPA 1696  #REF!          chr10   89725130 PTEN    C
                                                       1113         371     D
NULL    No      No      6       46      13
PAPA 1696  #REF!          chr17   7577532  TP53    G
                    A                                  749          250     P       L
      No      No      13      119     11
PAPA 1696  #REF!          chr5    67591105 PIK3R1  TAA
                                                       1698         566     I
NULL    No      No      22      43      51
PAPA 1697  #REF!          chr17   7577094  TP53    G
                    A                                  844          282     R       W
      No      No      2       22      9
PAPA 1697  #REF!          chr17   7578370  TP53    C
                    T                                  0            0       NULL
NULL    Yes     No      65      100     65
PAPA 1697  #REF!          chr17   7579457  TP53    G
                    T                                  230          77      P       Q
      No      No      2       39      5
PAPA 1698  #REF!          chr17   7577153  TP53    CCAC
                                                       785          262     G
NULL    No      No      13      57      23
PAPA 1699  #REF!          chr17   7576921  TP53    G
                                                       925          309     P
```

Table16.txt

```
NULL    No      No      6       12      50
PAPA 1700  #REF!           chr17   7578247  TP53    A
                   T                                    602          201     L       *
      No      No      16      25      64
PAPA 1700  #REF!           chr17   7579365  TP53    C
                   A                                    322          108     G       C
      No      No      2       38      5
PAPA 1701  #REF!           chr17   7577548  TP53    C
                   T                                    733          245     G       S
      No      No      212     428     50
PAPA 1702  #REF!           chr17   7577547  TP53    C
                   T                                    734          245     G       D
      No      No      312     360     87
PAPA 1702  #REF!           chr19   52716328 PPP2R1A C
                   T                                    772          258     R       C
      No      No      4       35      11
PAPA 1703  #REF!           chr17   7577022  TP53    G
                   A                                    916          306     R       *
      No      No      424     1296    33
PAPA 1705  #REF!           chr10   89717716 PTEN
                   A                                    741          247     L
NULL    No      No      4       19      21
PAPA 1706  #REF!           chr17   7578555  TP53    C
                   T                                    0            0       NULL
NULL    Yes     No      39      1096    4
PAPA 1707  #REF!           chr17   7577114  TP53    C
                   A                                    824          275     C       F
      No      No      3       6       50
PAPA 1712  #REF!           chr17   7577105  TP53    G
                   C                                    833          278     P       R
      No      No      115     169     68
PAPA 1712  #REF!           chr5    67588981 PIK3R1  C
                   T                                    1072         358     R       *
      No      No      6       115     5
PAPA 1715  #REF!           chr12   133250289POLE    C
                   A                                    1231         411     V       L
      No      No      26      52      50
PAPA 1715  #REF!           chr3    178952074PIK3CA  G
                   T                                    3129         1043    M       I
      No      No      18      90      20
PAPA 1717  #REF!           chr17   7577100  TP53    T
                   C                                    838          280     R       G
      No      No      495     604     82
PAPA 1720  #REF!           chr17   7578406  TP53    C
                   T                                    524          175     R       H
      No      No      243     366     66
PAPA 1724  #REF!           chr17   7576897  TP53    G
                   A                                    949          317     Q       *
```

Table16.txt

	No	No	104	170	61								
PAPA	1725	#REF!		chr12	25398284	KRAS	C						
			A					35		12	G		V
	No	No	1357	2479	55								
PAPA	1730	#REF!		chr17	7578535	TP53	T						
			C					395		132	K		R
	No	No	306	476	64								
PAPA	1732	#REF!		chr17	7578534	TP53	C						
			A					396		132	K		N
	No	No	26	67	39								
PAPA	1734	#REF!		chr17	7577560	TP53	A						
			C					721		241	S		A
	No	No	1170	1285	91								
PAPA	1735	#REF!		chr12	25398284	KRAS	C						
			A					35		12	G		V
	No	No	103	197	52								
PAPA	1736	#REF!		chr19	52715983	PPP2R1A	G						
			A					548		183	R		Q
	No	No	207	751	28								
PAPA	1736	#REF!		chr3	41266101	CTNNB1	C						
			T					98		33	S		F
	No	No	23	73	32								
PAPA	1738	#REF!		chr10	89717729	PTEN	G						
			T					754		252	D		Y
	No	No	2	17	12								
PAPA	1738	#REF!		chr17	7577144	TP53	A						
			G					794		265	L		P
	No	No	12	56	21								
PAPA	1739	#REF!		chr17	7577124	TP53	C						
			A					814		272	V		L
	No	No	36	182	20								
PAPA	1739	#REF!		chr9	21974778	CDKN2A	CCAG						
								49		17	A		
NULL	No	No	203	1138	18								
PAPA	1739	#REF!		chr9	21974782	CDKN2A	CCAG						
								45		15	W		
NULL	No	No	348	1317	26								
PAPA	1816	#REF!		chr10	89692904	PTEN	C						
			G					388		130	R		G
	No	No	449	2817	16								
PAPA	1816	#REF!		chr10	89692905	PTEN	G						
			A					389		130	R		Q
	No	No	515	2817	18								
PAPA	1816	#REF!		chr3	178936074	PIK3CA	C						
			G					1616		539	P		R
	No	No	192	642	30								
PAPA	1816	#REF!		chr3	178936091	PIK3CA	G						
			A					1633		545	E		K

Table16.txt

```
      No      No      192     642     30
PAPA 1819  #REF!          chr17   7577527  TP53    GGA
                                                    754           252     L
NULL    No      No      719     1833    39
PAPA 1820  #REF!          chr12   25398284 KRAS    C
                  A                                 35            12      G       V
      No      No      2737    3249    84
PAPA 1820  #REF!          chr17   7578271  TP53    T
                  A                                 578           193     H       L
      No      No      451     546     83
PAPA 1821  #REF!          chr17   7577534  TP53    C
                  A                                 747           249     R       S
      No      No      772     1903    41
PAPA 1823  #REF!          chr17   7578203  TP53    C
                  T                                 646           216     V       M
      No      No      387     416     93
PAPA 1826  #REF!          chr5    67591134 PIK3R1  CGA
                                                    1727          576     T
NULL    No      No      169     333     51
PAPA 1828  #REF!          chr17   7578190  TP53    T
                  C                                 659           220     Y       C
      No      No      75      124     60
PAPA 1834  #REF!          chr1    115256529NRAS    T
                  C                                 182           61      Q       R
      No      No      1111    2402    46
PAPA 1836  #REF!          chr10   89685316 PTEN    T
                  C                                 0             0       NULL
NULL    Yes     No      7       15      47
PAPA 1836  #REF!          chr10   89692794 PTEN    A
                  G                                 278           93      H       R
      No      No      18      50      36
PAPA 1836  #REF!          chr3    178952085PIK3CA  A
                  T                                 3140          1047    H       L
      No      No      223     611     36
PAPA 1836  #REF!          chr3    41266101 CTNNB1  C
                  T                                 98            33      S       F
      No      No      324     870     37
PAPA 1837  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      1395    2241    62
PAPA 1837  #REF!          chr3    178952085PIK3CA  A
                  G                                 3140          1047    H       R
      No      No      316     1085    29
PAPA 1839  #REF!          chr10   123279677FGFR2   G
                  C                                 755           252     S       W
      No      No      85      370     23
PAPA 1839  #REF!          chr10   89692961 PTEN    C
                  T                                 445           149     Q       *
```

Table16.txt

```
      No      No      315     1629    19
PAPA 1839  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
NULL    No      No      149     561     27
PAPA 1839  #REF!          chr5    67592055 PIK3R1
                  TG                                1871          624     W
NULL    No      No      45      188     24
PAPA 1840  #REF!          chr10   89717708 PTEN    C
                  T                                 733           245     Q       *
      No      No      267     816     33
PAPA 1840  #REF!          chr5    112175957APC     A
                                                    4666          1556    T
NULL    No      No      667     843     79
PAPA 1842  #REF!          chr10   89720875 PTEN    G
                  T                                 1026          342     K       N
      No      Yes     230     269     86
PAPA 1842  #REF!          chr19   52715982 PPP2R1A C
                  T                                 547           183     R       W
      No      No      238     586     41
PAPA 1842  #REF!          chr3    41266113 CTNNB1  C
                  T                                 110           37      S       F
      No      No      809     1952    41
PAPA 1842  #REF!          chr5    67591130 PIK3R1  AAGACGAGA
                                                    1723          575     K
NULL    No      No      362     661     55
PAPA 1843  #REF!          chr10   89692904 PTEN    C
                  G                                 388           130     R       G
      No      No      263     2865    9
PAPA 1843  #REF!          chr10   89692905 PTEN    GAACTGGTGTAATGATATGTG (SEQ ID
NO:803)                                                 389           130     R
 NULL    No      No      142     2865    5
PAPA 1844  #REF!          chr17   7578437  TP53    G
                  A                                 493           165     Q       *
      No      No      538     1331    40
PAPA 1845  #REF!          chr17   7578223  TP53    CT
                                                    626           209     R
NULL    No      No      211     320     66
PAPA 1847  #REF!          chr10   89692905 PTEN    G
                  C                                 389           130     R       P
      No      No      1129    3063    37
PAPA 1847  #REF!          chr12   25398284 KRAS    C
                  G                                 35            12      G       A
      No      No      1926    3031    64
PAPA 1848  #REF!          chr10   89717716 PTEN    A
                                                    741           247     L
NULL    No      No      70      147     48
PAPA 1848  #REF!          chr17   56435167 RNF43   C
                                                    1970          657     R
```

Table16.txt

```
NULL    No      No      149     184     81
PAPA 1849  #REF!           chr14   105246551AKT1   C
                  T                                 49          17      E       K
      No      No      3324    3551    94
PAPA 1849  #REF!           chr17   7577082  TP53   C
                  T                                 856         286     E       K
      No      No      296     566     52
PAPA 1849  #REF!           chr19   52715983 PPP2R1A G
                  A                                 548         183     R       Q
      No      No      186     470     40
PAPA 1850  #REF!           chr17   7579424  TP53   G
                                                    263         88      A
NULL    No      No      227     376     60
PAPA 1852  #REF!           chr10   89692904 PTEN   C
                  G                                 388         130     R       G
      No      No      4525    8643    52
PAPA 1852  #REF!           chr3    178952074PIK3CA G
                  A                                 3129        1043    M       I
      No      No      575     1327    43
PAPA 1855  #REF!           chr10   89692904 PTEN   C
                  G                                 388         130     R       G
      No      No      1536    4058    38
PAPA 1855  #REF!           chr12   25398284 KRAS   C
                  A                                 35          12      G       V
      No      No      1067    2642    40
PAPA 1855  #REF!           chr3    178916876PIK3CA G
                  A                                 263         88      R       Q
      No      No      12      194     6
PAPA 1856  #REF!           chr17   7578432  TP53   TG
                                                    498         166     S
NULL    No      No      814     1083    75
PAPA 1857  #REF!           chr17   7578551  TP53   A
                  G                                 379         127     S       P
      No      No      3077    3794    81
PAPA 1857  #REF!           chr19   52715971 PPP2R1A C
                  G                                 536         179     P       R
      No      No      1023    2388    43
PAPA 1857  #REF!           chr3    178952074PIK3CA G
                  T                                 3129        1043    M       I
      No      No      1125    2292    49
PAPA 1858  #REF!           chr10   89692803 PTEN   C
                  T                                 287         96      P       L
      No      No      18      53      34
PAPA 1858  #REF!           chr10   89692929 PTEN   A
                  G                                 413         138     Y       C
      No      No      581     2659    22
PAPA 1858  #REF!           chr3    178952085PIK3CA A
                  T                                 3140        1047    H       L
```

Table16.txt

	No	No	550	1390	40							
PAPA	1859	#REF!		chr10	123258034	FGFR2	A					
			T					1647	549	N	K	
	No	No	424	542	78							
PAPA	1859	#REF!		chr10	89720737	PTEN	T					
			A					888	296	C	*	
	No	No	111	156	71							
PAPA	1859	#REF!		chr17	7577538	TP53	C					
			T					743	248	R	Q	
	No	No	71	587	12							
PAPA	1859	#REF!		chr3	178916876	PIK3CA	G					
			A					263	88	R	Q	
	No	No	50	97	52							
PAPA	1860	#REF!		chr10	89692905	PTEN	G					
			A					389	130	R	Q	
	No	No	1785	12774	14							
PAPA	1860	#REF!		chr3	41266113	CTNNB1	C					
			T					110	37	S	F	
	No	No	439	2901	15							
PAPA	1861	#REF!		chr10	89720875	PTEN	GGTCAGTTAAA (SEQ ID NO:804)					
								1026	342	K		
NULL	No	Yes	4	9	44							
PAPA	1862	#REF!		chr10	89720845	PTEN						
			A					996	332	K		
NULL	No	No	30	2146	1							
PAPA	1864	#REF!		chr17	7574018	TP53	G					
			A					1009	337	R	C	
	No	No	682	823	83							
PAPA	1865	#REF!		chr10	89692935	PTEN	T					
			G					419	140	L	*	
	No	No	1163	4946	24							
PAPA	1865	#REF!		chr17	7577120	TP53	C					
			T					818	273	R	H	
	No	No	1002	1410	71							
PAPA	1865	#REF!		chr5	67589590	PIK3R1	ATA					
								1353	451	E		
NULL	No	No	359	921	39							
PAPA	1867	#REF!		chr12	25398284	KRAS	C					
			A					35	12	G	V	
	No	No	2239	5424	41							

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

Table17.txt

Table 17. Mutations identified in the plasma of ovarian cancer patients.

Patient ID	Sample Type	Chrom	WT Position*	Mutant MutType	WT Exon Base	MT Base	Mutation in # SM	# UIDs	% MAF
Gene	Nucleotide	Codon	Codon	Codon	end		Primary Tumor		
PAP 184	Ovarian	chr3	41266113	SBS	C	T	56	25208	0.22
CTNNB1	110	37	S	F	No		Present		
PAP 184	Ovarian	chr3	178952085	SBS	A	G	126	36828	0.34
PIK3CA	3140	1047	H	R	No		Present		
PAP 186	Ovarian	chr17	7579589	Indel	G		342	8297	4.12
TP53	98	33	S	NULL	No		Present		
PAP 193	Ovarian	chr20	57484421	SBS	G	A	30	17222	0.17
GNAS	602	201	R	H	No		Insufficient sequence coverage at mutated position		
PAP 196	Ovarian	chr17	7578290	SBS	C	A	1478	13739	10.76
TP53	0	0	NULL	NULL	No		Present		
PAP 197	Ovarian	chr17	7578190	SBS	T	C	3113	27587	11.28
TP53	659	220	Y	C	No		Present		
PAP 198	Ovarian	chr17	7574027	Indel		C	1049	20825	5.04
TP53	1000	334	G	NULL	No		Present		
PAP 199	Ovarian	chr17	7578265	SBS	A	G	381	28760	1.32
TP53	584	195	I	T	No		Present		
PAP 210	Ovarian	chr12	25398284	SBS	C	A	48	20549	0.23
KRAS	35	12	G	V	No		Present		
PAP 250	Ovarian	chr17	7577022	SBS	G	A	19	28710	0.07
TP53	916	306	R	*	No		Present		
PAP 251	Ovarian	chr17	7577556	SBS	C	T	261	53994	0.48
TP53	725	242	C	Y	No		Present		
PAP 255	Ovarian	chr17	7577102	SBS	C	T	3381	53914	6.27
TP53	836	279	G	E	No		Present		
PAP 255	Ovarian	chr17	7579313	SBS	G	A	4	44170	0.01
TP53	374	125	T	M	No		Not present		
PAP 255	Ovarian	chr17	7578406	SBS	C	T	12	40047	0.03
TP53	524	175	R	H	No		Not present		
PAP 261	Ovarian	chr17	7578530	SBS	A	G	5574	17965	31.03
TP53	400	134	F	L	No		Present		
PAP 262	Ovarian	chr17	7574004	Indel	G		18	2693	0.67
TP53	1023	341	F	NULL	No		Present		
PAP 642	Ovarian	chr3	178936082	SBS	G	A	402	11738	3.42
PIK3CA	1624	542	E	K	No		Present		
PAP 642	Ovarian	chr19	52715982	SBS	C	T	66	2713	2.43
PPP2R1A	547	183	R	W	No		Present		
PAP 643	Ovarian	chr17	7578212	SBS	G	A	39	740	5.27
TP53	637	213	R	*	No		Present		
PAP 644	Ovarian	chr17	7578442	SBS	T	C	23	6577	0.35
TP53	488	163	Y	C	No		Not present		
PAP 645	Ovarian	chr12	25398285	SBS	C	T	412	12252	3.36
KRAS	34	12	G	S	No		Present		

Table17.txt

PAP 707	Ovarian	chr17	7578271	SBS	T	C	57	1580	
3.61	TP53	578	193	H	R	No	Present		
PAP 711	Ovarian	chr17	7578429	Indel	C		11	515	
2.14	TP53	501	167	Q	NULL	No	Present		
PAPA 1037	Ovarian	chr17	7577117	SBS	A	C	193	5079	
3.80	TP53	821	274	V	G	No	Present		
PAPA 1096	Ovarian	chr17	7577595	Indel	CA		31	1417	
2.19	TP53	686	229	C	NULL	No	Present		
PAPA 1113	Ovarian	chr3	178952088	SBS	A	G	17	4948	
0.34	PIK3CA	3143	1048	H	R	No	Not present		
PAPA 1115	Ovarian	chr17	7578263	SBS	G	A	324	4708	
6.88	TP53	586	196	R	*	No	Present		
PAPA 1117	Ovarian	chr17	7574003	SBS	G	A	1385	7203	
19.23	TP53	1024	342	R	*	No	Present		
PAPA 1122	Ovarian	chr3	178936094	SBS	C	A	88	24147	
0.36	PIK3CA	1636	546	Q	K	No	Present		
PAPA 1213	Ovarian	chr17	7577090	SBS	C	G	54	13066	
0.41	TP53	848	283	R	P	No	Present		
PAPA 1237	Ovarian	chr17	7578177	SBS	C	T	21	1248	
1.68	TP53	672	224	E	E	Yes	Insufficient		
neoplastic cell content									
PAPA 1240	Ovarian	chr17	7577124	SBS	C	A	19	12092	
0.16	TP53	814	272	V	L	No	Present		
PAPA 1292	Ovarian	chr17	7577536	SBS	T	C	1759	19535	
9.00	TP53	745	249	R	G	No	Not present		
PAPA 1297	Ovarian	chr17	7577556	SBS	C	G	815	8502	
9.59	TP53	725	242	C	S	No	Present		
PAPA 1298	Ovarian	chr3	178936092	SBS	A	G	10787	45561	
23.68	PIK3CA	1634	545	E	G	No	Not present		
PAPA 1298	Ovarian	chr17	7578406	SBS	C	T	64	72229	
0.09	TP53	524	175	R	H	No	Not present		
PAPA 1320	Ovarian	chr3	178936094	SBS	C	A	163	51374	
0.32	PIK3CA	1636	546	Q	K	No	Insufficient		
neoplastic cell content									
PAPA 1320	Ovarian	chr17	7578212	SBS	G	A	44	20478	
0.21	TP53	637	213	R	*	No	Insufficient		
neoplastic cell content									
PAPA 1321	Ovarian	chr17	7579414	SBS	C	T	49	32568	
0.15	TP53	273	91	W	*	No	Present		
PAPA 1322	Ovarian	chr17	7578403	SBS	C	T	188	34709	
0.54	TP53	527	176	C	Y	No	Not present		
PAPA 1322	Ovarian	chr17	7578271	SBS	T	C	56	13864	
0.40	TP53	578	193	H	R	No	Present		
PAPA 1326	Ovarian	chr5	112175639	SBS	C	T	342	40062	
0.85	APC	4348	1450	R	*	No	Present		
PAPA 1327	Ovarian	chr3	178916854	SBS	G	A	243	59582	
0.41	PIK3CA	241	81	E	K	No	Present		
PAPA 1327	Ovarian	chr10	89692905	SBS	G	A	191	39079	

Table17.txt

0.49 PTEN 389 130 R Q No Present
PAPA 1327 Ovarian chr17 7579528 SBS C T 82 9384
0.87 TP53 159 53 W * No Present
*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

Table18.txt

Table 18. Demographic and clinical features of the BC Early Detection Cohort

BV #	Source	Sex	Age	Clinical Indication	Cytology Diagnosis	Tumor Diagnosis	Tumor Stage	Tumor Grade	Detected UroSEEK analysis and clinical detection	Detected Time between (months)
BLD 147	U JHH	M	57	Hematuria	1	INTCC	pT1	HG		6.91
BLD 152	U JHH	F	62	Hematuria	2	N/A	N/A	N/A		N/A
BLD 162	U JHH	M	54	Hematuria	0	N/A	N/A	N/A		N/A
BLD 163	U JHH	M	63	Hematuria	2	N/A	N/A	N/A		N/A
BLD 166	U JHH	M	65	Hematuria	0	N/A	N/A	N/A		N/A
BLD 169	U JHH	F	66	Other	0	N/A	N/A	N/A		N/A
BLD 172	U JHH	M	61	Hematuria	2	N/A	N/A	N/A		N/A
BLD 173	U JHH	F	61	Hematuria	0	N/A	N/A	N/A		N/A
BLD 178	U JHH	M	62	Other	0	N/A	N/A	N/A		N/A
BLD 180	U JHH	M	61	Hematuria	0	N/A	N/A	N/A		N/A
BLD 183	U JHH	F	51	Hematuria	0	N/A	N/A	N/A		N/A
BLD 184	U JHH	M	77	Other	0	N/A	N/A	N/A		N/A
BLD 186	U JHH	M	76	Hematuria	2	N/A	N/A	N/A		N/A
BLD 188	U JHH	M	42	Hematuria	2	N/A	N/A	N/A		N/A
BLD 200	U JHH	M	72	Hematuria	2	N/A	N/A	N/A		N/A
BLD 203	U JHH	F	41	Hematuria	2	N/A	N/A	N/A		N/A
BLD 206	U JHH	M	64	Hematuria	0	N/A	N/A	N/A		N/A
BLD 208	U JHH	F	35	Hematuria	0	N/A	N/A	N/A		1.16
BLD 224	U JHH	M	44	Hematuria	2	N/A	N/A	N/A		N/A
BLD 228	U JHH	F	24	Hematuria	0	N/A	N/A	N/A		N/A
BLD 229	U JHH	F	41	Hematuria	2	N/A	N/A	N/A		

Table18.txt

N/A								
BLD 230 U JHH	M	56	Hematuria	2	N/A	N/A	N/A	
N/A								
BLD 231 U JHH	M	51	Other	2	N/A	N/A	N/A	
N/A								
BLD 232 U JHH	M	31	Other	2	N/A	N/A	N/A	
N/A								
BLD 233 U JHH	F	65	LUTS	0	N/A	N/A	N/A	
N/A								
BLD 235 U JHH	M	67	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 236 U1JHH	M	53	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 237 U1JHH	M	44	Hematuria	1	INTCC	pT4	HG	
6.27								
BLD 241 U1JHH	M	57	Hematuria	2	N/A	N/A	N/A	
N/A								
BLD 243 U1JHH	F	80	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 244 U1JHH	M	69	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 250 U1JHH	M	28	Other	0	N/A	N/A	N/A	
N/A								
BLD 251 U1JHH	F	53	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 252 U1JHH	M	69	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 253 U1JHH	M	54	Hematuria	1	HGTCC	pTa	HG	
3.87								
BLD 261 U1JHH	M	63	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 263 U1JHH	M	67	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 264 U1JHH	M	78	Other	0	N/A	N/A	N/A	
N/A								
BLD 267 U1JHH	M	79	Other	0	N/A	N/A	N/A	
N/A								
BLD 268 U1JHH	M	78	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 271 U1JHH	M	52	Hematuria	2	N/A	N/A	N/A	
N/A								
BLD 273 U1JHH	M	66	Hematuria	2	N/A	N/A	N/A	
N/A								
BLD 274 U1JHH	M	81	Hematuria	0	N/A	N/A	N/A	
N/A								
BLD 277 U1JHH	N/A	N/A	Hematuria	1	N/A	N/A	N/A	
1.5								
BLD 278 U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A	

Table18.txt

N/A								
BLD 283	U1JHH	M	76	Hematuria	1	CIS	pTis	HG
9.77								
BLD 288	U1JHH	M	74	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 293	U1JHH	M	54	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 296	U1JHH	F	24	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 297	U1JHH	N/A	N/A	Hematuria	1	HGTCC	pTa	HG
0.2								
BLD 304	U1JHH	M	66	Hematuria	1	INTCC	pT3	HG
7.5								
BLD 308	U1JHH	F	63	Other	2	N/A	N/A	N/A
N/A								
BLD 315	U1JHH	F	34	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 316	U1JHH	M	84	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 319	U1JHH	M	63	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 333	U1JHH	F	72	Hematuria	1	INTCC	pT2	HG
2								
BLD 336	U1JHH	F	61	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 337	U1JHH	M	70	Other	0	N/A	N/A	N/A
N/A								
BLD 342	U1JHH	M	25	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 343	U1JHH	M	56	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 344	U1JHH	F	18	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 346	U1JHH	F	61	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 357	U1JHH	M	76	Other	2	N/A	N/A	N/A
N/A								
BLD 359	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 362	U1JHH	M	65	Hematuria	1	INTCC	pT1	HG
0.63								
BLD 363	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 364	U1JHH	F	77	LUTS	0	N/A	N/A	N/A
N/A								
BLD 366	U1JHH	M	54	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 368	U1JHH	M	72	Hematuria	0	N/A	N/A	N/A

Table18.txt

N/A								
BLD 370	U1JHH	M	69	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 371	U1JHH	M	38	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 373	U1JHH	M	67	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 375	U1JHH	M	63	Other	0	N/A	N/A	N/A
N/A								
BLD 376	U1JHH	M	42	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 377	U1JHH	M	69	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 389	U1JHH	F	55	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 392	U1JHH	F	52	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 394	U1JHH	M	68	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 395	U1JHH	M	54	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 396	U1JHH	M	74	hematuria	0	N/A	N/A	N/A
N/A								
BLD 398	U1JHH	M	71	LUTS	0	N/A	N/A	N/A
N/A								
BLD 400	U1JHH	M	60	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 402	U1JHH	M	65	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 403	U1JHH	M	71	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 406	U1JHH	M	61	Hematuria	1	CIS	pTis	HG
4.27								
BLD 411	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 412	U1JHH	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 414	U1JHH	F	65	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 416	U1JHH	M	63	Other	0	N/A	N/A	N/A
N/A								
BLD 417	U1JHH	F	68	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 418	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 421	U1JHH	F	28	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 423	U1JHH	F	69	Other	2	N/A	N/A	N/A

Table18.txt

N/A								
BLD 426	U1JHH	M	35	Other	0	N/A	N/A	N/A
N/A								
BLD 427	U1JHH	M	64	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 428	U1JHH	F	89	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 429	U1JHH	M	77	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 430	U1JHH	F	44	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 432	U1JHH	F	50	Other	0	N/A	N/A	N/A
N/A								
BLD 436	U1JHH	M	80	Other	2	INTCC	pT1	HG
2.53								
BLD 437	U1JHH	M	53	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 443	U1JHH	M	63	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 452	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 458	U1JHH	F	5	Hematuria	2	HGTCC	pTa	HG
18.17								
BLD 459	U1JHH	F	60	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 465	U1JHH	M	57	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 468	U1JHH	M	48	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 474	U1JHH	M	47	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 477	U1JHH	M	58	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 481	U1JHH	F	20	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 486	U1JHH	M	58	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 488	U1JHH	F	45	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 491	U1JHH	F	59	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 494	U1JHH	M	73	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 496	U1JHH	F	59	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 499	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 503	U1JHH	M	71	Hematuria	0	N/A	N/A	N/A

Table18.txt

N/A								
BLD 505	U1JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 506	U1JHH	M	40	Hematuria	2	LGTCC	pTa	LG
0.53								
BLD 511	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 515	U1JHH	M	46	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 516	U1JHH	M	80	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 523	U1JHH	M	88	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 524	U1JHH	M	82	Other	N/A	N/A	N/A	N/A
N/A								
BLD 532	U1JHH	M	53	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 533	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.07								
BLD 534	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.03								
BLD 535	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLD 536	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0								
BLD 537	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.1								
BLD 538	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG
3.33								
BLD 539	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.03								
BLD 540	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLD 541	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLD 542	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLD 543	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.03								
BLD 544	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.1								
BLD 545	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.23								
BLD 546	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0								
BLD 547	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.13								
BLD 548	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG

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0.13								
BLD 549	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.03								
BLD 550	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.03								
BLD 551	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.13								
BLD 552	U1Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.13								
BLD 553	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.2								
BLD 554	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLD 555	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.03								
BLD 556	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.13								
BLD 557	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.1								
BLD 558	U1Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.13								
BLD 559	U1Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0								
BLD 597	U1JHH	M	69	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 600	U1JHH	M	76	LUTS	2	N/A	N/A	N/A
N/A								
BLD 601	U1JHH	M	54	Other	0	LGTCC	pTa	LG
0.43								
BLD 605	U1JHH	M	69	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 606	U1JHH	N/A	N/A	Hematuria	0	HGTCC	pTa	HG
2.9								
BLD 611	U1JHH	M	66	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 613	U1JHH	F	73	Other	0	N/A	N/A	N/A
N/A								
BLD 615	U1JHH	F	62	Other	2	N/A	N/A	N/A
N/A								
BLD 617	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 618	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 619	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 620	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 621	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A

Table18.txt

N/A								
BLD 622	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 623	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 624	U1Turkey	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
13								
BLD 625	U1Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
12.97								
BLD 626	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 627	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 628	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 629	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 630	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 631	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 632	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 633	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 634	U1Turkey	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
12.43								
BLD 635	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 636	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 637	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 638	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 639	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 640	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 641	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 642	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 643	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 644	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 645	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A

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N/A								
BLD 646	U1Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
12.04								
BLD 647	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 648	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 649	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 650	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 651	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 652	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 655	U1JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 656	U1JHH	M	34	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 657	U1JHH	M	57	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 658	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 659	U1JHH	F	46	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 661	U1JHH	M	62	LUTS	2	N/A	N/A	N/A
N/A								
BLD 664	U1JHH	F	38	Other	0	N/A	N/A	N/A
N/A								
BLD 667	U1JHH	F	62	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 671	U1JHH	M	76	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 673	U1JHH	F	73	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 675	U1JHH	F	46	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 676	U1JHH	F	50	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 677	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 679	U1JHH	M	62	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 680	U1JHH	M	58	Other	0	N/A	N/A	N/A
N/A								
BLD 693	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 695	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A

Table18.txt

	N/A							
BLD 699	U1JHH	M	64	LUTS	0	N/A	N/A	N/A
	N/A							
BLD 707	U1JHH	M	40	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 708	U1JHH	M	63	LUTS	2	N/A	N/A	N/A
	N/A							
BLD 711	U1JHH	M	67	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 718	U1JHH	M	55	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 720	U1JHH	M	60	LUTS	0	N/A	N/A	N/A
	N/A							
BLD 721	U1JHH	F	68	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 727	U1JHH	M	55	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 732	U1JHH	F	21	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 734	U1JHH	F	43	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 742	U1JHH	F	78	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 745	U1JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 746	U1JHH	F	71	Hematuria	2	INTCC	pT1	HG
	0.73							
BLD 751	U1JHH	M	75	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 752	U1JHH	M	73	Other	0	N/A	N/A	N/A
	N/A							
BLD 754	U1JHH	F	44	Hematuria	0	PUNLMP	pTa	N/A
	0.9							
BLD 756	U1JHH	M	66	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 765	U1JHH	N/A	N/A	LUTS	0	N/A	N/A	N/A
	N/A							
BLD 767	U1JHH	M	43	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 769	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 772	U1JHH	M	58	hematuria	2	N/A	N/A	N/A
	N/A							
BLD 774	U1JHH	M	49	Hematuria	0	N/A	N/A	N/A
	N/A							
BLD 782	U1JHH	M	34	Hematuria	2	N/A	N/A	N/A
	N/A							
BLD 783	U1JHH	M	71	Hematuria	0	N/A	N/A	N/A

Table18.txt

N/A								
BLD 784	U1JHH	F	28	hematuria	2	N/A	N/A	N/A
N/A								
BLD 786	U1JHH	M	55	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 787	U1JHH	F	44	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 789	U1JHH	M	43	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 790	U1JHH	M	63	Other	2	HGTCC	pTa	HG
1.13								
BLD 792	U1JHH	M	64	LUTS	0	N/A	N/A	N/A
N/A								
BLD 793	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 794	U1JHH	N/A	N/A	hematuria	2	N/A	N/A	N/A
N/A								
BLD 796	U1JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 799	U1JHH	M	79	Hematuria	2	N/A	N/A	N/A
N/A								
BLD 805	U1JHH	M	53	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 825	U1JHH	F	38	Hematuria	0	N/A	N/A	N/A
N/A								
BLD 831	U1JHH	M	71	Hematuria	1	N/A	N/A	N/A
0								
BLD 832	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 833	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 834	U1Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
12.00								
BLD 835	U1Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG
10.37								
BLD 836	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 837	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 838	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 839	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
9.2								
BLD 840	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLD 841	U1Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
9.07								
BLD 842	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A

Table18.txt

	N/A							
BLD 843	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 844	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 845	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	9							
BLD 846	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 847	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 848	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 849	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 850	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 851	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 853	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 854	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 855	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 856	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 857	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 858	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 859	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	8.47							
BLD 860	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 861	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	0.07							
BLD 862	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 863	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 864	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 865	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	N/A							
BLD 866	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
	8.07							
BLD 867	U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A

Table18.txt

N/A							
BLD 868 U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
8							
BLD 869 U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLD 870 U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLD 871 U1Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLD 981 U1Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1005 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1007 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1051 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1063 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1081 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1094 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1095 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1102 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1108 Brazil	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1120 JHH	M	78	hematuria	2	HGTCC	pTa	HG
0.9							
BLDA 1121 JHH	N/A	N/A	LUTS	0	N/A	N/A	N/A
N/A							
BLDA 1123 JHH	M	69	Hematuria	0	N/A	N/A	N/A
N/A							
BLDA 1125 JHH	F	38	Hematuria	0	N/A	N/A	N/A
N/A							
BLDA 1126 JHH	M	46	Hematuria	0	N/A	N/A	N/A
N/A							
BLDA 1127 JHH	M	80	Hematuria	0	N/A	N/A	N/A
N/A							
BLDA 1128 JHH	M	48	Hematuria	N/A	N/A	N/A	N/A
N/A							
BLDA 1133 JHH	F	78	Other	2	N/A	N/A	N/A
N/A							
BLDA 1137 JHH	F	61	LUTS	2	CIS	pTis	HG
6.63							
BLDA 1138 JHH	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A

Table18.txt

N/A								
BLDA 1143 JHH	F	61	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1145 JHH	M	61	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1149 JHH	M	56	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1153 JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1156 JHH	M	41	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1158 JHH	M	39	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1159 JHH	M	52	Other	0	N/A	N/A	N/A	
N/A								
BLDA 1161 JHH	M	61	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1164 JHH	M	76	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1173 JHH	M	60	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1174 JHH	F	48	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1183 JHH	M	83	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1185 JHH	F	42	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1186 JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1195 JHH	F	33	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1199 JHH	F	47	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1200 JHH	F	21	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1204 JHH	F	61	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1206 JHH	M	65	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1208 JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1209 JHH	M	62	Hematuria	0	N/A	N/A	N/A	
N/A								
BLDA 1212 JHH	F	84	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1213 JHH	M	32	Hematuria	2	N/A	N/A	N/A	
N/A								
BLDA 1214 JHH	M	57	Hematuria	2	N/A	N/A	N/A	

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N/A								
BLDA 1215	JHH	M	56	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1220	JHH	M	57	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1222	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1228	JHH	M	58	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1229	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1230	JHH	F	75	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1231	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1234	JHH	M	51	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1235	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1246	JHH	F	54	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1248	JHH	F	22	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1257	JHH	M	59	Hematuria	2	INTCC	pT1	HG
1.43								
BLDA 1259	JHH	M	56	Other	2	N/A	N/A	N/A
N/A								
BLDA 1262	JHH	M	62	Other	0	N/A	N/A	N/A
N/A								
BLDA 1264	JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1265	JHH	F	62	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1267	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1268	JHH	F	49	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1271	JHH	F	60	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1272	JHH	M	70	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1274	JHH	M	52	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1276	JHH	M	63	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1277	JHH	M	57	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1282	JHH	M	37	Hematuria	0	N/A	N/A	N/A

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N/A								
BLDA 1288	JHH	M	35	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1295	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1297	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1298	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1300	JHH	M	60	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1301	JHH	F	58	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1303	JHH	M	78	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1305	JHH	M	55	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1315	JHH	F	15	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1318	JHH	M	12	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1320	JHH	F	64	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1323	JHH	M	63	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1325	JHH	M	67	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1326	JHH	M	51	Hematuria	0	CIS	pTis	HG
1.4								
BLDA 1329	JHH	M	74	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1331	JHH	M	52	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1336	JHH	M	62	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1338	JHH	M	63	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1339	JHH	M	75	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1340	JHH	M	73	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1344	JHH	F	38	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1345	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1346	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1348	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A

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N/A								
BLDA 1353	JHH	M	89	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1357	JHH	F	54	Hematuria	0	LGTCC	pTa	LG
1.03								
BLDA 1358	JHH	M	73	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1361	JHH	M	71	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1365	JHH	F	35	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1366	JHH	F	53	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1368	JHH	M	67	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1374	JHH	M	50	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1377	JHH	F	34	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1380	JHH	M	84	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1384	JHH	M	52	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1385	JHH	M	64	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1390	JHH	M	62	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1391	JHH	M	55	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1394	JHH	M	77	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1396	JHH	F	46	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1398	JHH	M	62	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1402	JHH	M	53	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1403	JHH	M	69	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1404	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1405	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1406	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1408	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1410	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A

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N/A								
BLDA 1411	JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1412	JHH	M	59	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1413	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1414	JHH	M	37	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1438	JHH	F	24	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1439	JHH	F	36	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1443	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1450	JHH	M	44	Other	0	N/A	N/A	N/A
N/A								
BLDA 1451	JHH	F	40	Other	0	N/A	N/A	N/A
N/A								
BLDA 1462	JHH	F	53	Other	2	N/A	N/A	N/A
N/A								
BLDA 1470	JHH	M	50	Other	0	N/A	N/A	N/A
N/A								
BLDA 1473	JHH	M	54	Other	0	N/A	N/A	N/A
N/A								
BLDA 1474	JHH	F	30	Other	2	N/A	N/A	N/A
N/A								
BLDA 1475	JHH	F	51	Other	2	N/A	N/A	N/A
N/A								
BLDA 1484	JHH	F	63	Other	0	N/A	N/A	N/A
N/A								
BLDA 1486	JHH	N/A	N/A	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1489	JHH	N/A	N/A	Other	2	N/A	N/A	N/A
N/A								
BLDA 1490	JHH	N/A	N/A	Other	0	N/A	N/A	N/A
N/A								
BLDA 1491	JHH	N/A	N/A	Other	0	N/A	N/A	N/A
N/A								
BLDA 1789	Japan	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 1790	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 1791	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0								
BLDA 1792	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.1								
BLDA 1793	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG

Table18.txt

	0.13								
BLDA 1794	Japan	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A	
	N/A								
BLDA 1795	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG	
	0.03								
BLDA 1796	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.13								
BLDA 1797	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG	
	2.7								
BLDA 1798	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.07								
BLDA 1799	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.17								
BLDA 1800	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0								
BLDA 1801	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG	
	0.03								
BLDA 1802	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG	
	0.03								
BLDA 1803	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.13								
BLDA 1804	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG	
	0								
BLDA 1805	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.03								
BLDA 1806	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0								
BLDA 1807	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0								
BLDA 1808	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG	
	0								
BLDA 1809	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.03								
BLDA 1810	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0								
BLDA 1811	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG	
	0.03								
BLDA 1812	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.07								
BLDA 1813	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.1								
BLDA 1814	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.07								
BLDA 1815	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0								
BLDA 1816	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	
	0.03								
BLDA 1817	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG	

Table18.txt

0								
BLDA 1818	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 1819	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 1820	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 1821	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0								
BLDA 1822	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
1.53								
BLDA 1833	JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1841	JHH	M	42	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1843	JHH	F	50	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1844	JHH	M	76	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1853	JHH	M	48	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1855	JHH	M	77	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1857	JHH	M	47	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1866	JHH	M	62	Hematuria	2	INTCC	pT2	HG
12.6								
BLDA 1872	JHH	F	46	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1877	JHH	M	63	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1879	JHH	M	73	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1892	JHH	F	61	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1899	JHH	N/A	N/A	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1903	JHH	M	64	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1904	JHH	F	54	Hematuria	0	N/A	N/A	N/A
N/A								
BLDA 1909	JHH	M	56	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1910	JHH	M	69	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 1915	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 1924	Turkey	N/A	N/A	Hematuria	N/A	PUNLMP	pTa	N/A

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7.8								
BLDA 1925	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
10.83								
BLDA 1926	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
7.33								
BLDA 1928	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
10.8								
BLDA 1934	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
10								
BLDA 1935	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
10								
BLDA 1938	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
10.8								
BLDA 1940	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 1943	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
9.47								
BLDA 1944	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
9.4								
BLDA 1945	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
9								
BLDA 1970	JHH	M	73	Other	2	N/A	N/A	N/A
N/A								
BLDA 1983	JHH	M	52	Other	2	HGTCC	pTa	HG
7.1								
BLDA 2012	JHH	M	47	LUTS	2	N/A	N/A	N/A
0								
BLDA 2146	JHH	M	82	Hematuria	2	HGTCC	pTa	HG
10.43								
BLDA 2158	JHH	N/A	N/A	Hematuria	1	INTCC	pT1	HG
0.73								
BLDA 2182	JHH	N/A	N/A	hematuria	2	LGTCC	pTa	LG
1								
BLDA 2194	JHH	M	61	Hematuria	1	INTCC	pT1	HG
0.27								
BLDA 2263	JHH	M	62	Other	2	HGTCC	pTa	HG
1.53								
BLDA 2281	JHH	M	70	Hematuria	2	INTCC	pT1	HG
1.03								
BLDA 2289	JHH	M	60	Hematuria	2	N/A	N/A	N/A
N/A								
BLDA 2443	JHH	M	83	Other	1	INTCC	pT1	HG
1.73								
BLDA 2476	JHH	F	49	Hematuria	2	LGTCC	pTa	LG
1.97								
BLDA 2489	JHH	M	54	Hematuria	1	N/A	N/A	N/A
0								
BLDA 2569	JHH	N/A	N/A	Other	2	CIS	pTis	HG

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1.67								
BLDA 2614	JHH	M	68	Hematuria	1	INTCC	pT1	HG
1.33								
BLDA 2647	JHH	M	71	Other	1	INTCC	pT1	HG
1.23								
BLDA 2671	JHH	M	75	Other	2	N/A	N/A	N/A
0								
BLDA 2719	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLDA 2720	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 2721	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.13								
BLDA 2722	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG
19.03								
BLDA 2723	Japan	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 2724	Japan	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 2725	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0.1								
BLDA 2726	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.13								
BLDA 2727	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.1								
BLDA 2728	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG
0.13								
BLDA 2729	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0								
BLDA 2730	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0								
BLDA 2731	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 2732	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.13								
BLDA 2733	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.03								
BLDA 2734	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.03								
BLDA 2735	Japan	N/A	N/A	Hematuria	N/A	CIS	pTis	HG
0								
BLDA 2737	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLDA 2738	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.07								
BLDA 2739	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLDA 2740	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG

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0.13								
BLDA 2741	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT3	HG
0.03								
BLDA 2742	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0								
BLDA 2743	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.1								
BLDA 2744	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLDA 2745	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.13								
BLDA 2746	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.13								
BLDA 2747	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT2	HG
0.1								
BLDA 2748	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.03								
BLDA 2749	Japan	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG
0.07								
BLDA 2750	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.03								
BLDA 2751	Japan	N/A	N/A	Hematuria	N/A	HGTCC	pTa	HG
0.03								
BLDA 2752	Japan	N/A	N/A	Hematuria	N/A	LGTCC	pTa	LG
0								
BLDA 2766	JHH	M	54	hematuria	1	HGTCC	pTa	HG
0.93								
BLDA 2781	JHH	M	32	LUTS	1	N/A	N/A	N/A
0.73								
BLDA 2787	JHH	M	81	Hematuria	2	INTCC	pT2	HG
1.2								
BLDA 2793	JHH	M	56	Hematuria	1	HGTCC	pTa	HG
0.53								
BLDA 2824	JHH	M	72	Hematuria	0	N/A	N/A	N/A
0.03								
BLDA 2867	JHH	F	57	Hematuria	2	INTCC	pT4	HG
3.57								
BLDA 2901	JHH	N/A	N/A	Hematuria	1	CIS	pTis	HG
1.2								
BLDA 3208	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
7.2								
BLDA 3209	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 3210	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 3211	Turkey	N/A	N/A	Hematuria	N/A	N/A	N/A	N/A
N/A								
BLDA 3212	Turkey	N/A	N/A	Hematuria	N/A	INTCC	pT1	HG

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3.03
BLDA 3213 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3214 Turkey N/A N/A Hematuria N/A HGTCC pTa HG
0.8
BLDA 3215 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3216 Turkey N/A N/A Hematuria N/A LGTCC pTa LG
0.53
BLDA 3217 Turkey N/A N/A Hematuria N/A INTCC pT1 HG
0.2
BLDA 3218 Turkey N/A N/A Hematuria N/A LGTCC pTa LG
0.9
BLDA 3220 Turkey N/A N/A Hematuria N/A LGTCC pTa LG
0.63
BLDA 3221 Turkey N/A N/A Hematuria N/A INTCC pT1 HG
0.47
BLDA 3222 Turkey N/A N/A Hematuria N/A INTCC pT1 HG
0
BLDA 3223 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3224 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3225 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3226 Turkey N/A N/A Hematuria N/A INTCC pT1 HG
0.07
BLDA 3227 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3228 Turkey N/A N/A Hematuria N/A LGTCC pTa LG
0.67
BLDA 3230 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3231 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3235 Turkey N/A N/A Hematuria N/A LGTCC pTa LG
1.1
BLDA 3237 Turkey N/A N/A Hematuria N/A N/A N/A N/A
0.43
BLDA 3239 Turkey N/A N/A Hematuria N/A N/A N/A N/A
N/A
BLDA 3242 Turkey N/A N/A Hematuria N/A INTCC pT1 HG
0
N/A Not Available
Cytology Diagnosis:
0 Negative
2 Atypical
1 Positive

Table19.txt

Table 19. Mutations detected by the 10-gene Multiplex Assay in urine samples from the Early Detection cohort.

Urine Sample	Patient	PT Sample	Gene	Chr	Reference hg19 Position	Variant base	Codon	Reference amino acid	Variant amino acid	Mutant allele frequency	# unique templates	Found in the matched primary tumor
BLD 147 U	BLD 147	BLD 147 PT	TP53	chr17	7574003	G	A	342	R	*	79.13%	6108	Yes
BLD 237 U1	BLD 237	BLD 237 PT	TP53	chr17	7577121	G	A	273	R	C	7.61%	13834	Yes
BLD 253 U1	BLD 253	BLD 253 PT	ERBB2	chr17	37868208	C	T	310	S	F	46.87%	11015	Yes
BLD 253 U1	BLD 253	BLD 253 PT	PIK3CA	chr3	178936082	G	A	542	E	K	38.85%	7415	Yes
BLD 283 U1	BLD 283	BLDA 3024 PT1	TP53	chr17	7577571	ATGTAGTTGTAGTG (SEQ ID NO:725)	NULL	237	M	NULL	2.09%	52881	Yes
BLD 297 U1	BLD 297	NULL	CDKN2A	chr9	21971036	C	G	108	D	H	6.49%	10367	NULL
BLD 297 U1	BLD 297	NULL	TP53	chr17	7578253	C	A	199	G	V	11.55%	16116	NULL
BLD 333 U1	BLD 333	BLD 333 PT	TP53	chr17	7574012	C	A	339	E	*	83.62%	15991	No
BLD 359 U1	BLD 359	NULL	FGFR3	chr4	1803568	C	G	249	S	C	9.42%	6930	NULL
BLD 362 U1	BLD 362	BLD 362 PT	TP53	chr17	7577085	C	T	285	E	K	73.66%	12529	No
BLD 362 U1	BLD 362	BLD 362 PT	TP53	chr17	7577506	C	G	259	D	H	23.56%	5744	No
BLD 406 U1	BLD 406	BLD 406 PT	ERBB2	chr17	37868208	C	A	310	S	Y	0.49%	42219	No
BLD 406 U1	BLD 406	BLD 406 PT	ERBB2	chr17	37868208	C							

Table19.txt

			T	310	S	F	1.40%	42219	No		
BLD 423 U1	BLD 423	NULL		KRAS	chr12	25398284	C				
			T	12	G	D	1.24%	7796	NULL		
BLD 436 U1	BLD 436	BLD 436 PT		TP53	chr17	7577559	G				
			A	241	S	F	2.25%	44299	Yes		
BLD 506 U1	BLD 506	BLDA 3041 PT1PIK3CA			chr3	178936091	G				
			A	545	E	K	29.85%	6852	Yes		
BLD 506 U1	BLD 506	BLDA 3041 PT1FGFR3			chr4	1803568	C				
			G	249	S	C	34.35%	9633	Yes		
BLD 515 U1	BLD 515	NULL		TP53	chr17	7577559	G				
			T	241	S	Y	1.20%	18219	NULL		
BLD 533 U1	BLD 533	NULL		TP53	chr17	7578437	G				
			A	165	Q	*	16.57%	17360	NULL		
BLD 535 U1	BLD 535	BLDA 2902 PT1TP53			chr17	7578513	C				
			A	139	K	N	57.23%	15052	Yes		
BLD 535 U1	BLD 535	BLDA 2902 PT1KRAS			chr12	25398284	C				
			T	12	G	D	46.06%	14356	Yes		
BLD 537 U1	BLD 537	BLDA 2920 PT1TP53			chr17	7578190	T				
			C	220	Y	C	3.28%	13996	Yes		
BLD 538 U1	BLD 538	NULL		PIK3CA	chr3	178936091	G				
			A	545	E	K	0.59%	17532	NULL		
BLD 539 U1	BLD 539	BLDA 2906 PT1TP53			chr17	7578382	G				
			C	183	S	*	16.87%	14342	Yes		
BLD 539 U1	BLD 539	BLDA 2906 PT1VHL			chr3	10183565	G				
			A	12	E	K	7.46%	29957	Yes		
BLD 539 U1	BLD 539	BLDA 2906 PT1TP53			chr17	7579340	G				
			C	116	S	C	16.54%	19364	Yes		
BLD 540 U1	BLD 540	BLDA 2905 PT1TP53			chr17	7574021	C				
			A	336	E	*	11.54%	23523	Yes		
BLD 542 U1	BLD 542	BLDA 2908 PT1KRAS			chr12	25398284	C				
			A	12	G	V	1.51%	10513	Yes		
BLD 542 U1	BLD 542	BLDA 2908 PT1PIK3CA			chr3	178936082	G				

Table19.txt

```
                                A       542     E       K       1.83%       16561
   Yes
BLD 544 U1    BLD 544       BLDA 2910 PT1PIK3CA  chr3    178936082  G
                                A       542     E       K       44.64%      6093
   Yes
BLD 544 U1    BLD 544       BLDA 2910 PT1FGFR3   chr4    1806099    A
                                G       373     Y       C       70.92%      9723
   Yes
BLD 544 U1    BLD 544       BLDA 2910 PT1CDKN2A  chr9    21971120   G
                                A       80      R       *       3.34%       1675
   No
BLD 545 U1    BLD 545       BLDA 2911 PT1FGFR3   chr4    1806099    A
                                G       373     Y       C       15.71%      13069
   Yes
BLD 546 U1    BLD 546       BLDA 2912 PT1HRAS    chr11   534285     C
                                A       13      G       V       11.69%      3532
   Yes
BLD 548 U1    BLD 548       NULL        PIK3CA   chr3    178936082  G
                                A       542     E       K       11.93%      13541
   NULL
BLD 548 U1    BLD 548       NULL        CDKN2A   chr9    21971120   G
                                A       80      R       *       13.69%      1030
   NULL
BLD 549 U1    BLD 549       BLDA 2914 PT1TP53    chr17   7577559    G
                                A       241     S       F       1.62%       45374
   Yes
BLD 553 U1    BLD 553       BLDA 2921 PT1FGFR3   chr4    1806099    A
                                G       373     Y       C       1.03%       7577
   Yes
BLD 554 U1    BLD 554       BLDA 2918 PT1TP53    chr17   7577543    C
                                G       246     M       I       39.15%      258
   Yes
BLD 554 U1    BLD 554       BLDA 2918 PT1TP53    chr17   7577506    C
                                T       259     D       N       39.15%      258
   Yes
BLD 555 U1    BLD 555       BLDA 2922 PT1HRAS    chr11   533874     T
                                A       61      Q       L       19.03%      49836
   Yes
BLD 556 U1    BLD 556       BLDA 2923 PT1TP53    chr17   7577596    A
                                G       229     C       R       47.15%      3758
   Yes
BLD 557 U1    BLD 557       BLDA 2924 PT1TP53    chr17   7579542    C
                                G       49      D       H       48.80%      17946
   No
BLD 559 U1    BLD 559       BLDA 2926 PT1TP53    chr17   7574018    G
                                A       337     R       C       3.29%       15672
   Yes
BLD 559 U1    BLD 559       BLDA 2926 PT1FGFR3   chr4    1803568    C
```

Table19.txt

```
                    G       249     S       C       2.87%       6071
   Yes
BLD 559 U1    BLD 559     BLDA 2926 PT1CDKN2A  chr9    21971036   C
                    G       108     D       H       2.30%       2651
   Yes
BLD 601 U1    BLD 601     BLD 601 PT1  PIK3CA  chr3    178936091  G
                    A       545     E       K       6.05%       26186
   Yes
BLD 606 U1    BLD 606     NULL         FGFR3   chr4    1803568    C
                    G       249     S       C       5.26%       9838
   NULL
BLD 646 U1    BLD 646     BLD 646 PT1  TP53    chr17   7574000    C
                    A       343     E       *       53.55%      19924
   No
BLD 711 U1    BLD 711     NULL         CDKN2A  chr9    21971186   G
                    A       58      R       *       4.16%       18369
   NULL
BLD 790 U1    BLD 790     BLDA 3025 PT1FGFR3   chr4    1803568    C
                    G       249     S       C       40.34%      17782
   Yes
BLD 834 U1    BLD 834     BLD 834 PT1  KRAS    chr12   25398284   C
                    A       12      G       V       1.15%       15889
   No
BLD 835 U1    BLD 835     BLD 835 PT1  TP53    chr17   7572968    T
                    NULL    381     K       NULL    3.94%       18795
   No
BLD 835 U1    BLD 835     BLD 835 PT1  TP53    chr17   7579362    A
                    C       109     F       V       0.37%       17449
   No
BLD 835 U1    BLD 835     BLD 835 PT1  CDKN2A  chr9    21971096   C
                    T       88      E       K       5.41%       9785
   No
BLD 835 U1    BLD 835     BLD 835 PT1  CDKN2A  chr9    21971108   C
                    A       84      D       Y       5.36%       9785
   No
BLD 835 U1    BLD 835     BLD 835 PT1  CDKN2A  chr9    21971132   NULL
                    C       76      A       NULL    3.14%       15721
   No
BLD 835 U1    BLD 835     BLD 835 PT1  TP53    chr17   7577130    A
                    G       270     F       L       1.06%       17089
   No
BLD 835 U1    BLD 835     BLD 835 PT1  TP53    chr17   7578275    G
                    A       192     Q       *       1.26%       16239
   No
BLD 835 U1    BLD 835     BLD 835 PT1  PIK3CA  chr3    178936091  G
                    A       545     E       K       2.18%       5634
   No
BLD 835 U1    BLD 835     BLD 835 PT1  FGFR3   chr4    1803568    C
```

Table19.txt

				G	249	S		C	0.48%	16623	
Yes											
BLD 841 U1	BLD 841	BLD 841 PT1	ERBB2	chr17	37868208	C					
				T	310	S		F	7.20%	8474	
No											
BLD 845 U1	BLD 845	NULL	PIK3CA	chr3	178952085	A					
				T	1047	H		L	25.64%	1962	
NULL											
BLD 845 U1	BLD 845	NULL	FGFR3	chr4	1806089	G					
				T	370	G		C	36.60%	2902	
NULL											
BLD 859 U1	BLD 859	BLD 859 PT1	TP53	chr17	7578524	G					
				A	136	Q		*	15.34%	14883	
Yes											
BLD 861 U1	BLD 861	NULL	FGFR3	chr4	1806099	A					
				G	373	Y		C	11.34%	16892	
NULL											
BLD 866 U1	BLD 866	BLD 866 PT1	TP53	chr17	7576876	C					
				T	324	D		N	1.27%	18827	
Yes											
BLD 866 U1	BLD 866	BLD 866 PT1	TP53	chr17	7576885	NULL					
				T	321	K		NULL	1.26%	18827	
Yes											
BLD 866 U1	BLD 866	BLD 866 PT1	TP53	chr17	7578205	C					
				T	215	S		N	0.36%	22479	
No											
BLD 866 U1	BLD 866	BLD 866 PT1	FGFR3	chr4	1803568	C					
				G	249	S		C	1.39%	18508	
Yes											
BLD 868 U1	BLD 868	NULL	KRAS	chr12	25398285	C					
				A	12	G		C	4.07%	15067	
NULL											
BLD 868 U1	BLD 868	NULL	TP53	chr17	7577117	A					
				NULL	274	V		NULL	1.36%	15275	
NULL											
BLDA 1120 U1	BLDA 1120	NULL	FGFR3	chr4	1806099	A					
				G	373	Y		C	24.61%	191	
NULL											
BLDA 1137 U1	BLDA 1137	BLDA 3059 PT1	TP53	chr17	7577120	C					
				T	273	R		H	5.00%	8475	
Yes											
BLDA 1212 U1	BLDA 1212	NULL	KRAS	chr12	25398284	C					
				T	12	G		D	1.16%	8592	
NULL											
BLDA 1257 U1	BLDA 1257	NULL	TP53	chr17	7577099	C					
				G	280	R		T	8.05%	13744	
NULL											
BLDA 1257 U1	BLDA 1257	NULL	ERBB2	chr17	37868208	C					

Table19.txt

T 310 S F 7.34% 13272
NULL
BLDA 1257 U1 BLDA 1257 NULL PIK3CA chr3 178936091 G
A 545 E K 0.59% 26080
NULL
BLDA 1792 U1 BLDA 1792 BLDA 2930 PT1TP53 chr17 7577565 T
C 239 N S 46.88% 19363
Yes
BLDA 1792 U1 BLDA 1792 BLDA 2930 PT1KRAS chr12 25398281 C
T 13 G D 47.64% 22096
Yes
BLDA 1792 U1 BLDA 1792 BLDA 2930 PT1TP53 chr17 7579556
ATCAAATCATCCATTGCTTG (SEQ ID NO: 726) NULL 44 M NULL
1.93% 16982 No
BLDA 1792 U1 BLDA 1792 BLDA 2930 PT1PIK3CA chr3 178936091 G
A 545 E K 92.81% 11723
Yes
BLDA 1796 U1 BLDA 1796 BLDA 2934 PT1FGFR3 chr4 1806099 A
G 373 Y C 35.56% 9481
Yes
BLDA 1797 U1 BLDA 1797 BLDA 2933 PT1PIK3CA chr3 178936082 G
A 542 E K 7.27% 17935
No
BLDA 1797 U1 BLDA 1797 BLDA 2933 PT1PIK3CA chr3 178936091 G
A 545 E K 5.84% 17935
No
BLDA 1797 U1 BLDA 1797 BLDA 2933 PT1FGFR3 chr4 1803568 C
G 249 S C 5.43% 4552
No
BLDA 1799 U1 BLDA 1799 NULL TP53 chr17 7577085 C
A 285 E * 2.81% 16825
NULL
BLDA 1799 U1 BLDA 1799 NULL TP53 chr17 7578463 C
G 156 R P 36.85% 13715
NULL
BLDA 1799 U1 BLDA 1799 NULL TP53 chr17 7573934 G
T 365 H N 1.66% 14204
NULL
BLDA 1800 U1 BLDA 1800 BLDA 2936 PT1TP53 chr17 7578437 G
A 165 Q * 5.72% 14014
Yes
BLDA 1801 U1 BLDA 1801 BLDA 2937 PT1TP53 chr17 7577099 C
G 280 R T 0.53% 15955
No
BLDA 1801 U1 BLDA 1801 BLDA 2937 PT1TP53 chr17 7574034 C
T 0 NULL NULL 0.62% 19270
No
BLDA 1801 U1 BLDA 1801 BLDA 2937 PT1PIK3CA chr3 178952085 A

Table19.txt

						G	1047	H	R	8.41%	26672				
Yes															
BLDA 1801 U1	BLDA 1801	BLDA 2937	PT1FGFR3	chr4	1803564	C									
						T	248	R	C	11.49%	4980				
Yes															
BLDA 1802 U1	BLDA 1802	BLDA 2938	PT1PIK3CA	chr3	178936091	G									
						C	545	E	Q	0.56%	28699				
Yes															
BLDA 1802 U1	BLDA 1802	BLDA 2938	PT1FGFR3	chr4	1806089	G									
						T	370	G	C	0.62%	8235				
Yes															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1KRAS	chr12	25380277	G									
						C	61	Q	E	1.59%	19979				
No															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1TP53	chr17	7577085	C									
						T	285	E	K	31.44%	21244				
Yes															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1TP53	chr17	7578275	G									
						A	192	Q	*	1.99%	17154				
No															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1TP53	chr17	7578406	C									
						T	175	R	H	20.70%	13637				
No															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1PIK3CA	chr3	178936091	G									
						A	545	E	K	0.76%	28000				
No															
BLDA 1803 U1	BLDA 1803	BLDA 2940	PT1TP53	chr17	7577065	C									
						G	291	K	N	0.48%	21244				
No															
BLDA 1805 U1	BLDA 1805	BLDA 2941	PT1TP53	chr17	7576855	G									
						A	331	Q	*	49.61%	10190				
Yes															
BLDA 1805 U1	BLDA 1805	BLDA 2941	PT1TP53	chr17	7578275	G									
						A	192	Q	*	41.01%	12351				
Yes															
BLDA 1806 U1	BLDA 1806	BLDA 2942	PT1TP53	chr17	7577574	T									
						A	236	Y	F	1.33%	19757				
Yes															
BLDA 1807 U1	BLDA 1807	BLDA 2943	PT1PIK3CA	chr3	178936091	G									
						A	545	E	K	0.33%	17758				
Yes															
BLDA 1807 U1	BLDA 1807	BLDA 2943	PT1CDKN2A	chr9	21971177	C									
						A	61	E	*	3.58%	6793				
Yes															
BLDA 1808 U1	BLDA 1808	BLDA 2944	PT1FGFR3	chr4	1806099	A									
						G	373	Y	C	98.94%	21247				
Yes															
BLDA 1810 U1	BLDA 1810	BLDA 2946	PT1TP53	chr17	7577095	G									

Table19.txt

					C	281	D	E	1.04%	14298			
No													
BLDA_1810_U1	BLDA_1810	BLDA_2946	PT1HRAS	chr11	533875	G							
					T	61	Q	K	0.61%	20474			
No													
BLDA_1812_U1	BLDA_1812	BLDA_2948	PT1FGFR3	chr4	1803568	C							
					G	249	S	C	1.21%	8753			
Yes													
BLDA_1813_U1	BLDA_1813	BLDA_2950	PT1TP53	chr17	7578407	G							
					C	175	R	G	2.72%	13994			
No													
BLDA_1813_U1	BLDA_1813	BLDA_2950	PT1TP53	chr17	7579589	G							
					NULL	33	S	NULL	41.47%	12907			
Yes													
BLDA_1813_U1	BLDA_1813	BLDA_2950	PT1PIK3CA	chr3	178952090	G							
					A	1049	G	S	2.13%	25909			
Yes													
BLDA_1814_U1	BLDA_1814	BLDA_2951	PT1TP53	chr17	7577541	T							
					A	247	N	I	12.59%	13290			
Yes													
BLDA_1815_U1	BLDA_1815	BLDA_2952	PT1TP53	chr17	7579882	C							
					G	11	E	Q	47.95%	14032			
Yes													
BLDA_1816_U1	BLDA_1816	BLDA_2954	PT1TP53	chr17	7577085	C							
					A	285	E	*	6.70%	1657			
No													
BLDA_1816_U1	BLDA_1816	BLDA_2954	PT1TP53	chr17	7578463	C							
					G	156	R	P	32.96%	1071			
No													
BLDA_1817_U1	BLDA_1817	NULL	TP53	chr17	7577539	G							
					A	248	R	W	2.87%	9579			
NULL													
BLDA_1818_U1	BLDA_1818	BLDA_2955	PT1TP53	chr17	7578419	C							
					A	171	E	*	16.66%	12080			
Yes													
BLDA_1818_U1	BLDA_1818	BLDA_2955	PT1TP53	chr17	7579882	C							
					G	11	E	Q	41.34%	11138			
Yes													
BLDA_1820_U1	BLDA_1820	BLDA_2957	PT1FGFR3	chr4	1803568	C							
					G	249	S	C	42.92%	3388			
Yes													
BLDA_1820_U1	BLDA_1820	BLDA_2957	PT1TP53	chr17	7577499	C							
					T	261	S	N	41.30%	10876			
Yes													
BLDA_1821_U1	BLDA_1821	BLDA_2958	PT1FGFR3	chr4	1806099	A							
					G	373	Y	C	45.00%	10374			
Yes													
BLDA_1822_U1	BLDA_1822	BLDA_2960	PT1FGFR3	chr4	1803568	C							

Table19.txt

				G	249	S		C		33.77%	3767
Yes											
BLDA_1866_U1	BLDA_1866	NULL		TP53	chr17	7578197		C			
				T	218	V		M		13.15%	3148
NULL											
BLDA_1925_U1	BLDA_1925	NULL		FGFR3	chr4	1806119		G			
				A	380	G		R		8.94%	15690
NULL											
BLDA_1926_U1	BLDA_1926	NULL		TP53	chr17	7576855		G			
				A	331	Q		*		22.64%	13384
NULL											
BLDA_1926_U1	BLDA_1926	NULL		TP53	chr17	7578534		C			
				G	132	K		N		21.17%	15379
NULL											
BLDA_1928_U1	BLDA_1928	NULL		TP53	chr17	7578382		G			
				C	183	S		*		56.88%	8400
NULL											
BLDA_1934_U1	BLDA_1934	NULL		TP53	chr17	7577099		C			
				T	280	R		K		61.58%	10582
NULL											
BLDA_1934_U1	BLDA_1934	NULL		TP53	chr17	7577559		G			
				NULL	241	S		NULL		6.63%	12425
NULL											
BLDA_1934_U1	BLDA_1934	NULL		ERBB2	chr17	37868208		C			
				T	310	S		F		0.48%	15577
NULL											
BLDA_1934_U1	BLDA_1934	NULL		PIK3CA	chr3	178916836		C			
				G	75	Q		E		40.31%	8601
NULL											
BLDA_1935_U1	BLDA_1935	NULL		TP53	chr17	7578275		G			
				A	192	Q		*		9.96%	3172
NULL											
BLDA_1935_U1	BLDA_1935	NULL		ERBB2	chr17	37868208		C			
				T	310	S		F		1.19%	10179
NULL											
BLDA_1938_U1	BLDA_1938	NULL		FGFR3	chr4	1803568		C			
				G	249	S		C		10.96%	5164
NULL											
BLDA_1943_U1	BLDA_1943	NULL		TP53	chr17	7577099		C			
				T	280	R		K		14.94%	2129
NULL											
BLDA_1944_U1	BLDA_1944	NULL		PIK3CA	chr3	178936082		G			
				A	542	E		K		8.32%	1911
NULL											
BLDA_1944_U1	BLDA_1944	NULL		PIK3CA	chr3	178936091		G			
				A	545	E		K		2.56%	1911
NULL											
BLDA_1944_U1	BLDA_1944	NULL		FGFR3	chr4	1803568		C			

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				G	249	S	C	10.84%	1781				
NULL													
BLDA 1945 U1	BLDA 1945	NULL		PIK3CA	chr3	178952085	A						
			T	1047	H	L	1.75%	19622					
NULL													
BLDA 1945 U1	BLDA 1945	NULL		FGFR3	chr4	1803568	C						
			G	249	S	C	1.67%	6774					
NULL													
BLDA 1983 U1	BLDA 1983	NULL		TP53	chr17	7577120	C						
			T	273	R	H	2.33%	7138					
NULL													
BLDA 1983 U1	BLDA 1983	NULL		FGFR3	chr4	1803568	C						
			G	249	S	C	86.00%	4399					
NULL													
BLDA 2146 U1	BLDA 2146	NULL		TP53	chr17	7577539	G						
			A	248	R	W	9.97%	10105					
NULL													
BLDA 2158 U1	BLDA 2158	NULL		TP53	chr17	7579313	G						
			A	125	T	M	8.49%	15681					
NULL													
BLDA 2182 U1	BLDA 2182	BLDA 3037		PT1FGFR3	chr4	1803568	C						
			G	249	S	C	11.93%	18158					
Yes													
BLDA 2194 U1	BLDA 2194	BLDA 3005		PT1TP53	chr17	7576855	G						
			A	331	Q	*	22.86%	9107					
Yes													
BLDA 2263 U1	BLDA 2263	BLDA 3021		PT1TP53	chr17	7577099	C						
			G	280	R	T	43.59%	17090					
Yes													
BLDA 2263 U1	BLDA 2263	BLDA 3021		PT1TP53	chr17	7577099	C						
			T	280	R	K	46.01%	17090					
Yes													
BLDA 2263 U1	BLDA 2263	BLDA 3021		PT1TP53	chr17	7577599	C						
			G	228	D	H	45.15%	3847					
Yes													
BLDA 2281 U1	BLDA 2281	BLDA 3016		PT1TP53	chr17	7576897	G						
			A	317	Q	*	18.01%	7347					
Yes													
BLDA 2281 U1	BLDA 2281	BLDA 3016		PT1VHL	chr3	10183725	C						
			G	65	S	W	3.88%	14849					
Yes													
BLDA 2289 U1	BLDA 2289	BLDA 3017		PT1TP53	chr17	7579476	G						
			NULL	71	P	NULL	52.74%	5383					
Yes													
BLDA 2443 U1	BLDA 2443	NULL		TP53	chr17	7577099	C						
			G	280	R	T	9.01%	32960					
NULL													
BLDA 2443 U1	BLDA 2443	NULL		TP53	chr17	7578394	T						

Table19.txt

```
                                C       179     H       R       3.66%   31088
   NULL
BLDA 2443 U1  BLDA 2443    NULL          TP53    chr17   7576889    C
                                A       319     K       N       9.43%   29746
   NULL
BLDA 2476 U1  BLDA 2476    BLDA 3095 PT1ERBB2   chr17   37868208   C
                                A       310     S       Y       0.48%   35212
   Yes
BLDA 2476 U1  BLDA 2476    BLDA 3095 PT1PIK3CA  chr3    178936091  G
                                A       545     E       K       1.31%   4285
   No
BLDA 2476 U1  BLDA 2476    BLDA 3095 PT1FGFR3   chr4    1803568    C
                                G       249     S       C       8.11%   22206
   Yes
BLDA 2489 U1  BLDA 2489    NULL          KRAS    chr12   25398285   C
                                G       12      G       R       0.29%   17057
   NULL
BLDA 2489 U1  BLDA 2489    NULL          TP53    chr17   7578264    G
                                NULL    195     I       NULL    5.24%   15352
   NULL
BLDA 2489 U1  BLDA 2489    NULL          PIK3CA  chr3    178952085  A
                                G       1047    H       R       0.54%   28709
   NULL
BLDA 2569 U1  BLDA 2569    NULL          KRAS    chr12   25398285   C
                                T       12      G       S       2.61%   15250
   NULL
BLDA 2569 U1  BLDA 2569    NULL          TP53    chr17   7578479    G
                                A       151     P       S       1.06%   22528
   NULL
BLDA 2614 U1  BLDA 2614    NULL          TP53    chr17   7574034    C
                                T       0       NULL    NULL    65.42%  32807
   NULL
BLDA 2647 U1  BLDA 2647    NULL          CDKN2A  chr9    21971123   NULL
                                T       79      T       NULL    32.35%  3910
   NULL
BLDA 2671 U1  BLDA 2671    NULL          PIK3CA  chr3    178936091  G
                                A       545     E       K       2.42%   6484
   NULL
BLDA 2671 U1  BLDA 2671    NULL          FGFR3   chr4    1803568    C
                                G       249     S       C       8.33%   20637
   NULL
BLDA 2671 U1  BLDA 2671    NULL          FGFR3   chr4    1806089    G
                                T       370     G       C       7.78%   16161
   NULL
BLDA 2719 U1  BLDA 2719    BLDA 2959 PT1TP53    chr17   7577099    C
                                T       280     R       K       17.68%  74146
   Yes
BLDA 2719 U1  BLDA 2719    BLDA 2959 PT1TP53    chr17   7578442    T
```

Table19.txt

```
                                C       163     Y       C       18.94%      54337
   Yes
BLDA 2721 U1  BLDA 2721    NULL          FGFR3   chr4    1803568    C
                                G       249     S       C       24.99%      27512
   NULL
BLDA 2725 U1  BLDA 2725    BLDA 2962 PT1FGFR3   chr4    1803568    C
                                G       249     S       C       27.31%      18737
   Yes
BLDA 2725 U1  BLDA 2725    BLDA 2962 PT1TP53    chr17   7578286    A
                                NULL    188     L       NULL    4.47%       12439
   No
BLDA 2726 U1  BLDA 2726    BLDA 2963 PT1ERBB2   chr17   37868208   C
                                A       310     S       Y       0.35%       29340
   No
BLDA 2726 U1  BLDA 2726    BLDA 2963 PT1FGFR3   chr4    1803568    C
                                G       249     S       C       2.34%       15176
   Yes
BLDA 2726 U1  BLDA 2726    NULL          TP53    chr17   7577079    C
                                T       287     E       K       9.52%       39659
   NULL
BLDA 2727 U1  BLDA 2727    BLDA 2964 PT1CDKN2A  chr9    21971177   C
                                A       61      E       *       2.65%       71114
   Yes
BLDA 2727 U1  BLDA 2727    BLDA 2964 PT1PIK3CA  chr3    178936091  G
                                A       545     E       K       0.97%       12265
   No
BLDA 2729 U1  BLDA 2729    BLDA 2965 PT1ERBB2   chr17   37868208   C
                                T       310     S       F       3.93%       259667
   No
BLDA 2729 U1  BLDA 2729    BLDA 2965 PT1TP53    chr17   7577085    C
                                T       285     E       K       31.90%      47871
   Yes
BLDA 2729 U1  BLDA 2729    BLDA 2965 PT1TP53    chr17   7574034    C
                                G       0       NULL    NULL    30.99%      52151
   Yes
BLDA 2729 U1  BLDA 2729    NULL          TP53    chr17   7577065    C
                                G       291     K       N       29.45%      47871
   NULL
BLDA 2729 U1  BLDA 2729    NULL          TP53    chr17   7577077    C
                                G       287     E       D       2.45%       47871
   NULL
BLDA 2730 U1  BLDA 2730    BLDA 2966 PT1FGFR3   chr4    1803568    C
                                G       249     S       C       30.19%      47419
   No
BLDA 2730 U1  BLDA 2730    BLDA 2966 PT1PIK3CA  chr3    178936082  G
                                A       542     E       K       44.53%      14521
   Yes
BLDA 2730 U1  BLDA 2730    BLDA 2966 PT1PIK3CA  chr3    178952074  G
```

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```
                                A       1043    M       I       0.17%       41854
   No
BLDA 2732 U1  BLDA 2732    BLDA 2969 PT1PIK3CA  chr3    178936091  G
                                A       545     E       K       0.89%       10843
   No
BLDA 2732 U1  BLDA 2732    BLDA 2969 PT1FGFR3   chr4    1803568    C
                                G       249     S       C       0.53%       38069
   No
BLDA 2732 U1  BLDA 2732    BLDA 2969 PT1KRAS    chr12   25380282   G
                                C       59      A       G       1.03%       43340
   No
BLDA 2733 U1  BLDA 2733    BLDA 2970 PT1ERBB2   chr17   37868208   C
                                A       310     S       Y       0.98%       26922
   No
BLDA 2734 U1  BLDA 2734    BLDA 2971 PT1FGFR3   chr4    1806089    G
                                T       370     G       C       0.67%       36036
   Yes
BLDA 2737 U1  BLDA 2737    BLDA 2975 PT1FGFR3   chr4    1803564    C
                                T       248     R       C       17.97%      46690
   Yes
BLDA 2740 U1  BLDA 2740    BLDA 2949 PT1FGFR3   chr4    1803564    C
                                T       248     R       C       3.80%       51394
   Yes
BLDA 2740 U1  BLDA 2740    BLDA 2949 PT1TP53    chr17   7578449    C
                                T       161     A       T       3.88%       30398
   Yes
BLDA 2741 U1  BLDA 2741    NULL        CDKN2A   chr9    21971036   C
                                G       108     D       H       69.63%      25644
   NULL
BLDA 2741 U1  BLDA 2741    NULL        PIK3CA   chr3    178952085  A
                                G       1047    H       R       43.15%      36886
   NULL
BLDA 2741 U1  BLDA 2741    NULL        KRAS     chr12   25398284   C
                                G       12      G       A       44.54%      58411
   NULL
BLDA 2741 U1  BLDA 2741    NULL        TP53     chr17   7579882    C
                                G       11      E       Q       48.80%      39772
   NULL
BLDA 2744 U1  BLDA 2744    NULL        TP53     chr17   7577559    G
                                T       241     S       Y       11.38%      32002
   NULL
BLDA 2745 U1  BLDA 2745    NULL        TP53     chr17   7577127    C
                                T       271     E       K       22.38%      24166
   NULL
BLDA 2746 U1  BLDA 2746    NULL        FGFR3    chr4    1803568    C
                                G       249     S       C       1.32%       31572
   NULL
BLDA 2747 U1  BLDA 2747    NULL        ERBB2    chr17   37868208   C
```

Table19.txt

				T	310	S	F	6.98%	46867	NULL	
BLDA 2747 U1	BLDA 2747	NULL		ERBB2	chr17	37868208	C				
				A	310	S	Y	2.92%	46867	NULL	
BLDA 2748 U1	BLDA 2748	NULL		TP53	chr17	7578272	G				
				A	193	H	Y	30.87%	18856	NULL	
BLDA 2751 U1	BLDA 2751	NULL		TP53	chr17	7577099	C				
				T	280	R	K	88.79%	29417	NULL	
BLDA 2781 U1	BLDA 2781	NULL		TP53	chr17	7577548	C				
				T	245	G	S	7.47%	6577	NULL	
BLDA 2781 U1	BLDA 2781	NULL		TP53	chr17	7578407	G				
				A	175	R	C	6.34%	6104	NULL	
BLDA 2787 U1	BLDA 2787	BLDA 3207 PT1TP53			chr17	7577085	C				
				A	285	E	*	3.17%	18963	Yes	
BLDA 2793 U1	BLDA 2793	NULL		TP53	chr17	7577538	C				
				T	248	R	Q	41.40%	9514	NULL	
BLDA 2793 U1	BLDA 2793	NULL		PIK3CA	chr3	178936082	G				
				A	542	E	K	39.84%	6873	NULL	
BLDA 2793 U1	BLDA 2793	NULL		FGFR3	chr4	1803568	C				
				G	249	S	C	9.50%	12593	NULL	
BLDA 2867 U1	BLDA 2867	BLDA 3076 PT1TP53			chr17	7579447	A				
				NULL	80	P	NULL	0.57%	9816	Yes	
BLDA 3208 U1	BLDA 3208	NULL		PIK3CA	chr3	178936091	G				
				A	545	E	K	31.42%	2183	NULL	
BLDA 3208 U1	BLDA 3208	NULL		FGFR3	chr4	1807890	A				
				C	650	K	T	27.47%	1558	NULL	
BLDA 3216 U1	BLDA 3216	NULL		FGFR3	chr4	1803568	C				
				G	249	S	C	16.56%	912	NULL	
BLDA 3217 U1	BLDA 3217	NULL		PIK3CA	chr3	178936091	G				
				A	545	E	K	24.16%	4185	NULL	
BLDA 3217 U1	BLDA 3217	NULL		FGFR3	chr4	1803564	C				
				T	248	R	C	26.33%	22301	NULL	
BLDA 3217 U1	BLDA 3217	NULL		CDKN2A	chr9	21971127	AG				

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```
                              NULL    77      T       NULL    56.12%      3236
   NULL
BLDA 3217 U1  BLDA 3217    NULL        CDKN2A  chr9    21971192
TGCCCATCATCATGACCTGCCAGAG (SEQ ID NO:727)      NULL    56      S       NULL
13.28%      11334      NULL
BLDA 3222 U1  BLDA 3222    NULL        KRAS    chr12   25398284   C
                              T       12      G       D       8.03%       4884
   NULL
BLDA 3222 U1  BLDA 3222    NULL        TP53    chr17   7578203    C
                              T       216     V       M       5.06%       4232
   NULL
BLDA 3222 U1  BLDA 3222    NULL        CDKN2A  chr9    21974676   C
                              T       0       NULL    NULL    13.79%      4192
   NULL
BLDA 3225 U1  BLDA 3225    NULL        TP53    chr17   7577120    C
                              A       273     R       L       9.74%       1838
   NULL
BLDA 3225 U1  BLDA 3225    NULL        PIK3CA  chr3    178936083  A
                              T       542     E       V       9.94%       1398
   NULL
BLDA 3226 U1  BLDA 3226    NULL        PIK3CA  chr3    178936091  G
                              A       545     E       K       85.66%      9239
   NULL
BLDA 3226 U1  BLDA 3226    NULL        FGFR3   chr4    1803568    C
                              G       249     S       C       3.91%       11753
   NULL
BLDA 3242 U1  BLDA 3242    NULL        PIK3CA  chr3    178936091  G
                              A       545     E       K       22.77%      12191
   NULL
BLDA 3242 U1  BLDA 3242    NULL        FGFR3   chr4    1803568    C
                              G       249     S       C       25.86%      10998
   NULL
```

Table20.txt

Table 20. Mutations detected by the TERT Assay in urine samples from the Early Detection cohort.

Mutant Urine allele Sample frequency	# unique templates Patient analyzed	Found in Matched the matched Tumor primary tumor	Gene	Chr	hg 19 Position	Reference base	Variant base	
BLD 186 U 29326	BLD 186	NULL N/A	TERT	chr5	1295228	C	T	0.34%
BLD 237 U1 15372	BLD 237	BLD 237 PT Yes	TERT	chr5	1295228	C	T	7.41%
BLD 253 U1 26.00%	BLD 253	BLD 253 PT Yes	TERT	chr5	1295228	C	T	
BLD 274 U1 49448	BLD 274	NULL N/A	TERT	chr5	1295228	C	T	2.42%
BLD 274 U1 49448	BLD 274	NULL N/A	TERT	chr5	1295250	C	T	0.23%
BLD 288 U1 7748	BLD 288	NULL N/A	TERT	chr5	1295250	C	T	0.66%
BLD 333 U1 29.49%	BLD 333	BLD 333 PT Yes	TERT	chr5	1295228	C	T	
BLD 362 U1 54.29%	BLD 362	BLD 362 PT Yes	TERT	chr5	1295250	C	T	
BLD 402 U1 21354	BLD 402	NULL N/A	TERT	chr5	1295228	C	T	0.52%
BLD 406 U1 14.77%	BLD 406	BLD 406 PT Yes	TERT	chr5	1295228	C	T	
BLD 428 U1 9194	BLD 428	BLD 428 PT1 No	TERT	chr5	1295228	C	T	2.49%
BLD 436 U1 24086	BLD 436	BLD 436 PT Yes	TERT	chr5	1295228	C	T	1.09%
BLD 458 U1 10110	BLD 458	BLD 458 PT1 Yes	TERT	chr5	1295228	C	T	4.38%
BLD 506 U1 16.57%	BLD 506	BLDA 3041 PT Yes	TERT	chr5	1295228	C	T	
BLD 534 U1 82228	BLD 534	BLDA 2903 PT Yes	TERT	chr5	1295228	C	T	1.39%
BLD 538 U1 14742	BLD 538	NULL N/A	TERT	chr5	1295228	C	T	1.06%
BLD 539 U1 12.18%	BLD 539	BLDA 2906 PT Yes	TERT	chr5	1295243	C	T	
BLD 540 U1 14.86%	BLD 540	BLDA 2905 PT Yes	TERT	chr5	1295228	C	T	
BLD 542 U1 76675	BLD 542	BLDA 2908 PT Yes	TERT	chr5	1295250	C	T	2.28%
BLD 543 U1 42278	BLD 543	BLDA 2909 PT Yes	TERT	chr5	1295228	C	T	0.39%

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BLD 544 U1	BLD 544	BLDA 2910 PTTERT	chr5	1295228	C	T	44.03%	30360	Yes
BLD 545 U1	BLD 545	BLDA 2911 PTTERT	chr5	1295228	C	T	6.28%	24323	Yes
BLD 546 U1	BLD 546	BLDA 2912 PTTERT	chr5	1295228	C	T	2.06%	68155	Yes
BLD 547 U1	BLD 547	BLDA 2913 PTTERT	chr5	1295228	C	T	10.38%	33710	Yes
BLD 548 U1	BLD 548	NULL TERT	chr5	1295228	C	T	26.49%	6843	N/A
BLD 549 U1	BLD 549	BLDA 2914 PTTERT	chr5	1295228	C	T	1.03%	65332	Yes
BLD 551 U1	BLD 551	BLDA 2916 PTTERT	chr5	1295228	C	T	4.06%	8458	Yes
BLD 557 U1	BLD 557	BLDA 2924 PTTERT	chr5	1295250	C	T	1.87%	16017	Yes
BLD 601 U1	BLD 601	BLD 601 PT1 TERT	chr5	1295228	C	T	3.18%	9089	Yes
BLD 606 U1	BLD 606	NULL TERT	chr5	1295250	C	T	7.49%	12988	N/A
BLD 625 U1	BLD 625	BLD 625 PT1 TERT	chr5	1295228	C	T	0.82%	77790	Yes
BLD 639 U1	BLD 639	NULL TERT	chr5	1295228	C	T	0.35%	75999	N/A
BLD 646 U1	BLD 646	BLD 646 PT1 TERT	chr5	1295228	C	T	26.18%	30669	Yes
BLD 661 U1	BLD 661	NULL TERT	chr5	1295228	C	T	0.27%	30599	N/A
BLD 699 U1	BLD 699	NULL TERT	chr5	1295228	C	T	0.18%	15383	N/A
BLD 711 U1	BLD 711	NULL TERT	chr5	1295228	C	T	2.57%	41841	N/A
BLD 790 U1	BLD 790	BLDA 3025 PTTERT	chr5	1295250	C	T	48.48%	29005	Yes
BLD 835 U1	BLD 835	BLD 835 PT1 TERT	chr5	1295228	C	T	9.12%	16070	Yes
BLD 841 U1	BLD 841	BLD 841 PT1 TERT	chr5	1295250	C	T	6.19%	26278	Yes
BLD 850 U1	BLD 850	NULL TERT	chr5	1295228	C	T	0.84%	21560	N/A
BLD 850 U1	BLD 850	NULL TERT	chr5	1295250	C	T	0.62%	21560	N/A
BLD 859 U1	BLD 859	BLD 859 PT1 TERT	chr5	1295228	C	T	0.90%	15452	No
BLD 861 U1	BLD 861	NULL TERT	chr5	1295228	C	T	5.73%	33148	N/A
BLD 866 U1	BLD 866	BLD 866 PT1 TERT	chr5	1295228	C	T	2.02%	32459	Yes

Table20.txt

BLDA 1137	U1BLDA 1137	BLDA 3059	PTTERT	chr5	1295228	C	T	2.64%	8280	Yes	
BLDA 1153	U1BLDA 1153	NULL	TERT	chr5	1295228	C	T	0.45%	43330	N/A	
BLDA 1257	U1BLDA 1257	NULL	TERT	chr5	1295228	C	T	1.43%	15723	N/A	
BLDA 1326	U1BLDA 1326	BLDA 2991	PTTERT	chr5	1295250	C	T	0.54%	24993	Yes	
BLDA 1380	U1BLDA 1380	NULL	TERT	chr5	1295228	C	T	3.75%	7812	N/A	
BLDA 1405	U1BLDA 1405	NULL	TERT	chr5	1295228	C	T	0.46%	7832	N/A	
BLDA 1790	U1BLDA 1790	BLDA 2928	PTTERT	chr5	1295228	C	T	1.74%	2470	Yes	
BLDA 1793	U1BLDA 1793	BLDA 2931	PTTERT	chr5	1295228	C	T	3.42%	9483	Yes	
BLDA 1796	U1BLDA 1796	BLDA 2934	PTTERT	chr5	1295228	C	T	28.60%	7090	Yes	
BLDA 1798	U1BLDA 1798	BLDA 2935	PTTERT	chr5	1295228	C	T	1.76%	10040	Yes	
BLDA 1799	U1BLDA 1799	NULL	TERT	chr5	1295228	C	T	21.49%	8608	N/A	
BLDA 1801	U1BLDA 1801	BLDA 2937	PTTERT	chr5	1295228	C	T	5.06%	6939	Yes	
BLDA 1802	U1BLDA 1802	BLDA 2938	PTTERT	chr5	1295228	C	T	0.54%	17052	Yes	
BLDA 1803	U1BLDA 1803	BLDA 2940	PTTERT	chr5	1295228	C	T	56.91%	10061	Yes	
BLDA 1804	U1BLDA 1804	BLDA 2939	PTTERT	chr5	1295228	C	T	1.54%	5446	Yes	
BLDA 1805	U1BLDA 1805	BLDA 2941	PTTERT	chr5	1295228	C	T	50.56%	13771	No	
BLDA 1807	U1BLDA 1807	BLDA 2943	PTTERT	chr5	1295228	C	T	8.23%	8286	Yes	
BLDA 1808	U1BLDA 1808	BLDA 2944	PTTERT	chr5	1295250	C	T	73.37%	11699	Yes	
BLDA 1811	U1BLDA 1811	BLDA 2947	PTTERT	chr5	1295228	C	T	1.23%	12494	Yes	
BLDA 1812	U1BLDA 1812	BLDA 2948	PTTERT	chr5	1295250	C	T	1.81%	3869	Yes	
BLDA 1816	U1BLDA 1816	BLDA 2954	PTTERT	chr5	1295228	C	T	27.14%	667	Yes	
BLDA 1818	U1BLDA 1818	BLDA 2955	PTTERT	chr5	1295228	C	T	5.79%	7277	Yes	
BLDA 1820	U1BLDA 1820	BLDA 2957	PTTERT	chr5	1295250	C	T	48.52%	4462	Yes	
BLDA 1822	U1BLDA 1822	BLDA 2960	PTTERT	chr5	1295228	C	T	35.17%	3224	Yes	

Table20.txt

BLDA 1844 U1BLDA 1844	NULL	TERT	chr5	1295228	C	T	0.98%	5799 N/A
BLDA 1853 U1BLDA 1853	NULL	TERT	chr5	1295228	C	T	0.59%	13174 N/A
BLDA 1866 U1BLDA 1866	NULL	TERT	chr5	1295228	C	T	18.00%	9166 N/A
BLDA 1892 U1BLDA 1892	NULL	TERT	chr5	1295228	C	T	0.70%	38335 N/A
BLDA 1924 U1BLDA 1924	BLDA 1924	PTTERT	chr5	1295228	C	T	1.71%	1171 Yes
BLDA 1925 U1BLDA 1925	NULL	TERT	chr5	1295228	C	T	6.92%	5404 N/A
BLDA 1926 U1BLDA 1926	NULL	TERT	chr5	1295228	C	T	30.74%	4929 N/A
BLDA 1934 U1BLDA 1934	NULL	TERT	chr5	1295228	C	T	63.18%	4481 N/A
BLDA 1938 U1BLDA 1938	NULL	TERT	chr5	1295228	C	T	15.27%	1356 N/A
BLDA 1943 U1BLDA 1943	NULL	TERT	chr5	1295228	C	T	8.40%	1036 N/A
BLDA 1944 U1BLDA 1944	NULL	TERT	chr5	1295228	C	T	3.28%	1891 N/A
BLDA 1983 U1BLDA 1983	NULL	TERT	chr5	1295228	C	T	47.60%	10421 N/A
BLDA 2182 U1BLDA 2182	BLDA 3037	PTTERT	chr5	1295228	C	T	2.49%	25257 Yes
BLDA 2194 U1BLDA 2194	BLDA 3005	PTTERT	chr5	1295250	C	T	15.28%	16170 Yes
BLDA 2263 U1BLDA 2263	BLDA 3021	PTTERT	chr5	1295228	C	T	65.18%	20533 Yes
BLDA 2281 U1BLDA 2281	BLDA 3016	PTTERT	chr5	1295228	C	T	13.69%	17839 Yes
BLDA 2443 U1BLDA 2443	NULL	TERT	chr5	1295228	C	T	9.29%	49639 N/A
BLDA 2476 U1BLDA 2476	BLDA 3095	PTTERT	chr5	1295228	C	T	4.70%	30081 Yes
BLDA 2489 U1BLDA 2489	NULL	TERT	chr5	1295228	C	T	5.32%	20758 N/A
BLDA 2489 U1BLDA 2489	NULL	TERT	chr5	1295243	C	T	2.94%	20758 N/A
BLDA 2647 U1BLDA 2647	NULL	TERT	chr5	1295228	C	T	16.58%	34496 N/A
BLDA 2671 U1BLDA 2671	NULL	TERT	chr5	1295250	C	T	4.05%	108370 N/A
BLDA 2719 U1BLDA 2719	BLDA 2959	PTTERT	chr5	1295228	C	T	1.46%	32060 No
BLDA 2721 U1BLDA 2721	NULL	TERT	chr5	1295228	C	T	13.44%	38001 N/A

Table20.txt

BLDA 2725 U1BLDA 2725 BLDA 2962 PTTERT chr5 1295228 C T
16.75% 11935 Yes
BLDA 2726 U1BLDA 2726 BLDA 2963 PTTERT chr5 1295250 C T
12.35% 39783 Yes
BLDA 2727 U1BLDA 2727 BLDA 2964 PTTERT chr5 1295228 C T 5.24%
48868 Yes
BLDA 2728 U1BLDA 2728 BLDA 2968 PTTERT chr5 1295228 C T
15.93% 59242 Yes
BLDA 2729 U1BLDA 2729 BLDA 2965 PTTERT chr5 1295228 C T
24.23% 33141 Yes
BLDA 2729 U1BLDA 2729 BLDA 2965 PTTERT chr5 1295250 C T 6.98%
33141 Yes
BLDA 2730 U1BLDA 2730 BLDA 2966 PTTERT chr5 1295228 C T
23.29% 36717 No
BLDA 2732 U1BLDA 2732 BLDA 2969 PTTERT chr5 1295228 C T 9.69%
32463 Yes
BLDA 2733 U1BLDA 2733 BLDA 2970 PTTERT chr5 1295228 C T 5.27%
69282 Yes
BLDA 2737 U1BLDA 2737 BLDA 2975 PTTERT chr5 1295250 C T 0.55%
53172 No
BLDA 2738 U1BLDA 2738 BLDA 2976 PTTERT chr5 1295228 C T
11.02% 14772 Yes
BLDA 2744 U1BLDA 2744 NULL TERT chr5 1295228 C T 4.07%
53227 N/A
BLDA 2744 U1BLDA 2744 NULL TERT chr5 1295250 C T 0.20%
53227 N/A
BLDA 2745 U1BLDA 2745 NULL TERT chr5 1295228 C T
11.79% 32040 N/A
BLDA 2746 U1BLDA 2746 NULL TERT chr5 1295250 C T 6.34%
25555 N/A
BLDA 2746 U1BLDA 2746 NULL TERT chr5 1295243 C T 0.22%
25555 N/A
BLDA 2747 U1BLDA 2747 NULL TERT chr5 1295228 C T
26.13% 43462 N/A
BLDA 2751 U1BLDA 2751 NULL TERT chr5 1295228 C T
36.97% 56636 N/A
BLDA 2766 U1BLDA 2766 NULL TERT chr5 1295228 C T
27.68% 100423 N/A
BLDA 2793 U1BLDA 2793 NULL TERT chr5 1295228 C T
23.35% 71638 N/A
BLDA 2901 U1BLDA 2901 NULL TERT chr5 1295228 C T
33.84% 78556 N/A
BLDA 3208 U1BLDA 3208 NULL TERT chr5 1295228 C T
20.58% 14345 N/A
BLDA 3208 U1BLDA 3208 NULL TERT chr5 1295250 C T 2.34%
14345 N/A
BLDA 3212 U1BLDA 3212 NULL TERT chr5 1295228 C T 0.90%
9965 N/A

Table20.txt

BLDA 3214 U1BLDA 3214 NULL TERT chr5 1295228 C T 0.36%
26888 N/A
BLDA 3216 U1BLDA 3216 NULL TERT chr5 1295228 C A
23.22% 6162 N/A
BLDA 3217 U1BLDA 3217 NULL TERT chr5 1295228 C T
16.01% 91266 N/A
BLDA 3220 U1BLDA 3220 NULL TERT chr5 1295228 C T
65.06% 9265 N/A
BLDA 3225 U1BLDA 3225 NULL TERT chr5 1295228 C T
13.34% 12843 N/A
BLDA 3225 U1BLDA 3225 NULL TERT chr5 1295250 C T 0.78%
12843 N/A
BLDA 3226 U1BLDA 3226 NULL TERT chr5 1295250 C T
77.60% 11351 N/A
BLDA 3242 U1BLDA 3242 NULL TERT chr5 1295228 C T
31.77% 23748 N/A
N/A Not Available

Table21.txt

Table 21. Chromosome arm gains and losses detected by the Aneuploidy Assay

Urine Sample	Patient	Aneuploidy Score	Gains	Losses	# unique templates analyzed
BLD 147 U	BLD 147	1.00	15	9	7652738
BLD 237 U1	BLD 237	0.83	2	0	6301336
BLD 253 U1	BLD 253	1.00	3	2	7578012
BLD 277 U1	BLD 277	1.00	5	6	7208509
BLD 297 U1	BLD 297	1.00	5	2	5407224
BLD 304 U1	BLD 304	1.00	13	12	3743211
BLD 333 U1	BLD 333	1.00	13	14	4503069
BLD 458 U1	BLD 458	0.85	2	2	6885328
BLD 506 U1	BLD 506	1.00	0	3	1705267
BLD 535 U1	BLD 535	1.00	7	5	7671847
BLD 536 U1	BLD 536	1.00	3	4	5608276
BLD 537 U1	BLD 537	0.88	9	3	5783187
BLD 538 U1	BLD 538	1.00	5	8	7416559
BLD 542 U1	BLD 542	1.00	8	6	8227342
BLD 543 U1	BLD 543	1.00	8	8	7555432
BLD 546 U1	BLD 546	1.00	5	4	6698390
BLD 548 U1	BLD 548	1.00	4	5	4326424
BLD 550 U1	BLD 550	1.00	6	3	6005217
BLD 551 U1	BLD 551	1.00	14	8	6785716
BLD 613 U1	BLD 613	1.00	2	6	7726944
BLD 644 U1	BLD 644	1.00	16	9	3569597
BLD 649 U1	BLD 649	1.00	20	11	6798823
BLD 746 U1	BLD 746	1.00	7	8	7216224
BLD 790 U1	BLD 790	1.00	21	9	11599984
BLD 834 U1	BLD 834	0.82	3	0	11486861
BLD 835 U1	BLD 835	1.00	8	5	10663555
BLD 859 U1	BLD 859	1.00	8	4	7117473
BLDA 1128 U1	BLDA 1128	0.79	4	1	7621600
BLDA 1257 U1	BLDA 1257	0.88	7	3	4536566
BLDA 1380 U1	BLDA 1380	1.00	4	0	5405650
BLDA 1792 U1	BLDA 1792	1.00	1	0	3497578
BLDA 1796 U1	BLDA 1796	1.00	1	2	10234096
BLDA 1797 U1	BLDA 1797	1.00	3	3	10391245
BLDA 1799 U1	BLDA 1799	1.00	7	4	6843547
BLDA 1800 U1	BLDA 1800	1.00	3	5	10865287
BLDA 1803 U1	BLDA 1803	1.00	11	7	9485173
BLDA 1805 U1	BLDA 1805	1.00	14	12	9978133
BLDA 1807 U1	BLDA 1807	1.00	4	2	10410863
BLDA 1808 U1	BLDA 1808	1.00	2	2	3497076
BLDA 1810 U1	BLDA 1810	1.00	12	7	9230917
BLDA 1818 U1	BLDA 1818	1.00	10	7	8367556
BLDA 1820 U1	BLDA 1820	1.00	8	8	9053725
BLDA 1821 U1	BLDA 1821	0.87	3	0	9694865
BLDA 1822 U1	BLDA 1822	1.00	7	5	9138123

Table21.txt

BLDA 1866 U1	BLDA 1866	1.00	15	11	4778332
BLDA 1926 U1	BLDA 1926	1.00	17	9	4350585
BLDA 1928 U1	BLDA 1928	1.00	11	9	2795555
BLDA 1934 U1	BLDA 1934	1.00	13	13	3742850
BLDA 1935 U1	BLDA 1935	1.00	6	6	2729701
BLDA 1938 U1	BLDA 1938	1.00	3	2	2716864
BLDA 1943 U1	BLDA 1943	1.00	7	6	1387425
BLDA 1983 U1	BLDA 1983	1.00	16	9	4553823
BLDA 2146 U1	BLDA 2146	1.00	5	8	4113593
BLDA 2158 U1	BLDA 2158	0.88	5	6	6549218
BLDA 2182 U1	BLDA 2182	1.00	2	1	6753229
BLDA 2194 U1	BLDA 2194	1.00	10	8	6154967
BLDA 2263 U1	BLDA 2263	1.00	13	10	3188571
BLDA 2281 U1	BLDA 2281	1.00	7	6	5237813
BLDA 2443 U1	BLDA 2443	1.00	8	6	6066336
BLDA 2489 U1	BLDA 2489	0.88	4	2	6122252
BLDA 2614 U1	BLDA 2614	1.00	13	8	10513445
BLDA 2647 U1	BLDA 2647	1.00	13	10	9617669
BLDA 2719 U1	BLDA 2719	1.00	10	10	6989800
BLDA 2721 U1	BLDA 2721	1.00	7	5	6189883
BLDA 2725 U1	BLDA 2725	1.00	5	5	4563241
BLDA 2726 U1	BLDA 2726	1.00	7	7	5896294
BLDA 2727 U1	BLDA 2727	0.87	2	3	5881662
BLDA 2728 U1	BLDA 2728	1.00	5	6	6997056
BLDA 2729 U1	BLDA 2729	1.00	12	9	6516188
BLDA 2730 U1	BLDA 2730	1.00	6	13	6150215
BLDA 2732 U1	BLDA 2732	1.00	13	9	6706768
BLDA 2733 U1	BLDA 2733	1.00	9	8	6744958
BLDA 2738 U1	BLDA 2738	1.00	6	6	5499438
BLDA 2744 U1	BLDA 2744	1.00	5	5	6223566
BLDA 2745 U1	BLDA 2745	1.00	6	5	5731845
BLDA 2747 U1	BLDA 2747	1.00	13	12	5653510
BLDA 2748 U1	BLDA 2748	1.00	14	12	5708567
BLDA 2749 U1	BLDA 2749	0.88	6	5	6157887
BLDA 2751 U1	BLDA 2751	1.00	16	8	5211071
BLDA 2766 U1	BLDA 2766	1.00	8	7	6373866
BLDA 2793 U1	BLDA 2793	1.00	13	10	6594128
BLDA 2901 U1	BLDA 2901	1.00	11	10	6200522
BLDA 3208 U1	BLDA 3208	1.00	2	3	2597055
BLDA 3220 U1	BLDA 3220	1.00	3	3	3317874
BLDA 3225 U1	BLDA 3225	1.00	1	1	1443235
BLDA 3226 U1	BLDA 3226	1.00	2	1	5245159
BLDA 3242 U1	BLDA 3242	1.00	12	12	4521910

Table22.txt

Table 22. Mutations detected by Multiplex Assay in primary tumor tissues from the Early Detection cohort.

Tumor Sample	Variant base	Patient	Gene Codon	Reference amino acid	chrom	Variant amino acid	hg 19 Position	Mutant allele frequency	# unique Reference templates analyzed	Detectable Variant in urine
BLD 147 PT	A	BLD 147	TP53 342	R	chr17	*	7574003 G 88%		2654	Yes
BLD 237 PT	A	BLD 237	TP53 273	R	chr17	C	7577121 G 34%		1575	Yes
BLD 253 PT	A	BLD 253	TP53 47	P	chr17	S	7579548 G 51%		4127	No
BLD 253 PT	A	BLD 253	PIK3CA 542	E	chr3	K	178936082 G 10%		2925	Yes
BLD 253 PT	T	BLD 253	ERBB2 310	S	chr17	F	37868208 C 37%		1521	Yes
BLD 333 PT	G	BLD 333	TP53 280	R	chr17	T	7577099 C 14%		116	No
BLD 333 PT	A	BLD 333	TP53 283	R	chr17	C	7577091 G 5%		116	No
BLD 333 PT	G	BLD 333	TP53 345	N	chr17	H	7573994 T 5%		74	No
BLD 436 PT	A	BLD 436	TP53 241	S	chr17	F	7577559 G 64%		1800	Yes
BLD 601 PT1	G	BLD 601	FGFR3 650	K	chr4	E	1807889 A 47%		5311	No
BLD 601 PT1	A	BLD 601	PIK3CA 545	E	chr3	K	178936091 G 46%		3085	Yes
BLD 601 PT1	G	BLD 601	CDKN2A 66	H	chr9	P	21971161 T 6%		336	No
BLD 624 PT1	G	BLD 624	TP53 249	R	chr17	S	7577534 C 18%		4230	No
BLD 634 PT1	C	BLD 634	HRAS 61	Q	chr11	R	533874 T 24%		4421	No
BLD 835 PT1	G	BLD 835	FGFR3 249	S	chr4	C	1803568 C 20%		2274	Yes
BLD 841 PT1	T	BLD 841	TP53 273	R	chr17	H	7577120 C 32%		4682	No
BLD 841 PT1	G	BLD 841	CDKN2A 66	H	chr9	P	21971161 T 5%		352	No
BLD 859 PT1	A	BLD 859	TP53 136	Q	chr17	*	7578524 G 54%		1617	Yes
BLD 866 PT1	G	BLD 866	FGFR3 249	S	chr4	C	1803568 C 11%		195	Yes
BLD 866 PT1	T	BLD 866	TP53 321	K	chr17	NULL	7576885 fs 9%		183	No

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BLD 866 PT1	T	BLD 866	TP53	324	D	chr17	7576876	C	N	9%	183	Yes
BLD 866 PT1	A	BLD 866	TP53	53	W	chr17	7579528	C	C	7%	135	No
BLDA 1924 PT1	G	BLDA 1924	FGFR3	249	S	chr4	1803568	C	C	30%	6711	No
BLDA 1924 PT1	G	BLDA 1924	CDKN2A	66	H	chr9	21971161	T	P	7%	673	No
BLDA 2902 PT1	T	BLD 535	KRAS	12	G	chr12	25398284	C	D	26%	5314	Yes
BLDA 2902 PT1	A	BLD 535	TP53	139	K	chr17	7578513	C	N	32%	3441	Yes
BLDA 2903 PT1	G	BLD 534	FGFR3	249	S	chr4	1803568	C	C	22%	1751	No
BLDA 2905 PT1	A	BLD 540	TP53	336	E	chr17	7574021	C	*	37%	682	Yes
BLDA 2905 PT1	T	BLD 540	ERBB2	310	S	chr17	37868208	C	F	26%	402	No
BLDA 2906 PT1	C	BLD 539	TP53	183	S	chr17	7578382	G	*	48%	2623	Yes
BLDA 2906 PT1	C	BLD 539	TP53	116	S	chr17	7579340	G	C	52%	2395	Yes
BLDA 2907 PT1	C	BLD 541	TP53	163	Y	chr17	7578442	T	C	58%	1160	No
BLDA 2908 PT1	A	BLD 542	KRAS	12	G	chr12	25398284	C	V	41%	3708	Yes
BLDA 2908 PT1	A	BLD 542	PIK3CA	542	E	chr3	178936082	G	K	46%	853	Yes
BLDA 2909 PT1	G	BLD 543	FGFR3	249	S	chr4	1803568	C	C	54%	8815	No
BLDA 2909 PT1	A	BLD 543	PIK3CA	545	E	chr3	178936091	G	K	49%	1034	No
BLDA 2910 PT1	G	BLD 544	FGFR3	373	Y	chr4	1806099	A	C	43%	3686	Yes
BLDA 2910 PT1	A	BLD 544	PIK3CA	542	E	chr3	178936082	G	K	46%	335	Yes
BLDA 2911 PT1	G	BLD 545	FGFR3	373	Y	chr4	1806099	A	C	31%	51	Yes
BLDA 2912 PT1	A	BLD 546	HRAS	13	G	chr11	534285	C	V	65%	14639	Yes
BLDA 2913 PT1	A	BLD 547	HRAS	61	Q	chr11	533874	T	L	5%	58	No
BLDA 2914 PT1	A	BLD 549	TP53	241	S	chr17	7577559	G	F	25%	3099	Yes
BLDA 2915 PT1	G	BLD 550	FGFR3	373	Y	chr4	1806099	A	C	41%	241	No
BLDA 2917 PT1	G	BLD 552	FGFR3	249	S	chr4	1803568	C	C	52%	2853	No

Table22.txt

BLDA 2918	PT1	BLD 554	TP53		chr17	7577543	C				
	G		246	M		I	61%		2066		Yes
BLDA 2918	PT1	BLD 554	TP53		chr17	7577506	C				
	T		259	D		N	61%		2066		Yes
BLDA 2920	PT1	BLD 537	TP53		chr17	7578190	T				
	C		220	Y		C	20%		4824		Yes
BLDA 2921	PT1	BLD 553	FGFR3		chr4	1806099	A				
	G		373	Y		C	17%		102		Yes
BLDA 2922	PT1	BLD 555	HRAS		chr11	533874	T				
	A		61	Q		L	33%		5856		Yes
BLDA 2923	PT1	BLD 556	TP53		chr17	7577596	A				
	G		229	C		R	62%		1762		Yes
BLDA 2924	PT1	BLD 557	TP53		chr17	7579542	C				
	G		49	D		H	23%		81		Yes
BLDA 2925	PT1	BLD 558	FGFR3		chr4	1803568	C				
	G		249	S		C	43%		1073		No
BLDA 2925	PT1	BLD 558	PIK3CA		chr3	178952085	A				
	T		1047	H		L	47%		277		No
BLDA 2925	PT1	BLD 558	TP53		chr17	7579705	C				
	T		31	V		I	42%		176		No
BLDA 2926	PT1	BLD 559	FGFR3		chr4	1803568	C				
	G		249	S		C	32%		12278		Yes
BLDA 2926	PT1	BLD 559	CDKN2A		chr9	21971036	C				
	G		108	D		H	51%		10707		Yes
BLDA 2926	PT1	BLD 559	TP53		chr17	7574018	G				
	A		337	R		C	55%		6161		Yes
BLDA 2928	PT1	BLDA 1790	TP53		chr17	7578263	G				
	A		196	R		*	48%		3662		No
BLDA 2929	PT1	BLDA 1791	FGFR3		chr4	1803568	C				
	G		249	S		C	23%		1560		No
BLDA 2930	PT1	BLDA 1792	TP53		chr17	7577565	T				
	C		239	N		S	38%		2726		Yes
BLDA 2930	PT1	BLDA 1792	PIK3CA		chr3	178936091	G				
	A		545	E		K	71%		773		Yes
BLDA 2931	PT1	BLDA 1793	TP53		chr17	7577548	C				
	T		245	G		S	35%		4674		No
BLDA 2934	PT1	BLDA 1796	FGFR3		chr4	1806099	A				
	G		373	Y		C	34%		1656		Yes
BLDA 2936	PT1	BLDA 1800	TP53		chr17	7578437	G				
	A		165	Q		*	57%		2394		Yes
BLDA 2937	PT1	BLDA 1801	FGFR3		chr4	1803564	C				
	T		248	R		C	44%		21650		Yes
BLDA 2937	PT1	BLDA 1801	PIK3CA		chr3	178952085	A				
	G		1047	H		R	74%		9942		Yes
BLDA 2938	PT1	BLDA 1802	FGFR3		chr4	1806089	G				
	T		370	G		C	46%		8862		Yes
BLDA 2939	PT1	BLDA 1804	FGFR3		chr4	1803568	C				
	G		249	S		C	34%		800		No

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BLDA 2939	PT1	A	BLDA 1804	PIK3CA	545	chr3	E	178936091	K	G	A
								8%		78	No
BLDA 2941	PT1	A	BLDA 1805	TP53	192	chr17	Q	7578275	*	G	A
								33%		2612	Yes
BLDA 2941	PT1	A	BLDA 1805	TP53	331	chr17	Q	7576855	*	G	A
								47%		1373	Yes
BLDA 2942	PT1	T	BLDA 1806	ERBB2	310	chr17	S	37868208	F	C	T
								32%		2524	No
BLDA 2942	PT1	A	BLDA 1806	TP53	248	chr17	R	7577539	W	G	A
								62%		2192	No
BLDA 2942	PT1	A	BLDA 1806	TP53	236	chr17	Y	7577574	F	T	A
								62%		2192	Yes
BLDA 2943	PT1	A	BLDA 1807	PIK3CA	545	chr3	E	178936091	K	G	A
								12%		76	Yes
BLDA 2944	PT1	G	BLDA 1808	FGFR3	373	chr4	Y	1806099	C	A	G
								72%		4506	Yes
BLDA 2948	PT1	G	BLDA 1812	FGFR3	249	chr4	S	1803568	C	C	G
								26%		2353	Yes
BLDA 2949	PT1	T	BLDA 2740	FGFR3	248	chr4	R	1803564	C	C	T
								25%		6945	Yes
BLDA 2950	PT1	fs	BLDA 1813	TP53	33	chr17	S	7579589	NULL	G	-
								77%		5109	No
BLDA 2951	PT1	A	BLDA 1814	TP53	247	chr17	N	7577541	I	T	A
								49%		354	Yes
BLDA 2952	PT1	G	BLDA 1815	TP53	11	chr17	E	7579882	Q	C	G
								11%		1296	Yes
BLDA 2952	PT1	fs	BLDA 1815	TP53	253	chr17	T	7577524	NULL	T	-
								77%		1054	No
BLDA 2955	PT1	A	BLDA 1818	TP53	171	chr17	E	7578419	*	C	A
								50%		2683	Yes
BLDA 2955	PT1	G	BLDA 1818	TP53	11	chr17	E	7579882	Q	C	G
								21%		2308	Yes
BLDA 2957	PT1	G	BLDA 1820	FGFR3	249	chr4	S	1803568	C	C	G
								24%		2090	Yes
BLDA 2957	PT1	T	BLDA 1820	TP53	261	chr17	S	7577499	N	C	T
								15%		207	Yes
BLDA 2958	PT1	G	BLDA 1821	FGFR3	373	chr4	Y	1806099	C	A	G
								42%		5259	Yes
BLDA 2959	PT1	T	BLDA 2719	TP53	280	chr17	R	7577099	K	C	T
								29%		5341	Yes
BLDA 2959	PT1	C	BLDA 2719	TP53	163	chr17	Y	7578442	C	T	C
								34%		3813	Yes
BLDA 2960	PT1	G	BLDA 1822	FGFR3	249	chr4	S	1803568	C	C	G
								58%		6673	Yes
BLDA 2962	PT1	G	BLDA 2725	FGFR3	249	chr4	S	1803568	C	C	G
								56%		9598	Yes
BLDA 2963	PT1	G	BLDA 2726	FGFR3	249	chr4	S	1803568	C	C	G
								6%		10711	Yes

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BLDA 2963	PT1	T	BLDA 2726	TP53	287	E	chr17	7577079	C	K	64%	4170	Yes
BLDA 2965	PT1	G	BLDA 2729	TP53	291	K	chr17	7577065	C	N	25%	4351	Yes
BLDA 2966	PT1	A	BLDA 2730	PIK3CA	542	E	chr3	178936082	G	K	10%	105	Yes
BLDA 2971	PT1	T	BLDA 2734	FGFR3	370	G	chr4	1806089	G	C	32%	20752	Yes
BLDA 2974	PT1	T	BLDA 2742	TP53	237	M	chr17	7577570	C	I	63%	5045	No
BLDA 2975	PT1	T	BLDA 2737	FGFR3	248	R	chr4	1803564	C	C	43%	4902	Yes
BLDA 2992	PT1	G	BLDA 1357	FGFR3	249	S	chr4	1803568	C	C	43%	2688	No
BLDA 3005	PT1	A	BLDA 2194	TP53	331	Q	chr17	7576855	G	*	49%	1829	Yes
BLDA 3016	PT1	A	BLDA 2281	TP53	317	Q	chr17	7576897	G	*	91%	4110	Yes
BLDA 3016	PT1	G	BLDA 2281	VHL	65	S	chr3	10183725	C	W	24%	1118	Yes
BLDA 3021	PT1	G	BLDA 2263	TP53	280	R	chr17	7577099	C	T	36%	11855	Yes
BLDA 3021	PT1	T	BLDA 2263	TP53	280	R	chr17	7577099	C	K	49%	11855	Yes
BLDA 3021	PT1	G	BLDA 2263	TP53	228	D	chr17	7577599	C	H	42%	1583	Yes
BLDA 3024	PT1	fs	BLD 283	TP53	237	M	chr17	7577571	ATGTAGTTGTAGTG (SEQ ID NO:728)	NULL	8%	1174	No
BLDA 3025	PT1	G	BLD 790	FGFR3	249	S	chr4	1803568	C	C	51%	1219	Yes
BLDA 3037	PT1	G	BLDA 2182	FGFR3	249	S	chr4	1803568	C	C	46%	5098	Yes
BLDA 3041	PT1	G	BLD 506	FGFR3	249	S	chr4	1803568	C	C	41%	5112	Yes
BLDA 3041	PT1	A	BLD 506	PIK3CA	545	E	chr3	178936091	G	K	32%	561	Yes
BLDA 3059	PT1	T	BLDA 1137	TP53	273	R	chr17	7577120	C	H	12%	1648	Yes
BLDA 3076	PT1	fs	BLDA 2867	TP53	80	P	chr17	7579447	A	NULL	35%	789	No
BLDA 3076	PT1	G	BLDA 2867	CDKN2A	66	H	chr9	21971161	T	P	6%	146	No
BLDA 3095	PT1	A	BLDA 2476	ERBB2	310	S	chr17	37868208	C	Y	42%	1770	Yes
BLDA 3095	PT1	G	BLDA 2476	FGFR3	249	S	chr4	1803568	C	C	42%	1278	Yes
BLDA 3207	PT1	A	BLDA 2787	TP53	285	E	chr17	7577085	C	*	59%	5322	Yes

Table22.txt

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Table23.txt

Table 23. Mutations detected by TERT Assay in primary tumor tissues from the Early Detection cohort.

Tumor Sample	Patient	Gene	chrom	hg 19 Position	Reference base	Variant base	Mutant allele frequency	# unique Detectable templatesin analyzed urine
BLD 237 PT 6225	BLD 237	TERT	chr5	1295228	C	T	24.51%	Yes
BLD 253 PT 7169	BLD 253	TERT	chr5	1295228	C	T	41.57%	Yes
BLD 333 PT 22836	BLD 333	TERT	chr5	1295228	C	T	64.48%	Yes
BLD 362 PT 5576	BLD 362	TERT	chr5	1295250	C	T	39.42%	Yes
BLD 436 PT 6632	BLD 436	TERT	chr5	1295228	C	T	31.74%	Yes
BLD 458 PT1 633	BLD 458	TERT	chr5	1295228	C	T	43.92%	Yes
BLDA 3041 PT1 5030	BLD 506	TERT	chr5	1295228	C	T	42.33%	Yes
BLDA 2906 PT1 1559	BLD 539	TERT	chr5	1295243	C	T	36.43%	Yes
BLDA 2905 PT1 30	BLD 540	TERT	chr5	1295228	C	T	76.67%	Yes
BLDA 2908 PT1 2331	BLD 542	TERT	chr5	1295250	C	T	46.03%	Yes
BLDA 2909 PT1 483	BLD 543	TERT	chr5	1295228	C	T	43.89%	Yes
BLDA 2910 PT1 130	BLD 544	TERT	chr5	1295228	C	T	46.15%	Yes
BLDA 2912 PT1 2482	BLD 546	TERT	chr5	1295228	C	T	29.29%	Yes
BLDA 2913 PT1 40	BLD 547	TERT	chr5	1295228	C	T	50.00%	Yes
BLDA 2914 PT1 1822	BLD 549	TERT	chr5	1295228	C	T	11.86%	Yes
BLDA 2916 PT1 712	BLD 551	TERT	chr5	1295228	C	T	37.50%	Yes
BLDA 2921 PT1 299	BLD 553	TERT	chr5	1295228	C	T	44.15%	No
BLDA 2923 PT1 1627	BLD 556	TERT	chr5	1295228	C	T	12.23%	No
BLDA 2924 PT1 45	BLD 557	TERT	chr5	1295250	C	T	44.44%	Yes
BLD 601 PT1 3090	BLD 601	TERT	chr5	1295228	C	T	37.86%	Yes

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BLD 625 PT1	BLD 625	TERT	chr5	1295228	C	T	34.88%	17157 Yes
BLD 646 PT1	BLD 646	TERT	chr5	1295228	C	T	21.57%	5002 Yes
BLDA 3025 PT1	BLD 790	TERT	chr5	1295250	C	T	54.97%	1419 Yes
BLD 835 PT1	BLD 835	TERT	chr5	1295228	C	T	23.48%	7500 Yes
BLD 841 PT1	BLD 841	TERT	chr5	1295250	C	T	20.64%	4211 Yes
BLD 866 PT1	BLD 866	TERT	chr5	1295228	C	A	7.21%	458 No
BLD 866 PT1	BLD 866	TERT	chr5	1295228	C	T	6.11%	458 Yes
BLDA 3059 PT1	BLDA 1137	TERT	chr5	1295228	C	T	10.66%	1473 Yes
BLDA 2928 PT1	BLDA 1790	TERT	chr5	1295228	C	T	26.73%	550 Yes
BLDA 2931 PT1	BLDA 1793	TERT	chr5	1295228	C	T	32.06%	1073 Yes
BLDA 2934 PT1	BLDA 1796	TERT	chr5	1295228	C	T	33.33%	351 Yes
BLDA 2935 PT1	BLDA 1798	TERT	chr5	1295228	C	T	66.61%	542 Yes
BLDA 2937 PT1	BLDA 1801	TERT	chr5	1295228	C	T	43.11%	4231 Yes
BLDA 2940 PT1	BLDA 1803	TERT	chr5	1295228	C	T	48.50%	2961 Yes
BLDA 2939 PT1	BLDA 1804	TERT	chr5	1295228	C	T	41.49%	617 Yes
BLDA 2943 PT1	BLDA 1807	TERT	chr5	1295228	C	T	64.94%	328 Yes
BLDA 2944 PT1	BLDA 1808	TERT	chr5	1295250	C	T	48.30%	2534 Yes
BLDA 2947 PT1	BLDA 1811	TERT	chr5	1295228	C	T	22.99%	1592 Yes
BLDA 2948 PT1	BLDA 1812	TERT	chr5	1295250	C	T	42.38%	925 Yes
BLDA 2954 PT1	BLDA 1816	TERT	chr5	1295228	C	T	12.76%	1442 Yes
BLDA 2955 PT1	BLDA 1818	TERT	chr5	1295228	C	T	8.25%	618 Yes
BLDA 2957 PT1	BLDA 1820	TERT	chr5	1295250	C	T	25.12%	430 Yes
BLDA 2960 PT1	BLDA 1822	TERT	chr5	1295228	C	T	33.47%	3370 Yes
BLDA 1924 PT1	BLDA 1924	TERT	chr5	1295228	C	T	32.20%	1817 Yes

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BLDA 3037 PT1	BLDA 2182	TERT	chr5	1295228	C	T	45.06%	4774 Yes
BLDA 3005 PT1	BLDA 2194	TERT	chr5	1295250	C	T	44.60%	982 Yes
BLDA 3021 PT1	BLDA 2263	TERT	chr5	1295228	C	T	73.99%	16586 Yes
BLDA 3016 PT1	BLDA 2281	TERT	chr5	1295228	C	T	59.32%	1460 Yes
BLDA 3095 PT1	BLDA 2476	TERT	chr5	1295228	C	T	47.37%	7573 Yes
BLDA 2962 PT1	BLDA 2725	TERT	chr5	1295228	C	T	53.66%	41 Yes
BLDA 2963 PT1	BLDA 2726	TERT	chr5	1295250	C	T	29.30%	7646 Yes
BLDA 2964 PT1	BLDA 2727	TERT	chr5	1295228	C	T	5.86%	4200 Yes
BLDA 2968 PT1	BLDA 2728	TERT	chr5	1295228	C	T	38.13%	1280 Yes
BLDA 2965 PT1	BLDA 2729	TERT	chr5	1295228	C	T	28.43%	1780 Yes
BLDA 2969 PT1	BLDA 2732	TERT	chr5	1295228	C	T	12.75%	2032 Yes
BLDA 2970 PT1	BLDA 2733	TERT	chr5	1295228	C	T	33.61%	238 Yes
BLDA 2976 PT1	BLDA 2738	TERT	chr5	1295228	C	T	22.35%	7003 Yes

Table24.txt

Table 24. Demographic and clinical features of the Surveillance Cohort

Initial Tumor BV #	Initial Tumor Grade	Recurrence Tumor Source	Recurrence Tumor Diagnosis	Recurrence Tumor Sex	Recurrence Tumor Stage	Recurrence Tumor Age	Time between Initial Tumor and Recurrence Tumor Diagnosis (months)	Initial Urine Cytology Diagnosis	Initial Urine sample collection and tumor detection Tumor Diagnosis	Initial Tumor Stage	Initial Tumor Grade
BLD 093	U	JHH	HGTCC	F	pTa	52	0.00	N/A	HGTCC	pTa	HG
BLD 094	U	JHH	INTCC	F	pT2	73	0.00	N/A	HGTCC	pTa	HG
BLD 095	U	JHH	INTCC	M	pT1	32	0.00	N/A	INTCC	pT1	HG
BLD 096	U	JHH	CIS	M	pTis	57	0.00	N/A	INTCC	pT3	HG
BLD 097	U	JHH	INTCC	M	pT2	29	0.00	N/A	INTCC	pT1	HG
BLD 098	U	JHH	LGTCC	M	pTa	69	0.00	N/A	INTCC	pT1	HG
BLD 099	U	JHH	HGTCC	M	pTa	60	0.00	N/A	INTCC	pT2	HG
BLD 100	U	JHH	HGTCC	M	pTa	67	0.00	N/A	HGTCC	pTa	HG
BLD 101	U	JHH	INTCC	F	pT2	44	0.00	N/A	INTCC	pT2	HG
BLD 102	U	JHH	N/A	M	N/A	77	N/A	N/A	INTCC	PT1	HG
BLD 103	U	JHH	N/A	M	N/A	85	N/A	N/A	INTCC	pT1	HG
BLD 104	U	JHH	CIS	M	ptis	55	0.00	N/A	INTCC	pT1	HG
BLD 105	U	JHH	LGTCC	M	pTa	59	0.00	N/A	HGTCC	pTa	HG
BLD 106	U	JHH	N/A	M	N/A	77	N/A	N/A	HGTCC	pTa	HG
BLD 108	U	JHH	INTCC	F	pT1	37	0.00	N/A	INTCC	pT1	HG
BLD 109	U	JHH	HGTCC	F	pTa	66	0.00	N/A	HGTCC	pTa	HG
BLD 148	U	JHH	INTCC	M	pT1	63	0.00	1	INTCC	pT1	HG
BLD 149	U	JHH	INTCC	M	pT1	87	0.00	1	INTCC	pT1	HG
BLD 153	U	JHH	HGTCC	M	pTa	62	0.00	2	HGTCC	pTa	HG
BLD 160	U	JHH		F		41		0	INTCC	pT1	HG

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	N/A	N/A	N/A	N/A				
BLD 164	U	JHH	F	54	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 165	U	JHH	M	29	0	INTCC	pT3	HG
	INTCC	pT1	HG	0.00				
BLD 167	U	JHH	M	63	2	LGTCC	pTa	LG
	N/A	N/A	N/A	0.00				
BLD 168	U	JHH	F	56	2	LGTCC	pTa	LG
	LGTCC	pTa	LG	0.00				
BLD 170	U	JHH	M	74	0	LGTCC	pTa	LG
	LGTCC	pTa	LG	0.00				
BLD 174	U	JHH	M	67	2	HGTCC	pTa	HG
	HGTCC	pTa	HG	0.00				
BLD 176	U	JHH	F	74	0	INTCC	pT3	HG
	INTCC	pT3	HG	0.00				
BLD 182	U	JHH	F	51	0	HGTCC	pTa	HG
	N/A	N/A	N/A	N/A				
BLD 190	U	JHH	M	51	0	HGTCC	pTa	HG
	N/A	N/A	N/A	N/A				
BLD 191	U	JHH	M	75	2	INTCC	pT2	HG
	HGTCC	pTa	HG	0.00				
BLD 194	U	JHH	M	38	0	INTCC	pT1	HG
	HGTCC	pTa	HG	0.00				
BLD 195	U	JHH	M	63	0	LGTCC	pTa	LG
	N/A	N/A	N/A	N/A				
BLD 196	U	JHH	M	59	0	LGTCC	pTa	LG
	LGTCC	pTa	LG	0.00				
BLD 197	U	JHH	M	66	2	HGTCC	pTa	HG
	N/A	N/A	N/A	N/A				
BLD 198	U	JHH	M	58	1	INTCC	pT3	HG
	N/A	N/A	N/A	0.00				
BLD 199	U	JHH	F	56	0	HGTCC	pTa	HG
	N/A	N/A	N/A	N/A				
BLD 201	U	JHH	M	54	0	LGTCC	pTa	LG
	LGTCC	pTa	LG	0.00				
BLD 202	U	JHH	M	57	0	HGTCC	pTa	HG
	N/A	N/A	N/A	0.00				
BLD 207	U	JHH	F	65	1	INTCC	pT2	HG
	INTCC	pT1	HG	0.00				
BLD 209	U	JHH	M	67	0	CIS	pTis	HG
	N/A	N/A	N/A	N/A				
BLD 212	U	JHH	M	32	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 213	U	JHH	M	66	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 218	U	JHH	M	79	0	LGTCC	pTa	LG
	LGTCC	pTa	HG	0.00				
BLD 220	U	JHH	M	68	0	LGTCC	pTa	LG

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        N/A         N/A         N/A         N/A
BLD 221 U       JHH     M       67      2           INTCC           pT2         HG
        N/A         N/A         N/A         N/A
BLD 223 U       JHH     F       58      2           LGTCC           pTa         LG
        LGTCC       pTa         LG          0.00
BLD 225 U       JHH     F       55      2           INTCC           pT1         HG
        HGTCC       pTa         HG          0.00
BLD 227 U       JHH     M       57      0           N/A             N/A         N/A
        LGTCC       pTa         LG          0.00
BLD 234 U       JHH     F       62      2           INTCC           pT1         HG
        INTCC       pT1         HG          0.00
BLD 238 U1      JHH     F       51      0           LGTCC           pTa         LG
        N/A         N/A         N/A         N/A
BLD 239 U1      JHH     M       62      2           HGTCC           pTa         HG
        CIS         pTis        HG          0.00
BLD 242 U1      JHH     M       28      2           LGTCC           pTa         LG
        N/A         N/A         N/A         N/A
BLD 247 U1      JHH     M       65      2           INTCC           pT1         HG
        INTCC       pT1         HG          0.00
BLD 248 U1      JHH     F       45      2           INTCC           pT2         HG
        N/A         N/A         N/A         N/A
BLD 254 U1      JHH     F       57      2           HGTCC           pTa         HG
        N/A         N/A         N/A         N/A
BLD 255 U1      JHH     M       62      2           PUNLMP          pTa
PUNLMP      N/A         N/A         N/A         N/A
BLD 256 U1      JHH     M       30      0           PUNLMP          pTa
PUNLMP      N/A         N/A         N/A         N/A
BLD 257 U1      JHH     M       58      2           INTCC           pT1         HG
        HGTCC       pTa         HG          0.00
BLD 259 U1      JHH     F       76      2           INTCC           pT2         HG
        N/A         N/A         N/A         N/A
BLD 262 U1      JHH     M       65      0           CIS             pTis        HG
        N/A         N/A         N/A         N/A
BLD 265 U1      JHH     M       61      0           LGTCC           pTa         LG
        N/A         N/A         N/A         N/A
BLD 270 U1      JHH     N/A     N/A     0           INTCC           pT2         HG
        N/A         N/A         N/A         N/A
BLD 276 U1      JHH     N/A     N/A     1           INTCC           pT1         HG
        HGTCC       pTa         HG          0.00
BLD 279 U1      JHH     N/A     N/A     2           LGTCC           pTa         LG
        N/A         N/A         N/A         N/A
BLD 289 U1      JHH     F       22      0           INTCC           pT1         HG
        N/A         N/A         N/A         N/A
BLD 291 U1      JHH     M       72      0           LGTCC           pTa         LG
        N/A         N/A         N/A         N/A
BLD 292 U1      JHH     M       63      1           HGTCC           pTa         HG
        HGTCC       pTa         HG          0.00
BLD 294 U1      JHH     M       65      2           CIS             pTis        HG
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	N/A		N/A		N/A		N/A		
BLD	299	U1	JHH	N/A	N/A	2	HGTCC	pTa	HG
	LGTCC		pTa		LG		0.00		
BLD	302	U1	JHH	N/A	N/A	2	LGTCC	pTa	LG
	N/A		N/A		N/A		0.00		
BLD	303	U1	JHH	M	54	2	INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD	305	U1	JHH	M	54	0	LGTCC	pTa	LG
	N/A		N/A		N/A		N/A		
BLD	307	U1	JHH	M	62	0	INTCC	pT2	HG
	N/A		N/A		N/A		0.00		
BLD	309	U1	JHH	F	55	0	INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD	311	U1	JHH	M	68	1	CIS	pTis	HG
	HGTCC		pTa		HG		0.00		
BLD	313	U1	JHH	M	52	2	INTCC	pT2	HG
	N/A		N/A		N/A		N/A		
BLD	318	U1	JHH	M	63	0	HGTCC	pTa	HG
	N/A		N/A		N/A		N/A		
BLD	322	U1	JHH	M	83	2	N/A	N/A	N/A
	LGTCC		pTa		LG		0.00		
BLD	324	U1	JHH	F	45	2	INTCC	pT1	HG
	INTCC		pT1		HG		0.00		
BLD	330	U1	JHH	M	29	0	LGTCC	pTa	LG
	N/A		N/A		N/A		N/A		
BLD	334	U1	JHH	M	65	1	INTCC	pT1	HG
	CIS		pTis		HG		0.00		
BLD	353	U1	JHH	M	58	0	INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD	354	U1	JHH	M	34	2	LGTCC	pTa	LG
	N/A		N/A		N/A		N/A		
BLD	355	U1	JHH	F	63	2	LGTCC	pTa	LG
	PUNLMP		pTa		N/A		0.03		
BLD	360	U1	JHH	M	59	2	HGTCC	pTa	HG
	INTCC		pT1		HG		0.03		
BLD	383	U1	JHH	M	79	2	N/A	N/A	N/A
	N/A		N/A		N/A		N/A		
BLD	386	U1	JHH	M	69	2	CIS	pTis	HG
	CIS		pTis		HG		0.03		
BLD	387	U1	JHH	F	57	0	INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD	388	U1	JHH	M	73	0	INTCC	pT2	HG
	N/A		N/A		N/A		N/A		
BLD	390	U1	JHH	M	63	0	CIS	pTis	HG
	N/A		N/A		N/A		N/A		
BLD	405	U1	JHH	F	68	0	INTCC	pT3	HG
	INTCC		pT3		HG		0.03		
BLD	408	U1	JHH	M	58	0	INTCC	pT1	HG

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	N/A		N/A		N/A		N/A		
BLD 419	U1	JHH	M		77	0		HGTCC	pTa	HG
	N/A		N/A		N/A		N/A		
BLD 420	U1	JHH	M		68	0		INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD 425	U1	JHH	F		65	1		INTCC	pT1	HG
	CIS		pTis		HG		0.03		
BLD 434	U1	JHH	M		58	2		INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD 440	U1	JHH	M		62	1		HGTCC	pTa	HG
	HGTCC		pTa		HG		0.23		
BLD 448	U1	JHH	M		59	2		LGTCC	pTa	LG
	LGTCC		pTa		LG		0.33		
BLD 451	U1	JHH	M		53	0		PUNLMP	pTa	
PUNLMP		N/A		N/A		N/A		N/A		
BLD 454	U1	JHH	N/A		N/A	2		LGTCC	pTa	LG
	LGTCC		pTa		LG		0.33		
BLD 461	U1	JHH	F		70	1		INTCC	pT1	HG
	CIS		pTis		HG		0.40		
BLD 471	U1	JHH	M		77	2		HGTCC	pTa	HG
	HGTCC		pTa		HG		0.43		
BLD 473	U1	JHH	M		67	2		PUNLMP	pTa	
PUNLMP		LGTCC		pTa		LG		0.47		
BLD 480	U1	JHH	M		20	2		INTCC	pT2	HG
	INTCC		pT2		HG		0.50		
BLD 484	U1	JHH	M		58	2		LGTCC	pTa	LG
	LGTCC		pTa		LG		0.50		
BLD 489	U1	JHH	M		40	2		N/A	N/A	N/A
	LGTCC		pTa		LG		0.50		
BLD 493	U1	JHH	M		69	0		INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD 498	U1	JHH	M		64	0		INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD 500	U1	JHH	M		42	0		INTCC	pT1	HG
	N/A		N/A		N/A		N/A		
BLD 513	U1	JHH	M		74	2		INTCC	pT3	HG
	HGTCC		pTa		HG		0.57		
BLD 518	U1	JHH	N/A		N/A	2		INTCC	pT3	HG
	N/A		N/A		N/A		N/A		
BLD 527	U1	JHH	M		39	2		INTCC	pT1	HG
	HGTCC		pTa		HG		0.60		
BLD 529	U1	JHH	M		77	2		INTCC	pT2	HG
	N/A		N/A		N/A		N/A		
BLD 531	U1	JHH	M		61	0		PUNLMP	pTa	
PUNLMP		LGTCC		pTa		LG		0.67		
BLD 560	U1	JHH	M		41	2		LGTCC	pta	LG
	LGTCC		pTa		LG		0.70		
BLD 561	U2	JHH	F		34	2		LGTCC	pta	LG

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	N/A	N/A	N/A	N/A				
BLD 562	U1	JHH	M	72	N/A	HGTCC	pta	HG
	LGTCC	pTa	LG	0.70				
BLD 563	U1	JHH	M	63	0	INTCC	pt1	HG
	N/A	N/A	N/A	N/A				
BLD 565	U1	JHH	M	71	N/A	INTCC	pT2	HG
	INTCC	pT2	HG	0.73				
BLD 568	U1	JHH	F	68	2	HGTCC	pta	HG
	HGTCC	pTa	HG	0.73				
BLD 569	U1	JHH	N/A	N/A	N/A	CIS	pTis	HG
	HGTCC	pTa	HG	0.77				
BLD 572	U1	JHH	M	60	N/A	LGTCC	pta	LG
	LGTCC	pTa	LG	0.80				
BLD 580	U1	JHH	M	51	N/A	CIS	pTis	HG
	CIS	pTis	HG	0.90				
BLD 581	U1	JHH	M	57	N/A	N/A	N/A	N/A
	LGTCC	pTa	LG	0.93				
BLD 582	U1	JHH	M	57	1	N/A	N/A	N/A
	CIS	pTis	HG	0.97				
BLD 584	U1	JHH	M	76	N/A	INTCC	pT4	HG
	INTCC	pT4	HG	1.00				
BLD 590	U1	JHH	M	55	0	PUNLMP	pTa	
PUNLMP	N/A	N/A	N/A	N/A				
BLD 591	U1	JHH	F	62	2	LGTCC	pta	LG
	LGTCC	pTa	LG	1.00				
BLD 603	U1	JHH	M	67	0	CIS	pTis	HG
	N/A	N/A	N/A	N/A				
BLD 604	U1	JHH	M	51	2	INTCC	pT3	HG
	N/A	N/A	N/A	N/A				
BLD 612	U1	JHH	M	53	1	INTCC	pT2	HG
	HGTCC	pTa	HG	1.00				
BLD 616	U1	JHH	N/A	N/A	2	LGTCC	pTa	LG
	LGTCC	pTa	LG	1.10				
BLD 660	U1	JHH	M	61	2	HGTCC	pTa	HG
	CIS	pTis	HG	1.20				
BLD 663	U1	JHH	F	65	2	LGTCC	pTa	LG
	LGTCC	pTa	LG	1.23				
BLD 672	U1	JHH	M	77	2	LGTCC	pTa	LG
	N/A	N/A	N/A	N/A				
BLD 682	U1	JHH	M	62	2	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 692	U1	JHH	M	31	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 694	U1	JHH	F	74	2	LGTCC	pTa	LG
	LGTCC	pTa	LG	1.27				
BLD 705	U1	JHH	M	68	0	INTCC	pT2	HG
	N/A	N/A	N/A	N/A				
BLD 722	U1	JHH	M	69	0	PUNLMP	pTa	

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PUNLMP	N/A	N/A	N/A	N/A					
BLD 726	U1	JHH	M	76	2		INTCC	pT1	HG
	N/A	N/A	N/A	N/A					
BLD 729	U1	JHH	F	66	2		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A					
BLD 735	U1	JHH	M	72	0		N/A	N/A	N/A
	N/A	N/A	N/A	N/A					
BLD 738	U1	JHH	M	64	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	1.30					
BLD 743	U1	JHH	M	63	2		HGTCC	pTa	HG
	CIS	pTis	HG	1.33					
BLD 761	U1	JHH	M	36	2		INTCC	pT2	HG
	N/A	N/A	N/A	N/A					
BLD 762	U1	JHH	M	33	0		LGTCC	pTa	LG
	LGTCC	pTa	LG	1.40					
BLD 763	U1	JHH	F	65	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	1.43					
BLD 766	U1	JHH	M	68	0		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A					
BLD 768	U1	JHH	M	32	0		HGTCC	pTa	HG
	N/A	N/A	N/A	N/A					
BLD 771	U1	JHH	F	56	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	1.53					
BLD 776	U1	JHH	M	69	2		INTCC	pT1	HG
	HGTCC	pTa	HG	1.57					
BLD 781	U1	JHH	M	66	2		INTCC	pT2	HG
	N/A	N/A	N/A	N/A					
BLD 800	U1	JHH	M	55	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	1.70					
BLD 801	U1	JHH	F	62	2		LGTCC	pTa	LG
	N/A	N/A	N/A	1.87					
BLD 803	U1	JHH	M	55	0		LGTCC	pTa	LG
	LGTCC	pTa	LG	2.00					
BLD 810	U1	JHH	M	36	2		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A					
BLD 816	U1	JHH	M	60	0		HGTCC	pTa	HG
	N/A	N/A	N/A	N/A					
BLD 821	U1	JHH	M	46	2		HGTCC	pTa	HG
	N/A	N/A	N/A	N/A					
BLD 872	U1	JHH	F	52	0		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A					
BLD 954	U1	Brazil	N/A	N/A	N/A		LGTCC	pta	LG
	PUNLMP	pTa	N/A	2.03					
BLD 955	U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A					
BLD 956	U1	Brazil	N/A	N/A	0		INTCC	pT1	HG
	N/A	N/A	N/A	N/A					
BLD 957	U1	Brazil	N/A	N/A	0		LGTCC	pta	LG

Table24.txt

	N/A	N/A	N/A	N/A				
BLD 958	U1	Brazil	N/A	N/A	N/A	LGTCC	pta	LG
	INTCC	pT1	HG	2.10				
BLD 961	U1	Brazil	N/A	N/A	N/A	HGTCC	pta	HG
	INTCC	pT1	HG	2.23				
BLD 962	U1	Brazil	N/A	N/A	N/A	HGTCC	pta	HG
	HGTCC	pTa	HG	2.27				
BLD 963	U1	Brazil	N/A	N/A	0	HGTCC	pta	HG
	HGTCC	pta	HG	2.60				
BLD 964	U1	Brazil	N/A	N/A	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 965	U1	Brazil	N/A	N/A	0	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 966	U1	Brazil	N/A	N/A	0	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 967	U1	Brazil	N/A	N/A	N/A	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 968	U1	Brazil	N/A	N/A	0	N/A	N/A	N/A
	N/A	N/A	N/A	N/A				
BLD 969	U1	Brazil	N/A	N/A	N/A	INTCC	pT1	HG
	INTCC	pT1	HG	2.63				
BLD 971	U1	Brazil	N/A	N/A	N/A	HGTCC	pta	HG
	HGTCC	pTa	HG	2.70				
BLD 974	U1	Brazil	N/A	N/A	0	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 976	U1	Brazil	N/A	N/A	N/A	HGTCC	pta	HG
	HGTCC	pTa	HG	3.10				
BLD 977	U1	Brazil	N/A	N/A	N/A	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 978	U1	Brazil	N/A	N/A	0	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 980	U1	Brazil	N/A	N/A	0	CIS	pTis	HG
	N/A	N/A	N/A	N/A				
BLD 982	U1	Brazil	N/A	N/A	N/A	INTCC	pT1	HG
	INTCC	pT1	HG	3.13				
BLD 984	U1	Brazil	N/A	N/A	N/A	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 985	U1	Brazil	N/A	N/A	N/A	N/A	N/A	N/A
	N/A	N/A	N/A	N/A				
BLD 987	U1	Brazil	N/A	N/A	0	LGTCC	pta	LG
	LGTCC	pTa	LG	3.30				
BLD 993	U1	Brazil	N/A	N/A	0	LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLD 995	U1	Brazil	N/A	N/A	N/A	INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLD 996	U1	Brazil	N/A	N/A	N/A	N/A	N/A	N/A
	INTCC	pT1	HG	3.47				
BLD 999	U1	Brazil	N/A	N/A	1	CIS	pTis	HG

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        N/A         N/A         N/A         N/A
BLDA 1001 U1    Brazil  N/A      N/A      N/A          LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1002 U1    Brazil  N/A      N/A      N/A          HGTCC           pta           HG
        HGTCC       pTa         HG          3.50
BLDA 1003 U1    Brazil  N/A      N/A      0            CIS             pTis          HG
        N/A         N/A         N/A         N/A
BLDA 1004 U1    Brazil  N/A      N/A      N/A          LGTCC           pta           LG
        LGTCC       pTa         LG          3.57
BLDA 1009 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1010 U1    Brazil  N/A      N/A      0            INTCC           pT1           HG
        N/A         N/A         N/A         N/A
BLDA 1011 U1    Brazil  N/A      N/A      N/A          INTCC           pT1           HG
        N/A         N/A         N/A         N/A
BLDA 1013 U1    Brazil  N/A      N/A      2            HGTCC           pta           HG
        HGTCC       pTa         HG          3.70
BLDA 1014 U1    Brazil  N/A      N/A      N/A          PUNLMP          pTa
PUNLMP        PUNLMP      pTa          N/A         3.83
BLDA 1016 U1    Brazil  N/A      N/A      0            HGTCC           pta           HG
        N/A         N/A         N/A         N/A
BLDA 1017 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1018 U1    Brazil  N/A      N/A      2            HGTCC           pta           HG
        N/A         N/A         N/A         N/A
BLDA 1019 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1021 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        LGTCC       pTa         LG          3.90
BLDA 1022 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1023 U1    Brazil  N/A      N/A      0            LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1024 U1    Brazil  N/A      N/A      0            HGTCC           pta           HG
        N/A         N/A         N/A         N/A
BLDA 1026 U1    Brazil  N/A      N/A      0            INTCC           pT1           HG
        INTCC       pT1         HG          4.10
BLDA 1028 U1    Brazil  N/A      N/A      N/A          LGTCC           pta           LG
        N/A         N/A         N/A         N/A
BLDA 1029 U1    Brazil  N/A      N/A      0            HGTCC           pta           HG
        INTCC       pT1         HG          4.20
BLDA 1030 U1    Brazil  N/A      N/A      N/A          LGTCC           pta           LG
        LGTCC       pTa         LG          4.90
BLDA 1031 U1    Brazil  N/A      N/A      N/A          INTCC           pT1           HG
        INTCC       pT1         HG          4.90
BLDA 1033 U1    Brazil  N/A      N/A      0            N/A             N/A           N/A
        N/A         N/A         N/A         N/A
BLDA 1035 U1    Brazil  N/A      N/A      0            HGTCC           pta           HG
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        N/A         N/A         N/A         N/A
BLDA 1037 U1    Brazil  N/A     N/A     0           PUNLMP          pTa
PUNLMP        N/A         N/A         N/A         N/A
BLDA 1038 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        HGTCC       pTa         HG          5.13
BLDA 1040 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        N/A         N/A         N/A         N/A
BLDA 1041 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        N/A         N/A         N/A         5.17
BLDA 1042 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        N/A         N/A         N/A         N/A
BLDA 1043 U1    Brazil  N/A     N/A     N/A         LGTCC           pta             LG
        LGTCC       pTa         LG          5.57
BLDA 1046 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        LGTCC       pTa         LG          5.70
BLDA 1050 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        LGTCC       pTa         LG          6.00
BLDA 1054 U1    Brazil  N/A     N/A     0           N/A             N/A             N/A
        N/A         N/A         N/A         N/A
BLDA 1055 U1    Brazil  N/A     N/A     N/A         LGTCC           pta             LG
        LGTCC       pTa         LG          6.13
BLDA 1056 U1    Brazil  N/A     N/A     N/A         INTCC           pT1             HG
        INTCC       pT1         HG          6.53
BLDA 1057 U1    Brazil  N/A     N/A     1           CIS             pTis            HG
        CIS         pTis        HG          6.57
BLDA 1059 U1    Brazil  N/A     N/A     N/A         HGTCC           pta             HG
        N/A         N/A         N/A         N/A
BLDA 1060 U1    Brazil  N/A     N/A     0           INTCC           pT1             HG
        CIS         pTis        HG          6.80
BLDA 1061 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
        N/A         N/A         N/A         N/A
BLDA 1062 U1    Brazil  N/A     N/A     N/A         HGTCC           pta             HG
        HGTCC       pTa         HG          6.90
BLDA 1064 U1    Brazil  N/A     N/A     N/A         INTCC           pT1             HG
        INTCC       PT1         HG          7.00
BLDA 1066 U1    Brazil  N/A     N/A     2           CIS             pTis            HG
        CIS         pTis        HG          7.13
BLDA 1067 U1    Brazil  N/A     N/A     0           HGTCC           pta             HG
        N/A         N/A         N/A         N/A
BLDA 1068 U1    Brazil  N/A     N/A     N/A         HGTCC           pta             HG
        N/A         N/A         N/A         N/A
BLDA 1069 U1    Brazil  N/A     N/A     0           PUNLMP          pTa
PUNLMP        N/A         N/A         N/A         7.20
BLDA 1070 U1    Brazil  N/A     N/A     0           HGTCC           pta             HG
        N/A         N/A         N/A         N/A
BLDA 1071 U1    Brazil  N/A     N/A     0           HGTCC           pta             HG
        N/A         N/A         N/A         N/A
BLDA 1072 U1    Brazil  N/A     N/A     0           LGTCC           pta             LG
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	LGTCC	pTa	LG	7.67				
BLDA 1073 U1	Brazil	N/A	N/A	0		HGTCC	pta	HG
	INTCC	pT1	HG	7.67				
BLDA 1074 U1	Brazil	N/A	N/A	0		CIS	pTis	HG
	N/A	N/A	N/A	N/A				
BLDA 1076 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1080 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1082 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	LGTCC	pTa	LG	7.83				
BLDA 1084 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1085 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	LGTCC	pTa	LG	8.07				
BLDA 1086 U1	Brazil	N/A	N/A	N/A		LGTCC	pta	LG
	LGTCC	pTa	LG	8.17				
BLDA 1087 U1	Brazil	N/A	N/A	0		HGTCC	pta	HG
	N/A	N/A	N/A	N/A				
BLDA 1088 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1089 U1	Brazil	N/A	N/A	1		LGTCC	pta	LG
	LGTCC	pTa	LG	8.20				
BLDA 1090 U1	Brazil	N/A	N/A	0		HGTCC	pta	HG
	N/A	N/A	N/A	N/A				
BLDA 1093 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1096 U1	Brazil	N/A	N/A	N/A		INTCC	pT1	HG
	LGTCC	pTa	LG	8.50				
BLDA 1098 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1099 U1	Brazil	N/A	N/A	0		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1100 U1	Brazil	N/A	N/A	2		INTCC	pT1	HG
	HGTCC	pTa	HG	9.10				
BLDA 1103 U1	Brazil	N/A	N/A	0		HGTCC	pta	HG
	HGTCC	pTa	HG	9.17				
BLDA 1104 U1	Brazil	N/A	N/A	N/A		INTCC	pT1	HG
	INTCC	pT1	HG	9.23				
BLDA 1105 U1	Brazil	N/A	N/A	N/A		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1107 U1	Brazil	N/A	N/A	0		HGTCC	pta	HG
	HGTCC	pTa	HG	9.43				
BLDA 1109 U1	Brazil	N/A	N/A	0		PUNLMP	pTa	
PUNLMP	N/A	N/A	N/A	N/A				
BLDA 1111 U1	Brazil	N/A	N/A	N/A		INTCC	pT2	HG
	N/A	N/A	N/A	9.47				
BLDA 1112 U1	Brazil	N/A	N/A	2		LGTCC	pta	LG

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	N/A	N/A	N/A	N/A				
BLDA 1113 U1	Brazil	N/A	N/A	N/A		LGTCC	pta	LG
	LGTCC	pTa	LG	9.50				
BLDA 1114 U1	Brazil	N/A	N/A	N/A		HGTCC	pta	HG
	HGTCC	pTa	HG	9.57				
BLDA 1115 U1	Brazil	N/A	N/A	N/A		LGTCC	pta	LG
	N/A	N/A	N/A	N/A				
BLDA 1141 U1	JHH	F	61	0		PUNLMP	pTa	
PUNLMP	N/A	N/A	N/A	N/A				
BLDA 1142 U1	JHH	M	82	2		CIS	pTis	HG
	N/A	N/A	N/A	9.60				
BLDA 1155 U1	JHH	F	61	0		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A				
BLDA 1157 U1	JHH	M	71	0		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A				
BLDA 1166 U1	JHH	M	65	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	9.80				
BLDA 1170 U1	JHH	M	56	0		LGTCC	pTa	LG
	N/A	N/A	N/A	N/A				
BLDA 1177 U1	JHH	M	67	2		INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLDA 1180 U1	JHH	M	70	1		INTCC	pT2	HG
	INTCC	pT2	HG	11.33				
BLDA 1187 U1	JHH	M	76	2		INTCC	pT3	HG
	N/A	N/A	N/A	11.40				
BLDA 1191 U1	JHH	F	63	0		LGTCC	PTa	LG
	N/A	N/A	N/A	N/A				
BLDA 1193 U1	JHH	M	63	0		INTCC	pT1	HG
	N/A	N/A	N/A	N/A				
BLDA 1194 U1	JHH	N/A	N/A	1		INTCC	pT1	HG
	INTCC	pT1	HG	11.63				
BLDA 1211 U1	JHH	M	69	2		INTCC	pT1	HG
	HGTCC	pTa	HG	12.50				
BLDA 1221 U1	JHH	F	39	2		LGTCC	PTa	LG
	LGTCC	pTa	LG	12.60				
BLDA 1232 U1	JHH	N/A	N/A	2		LGTCC	PTa	LG
	LGTCC	pTa	LG	12.77				
BLDA 1250 U1	JHH	M	72	2		INTCC	pT1	HG
	LGTCC	pTa	LG	13.07				
BLDA 1252 U1	JHH	M	50	1		CIS	pTis	HG
	CIS	pTis	HG	13.33				
BLDA 1256 U1	JHH	N/A	N/A	1		INTCC	pT1	HG
	INTCC	pT1	HG	13.53				
BLDA 1314 U1	JHH	M	70	2		HGTCC	pTa	HG
	CIS	pTis	HG	13.53				
BLDA 1409 U1	JHH	N/A	N/A	2		INTCC	pT1	HG
	INTCC	pT1	HG	13.77				
BLDA 1453 U1	JHH	F	86	0		LGTCC	PTa	LG

Table24.txt

	LGTCC	pTa	LG	13.77				
BLDA 1457 U1	JHH	F	49	0		HGTCC	PTa	HG
	HGTCC	pTa	HG	14.23				
BLDA 1463 U1	JHH	M	56	0		HGTCC	PTa	HG
	LGTCC	pTa	LG	14.37				
BLDA 1481 U1	JHH	F	73	0		LGTCC	pta	LG
	PUNLMP	pTa	N/A	14.43				
BLDA 1828 U1	JHH	F	63	1		INTCC	pT2	HG
	HGTCC	pTa	HG	14.80				
BLDA 1854 U1	JHH	M	51	1		CIS	pTis	HG
	CIS	pTis	HG	15.20				
BLDA 1859 U1	JHH	M	61	2		CIS	pTis	HG
	INTCC	pT2	HG	16.00				
BLDA 1865 U1	JHH	M	63	0		LGTCC	pTa	LG
	LGTCC	pTa	LG	16.20				
BLDA 1880 U1	JHH	M	53	1		HGTCC	pTa	HG
	HGTCC	pTa	HG	16.37				
BLDA 1883 U1	JHH	M	59	0		LGTCC	pTa	LG
	LGTCC	pTa	HG	16.80				
BLDA 1890 U1	JHH	M	69	0		LGTCC	pTa	LG
	LGTCC	pTa	LG	16.83				
BLDA 2015 U1	JHH	M	67	2		CIS	pTis	HG
	CIS	pTis	HG	17.73				
BLDA 2020 U1	JHH	F	93	2		LGTCC	pta	LG
	LGTCC	pTa	LG	18.87				
BLDA 2023 U1	JHH	N/A	N/A	2		LGTCC	pta	LG
	LGTCC	pTa	LG	19.03				
BLDA 2072 U1	JHH	M	76	1		CIS	pTis	HG
	CIS	pTis	HG	19.10				
BLDA 2132 U1	JHH	N/A	N/A	2		HGTCC	pTa	HG
	CIS	pTis	HG	21.13				
BLDA 2148 U1	JHH	M	65	1		INTCC	pT1	HG
	CIS	pTis	HG	21.63				
BLDA 2175 U1	JHH	M	64	1		CIS	pTis	HG
	HGTCC	pTa	HG	21.97				
BLDA 2176 U1	JHH	M	54	2		CIS	pTis	HG
	CIS	pTis	HG	22.20				
BLDA 2177 U1	JHH	M	72	2		CIS	pTis	HG
	CIS	pTis	HG	22.33				
BLDA 2197 U1	JHH	F	72	2		LGTCC	pTa	LG
	INTCC	pT3	HG	22.63				
BLDA 2216 U1	JHH	N/A	N/A	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	22.73				
BLDA 2221 U1	JHH	M	73	2		HGTCC	pTa	HG
	INTCC	pT1	HG	22.90				
BLDA 2231 U1	JHH	M	73	1		INTCC	pT1	HG
	INTCC	pT1	HG	23.00				
BLDA 2304 U1	JHH	N/A	N/A	1		INTCC	pT1	HG

Table24.txt

	CIS	pTis	HG	23.37				
BLDA 2326 U1	JHH	M	51	0		LGTCC	pTa	LG
	LGTCC	pTa	LG	23.57				
BLDA 2346 U1	JHH	N/A	N/A	2		HGTCC	pTa	HG
	CIS	pTis	HG	25.03				
BLDA 2395 U1	JHH	F	62	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	25.93				
BLDA 2401 U1	JHH	M	77	2		CIS	pTis	HG
	CIS	pTis	HG	26.3				
BLDA 2441 U1	JHH	M	44	1		INTCC	pT2	HG
	INTCC	pT2	HG	26.83				
BLDA 2581 U1	JHH	F	75	1		INTCC	pT1	HG
	INTCC	pT1	HG	26.83				
BLDA 2622 U1	JHH	N/A	N/A	2		INTCC	pT2	HG
	INTCC	pT2	HG	31.50				
BLDA 2642 U1	JHH	N/A	N/A	2		LGTCC	pTa	LG
	LGTCC	pTa	LG	31.57				
BLDA 2709 U1	JHH	M	76	2		INTCC	pT1	HG
	HGTCC	pTa	HG	34.97				
BLDA 2761 U1	JHH	F	62	1		HGTCC	pTa	HG
	HGTCC	pTa	HG	36.03				
BLDA 2762 U1	JHH	M	66	2		INTCC	pT1	HG
	HGTCC	pTa	HG	38.30				
BLDA 2765 U1	JHH	M	81	1		INTCC	pT1	HG
	INTCC	pT1	HG	39.97				
BLDA 2852 U1	JHH	M	54	2		HGTCC	pTa	HG
	HGTCC	pTa	HG	50.23				
BLDA 2877 U1	JHH	M	40	1		INTCC	pT1	HG
	HGTCC	pTa	HG	51.07				

N/A Not Available
Cytology Diagnosis:
0 Negative
2 Atypical
1 Positive

Table25.txt

Table 25. Mutations detected by the 10-gene Multiplex Assay on urine samples from the Surveillance cohort.

Urine Sample	Patient	PT Variant Sample base	Codon	Gene	Chr	Reference amino acid	hg19 Position	Variant amino acid	Mutant Reference allele frequency	# unique templates analyzed	Found in the matched primary tumor
BLD 093 U	BLD 093	BLD 093 PT1 G	249	FGFR3	chr4	S	1803568	C	C 57.87%	38933	Yes
BLD 096 U	BLD 096	BLD 096 PT1 G	249	FGFR3	chr4	S	1803568	C	C 4.58%	7035	Yes
BLD 098 U	BLD 098	BLD 098 PT1 A	282	TP53	chr17	R	7577094	G	W 6.85%	23033	Yes
BLD 099 U	BLD 099	BLD 099 PT1 G	650	FGFR3	chr4	K	1807889	A	E 33.54%	3494	Yes
BLD 102 U	BLD 102	BLD 102 PT1 G	373	FGFR3	chr4	Y	1806099	A	C 0.12%	8190	Yes
BLD 165 U	BLD 165	BLD 165 PT C	113	TP53	chr17	F	7579348	G	L 0.48%	5606	Yes
BLD 168 U	BLD 168	BLD 168 PT G	249	FGFR3	chr4	S	1803568	C	C 2.20%	6305	Yes
BLD 174 U	BLD 174	BLD 174 PT A	1043	PIK3CA	chr3	M	178952074	G	I 0.14%	21406	Yes
BLD 182 U	BLD 182	BLD 182 PT G	249	FGFR3	chr4	S	1803568	C	C 0.26%	10378	Yes
BLD 190 U	BLD 190	BLD 190 PT G	249	FGFR3	chr4	S	1803568	C	C 7.02%	4489	Yes
BLD 196 U	BLD 196	BLD 196 PT G	373	FGFR3	chr4	Y	1806099	A	C 18.15%	573	Yes
BLD 207 U	BLD 207	BLD 207 PT G	249	FGFR3	chr4	S	1803568	C	C 14.09%	3577	Yes
BLD 212 U	BLD 212	BLD 594 PT1		TP53	chr17		7578265	A			

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				C	195	I		S	0.32%		
8462	Yes										
BLD 218 U		BLD 218	BLD 218 PT		KRAS	chr12	25398284		C		
				T	12	G		D	1.15%		
4340	Yes										
BLD 218 U		BLD 218	BLD 218 PT		PIK3CA	chr3	178936091		G		
				A	545	E		K	1.68%		
4176	Yes										
BLD 225 U		BLD 225	BLD 225 PT		FGFR3	chr4	1803568		C		
				G	249	S		C	44.40%		
23064	Yes										
BLD 227 U		BLD 227	BLD 227 PT		FGFR3	chr4	1803568		C		
				G	249	S		C	0.97%		
12519	Yes										
BLD 234 U		BLD 234	BLD 234 PT		ERBB2	chr17	37868208		C		
				T	310	S		F	18.35%		
41380	Yes										
BLD 234 U		BLD 234	BLD 234 PT		TP53	chr17	7577082		C		
				G	286	E		Q	14.89%		
4547	Yes										
BLD 276 U1		BLD 276	BLD 276 PT1		TP53	chr17	7579415		C		
				T	91	W		*	21.56%		
11942	Yes										
BLD 292 U1		BLD 292	BLD 292 PT		TP53	chr17	7577569		A		
				G	238	C		R	7.54%		
42353	Yes										
BLD 311 U1		BLD 311	BLD 311 PT		FGFR3	chr4	1803568		C		
				G	249	S		C	40.23%		
26988	Yes										
BLD 324 U1		BLD 324	BLD 324 PT		KRAS	chr12	25398284		C		
				A	12	G		V	0.24%		
11478	Yes										
BLD 334 U1		BLD 334	BLD 334 PT		HRAS	chr11	533874		T		
				C	61	Q		R	37.08%		
1826	Yes										
BLD 355 U1		BLD 355	BLD 355 PT		FGFR3	chr4	1803568		C		
				G	249	S		C	1.01%		
5228	Yes										
BLD 355 U1		BLD 355	BLD 355 PT		PIK3CA	chr3	178952085		A		
				G	1047	H		R	3.15%		
3143	Yes										
BLD 471 U1		BLD 471	BLDA 2514 PT1		FGFR3	chr4	1803568		C		
				G	249	S		C	1.94%		
14567	Yes										
BLD 473 U1		BLD 473	BLD 473 PT1		FGFR3	chr4	1803568		C		
				G	249	S		C	0.33%		
14629	Yes										
BLD 484 U1		BLD 484	BLD 484 PT1		FGFR3	chr4	1803568		C		

Table25.txt

			G	249	S		C	0.08%	
12356	Yes								
BLD 484 U1		BLD 484	BLD 484 PT1		PIK3CA	chr3	178952085	A	
			G	1047	H		R	0.12%	
17948	Yes								
BLD 489 U1		BLD 489	BLD 489 PT1		KRAS	chr12	25398284	C	
			A	12	G		V	1.20%	
5578	Yes								
BLD 489 U1		BLD 489	BLD 489 PT1		PIK3CA	chr3	178936082	G	
			A	542	E		K	1.70%	
8023	Yes								
BLD 560 U1		BLD 560	BLD 560 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	2.21%	
3354	Yes								
BLD 562 U1		BLD 562	BLD 562 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	3.06%	
2220	Yes								
BLD 580 U1		BLD 580	BLD 580 PT1		TP53	chr17	7579317	AAG	
			NULL	124	C		NULL	66.12%	
23937	Yes								
BLD 581 U1		BLD 581	BLD 581 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	27.48%	
11661	Yes								
BLD 582 U1		BLD 582	BLD 582 PT1		TP53	chr17	7577099	C	
			G	280	R		T	50.14%	
11568	Yes								
BLD 584 U1		BLD 584	BLD 584 PT1		TP53	chr17	7579699	C	
			A	0	NULL		NULL	12.87%	
17021	Yes								
BLD 660 U1		BLD 660	BLD 660 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	14.84%	
23989	Yes								
BLD 692 U1		BLD 692	BLD 692 PT1		CDKN2A	chr9	21971018	G	
			A	114	P		S	3.05%	
328	Yes								
BLD 738 U1		BLD 738	BLD 738 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	1.92%	
19926	Yes								
BLD 738 U1		BLD 738	BLD 738 PT1		PIK3CA	chr3	178936091	G	
			A	545	E		K	3.03%	
7422	Yes								
BLD 743 U1		BLD 743	BLDA 3045 PT1		FGFR3	chr4	1806092	A	
			T	371	S		C	0.75%	
21779	Yes								
BLD 762 U1		BLD 762	BLD 762 PT1		FGFR3	chr4	1803568	C	
			G	249	S		C	10.63%	
19000	Yes								
BLD 776 U1		BLD 776	BLD 776 PT1		FGFR3	chr4	1803568	C	

Table25.txt

			G	249	S		C	17.57%	
17008	Yes								
BLD 801 U1	BLD 801	BLD 801 PT1	FGFR3	chr4	1806099	A			
			G	373	Y		C	24.19%	
15116	Yes								
BLD 801 U1	BLD 801	BLD 801 PT1	PIK3CA	chr3	178936091	G			
			A	545	E		K	16.16%	
8724	Yes								
BLD 810 U1	BLD 810	BLD 810 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	0.29%	
5253	Yes								
BLD 958 U1	BLD 958	BLD 958 PT1	PIK3CA	chr3	178936091	G			
			A	545	E		K	23.60%	
4656	Yes								
BLD 958 U1	BLD 958	BLD 958 PT1	TP53	chr17	7577538	C			
			T	248	R		Q	50.94%	
24319	Yes								
BLD 961 U1	BLD 961	BLD 961 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	74.06%	
46523	Yes								
BLD 961 U1	BLD 961	BLD 961 PT1	TP53	chr17	7578211	C			
			T	213	R		Q	12.47%	
13126	Yes								
BLD 962 U1	BLD 962	BLD 962 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	3.24%	
20372	Yes								
BLD 965 U1	BLD 965	BLD 965 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	0.26%	
19136	Yes								
BLD 965 U1	BLD 965	BLD 965 PT1	PIK3CA	chr3	178936082	G			
			A	542	E		K	0.45%	
20709	Yes								
BLD 969 U1	BLD 969	BLD 969 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	30.43%	
15956	Yes								
BLD 969 U1	BLD 969	BLD 969 PT1	TP53	chr17	7577534	C			
			A	249	R		S	23.63%	
24431	Yes								
BLD 971 U1	BLD 971	BLD 971 PT1	FGFR3	chr4	1803568	C			
			G	249	S		C	0.52%	
19419	Yes								
BLD 976 U1	BLD 976	BLD 976 PT1	KRAS	chr12	25398281	C			
			T	13	G		D	0.89%	
11743	Yes								
BLD 976 U1	BLD 976	BLD 976 PT1	TP53	chr17	7577077	C			
			G	287	E		D	47.52%	
33227	Yes								
BLD 976 U1	BLD 976	BLD 976 PT1	TP53	chr17	7577085	C			

Table25.txt

			T	285	E		K	47.48%	
33227	Yes								
BLD 976 U1	BLD 976	BLD 976 PT1	TP53	chr17	7577514	GTG			
		NULL	256	T		NULL	31.82%		
28910	Yes								
BLD 982 U1	BLD 982	BLD 982 PT1	ERBB2	chr17	37868208	C			
		T	310	S		F	47.22%		
23824	Yes								
BLD 984 U1	BLD 984	BLD 984 PT1	FGFR3	chr4	1803568	C			
		G	249	S		C	5.61%		
19097	Yes								
BLD 987 U1	BLD 987	BLD 987 PT1	FGFR3	chr4	1806099	A			
		G	373	Y		C	0.62%		
5127	Yes								
BLDA 1010 U1	BLDA 1010	BLDA 1010 PT1	KRAS	chr12	25398284	C			
		A	12	G		V	50.48%		
4915	Yes								
BLDA 1013 U1	BLDA 1013	BLDA 1013 PT1	FGFR3	chr4	1803568	C			
		G	249	S		C	0.90%		
3676	Yes								
BLDA 1014 U1	BLDA 1014	BLDA 1014 PT1	CDKN2A	chr9	21971036	C			
		A	108	D		Y	0.15%		
22442	Yes								
BLDA 1014 U1	BLDA 1014	BLDA 1014 PT1	FGFR3	chr4	1803568	C			
		G	249	S		C	1.73%		
23708	Yes								
BLDA 1026 U1	BLDA 1026	BLDA 1026 PT1	FGFR3	chr4	1806099	A			
		G	373	Y		C	0.90%		
10751	Yes								
BLDA 1029 U1	BLDA 1029	BLDA 1029 PT1	KRAS	chr12	25398262	C			
		A	19	L		F	1.50%		
12012	Yes								
BLDA 1030 U1	BLDA 1030	BLDA 1030 PT1	FGFR3	chr4	1806089	G			
		T	370	G		C	0.78%		
11102	Yes								
BLDA 1030 U1	BLDA 1030	BLDA 1030 PT1	PIK3CA	chr3	178936094	C			
		A	546	Q		K	1.01%		
17824	Yes								
BLDA 1031 U1	BLDA 1031	BLDA 1031 PT1	FGFR3	chr4	1806089	G			
		T	370	G		C	93.08%		
29351	Yes								
BLDA 1031 U1	BLDA 1031	BLDA 1031 PT1	PIK3CA	chr3	178936091	G			
		A	545	E		K	46.09%		
4155	Yes								
BLDA 1055 U1	BLDA 1055	BLDA 1055 PT1	FGFR3	chr4	1806099	A			
		G	373	Y		C	0.49%		
14161	Yes								
BLDA 1056 U1	BLDA 1056	BLDA 1056 PT1	TP53	chr17	7576855	G			

Table25.txt

A 331 Q * 1.27%
3552 Yes
BLDA 1057 U1 BLDA 1057 BLDA 1057 PT1 TP53 chr17 7574021 C
A 336 E * 0.68%
8188 Yes
BLDA 1057 U1 BLDA 1057 BLDA 1057 PT1 TP53 chr17 7578534 C
G 132 K N 3.92%
12384 Yes
BLDA 1060 U1 BLDA 1060 BLDA 1060 PT1 TP53 chr17 7577539 G
A 248 R W 2.56%
13909 Yes
BLDA 1062 U1 BLDA 1062 BLDA 1062 PT1 PIK3CA chr3 178936091 G
A 545 E K 5.56%
5737 Yes
BLDA 1062 U1 BLDA 1062 BLDA 1062 PT1 TP53 chr17 7577100 T
C 280 R G 5.68%
7514 Yes
BLDA 1064 U1 BLDA 1064 BLDA 1064 PT1 FGFR3 chr4 1803564 C
T 248 R C 53.31%
13097 Yes
BLDA 1064 U1 BLDA 1064 BLDA 1064 PT1 TP53 chr17 7578391
TCATGGTGGGGGCAGCGC (SEQ ID NO:729) NULL 180 E NULL
9.40% 11479 Yes
BLDA 1073 U1 BLDA 1073 BLDA 1073 PT1 TP53 chr17 7576855 G
A 331 Q * 1.28%
4379 Yes
BLDA 1082 U1 BLDA 1082 BLDA 1082 PT1 FGFR3 chr4 1803568 C
G 249 S C 0.09%
14223 Yes
BLDA 1089 U1 BLDA 1089 BLDA 1089 PT1 FGFR3 chr4 1803568 C
G 249 S C 0.14%
13054 Yes
BLDA 1100 U1 BLDA 1100 BLDA 1100 PT1 TP53 chr17 7577099 C
A 280 R I 6.94%
23996 Yes
BLDA 1104 U1 BLDA 1104 BLDA 1104 PT1 TP53 chr17 7579313 G
A 125 T M 43.17%
7024 Yes
BLDA 1113 U1 BLDA 1113 BLDA 1113 PT1 KRAS chr12 25398284 C
A 12 G V 0.27%
9751 Yes
BLDA 1114 U1 BLDA 1114 BLDA 1114 PT1 FGFR3 chr4 1803568 C
G 249 S C 9.30%
4461 Yes
BLDA 1114 U1 BLDA 1114 BLDA 1114 PT1 PIK3CA chr3 178936091 G
A 545 E K 13.32%
5426 Yes
BLDA 1114 U1 BLDA 1114 BLDA 1114 PT1 TP53 chr17 7577099 C

Table25.txt

				G	280	R		T	21.42%	
13977	Yes									
BLDA 1180 U1	BLDA 1180	BLDA 1180 PT1	TP53	chr17	7578525	G				
				T	135	C		*	13.59%	
30413	Yes									
BLDA 1221 U1	BLDA 1221	BLDA 2984 PT1	FGFR3	chr4	1803564	C				
				T	248	R		C	7.22%	
9459	Yes									
BLDA 1232 U1	BLDA 1232	BLDA 3026 PT1	FGFR3	chr4	1803568	C				
				G	249	S		C	24.24%	
4492	Yes									
BLDA 1232 U1	BLDA 1232	BLDA 3026 PT1	PIK3CA	chr3	178952085	A				
				T	1047	H		L	25.90%	
12276	Yes									
BLDA 1250 U1	BLDA 1250	BLDA 2990 PT1	FGFR3	chr4	1803568	C				
				G	249	S		C	30.33%	
5615	Yes									
BLDA 1250 U1	BLDA 1250	BLDA 2990 PT1	PIK3CA	chr3	178936091	G				
				A	545	E		K	21.79%	
9690	Yes									
BLDA 1256 U1	BLDA 1256	BLDA 3035 PT1	TP53	chr17	7577099	C				
				G	280	R		T	70.40%	
6070	Yes									
BLDA 1409 U1	BLDA 1409	BLDA 3031 PT1	FGFR3	chr4	1803564	C				
				T	248	R		C	16.72%	
11220	Yes									
BLDA 1409 U1	BLDA 1409	BLDA 3031 PT1	TP53	chr17	7578534	C				
				A	132	K		N	40.46%	
16989	Yes									
BLDA 1457 U1	BLDA 1457	BLDA 3033 PT1	FGFR3	chr4	1803568	C				
				G	249	S		C	4.53%	
10671	Yes									
BLDA 1828 U1	BLDA 1828	BLDA 3063 PT1	FGFR3	chr4	1806099	A				
				G	373	Y		C	21.02%	
8915	Yes									
BLDA 1828 U1	BLDA 1828	BLDA 3063 PT1	TP53	chr17	7579471	NULL				
				C	72	P		NULL	21.04%	
28186	Yes									
BLDA 1865 U1	BLDA 1865	BLDA 3051 PT1	FGFR3	chr4	1803568	C				
				G	249	S		C	1.61%	
8113	Yes									
BLDA 1865 U1	BLDA 1865	BLDA 3051 PT1	PIK3CA	chr3	178952085	A				
				T	1047	H		L	0.42%	
23158	Yes									
BLDA 1880 U1	BLDA 1880	BLDA 3048 PT1	TP53	chr17	7577538	C				
				T	248	R		Q	19.32%	
10379	Yes									
BLDA 1880 U1	BLDA 1880	BLDA 3048 PT1	TP53	chr17	7579313	G				

Table25.txt

A 125 T M 15.73%
12426 Yes
BLDA 2015 U1 BLDA 2015 BLDA 2999 PT1 TP53 chr17 7577099 C
G 280 R T 17.91%
13877 Yes
BLDA 2020 U1 BLDA 2020 BLDA 3001 PT1 FGFR3 chr4 1803568 C
G 249 S C 0.48%
8618 Yes
BLDA 2023 U1 BLDA 2023 BLDA 3034 PT1 FGFR3 chr4 1806099 A
G 373 Y C 6.38%
14115 Yes
BLDA 2072 U1 BLDA 2072 BLDA 3088 PT1 TP53 chr17 7578203 C
T 216 V M 2.50%
25286 Yes
BLDA 2175 U1 BLDA 2175 BLDA 3068 PT1 TP53 chr17 7577543 C
T 246 M I 4.83%
12423 Yes
BLDA 2176 U1 BLDA 2176 BLDA 3067 PT1 PIK3CA chr3 178936091 G
A 545 E K 0.61%
10659 Yes
BLDA 2176 U1 BLDA 2176 BLDA 3067 PT1 TP53 chr17 7577544 A
T 246 M K 0.18%
9329 Yes
BLDA 2216 U1 BLDA 2216 BLDA 3036 PT1 FGFR3 chr4 1803564 C
T 248 R C 3.37%
3297 Yes
BLDA 2221 U1 BLDA 2221 BLDA 3006 PT1 HRAS chr11 533873 C
G 61 Q H 12.75%
15511 Yes
BLDA 2231 U1 BLDA 2231 BLDA 3007 PT1 TP53 chr17 7579710
TTTTCAGGAAGTCTG (SEQ ID NO:730) NULL 29 N NULL
22.29% 1364 Yes
BLDA 2304 U1 BLDA 2304 BLDA 3038 PT1 ERBB2 chr17 37868208 C
T 310 S F 3.14%
2801 Yes
BLDA 2326 U1 BLDA 2326 BLDA 3020 PT1 FGFR3 chr4 1803568 C
G 249 S C 1.33%
3758 Yes
BLDA 2326 U1 BLDA 2326 BLDA 3020 PT1 PIK3CA chr3 178916851 G
A 80 E K 0.10%
24879 Yes
BLDA 2395 U1 BLDA 2395 BLDA 3079 PT1 FGFR3 chr4 1803564 C
T 248 R C 27.99%
9228 Yes
BLDA 2395 U1 BLDA 2395 BLDA 3079 PT1 PIK3CA chr3 178936091 G
A 545 E K 15.43%
6040 Yes
BLDA 2441 U1 BLDA 2441 BLDA 3070 PT1 CDKN2A chr9 21971036 C

Table25.txt

			T	108	D		N	18.42%		
33119	Yes									
BLDA 2441 U1		BLDA 2441	BLDA 3070 PT1		TP53	chr17	7578394	T		
			C	179	H		R	73.55%		
42770	Yes									
BLDA 2581 U1		BLDA 2581	BLDA 3202 PT1		FGFR3	chr4	1803568	C		
			G	249	S		C	36.03%		
38644	Yes									
BLDA 2622 U1		BLDA 2622	BLDA 3074 PT1		TP53	chr17	7579313	G		
			A	125	T		M	25.32%		
38674	Yes									
BLDA 2642 U1		BLDA 2642	BLDA 3096 PT1		FGFR3	chr4	1803568	C		
			G	249	S		C	16.97%		
55601	Yes									
BLDA 2709 U1		BLDA 2709	BLDA 3084 PT1		TP53	chr17	7578394	T		
			C	179	H		R	3.00%		
12255	Yes									
BLDA 2761 U1		BLDA 2761	BLDA 3091 PT1		TP53	chr17	7578370	C		
			A	0	NULL		NULL	38.07%		
13334	Yes									
BLDA 2877 U1		BLDA 2877	BLDA 3203 PT1		HRAS	chr11	533874	T		
			A	61	Q		L	19.01%		
8825	Yes									

Table26.txt

Table 26. Mutations detected by the TERT Assay on urine samples from the BC Surveillance cohort.

Mutant Urine allele Sample	# unique templates Patient analyzed	Found in Matched Tumor	the matched primary tumor	Gene	Chr	hg 19 Position	Reference base	Variant base
BLD 093 U1 32.87%	BLD 093 6936	BLD 093 PT1	Yes	TERT	chr5	1295228	C	T
BLD 098 U1 4.92%	BLD 098 45438	BLD 098 PT1	Yes	TERT	chr5	1295228	C	T
BLD 099 U1 37.48%	BLD 099 46823	BLD 099 PT1	Yes	TERT	chr5	1295228	C	T
BLD 104 U1 37.29%	BLD 104 22601	BLD 104 PT1	Yes	TERT	chr5	1295228	C	T
BLD 106 U1 42.99%	BLD 106 31151	BLD 576 PT1	Yes	TERT	chr5	1295228	C	T
BLD 109 U1 1.39%	BLD 109 30080	BLD 109 PT1	Yes	TERT	chr5	1295250	C	T
BLD 168 U1 2.55%	BLD 168 33341	BLD 168 PT	Yes	TERT	chr5	1295228	C	T
BLD 191 U1 58.71%	BLD 191 21676	BLD 191 PT	Yes	TERT	chr5	1295228	C	T
BLD 196 U1 8.19%	BLD 196 537	BLD 196 PT	Yes	TERT	chr5	1295228	C	T
BLD 198 U1 2.78%	BLD 198 40906	BLD 198 PT	Yes	TERT	chr5	1295228	C	T
BLD 207 U1 16.05%	BLD 207 17921	BLD 207 PT	Yes	TERT	chr5	1295228	C	T
BLD 212 U1 4.36%	BLD 212 3299	BLD 594 PT1	Yes	TERT	chr5	1295228	C	T
BLD 218 U1 1.26%	BLD 218 38891	BLD 218 PT	Yes	TERT	chr5	1295250	C	T
BLD 225 U1 6.16%	BLD 225 31543	BLD 225 PT	Yes	TERT	chr5	1295250	C	T
BLD 234 U1 5.85%	BLD 234 8796	BLD 234 PT	Yes	TERT	chr5	1295250	C	T
BLD 259 U1 4.90%	BLD 259 9721	BLD 259 PT	Yes	TERT	chr5	1295228	C	T
BLD 262 U1 10.95%	BLD 262 74360	BLD 262 PT	Yes	TERT	chr5	1295228	C	T
BLD 276 U1 22.83%	BLD 276 35242	BLD 276 PT1	Yes	TERT	chr5	1295228	C	T
BLD 292 U1 7.10%	BLD 292 12706	BLD 292 PT	Yes	TERT	chr5	1295228	C	T
BLD 302 U1 13.02%	BLD 302 5247	BLD 302 PT	Yes	TERT	chr5	1295228	C	T

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BLD 311 U1	BLD 311	BLD 311 PT	TERT	chr5 1295250	C	T	
56.83%	16581	Yes					
BLD 322 U1	BLD 322	BLD 322 PT	TERT	chr5 1295228	C	T	
0.61%	33368	Yes					
BLD 334 U1	BLD 334	BLD 334 PT	TERT	chr5 1295228	C	T	
22.11%	4080	Yes					
BLD 355 U1	BLD 355	BLD 355 PT	TERT	chr5 1295250	C	T	
2.09%	1820	Yes					
BLD 360 U1	BLD 360	BLD 360 PT	TERT	chr5 1295228	C	T	
7.81%	24468	Yes					
BLD 425 U1	BLD 425	BLD 425 PT	TERT	chr5 1295228	C	T	
9.30%	18982	Yes					
BLD 425 U1	BLD 425	BLD 425 PT	TERT	chr5 1295250	C	T	
0.61%	18982	Yes					
BLD 448 U1	BLD 448	BLDA 1452 PT1	TERT	chr5 1295250	C	T	
0.67%	38710	Yes					
BLD 454 U1	BLD 454	BLD 697 PT1	TERT	chr5 1295228	C	T	
8.27%	10975	Yes					
BLD 461 U1	BLD 461	BLDA 3047 PT1	TERT	chr5 1295228	C	T	
10.24%	166	Yes					
BLD 473 U1	BLD 473	BLD 473 PT1	TERT	chr5 1295228	C	T	
1.50%	15393	Yes					
BLD 489 U1	BLD 489	BLD 489 PT1	TERT	chr5 1295228	C	T	
4.50%	6132	Yes					
BLD 562 U1	BLD 562	BLD 562 PT1	TERT	chr5 1295228	C	T	
4.79%	25161	Yes					
BLD 582 U1	BLD 582	BLD 582 PT1	TERT	chr5 1295228	C	T	
20.52%	27044	Yes					
BLD 584 U1	BLD 584	BLD 584 PT1	TERT	chr5 1295228	C	T	
9.31%	26664	Yes					
BLD 612 U1	BLD 612	BLD 612 PT1	TERT	chr5 1295228	C	T	
4.27%	17654	Yes					
BLD 660 U1	BLD 660	BLD 660 PT1	TERT	chr5 1295228	C	T	
4.81%	24867	Yes					
BLD 694 U1	BLD 694	BLD 694 PT1	TERT	chr5 1295228	C	T	
2.35%	3666	Yes					
BLD 738 U1	BLD 738	BLD 738 PT1	TERT	chr5 1295228	C	T	
1.81%	35192	Yes					
BLD 762 U1	BLD 762	BLD 762 PT1	TERT	chr5 1295228	C	T	
9.38%	50362	Yes					
BLD 771 U1	BLD 771	BLD 771 PT1	TERT	chr5 1295228	C	T	
2.57%	8982	Yes					
BLD 776 U1	BLD 776	BLD 776 PT1	TERT	chr5 1295228	C	T	
28.11%	25068	Yes					
BLD 800 U1	BLD 800	BLD 800 PT1	TERT	chr5 1295228	C	T	
5.20%	7460	Yes					
BLD 801 U1	BLD 801	BLD 801 PT1	TERT	chr5 1295228	C	T	
17.71%	6940	Yes					

Table26.txt

BLD 803 U1	BLD 803	BLD 803 PT1	TERT	chr5	1295228	C	T
7.69%	403	Yes					
BLD 958 U1	BLD 958	BLD 958 PT1	TERT	chr5	1295228	C	T
45.28%	13917	Yes					
BLD 961 U1	BLD 961	BLD 961 PT1	TERT	chr5	1295250	C	T
74.12%	18228	Yes					
BLD 962 U1	BLD 962	BLD 962 PT1	TERT	chr5	1295228	C	T
1.99%	33424	Yes					
BLD 965 U1	BLD 965	BLD 965 PT1	TERT	chr5	1295228	C	T
2.19%	1097	Yes					
BLD 967 U1	BLD 967	BLD 967 PT1	TERT	chr5	1295228	C	T
5.12%	7033	Yes					
BLD 974 U1	BLD 974	BLD 974 PT1	TERT	chr5	1295228	C	T
1.88%	48635	Yes					
BLD 976 U1	BLD 976	BLD 976 PT1	TERT	chr5	1295228	C	T
62.72%	18778	Yes					
BLD 982 U1	BLD 982	BLD 982 PT1	TERT	chr5	1295250	C	T
44.57%	28381	Yes					
BLD 984 U1	BLD 984	BLD 984 PT1	TERT	chr5	1295228	C	T
7.92%	41724	Yes					
BLD 985 U1	BLD 985	BLD 985 PT1	TERT	chr5	1295228	C	T
10.12%	14625	Yes					
BLD 995 U1	BLD 995	BLD 995 PT1	TERT	chr5	1295228	C	T
1.61%	8026	Yes					
BLD 996 U1	BLD 996	BLD 996 PT1	TERT	chr5	1295228	C	T
4.07%	13110	Yes					
BLDA 1010 U1	BLDA 1010	BLDA 1010 PT1	TERT	chr5	1295228	C	T
9.43%	9650	Yes					
BLDA 1011 U1	BLDA 1011	BLDA 1011 PT1	TERT	chr5	1295228	C	T
0.56%	22139	Yes					
BLDA 1013 U1	BLDA 1013	BLDA 1013 PT1	TERT	chr5	1295228	C	T
0.43%	42222	Yes					
BLDA 1014 U1	BLDA 1014	BLDA 1014 PT1	TERT	chr5	1295228	C	T
0.54%	26744	Yes					
BLDA 1030 U1	BLDA 1030	BLDA 1030 PT1	TERT	chr5	1295228	C	T
0.68%	16194	Yes					
BLDA 1031 U1	BLDA 1031	BLDA 1031 PT1	TERT	chr5	1295228	C	T
21.70%	15506	Yes					
BLDA 1050 U1	BLDA 1050	BLDA 1050 PT1	TERT	chr5	1295228	C	T
3.13%	3200	Yes					
BLDA 1055 U1	BLDA 1055	BLDA 1055 PT1	TERT	chr5	1295228	C	T
0.34%	45343	Yes					
BLDA 1056 U1	BLDA 1056	BLDA 1056 PT1	TERT	chr5	1295250	C	T
1.07%	40650	Yes					
BLDA 1057 U1	BLDA 1057	BLDA 1057 PT1	TERT	chr5	1295250	C	T
4.79%	43907	Yes					
BLDA 1060 U1	BLDA 1060	BLDA 1060 PT1	TERT	chr5	1295228	C	T
1.31%	14905	Yes					

Table26.txt

BLDA 1062	U1BLDA 1062	BLDA 1062 PT1 TERT	chr5	1295228	C	T
1.77%	18569	Yes				
BLDA 1064	U1BLDA 1064	BLDA 1064 PT1 TERT	chr5	1295228	C	T
22.01%	21728	Yes				
BLDA 1066	U1BLDA 1066	BLDA 1066 PT1 TERT	chr5	1295250	C	T
87.32%	22097	Yes				
BLDA 1073	U1BLDA 1073	BLDA 1073 PT1 TERT	chr5	1295228	C	T
0.80%	14041	Yes				
BLDA 1096	U1BLDA 1096	BLDA 1096 PT1 TERT	chr5	1295228	C	T
54.85%	44976	Yes				
BLDA 1100	U1BLDA 1100	BLDA 1100 PT1 TERT	chr5	1295250	C	T
4.76%	32355	Yes				
BLDA 1104	U1BLDA 1104	BLDA 1104 PT1 TERT	chr5	1295228	C	T
28.99%	9154	Yes				
BLDA 1107	U1BLDA 1107	BLDA 1107 PT1 TERT	chr5	1295228	C	T
2.27%	28997	Yes				
BLDA 1114	U1BLDA 1114	BLDA 1114 PT1 TERT	chr5	1295228	C	T
16.28%	4269	Yes				
BLDA 1157	U1BLDA 1157	BLDA 1157 PT1 TERT	chr5	1295228	C	T
1.74%	7522	Yes				
BLDA 1166	U1BLDA 1166	BLDA 1166 PT1 TERT	chr5	1295228	C	T
2.39%	31613	Yes				
BLDA 1177	U1BLDA 1177	BLDA 1177 PT1 TERT	chr5	1295228	C	T
0.52%	44461	Yes				
BLDA 1180	U1BLDA 1180	BLDA 1180 PT1 TERT	chr5	1295250	C	T
7.39%	28663	Yes				
BLDA 1194	U1BLDA 1194	BLDA 1194 PT1 TERT	chr5	1295250	C	T
5.86%	8655	Yes				
BLDA 1221	U1BLDA 1221	BLDA 2984 PT1 TERT	chr5	1295228	C	T
0.89%	8300	Yes				
BLDA 1250	U1BLDA 1250	BLDA 2990 PT1 TERT	chr5	1295228	C	T
3.95%	5219	Yes				
BLDA 1252	U1BLDA 1252	BLDA 2983 PT1 TERT	chr5	1295250	C	T
14.72%	8289	Yes				
BLDA 1256	U1BLDA 1256	BLDA 3035 PT1 TERT	chr5	1295228	C	T
9.71%	8850	Yes				
BLDA 1409	U1BLDA 1409	BLDA 3031 PT1 TERT	chr5	1295228	C	T
12.75%	5860	Yes				
BLDA 1457	U1BLDA 1457	BLDA 3033 PT1 TERT	chr5	1295250	C	T
2.31%	10071	Yes				
BLDA 1854	U1BLDA 1854	BLDA 3050 PT1 TERT	chr5	1295228	C	T
2.18%	14070	Yes				
BLDA 1880	U1BLDA 1880	BLDA 3048 PT1 TERT	chr5	1295228	C	T
20.98%	26799	Yes				
BLDA 2015	U1BLDA 2015	BLDA 2999 PT1 TERT	chr5	1295250	C	T
4.64%	5152	Yes				
BLDA 2023	U1BLDA 2023	BLDA 3034 PT1 TERT	chr5	1295228	C	T
6.66%	5634	Yes				

Table26.txt

BLDA 2072	U1BLDA 2072	BLDA 3088 PT1 TERT	chr5	1295228	C	T
2.41%	14293	Yes				
BLDA 2148	U1BLDA 2148	BLDA 3014 PT1 TERT	chr5	1295228	C	T
3.41%	13430	Yes				
BLDA 2175	U1BLDA 2175	BLDA 3068 PT1 TERT	chr5	1295228	C	T
1.99%	19631	Yes				
BLDA 2176	U1BLDA 2176	BLDA 3067 PT1 TERT	chr5	1295228	C	T
0.49%	15110	Yes				
BLDA 2177	U1BLDA 2177	BLDA 3066 PT1 TERT	chr5	1295228	C	T
4.47%	7658	Yes				
BLDA 2197	U1BLDA 2197	BLDA 3008 PT1 TERT	chr5	1295228	C	T
1.25%	38213	Yes				
BLDA 2221	U1BLDA 2221	BLDA 3006 PT1 TERT	chr5	1295228	C	T
9.57%	20625	Yes				
BLDA 2231	U1BLDA 2231	BLDA 3007 PT1 TERT	chr5	1295228	C	T
19.75%	13259	Yes				
BLDA 2304	U1BLDA 2304	BLDA 3038 PT1 TERT	chr5	1295228	C	T
3.28%	15977	Yes				
BLDA 2326	U1BLDA 2326	BLDA 3020 PT1 TERT	chr5	1295228	C	T
0.39%	26897	Yes				
BLDA 2346	U1BLDA 2346	BLDA 3039 PT1 TERT	chr5	1295228	C	T
3.04%	3616	Yes				
BLDA 2395	U1BLDA 2395	BLDA 3079 PT1 TERT	chr5	1295228	C	T
12.01%	34709	Yes				
BLDA 2441	U1BLDA 2441	BLDA 3070 PT1 TERT	chr5	1295228	C	T
42.57%	54227	Yes				
BLDA 2581	U1BLDA 2581	BLDA 3202 PT1 TERT	chr5	1295228	C	T
10.13%	38381	Yes				
BLDA 2642	U1BLDA 2642	BLDA 3096 PT1 TERT	chr5	1295250	C	T
17.78%	28331	Yes				
BLDA 2765	U1BLDA 2765	BLDA 3204 PT1 TERT	chr5	1295228	C	T
19.66%	116753	Yes				
BLDA 2852	U1BLDA 2852	BLDA 3199 PT1 TERT	chr5	1295228	C	T
2.55%	29236	Yes				
BLDA 2877	U1BLDA 2877	BLDA 3203 PT1 TERT	chr5	1295228	C	T
19.56%	76810	Yes				

Table27.txt

Table 27. Chromosome arm gains and losses detected by the Aneuploidy Assay in urine samples from the Surveillance cohort.

Urine Sample	Patient	Aneuploidy Score	Gains	Losses	# unique templates analyzed
BLD 093 U	BLD 093	1.00	7	4	5433661
BLD 102 U	BLD 102	1.00	2	1	13449089
BLD 106 U	BLD 106	1.00	13	7	7616104
BLD 191 U	BLD 191	1.00	3	0	7611193
BLD 207 U	BLD 207	1.00	6	7	4646608
BLD 225 U	BLD 225	0.87	2	2	7257598
BLD 234 U	BLD 234	1.00	9	5	4666644
BLD 276 U1	BLD 276	1.00	2	3	5300655
BLD 292 U1	BLD 292	1.00	8	5	4740385
BLD 311 U1	BLD 311	1.00	8	6	5193431
BLD 334 U1	BLD 334	1.00	9	10	3591078
BLD 360 U1	BLD 360	1.00	6	3	6056219
BLD 425 U1	BLD 425	1.00	5	6	6457877
BLD 454 U1	BLD 454	1.00	5	6	5719925
BLD 582 U1	BLD 582	1.00	2	2	6343093
BLD 590 U1	BLD 590	1.00	13	7	1834875
BLD 591 U1	BLD 591	1.00	12	7	2639687
BLD 660 U1	BLD 660	1.00	5	2	7138163
BLD 762 U1	BLD 762	1.00	4	1	11548238
BLD 776 U1	BLD 776	1.00	3	5	10370801
BLD 801 U1	BLD 801	1.00	2	4	8266150
BLD 961 U1	BLD 961	1.00	4	6	7162560
BLD 982 U1	BLD 982	1.00	10	9	7557810
BLD 996 U1	BLD 996	1.00	3	3	7115213
BLDA 1010 U1	BLDA 1010	1.00	12	12	7868167
BLDA 1031 U1	BLDA 1031	1.00	3	4	8805406
BLDA 1064 U1	BLDA 1064	1.00	15	10	7211487
BLDA 1066 U1	BLDA 1066	1.00	18	13	8057804
BLDA 1096 U1	BLDA 1096	1.00	18	10	8288852
BLDA 1100 U1	BLDA 1100	0.87	5	4	7307475
BLDA 1104 U1	BLDA 1104	1.00	16	10	7669494
BLDA 1111 U1	BLDA 1111	1.00	13	14	7310470
BLDA 1114 U1	BLDA 1114	1.00	3	5	7123273
BLDA 1180 U1	BLDA 1180	1.00	3	2	5091358
BLDA 1194 U1	BLDA 1194	1.00	3	3	5311402
BLDA 1232 U1	BLDA 1232	1.00	6	3	5153920
BLDA 1250 U1	BLDA 1250	1.00	0	2	5567451
BLDA 1252 U1	BLDA 1252	1.00	5	3	6039078
BLDA 1256 U1	BLDA 1256	1.00	11	9	5994872
BLDA 1409 U1	BLDA 1409	1.00	10	10	5826003
BLDA 1457 U1	BLDA 1457	1.00	4	1	5234679
BLDA 1828 U1	BLDA 1828	1.00	7	7	5059880
BLDA 1854 U1	BLDA 1854	0.88	7	3	6458510

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BLDA 1880	U1BLDA 18801.00	13	9	4599639
BLDA 2015	U1BLDA 20151.00	13	8	3924594
BLDA 2023	U1BLDA 20231.00	0	5	3189477
BLDA 2072	U1BLDA 20720.86	3	3	6377974
BLDA 2148	U1BLDA 21481.00	14	9	5979392
BLDA 2177	U1BLDA 21771.00	8	8	6209991
BLDA 2221	U1BLDA 22211.00	6	9	4761196
BLDA 2231	U1BLDA 22311.00	16	13	4772278
BLDA 2304	U1BLDA 23041.00	4	5	4240180
BLDA 2395	U1BLDA 23951.00	1	1	5877864
BLDA 2441	U1BLDA 24411.00	17	12	10582872
BLDA 2581	U1BLDA 25811.00	5	3	5522648
BLDA 2622	U1BLDA 26221.00	15	10	5852184
BLDA 2642	U1BLDA 26421.00	0	1	11058938
BLDA 2761	U1BLDA 27611.00	17	8	6454157
BLDA 2765	U1BLDA 27651.00	6	6	6939631
BLDA 2877	U1BLDA 28771.00	9	13	6156841

Table28.txt

Table 28. Individual clinical data for the UTUC cohort.

Case	Urine cytology	Age	Smoking	CKD	BC score per chemotherapy	Sex	LU, lower ureter (y)	UTUC history	UTUC stage	UTUC collection timing	Synch BC	BC grade	Synch BC stage	UTUC site	AL-dA adducts pre-surgery	P, renal pelvis UU, upper ureter Synch BC pre-surgery	Synch BC ureterovesical junctigrade chemotherapy drugs	Synch BC stage timing	Synch BC route
SB 136	Nil	F	84		No							3A	10.0						P
	Low	TaN0M0	12 h		Yes	High		Ta			None								None
											None								
SB 138	1N1S	M	60	40 pk-yr, quit for 3 yr								0-2	1.3+0.1						P,UU
	High	T3N0M0	12 h		No														
SB 139	6N	M	57	20 pk-yr, quit for 24 y								0-2	0.7+0.0						P
	High	T3N0M0	12 h		No														
SB 140	1N	M	74	20 pk-yr, current smoke								0-2	2.2+0.0						P
	High	TaN0M0	12 h		No														
SB 141	1N	F	50		No							3B	5+0.7						LU
	High	T3N2M1	12 h		Yes	High		T1			Systemic							Gemcitabine & cisplatin	5 mo before Nux
SB 149	4N	F	59		No							0-2	68.2						P
	Low	TaN0M0	12 h		No														
SB 151	Nil	M	84		No							3A	0.7						P,LU
	High	T1N0M0	12 h		Yes	High		T1			Intravesical Mitomycin, adriamycin, cisp			3 mo before Nux					
SB 156	1N	M	59	35 pk-yr, current smoke								3A	37.3						P
	High	T3N0M0	12 h & spot		No														
SB 157	3N2S	M	73	30 pk-yr, current smoke								3B	4.5						LU-UVJ
	High	T2N0M0	12 h & spot		Yes	High		T2			None								None
											None								
SB 160	2S1N	F	68		No							3A	0.4						UU,LU
	Low	T2N0M0	12 h		No														
SB 161	2N1P	M	80		No							3A	< LOQ						P
	High	T1N0M0	12 h		No														
SB 165	1N	M	61		No							0-2	2.6						P,UU,LU
	High	TaN0M0	12 h		Yes	High		Ta			None								None
											None								
SB 190	Nil	M	39		No							3A	17.0						P
	High	T3N0M0	12 h & spot		No														
SB 191	Nil	M	66		No							5	0.9						P,UU,LU
	High	T1N1M0	Bladder was		Yes	High		T1			None								None

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										None
SB 192	2N1S	M	64		No		0-2	1.8		LU
	High	T2N0M0	12 h & spot	Yes	High	T1		None		None
										None
SB 194	Nil	M	62		No		0-2	2.0		P,UU,LU
	High	T4N0M0	Spot	Yes	High	Ta		None		None
										None
SB 195	1N1A	F	45		No		0-2	5.5		P,UU
	High	T3N0M0	Spot	No						
SB 196	1A1S	F	79		No		3B	6.1		LU
	High	TaN0M0	Spot	No						
SB 197	4N	M	61		No		4	6.2		LU
	High	T2N0M0	Spot	Yes	High	T1		Intravesical Mitomycin, adriamycin, cisp3 mo before Nux		
SB 198	2A	F	78		No		3B	16.9		P
	High	T1aN0M0	Spot	No						
SB 201	2S	F	69		No		0-2	2.1		LU-UVJ
	High	T3N0M0	Spot	Yes	High	T3		None		None
										None
SB 202	1P	F	60		No		0-2	30.4		LU
	High	TaN0M0	Spot	No						
SB 203	4N	F	46		No		5	18.4		P,UU,LU
	High	T3N0M0	Spot	Yes	High	T1		None		None
										None
SB 204	1N	F	53		No		5	6.8		P
	High	T3N0M0	Spot	Yes	Low	T1		None		None
										None
SB 206	1N1A	F	71		No		0-2	12.9		P
	High	T2N0M0	Spot	No						
SB 208	1N	M	64		No		0-2	7.1		P
	High	T3N0M0	Spot	No						
SB 209	Nil	F	84		No		0-2	2.2		P,UU
	High	T4N0M0	Spot	No						
SB 210	Nil	F	79		No		3B	7.3		P,LU
	High	T3N0M0	Spot	Yes	High	T1		None		None
										None
SB 212	2N	F	64		No		0-2	2.7		P,UU
	High	T4N1M1	Spot	No						
SB 214	1N1A	F	72		No		0-2	24.5		P
	High	T3N0M0	Spot	No						
SB 216	1A	M	72		No		0-2	2.7		LU
	High	T3N0M0	Spot	No						
SB 217	2N	F	76		No		3B	3.8		LU
	High	T1N0M0	Spot	Yes	Low	Ta		Intravesical Mitomycin, adriamycin, cisp3 wk before Nux		
SB 218	1S	M	61		No		0-2	42.7		LU
	High	T3N0M0	Spot	No						
SB 219	4N	F	77		No		0-2	33.7		P

Table28.txt

	High	T3N0M0	Spot	Yes	High	T1	Intravesical Mitomycin, adriamycin, cisp3 mo before Nux				
SB 220	2N	F	62		No		0-2	20.6			P
	High	TaN0M0	Spot	No							
SB 221	Nil	F	61		No		0-2	6.8			P
	High	T3N0M0	Spot	No							
SB 222	Nil	F	61		No		3B	5.2			LU
	High	T2N0M0	Spot	No							
SB 223	5N1A	F	71		No		0-2	3.7			P
	High	T1N0M0	Spot	No							
SB 224	Nil	F	77		No		3B	1.1			LU
	High	T2N0M0	Spot	No							
SB 225	5N1A	M	62		No		3B	4.7			P
	Low	TaN0M0	Spot	No							
SB 226	2N	M	73	25 pk-yr, current smoke			3B	1.3			LU
	High	T2N0M0	Spot	Yes	High	T1	None				None
	None										
SB 227	4N1A	F	73		No		4	3.1			LU
	High	T2N0M0	Spot	No							
SB 228	3P	F	74		No		0-2	3.4			P,LU
	High	T3N0M0	Spot	No							
SB 296	1N	F	49		No		3A	5.2			LU
	Low	TaN0M0	Spot	Yes	High	T1	Intravesical Mitomycin, adriamycin, cisp3 mo before Nux				
SB 297	Nil	M	63		No		3A	2.3			LU
	High	T3N0M0	Spot	No							
SB 298	4N	F	85		No		3A	0.4			P,UU
	High	T3N0M0	Spot	No							
SB 300	1P	F	79		No		0-2	2.7			P
	High	T3N0M0	Spot	No							
SB 301	3N1A	M	63	25 pk-yr, current smoke			4	4.1			P
	High	T3N0M0	Spot	Yes	High	T1 with	Intravesical			Oncotice (BCG)	
	1 mo before Nux										
SB 302	Nil	M	69		No		0-2	24.5			LU
	High	T3N0M0	Spot	No							
SB 304	3N	F	79		No		3A	<LOQ			UU
	High	T1N0M0	Spot	No							
SB 306	Nil	F	70		No		4	1.0			P
	High	TaN0M0	Spot	Yes	Low	Ta	Systemic		Gemcitabine & cisplatin		
	3 mo before Nux										
SB 307	2N2A	F	76		No		3A	11.5			LU
	High	T3N0M0	Spot	No							
SB 309	Nil	M	72	50 pk-yr, current smoke			3A	15.7			P,LU
	High	T2N0M0	Spot	No							
SB 310	1A2N	M	68	40 pk-yr, current smoke			3A	4.3			P
	High	T3N2M0	Spot	No							
SB 312	2N	M	75	55 pk-yr, current smoke			3A	1.4			UU,LU
	Low	TaN0M0	Spot	Yes	Low	Ta	None				None

Table28.txt

None
SB 314 3N F 48 No 0-2 2.1 LU
High T1N0M0 Spot Yes High T1 Intravesical Oncotice
(BCG) 3 mo before Nux

Urine cytology score: N (negative); A (atypia); S (suspicious); P (positive); Nil, urine cytology data not available; numbers refer to the numbers of independent cytology samples that scored posi
Pk-yr, pack years.
CKD stage, chronic kidney disease stage (calculated with MDRD eGFR equation, see Methods).
AL-dA, aristolactam I-dA adduct levels in renal cortex.
nts, nucleotides.
UTUC, upper tract urothelial carcinoma.
Synch BC, synchronous bladder cancer defined as a bladder tumor diagnosis within three months prior to nephroureterectomy.
BCG, Bacillus Calmette?Gu?rin.
Nux, nephroureterectomy.

Table29.txt

Table 29. Mutations detected in urinary cell DNA from UTUC patients by the 10-gene multiplex assay.

Urine sample	Gene	Codon	ReferencVariant amino acid	Variant amino acid	Chr	Hg19 position	Reference base	# unique templates analyzed	Present in prima tumor
SB 138 U1	TP53	215	S	R	chr17	7578204	A	8849	Yes
T						6.93%			
SB 139 U1	PIK3CA	545	E	K	chr3	178936091	G	4054	Yes
A						21.26%			
SB 140 U1	FGFR3	249	S	C	chr4	1803568	C	9301	Yes
G						27.12%			
SB 141 U1	TP53	125	T	M	chr17	7579313	G	9442	Yes
A						17.71%			
SB 149 U1	FGFR3	249	S	C	chr4	1803568	C	25938	Yes
G						1.66%			
SB 156 U2	TP53	236	Y	C	chr17	7577574	T	26539	No
C						1.95%			
SB 160 U1	FGFR3	249	S	C	chr4	1803568	C	14191	Yes
G						1.08%			
SB 165 U1	FGFR3	249	S	C	chr4	1803568	C	23791	No
G						0.50%			
SB 190 U1**	TP53	280	R	S	chr17	7577098	T	14543	Yes
A						27.86%			
SB 190 U2**	TP53	280	R	S	chr17	7577098	T	9066	Yes
A						28.49%			
SB 190 U1**	TP53	179	H	L	chr17	7578394	T	12800	Yes
A						26.84%			
SB 190 U2**	TP53	179	H	L	chr17	7578394	T	9220	Yes
A						28.03%			
SB 191 U1	TP53	291	K	*	chr17	7577067	T	16405	Yes
A						10.73%			
SB 191 U1	TP53	164	K	*	chr17	7578440	T	9118	Yes
A						10.68%			
SB 192 U1**	KRAS	19	L	F	chr12	25398262	C	18420	Yes
G						0.65%			
SB 192 U2**	KRAS	19	L	F	chr12	25398262	C	12203	Yes
G						1.02%			
SB 195 U1	TP53	162	I	F	chr17	7578446	T	10323	Yes
A						39.68%			
SB 195 U1	ERBB2	310	S	F	chr17	37868208	C	12189	Yes
T						14.77%			
SB 196 U1	PIK3CA	545	E	K	chr3	178936091	G	2498	Yes
A						25.82%			
SB 196 U1	PIK3CA	1047	H	R	chr3	178952085	A	13416	No
G						1.19%			

Table29.txt

```
SB 197 U1   TP53     chr17   7577157   T
A       0       NULL    NULL    0.95%   8860      Yes
SB 202 U1   PIK3CA   chr3    178936091 G
A       545     E       K       15.71%  8289      Yes
SB 202 U1   PIK3CA   chr3    178952085 A
G       1047    H       R       0.45%   18518     No
SB 203 U1   TP53     chr17   7578235   T
A       205     Y       F       0.48%   18759     Yes
SB 204 U1   TP53     chr17   7578224   T
A       209     R       *       0.75%   10930     No
SB 204 U1   TP53     chr17   7578266   T
A       195     I       F       0.73%   14001     No
SB 204 U1   TP53     chr17   7578400   G
A       177     P       L       0.89%   12426     No
SB 204 U1   TP53     chr17   7578556   T
A       0       NULL    NULL    1.80%   13204     No
SB 204 U1   TP53     chr17   7579592   T
G       0       NULL    NULL    2.23%   6785      No
SB 204 U1   CDKN2A   chr9    21971204  T
A       52      M       L       0.57%   14201     No
SB 204 U1   MLL      chr11   118359365 A
T       1457    K       *       0.32%   11850     No
SB 206 U1   TP53     chr17   7579328   T
A       120     K       M       5.73%   13344     Yes
SB 210 U1   TP53     chr17   7577081   T
A       286     E       V       23.53%  10279     Yes
SB 210 U1   TP53     chr17   7577102   CCAGGACAGGCACAAACACGC (SEQ ID NO:731)
NULL    279     G       NULL    7.30%   3892      Yes
SB 216 U1   TP53     chr17   7578190   T
C       220     Y       C       2.91%   10282     Yes
SB 217 U1   TP53     chr17   7577581   A
T       234     Y       N       5.37%   24308     No
SB 217 U1   TP53     chr17   7579329   T
C       120     K       E       1.62%   6622      No
SB 218 U1   TP53     chr17   7577025   T
A       305     K       *       59.98%  25112     Yes
SB 220 U1   TP53     chr17   7577578   T
A       235     N       Y       0.30%   21908     No
SB 221 U1   FGFR3    chr4    1803568   C
G       249     S       C       53.41%  19615     Yes
SB 222 U1   TP53     chr17   7577126   T
A       271     E       V       2.52%   5359      Yes
SB 223 U1   HRAS     chr11   533874    T
A       61      Q       L       2.42%   44606     Yes
SB 224 U1   HRAS     chr11   533874    T
A       61      Q       L       0.73%   22532     Yes
SB 225 U1   FGFR3    chr4    1803564   C
T       248     R       C       13.15%  16041     Yes
```

Table29.txt

SB 225 U1	CDKN2A	chr9	21971069	GCACC				
NULL	97	L	NULL	2.13%	18250	No		
SB 226 U1	TP53	chr17	7578263	G				
A	196	R	*	5.16%	17371	Yes		
SB 228 U1	TP53	chr17	7577061	NULL				
C	293	G	NULL	8.61%	12658	Yes		
SB 228 U1	TP53	chr17	7579424	NULL				
G	88	A	NULL	8.62%	20333	Yes		
SB 297 U1	TP53	chr17	7577079	C				
G	287	E	Q	43.83%	5725	Yes		
SB 297 U1	TP53	chr17	7577085	C				
T	285	E	K	43.74%	5725	No		
SB 297 U1	TP53	chr17	7578257	C				
G	198	E	Q	42.75%	4826	Yes		
SB 300 U1	FGFR3	chr4	1803568	C				
G	249	S	C	80.30%	9154	Yes		
SB 302 U1	TP53	chr17	7578190	T				
C	220	Y	C	12.16%	17819	Yes		
SB 304 U1	FGFR3	chr4	1806099	A				
G	373	Y	C	1.07%	10352	No		
SB 304 U1	FGFR3	chr4	1806119	G				
A	380	G	R	4.61%	10352	Yes		
SB 309 U1	TP53	chr17	7577539	G				
A	248	R	W	5.43%	12813	Yes		
SB 309 U1	TP53	chr17	7577563	T				
A	240	S	C	3.25%	12813	Yes		
SB 309 U1	VHL	chr3	10191621	G				
A	205	R	H	45.41%	11611	Yes		
SB 312 U1	CDKN2A	chr9	21971029	C				
T	110	W	*	13.53%	12564	Yes		
SB 312 U1	CDKN2A	chr9	21971096	C				
A	88	E	*	20.38%	2713	Yes		

Table30.txt

Table 30. TERT promoter mutations identified in urinary cell DNA from UTUC patients.

Urine sample	Gene	Chr	Hg19 position	Reference base	Variant base	MAF	# unique templates analyzed	Present in primary tumor
SB 139 U1	TERT	chr5	1295250	C	T	18.49%	36861	Yes
SB 149 U1	TERT	chr5	1295228	C	T	0.59%	10842	Yes
SB 156 U1*	TERT	chr5	1295228	C	T	1.35%	60381	No
SB 156 U2*	TERT	chr5	1295228	C	T	1.40%	32282	No
SB 165 U1	TERT	chr5	1295228	C	T	24.58%	17406	Yes
SB 165 U1	TERT	chr5	1295250	C	T	0.83%	17406	No
SB 192 U1*	TERT	chr5	1295228	C	T	1.45%	49286	Yes
SB 192 U2*	TERT	chr5	1295228	C	T	1.40%	17442	Yes
SB 195 U1	TERT	chr5	1295228	C	T	5.94%	5438	Yes
SB 197 U1	TERT	chr5	1295243	C	T	0.68%	14050	Yes
SB 197 U1	TERT	chr5	1295250	C	G	0.68%	14050	Yes
SB 202 U1	TERT	chr5	1295228	C	T	3.44%	16476	Yes
SB 208 U1	TERT	chr5	1295250	C	T	4.55%	17026	Yes
SB 210 U1	TERT	chr5	1295228	C	T	2.98%	16329	Yes
SB 221 U1	TERT	chr5	1295228	C	T	23.37%	9858	Yes
SB 225 U1	TERT	chr5	1295228	C	T	1.42%	10477	Yes
SB 298 U1	TERT	chr5	1295228	C	T	12.95%	2286	Yes
SB 300 U1	TERT	chr5	1295250	C	T	46.33%	3050	Yes
SB 306 U1	TERT	chr5	1295228	C	T	1.15%	3223	Yes
SB 312 U1	TERT	chr5	1295228	C	T	22.24%	2441	Yes

Chr, chromosome; Hg19, human genome 19; MAF, mutant allele frequency.
*Matched spot urine sample and a 12-hour urine collection sample obtained from the same patient.

Table31.txt

Table 31. Urinary cell DNA samples from UTUC patients that scored positive for aneuploidy.

Urine sample	Score	Gains	Losses	# unique templates analyzed
SB 138 U1	1.00	3	1	6726601
SB 139 U1	0.78	0	2	5137893
SB 140 U1	1.00	5	5	10300465
SB 141 U1	1.00	14	9	7998866
SB 151 U1	1.00	3	1	5737160
SB 156 U2	1.00	9	6	4792486
SB 161 U1	1.00	1	4	4577916
SB 165 U1	1.00	6	1	5911260
SB 190 U1*	1.00	13	8	3606142
SB 190 U2*	1.00	10	8	2662871
SB 191 U1	1.00	7	6	6117370
SB 195 U1	1.00	10	9	3924640
SB 196 U1	1.00	6	3	4134609
SB 202 U1	1.00	5	5	7196399
SB 210 U1	1.00	8	8	7271219
SB 214 U1	1.00	8	5	4602340
SB 218 U1	1.00	13	9	6342046
SB 221 U1	1.00	19	10	4941180
SB 226 U1	0.87	5	3	7413224
SB 298 U1	1.00	7	5	9910445
SB 300 U1	1.00	4	6	11727639
SB 302 U1	1.00	11	9	11118503
SB 312 U1	1.00	2	0	12984080

GL, gains + losses; AI, allelic imbalance; GL-AI = gains + losses -
*Matched spot urine sample and a 12-hour urine collection sample
ob

Table32.txt

Table 32. Mutations detected in primary tumor DNA from UTUC patients by the 10-gene multiplex assay.

Tumor sample	Gene	Chr	Reference Hg19 position	Variant base	Reference amino acid	Variant amino acid	Codon	# unique templates analyzed	Present in urinary cells	Variant base
SB 136	PIK3CA	chr3	178952085	A	H	R	1047	11971	No	G
SB 136	FGFR3	chr4	1803568	C	S	C	249	5354	No	G
SB 138	TP53	chr17	7578204	A	S	R	215	1616	Yes	T
SB 139	PIK3CA	chr3	178936091	G	E	K	545	684	Yes	A
SB 140	FGFR3	chr4	1803568	C	S	C	249	2467	Yes	G
SB 141	TP53	chr17	7579313	G	T	M	125	1595	Yes	A
SB 149	FGFR3	chr4	1803568	C	S	C	249	4825	Yes	G
SB 151	TP53	chr17	7577540	G	N	NULL	247	9931	No	fs
SB 151	TP53	chr17	7577124	C	V	L	272	8016	No	G
SB 160	FGFR3	chr4	1803568	C	S	C	249	619	Yes	G
SB 190	TP53	chr17	7577098	T	R	S	280	10357	Yes	A
SB 190	TP53	chr17	7578394	T	H	L	179	6065	Yes	A
SB 191	TP53	chr17	7577067	T	K	*	291	2998	Yes	A
SB 191	TP53	chr17	7578440	T	K	*	164	2114	Yes	A
SB 192	KRAS	chr12	25398262	C	L	F	19	2660	Yes	G
SB 194	FGFR3	chr4	1806119	G	G	R	380	7153	No	A
SB 194	FGFR3	chr4	1803564	C	R	C	248	7099	No	T
SB 195	TP53	chr17	7578446	T	I	F	162	501	No	A
SB 195	ERBB2	chr17	37868208	C	S	F	310	488	Yes	T
SB 196	PIK3CA	chr3	178936091	G	E	K	545	155	Yes	A

Table32.txt

SB 197	TP53	chr17	7577157	T					A
0	NULL	NULL		90.2%	7246	Yes			
SB 198	HRAS	chr11	533874	T					A
61	Q	L		59.7%	1513	No			
SB 198	TP53	chr17	7578536	T					A
132	K	*		74.6%	556	No			
SB 202	PIK3CA	chr3	178936091	G					A
545	E	K		43.4%	302	Yes			
SB 203	TP53	chr17	7578235	T					A
205	Y	F		45.1%	1334	Yes			
SB 203	TP53	chr17	7578446	T					A
162	I	F		45.8%	907	No			
SB 204	TP53	chr17	7578271	T					A
193	H	L		40.2%	8117	No			
SB 204	TP53	chr17	7578440	T					A
164	K	*		46.1%	4952	No			
SB 206	TP53	chr17	7579328	T					A
120	K	M		10.3%	185	Yes			
SB 210	TP53	chr17	7577081	T					A
286	E	V		71.5%	326	Yes			
SB 210	TP53	chr17	7577102	CCAGGACAGGCACAAACACGC (SEQ ID NO:731)					NULL
279	G	NULL		72.2%	151	Yes			
SB 216	TP53	chr17	7578190	T					C
220	Y	C		41.1%	316	Yes			
SB 218	TP53	chr17	7577025	T					A
305	K	*		87.2%	1036	Yes			
SB 219	FGFR3	chr4	1806099	A					G
373	Y	C		60.1%	1447	No			
SB 219	PIK3CA	chr3	178936082	G					A
542	E	K		35.9%	482	No			
SB 220	HRAS	chr11	533873	C					A
61	Q	H		40.9%	934	No			
SB 221	FGFR3	chr4	1803568	C					G
249	S	C		38.4%	2214	Yes			
SB 222	TP53	chr17	7577126	T					A
271	E	V		11.9%	1529	Yes			
SB 223	HRAS	chr11	533874	T					A
61	Q	L		46.3%	2624	Yes			
SB 224	HRAS	chr11	533874	T					A
61	Q	L		28.8%	2375	Yes			
SB 225	FGFR3	chr4	1803564	C					T
248	R	C		85.2%	3355	Yes			
SB 226	TP53	chr17	7578263	G					A
196	R	*		88.0%	1672	Yes			
SB 227	TP53	chr17	7576928	T					A
0	NULL	NULL		91.8%	1145	No			
SB 228	TP53	chr17	7579424	NULL					G
88	A	NULL		37.7%	2295	Yes			

Table32.txt

SB 228	TP53	chr17	7577061	NULL				C
293	G	NULL		36.3%	2074	Yes		
SB 296	FGFR3	chr4	1803568	C				G
249	S	C		8.1%	2123	No		
SB 297	TP53	chr17	7577079	C				G
287	E	Q		38.9%	9973	Yes		
SB 297	TP53	chr17	7578257	C				G
198	E	Q		39.6%	5480	Yes		
SB 300	FGFR3	chr4	1803568	C				G
249	S	C		85.1%	4478	Yes		
SB 301	TP53	chr17	7578440	T				A
164	K	*		61.6%	4010	No		
SB 302	TP53	chr17	7578190	T				C
220	Y	C		92.9%	7469	Yes		
SB 304	FGFR3	chr4	1806119	G				A
380	G	R		45.7%	16894	Yes		
SB 306	TP53	chr17	7579536	C				A
51	E	*		82.9%	6040	No		
SB 307	TP53	chr17	7579328	T				A
120	K	M		35.7%	18917	No		
SB 309	VHL	chr3	10191621	G				A
205	R	H		28.5%	16953	Yes		
SB 309	TP53	chr17	7577539	G				A
248	R	W		80.7%	6953	Yes		
SB 309	TP53	chr17	7577563	T				A
240	S	C		12.3%	6953	Yes		
SB 310	TP53	chr17	7578235	T				C
205	Y	C		5.9%	11464	No		
SB 312	CDKN2A	chr9	21971029	C				T
110	W	*		46.9%	8049	Yes		
SB 312	CDKN2A	chr9	21971096	C				A
88	E	*		57.4%	1219	Yes		
SB 312	FGFR3	chr4	1803568	C				G
249	S	C		11.1%	859	No		
SB 314	FGFR3	chr4	1803564	C				T
248	R	C		21.5%	73907	No		

Chr, chromosome; Hg19, human genome 19; MAF, mutant allele frequency; UIDs, unique identifiers.
A>T transversions, characteristic of aristolochic acid-induced mutagenesis, are noted in red.

Table33.txt

Table 33. TERT promoter mutations identified in primary tumor DNA from UTUC patients.

Tumor sample	Gene	Chr	Hg19 position	Reference base	Variant base	MAF	# unique templates analyzed	Present in urinary cells
SB 136	TERT	chr5	1295243	C	T	42.71%	14255	No
SB 139	TERT	chr5	1295250	C	T	52.18%	9457	Yes
SB 149	TERT	chr5	1295228	C	T	31.75%	11318	Yes
SB 165	TERT	chr5	1295228	C	T	8.40%	3404	Yes
SB 192	TERT	chr5	1295228	C	T	17.87%	19564	Yes
SB 195	TERT	chr5	1295228	C	T	44.07%	71793	Yes
SB 197	TERT	chr5	1295243	C	T	50.26%	12151	Yes
SB 197	TERT	chr5	1295250	C	G	58.10%	12151	Yes
SB 198	TERT	chr5	1295228	C	T	50.56%	21954	No
SB 202	TERT	chr5	1295228	C	T	60.74%	24819	Yes
SB 208	TERT	chr5	1295250	C	T	3.08%	19674	Yes
SB 209	TERT	chr5	1295250	C	T	10.83%	7915	No
SB 210	TERT	chr5	1295228	C	T	26.92%	87910	Yes
SB 212	TERT	chr5	1295228	C	T	54.65%	10735	No
SB 217	TERT	chr5	1295228	C	T	68.69%	1236	No
SB 219	TERT	chr5	1295228	C	T	42.73%	2771	No
SB 221	TERT	chr5	1295228	C	T	52.19%	7957	Yes
SB 224	TERT	chr5	1295228	C	T	1.15%	6512	No
SB 225	TERT	chr5	1295228	C	T	45.92%	9593	Yes
SB 296	TERT	chr5	1295228	C	T	6.81%	7605	No
SB 298	TERT	chr5	1295228	C	T	38.77%	9192	Yes
SB 300	TERT	chr5	1295250	C	T	45.71%	9071	Yes
SB 306	TERT	chr5	1295228	C	T	70.60%	8559	Yes
SB 312	TERT	chr5	1295228	C	T	73.89%	6954	Yes

Chr, chromosome; Hg19, human genome 19; MAF, mutant allele frequency.

Table34.txt

Table 34. WALDO specificity and sensitivity

Chromosome Arm	Alteration	Threshold	Sensitivity (1% Cell Fraction)	Sensitivity (5% Cell Fraction)	Sensitivity (10% Cell Fraction)	Specificity
all	all	1.96> or <-1.96	0.222	0.965	0.993	0.969
all	all	3> or <-3	0.031	0.912	0.990	0.999
all	all	5> or <-5	0.000	0.667	0.952	1.000
chr1p	gain	1.96> or <-1.96	0.274	1.000	1.000	0.978
chr1p	gain	3> or <-3	0.081	1.000	1.000	0.999
chr1p	gain	5> or <-5	0.000	1.000	1.000	1.000
chr1p	loss	1.96> or <-1.96	0.355	1.000	1.000	0.978
chr1p	loss	3> or <-3	0.043	1.000	1.000	0.999
chr1p	loss	5> or <-5	0.000	1.000	1.000	1.000
chr1q	gain	1.96> or <-1.96	0.247	1.000	1.000	0.982
chr1q	gain	3> or <-3	0.016	1.000	1.000	1.000
chr1q	gain	5> or <-5	0.000	0.984	1.000	1.000
chr1q	loss	1.96> or <-1.96	0.333	1.000	1.000	0.982
chr1q	loss	3> or <-3	0.032	1.000	1.000	1.000
chr1q	loss	5> or <-5	0.000	1.000	1.000	1.000
chr2p	gain	1.96> or <-1.96	0.183	1.000	1.000	0.975
chr2p	gain	3> or <-3	0.000	1.000	1.000	0.999
chr2p	gain	5> or <-5	0.000	0.968	1.000	1.000
chr2p	loss	1.96> or <-1.96	0.398	1.000	1.000	0.975
chr2p	loss	3> or <-3	0.022	1.000	1.000	0.999
chr2p	loss	5> or <-5	0.000	1.000	1.000	1.000

Table34.txt

chr2q	gain	1.96> or <-1.96	0.349	1.000	1.000
0.993					
chr2q	gain	3> or <-3	0.011	1.000	1.000
1.000					
chr2q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr2q	loss	1.96> or <-1.96	0.694	1.000	1.000
0.993					
chr2q	loss	3> or <-3	0.199	1.000	1.000
1.000					
chr2q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr3p	gain	1.96> or <-1.96	0.392	1.000	1.000
0.987					
chr3p	gain	3> or <-3	0.032	1.000	1.000
1.000					
chr3p	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr3p	loss	1.96> or <-1.96	0.323	1.000	1.000
0.987					
chr3p	loss	3> or <-3	0.027	1.000	1.000
1.000					
chr3p	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr3q	gain	1.96> or <-1.96	0.403	1.000	1.000
0.982					
chr3q	gain	3> or <-3	0.022	1.000	1.000
1.000					
chr3q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr3q	loss	1.96> or <-1.96	0.457	1.000	1.000
0.982					
chr3q	loss	3> or <-3	0.038	1.000	1.000
1.000					
chr3q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr4p	gain	1.96> or <-1.96	0.215	1.000	1.000
0.987					
chr4p	gain	3> or <-3	0.016	1.000	1.000
1.000					
chr4p	gain	5> or <-5	0.000	0.738	1.000
1.000					
chr4p	loss	1.96> or <-1.96	0.156	1.000	1.000
0.987					
chr4p	loss	3> or <-3	0.032	1.000	1.000
1.000					
chr4p	loss	5> or <-5	0.000	0.792	1.000
1.000					

Table34.txt

chr4q	gain	1.96> or <-1.96	0.575	1.000	1.000
0.959					
chr4q	gain	3> or <-3	0.194	1.000	1.000
0.993					
chr4q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr4q	loss	1.96> or <-1.96	0.527	1.000	1.000
0.959					
chr4q	loss	3> or <-3	0.220	1.000	1.000
0.993					
chr4q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr5p	gain	1.96> or <-1.96	0.065	1.000	1.000
0.975					
chr5p	gain	3> or <-3	0.000	0.984	1.000
1.000					
chr5p	gain	5> or <-5	0.000	0.749	1.000
1.000					
chr5p	loss	1.96> or <-1.96	0.226	1.000	1.000
0.975					
chr5p	loss	3> or <-3	0.022	1.000	1.000
1.000					
chr5p	loss	5> or <-5	0.000	0.984	1.000
1.000					
chr5q	gain	1.96> or <-1.96	0.478	1.000	1.000
0.991					
chr5q	gain	3> or <-3	0.081	1.000	1.000
1.000					
chr5q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr5q	loss	1.96> or <-1.96	0.484	1.000	1.000
0.991					
chr5q	loss	3> or <-3	0.140	1.000	1.000
1.000					
chr5q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr6p	gain	1.96> or <-1.96	0.156	1.000	1.000
0.942					
chr6p	gain	3> or <-3	0.000	1.000	1.000
0.996					
chr6p	gain	5> or <-5	0.000	0.694	1.000
1.000					
chr6p	loss	1.96> or <-1.96	0.129	1.000	1.000
0.942					
chr6p	loss	3> or <-3	0.000	1.000	1.000
0.996					
chr6p	loss	5> or <-5	0.000	0.678	1.000
1.000					

Table34.txt

chr6q	gain	1.96> or <-1.96	0.489	1.000	1.000
0.981					
chr6q	gain	3> or <-3	0.070	1.000	1.000
1.000					
chr6q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr6q	loss	1.96> or <-1.96	0.392	1.000	1.000
0.981					
chr6q	loss	3> or <-3	0.048	1.000	1.000
1.000					
chr6q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr7p	gain	1.96> or <-1.96	0.016	1.000	1.000
0.972					
chr7p	gain	3> or <-3	0.000	0.989	1.000
1.000					
chr7p	gain	5> or <-5	0.000	0.464	1.000
1.000					
chr7p	loss	1.96> or <-1.96	0.199	1.000	1.000
0.972					
chr7p	loss	3> or <-3	0.027	1.000	1.000
1.000					
chr7p	loss	5> or <-5	0.000	0.749	1.000
1.000					
chr7q	gain	1.96> or <-1.96	0.312	1.000	1.000
0.978					
chr7q	gain	3> or <-3	0.016	1.000	1.000
1.000					
chr7q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr7q	loss	1.96> or <-1.96	0.376	1.000	1.000
0.978					
chr7q	loss	3> or <-3	0.070	1.000	1.000
1.000					
chr7q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr8p	gain	1.96> or <-1.96	0.070	1.000	1.000
0.982					
chr8p	gain	3> or <-3	0.016	0.956	1.000
1.000					
chr8p	gain	5> or <-5	0.000	0.290	1.000
1.000					
chr8p	loss	1.96> or <-1.96	0.124	1.000	1.000
0.982					
chr8p	loss	3> or <-3	0.022	0.984	1.000
1.000					
chr8p	loss	5> or <-5	0.000	0.514	1.000
1.000					

Table34.txt

chr8q	gain	1.96> or <-1.96	0.500	1.000	1.000
0.981					
chr8q	gain	3> or <-3	0.054	1.000	1.000
1.000					
chr8q	gain	5> or <-5	0.000	1.000	1.000
1.000					
chr8q	loss	1.96> or <-1.96	0.323	1.000	1.000
0.981					
chr8q	loss	3> or <-3	0.027	1.000	1.000
1.000					
chr8q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr9p	gain	1.96> or <-1.96	0.199	1.000	1.000
0.942					
chr9p	gain	3> or <-3	0.005	0.989	1.000
1.000					
chr9p	gain	5> or <-5	0.000	0.645	1.000
1.000					
chr9p	loss	1.96> or <-1.96	0.204	1.000	1.000
0.942					
chr9p	loss	3> or <-3	0.011	1.000	1.000
1.000					
chr9p	loss	5> or <-5	0.000	0.552	1.000
1.000					
chr9q	gain	1.96> or <-1.96	0.118	1.000	1.000
0.957					
chr9q	gain	3> or <-3	0.027	1.000	1.000
1.000					
chr9q	gain	5> or <-5	0.000	0.798	1.000
1.000					
chr9q	loss	1.96> or <-1.96	0.134	1.000	1.000
0.957					
chr9q	loss	3> or <-3	0.016	0.984	1.000
1.000					
chr9q	loss	5> or <-5	0.000	0.907	1.000
1.000					
chr10p	gain	1.96> or <-1.96	0.065	1.000	1.000
0.956					
chr10p	gain	3> or <-3	0.000	0.973	1.000
0.997					
chr10p	gain	5> or <-5	0.000	0.230	1.000
1.000					
chr10p	loss	1.96> or <-1.96	0.145	1.000	1.000
0.956					
chr10p	loss	3> or <-3	0.022	1.000	1.000
0.997					
chr10p	loss	5> or <-5	0.000	0.443	1.000
1.000					

Table34.txt

chr10q	gain	1.96> or <-1.96	0.215	1.000	1.000
0.969					
chr10q	gain	3> or <-3	0.016	1.000	1.000
1.000					
chr10q	gain	5> or <-5	0.000	0.940	1.000
1.000					
chr10q	loss	1.96> or <-1.96	0.349	1.000	1.000
0.969					
chr10q	loss	3> or <-3	0.043	1.000	1.000
1.000					
chr10q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr11p	gain	1.96> or <-1.96	0.167	1.000	1.000
0.919					
chr11p	gain	3> or <-3	0.016	0.984	1.000
0.994					
chr11p	gain	5> or <-5	0.000	0.754	1.000
1.000					
chr11p	loss	1.96> or <-1.96	0.210	1.000	1.000
0.919					
chr11p	loss	3> or <-3	0.016	1.000	1.000
0.994					
chr11p	loss	5> or <-5	0.000	0.847	1.000
1.000					
chr11q	gain	1.96> or <-1.96	0.280	1.000	1.000
0.988					
chr11q	gain	3> or <-3	0.022	1.000	1.000
1.000					
chr11q	gain	5> or <-5	0.000	0.956	1.000
1.000					
chr11q	loss	1.96> or <-1.96	0.210	1.000	1.000
0.988					
chr11q	loss	3> or <-3	0.016	1.000	1.000
1.000					
chr11q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr12p	gain	1.96> or <-1.96	0.048	1.000	1.000
0.969					
chr12p	gain	3> or <-3	0.000	0.978	1.000
1.000					
chr12p	gain	5> or <-5	0.000	0.242	1.000
1.000					
chr12p	loss	1.96> or <-1.96	0.145	1.000	1.000
0.969					
chr12p	loss	3> or <-3	0.000	1.000	1.000
1.000					
chr12p	loss	5> or <-5	0.000	0.367	1.000
1.000					

Table34.txt

chr12q	gain	1.96> or <-1.96	0.220	1.000	1.000
0.988					
chr12q	gain	3> or <-3	0.016	1.000	1.000
1.000					
chr12q	gain	5> or <-5	0.000	0.994	1.000
1.000					
chr12q	loss	1.96> or <-1.96	0.446	1.000	1.000
0.988					
chr12q	loss	3> or <-3	0.081	1.000	1.000
1.000					
chr12q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr13q	gain	1.96> or <-1.96	0.156	1.000	1.000
0.975					
chr13q	gain	3> or <-3	0.038	1.000	1.000
1.000					
chr13q	gain	5> or <-5	0.000	0.994	1.000
1.000					
chr13q	loss	1.96> or <-1.96	0.484	1.000	1.000
0.975					
chr13q	loss	3> or <-3	0.113	1.000	1.000
1.000					
chr13q	loss	5> or <-5	0.000	1.000	1.000
1.000					
chr14q	gain	1.96> or <-1.96	0.199	0.948	1.000
0.987					
chr14q	gain	3> or <-3	0.038	0.948	1.000
1.000					
chr14q	gain	5> or <-5	0.000	0.948	1.000
1.000					
chr14q	loss	1.96> or <-1.96	0.312	0.948	1.000
0.987					
chr14q	loss	3> or <-3	0.022	0.948	1.000
1.000					
chr14q	loss	5> or <-5	0.000	0.948	1.000
1.000					
chr15q	gain	1.96> or <-1.96	0.097	0.909	0.931
0.965					
chr15q	gain	3> or <-3	0.000	0.909	0.931
1.000					
chr15q	gain	5> or <-5	0.000	0.673	0.931
1.000					
chr15q	loss	1.96> or <-1.96	0.355	0.909	0.925
0.965					
chr15q	loss	3> or <-3	0.059	0.909	0.925
1.000					
chr15q	loss	5> or <-5	0.000	0.836	0.925
1.000					

Table34.txt

chr16p	gain	1.96> or <-1.96	0.134	1.000	0.909
0.942					
chr16p	gain	3> or <-3	0.022	0.807	0.909
0.994					
chr16p	gain	5> or <-5	0.000	0.100	0.909
1.000					
chr16p	loss	1.96> or <-1.96	0.081	0.907	0.915
0.942					
chr16p	loss	3> or <-3	0.005	0.747	0.915
0.994					
chr16p	loss	5> or <-5	0.000	0.060	0.896
1.000					
chr16q	gain	1.96> or <-1.96	0.038	0.927	1.000
0.979					
chr16q	gain	3> or <-3	0.000	0.853	1.000
0.999					
chr16q	gain	5> or <-5	0.000	0.140	1.000
1.000					
chr16q	loss	1.96> or <-1.96	0.151	0.980	1.000
0.979					
chr16q	loss	3> or <-3	0.022	0.980	1.000
0.999					
chr16q	loss	5> or <-5	0.000	0.300	1.000
1.000					
chr17p	gain	1.96> or <-1.96	0.134	0.789	0.967
0.941					
chr17p	gain	3> or <-3	0.000	0.476	0.933
0.994					
chr17p	gain	5> or <-5	0.000	0.000	0.713
1.000					
chr17p	loss	1.96> or <-1.96	0.065	0.741	0.960
0.941					
chr17p	loss	3> or <-3	0.000	0.456	0.953
0.994					
chr17p	loss	5> or <-5	0.000	0.007	0.700
1.000					
chr17q	gain	1.96> or <-1.96	0.016	1.000	0.980
0.966					
chr17q	gain	3> or <-3	0.000	1.000	0.980
1.000					
chr17q	gain	5> or <-5	0.000	0.201	0.980
1.000					
chr17q	loss	1.96> or <-1.96	0.194	1.000	0.980
0.966					
chr17q	loss	3> or <-3	0.005	1.000	0.980
1.000					
chr17q	loss	5> or <-5	0.000	0.479	0.980
1.000					

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chr18p	gain	1.96> or <-1.96	0.070	0.701	0.965
0.969					
chr18p	gain	3> or <-3	0.000	0.243	0.917
0.999					
chr18p	gain	5> or <-5	0.000	0.000	0.472
1.000					
chr18p	loss	1.96> or <-1.96	0.065	0.778	1.000
0.969					
chr18p	loss	3> or <-3	0.032	0.410	1.000
0.999					
chr18p	loss	5> or <-5	0.000	0.042	0.583
1.000					
chr18q	gain	1.96> or <-1.96	0.183	1.000	1.000
0.973					
chr18q	gain	3> or <-3	0.065	1.000	1.000
1.000					
chr18q	gain	5> or <-5	0.000	0.799	1.000
1.000					
chr18q	loss	1.96> or <-1.96	0.280	1.000	1.000
0.973					
chr18q	loss	3> or <-3	0.043	1.000	1.000
1.000					
chr18q	loss	5> or <-5	0.000	0.875	1.000
1.000					
chr19p	gain	1.96> or <-1.96	0.172	0.611	0.958
0.945					
chr19p	gain	3> or <-3	0.005	0.333	0.875
0.999					
chr19p	gain	5> or <-5	0.000	0.007	0.333
1.000					
chr19p	loss	1.96> or <-1.96	0.059	0.493	0.965
0.945					
chr19p	loss	3> or <-3	0.016	0.125	0.799
0.999					
chr19p	loss	5> or <-5	0.000	0.014	0.160
1.000					
chr19q	gain	1.96> or <-1.96	0.059	0.868	1.000
0.929					
chr19q	gain	3> or <-3	0.005	0.500	0.979
0.996					
chr19q	gain	5> or <-5	0.000	0.042	0.875
1.000					
chr19q	loss	1.96> or <-1.96	0.140	0.944	1.000
0.929					
chr19q	loss	3> or <-3	0.005	0.632	1.000
0.996					
chr19q	loss	5> or <-5	0.000	0.063	0.938
1.000					

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chr20p	gain	1.96> or <-1.96	0.091	1.000	1.000
0.982					
chr20p	gain	3> or <-3	0.005	0.854	1.000
1.000					
chr20p	gain	5> or <-5	0.000	0.069	1.000
1.000					
chr20p	loss	1.96> or <-1.96	0.032	1.000	1.000
0.982					
chr20p	loss	3> or <-3	0.000	0.944	1.000
1.000					
chr20p	loss	5> or <-5	0.000	0.056	1.000
1.000					
chr20q	gain	1.96> or <-1.96	0.022	0.847	1.000
0.969					
chr20q	gain	3> or <-3	0.000	0.556	1.000
0.999					
chr20q	gain	5> or <-5	0.000	0.021	0.806
1.000					
chr20q	loss	1.96> or <-1.96	0.108	0.938	1.000
0.969					
chr20q	loss	3> or <-3	0.000	0.667	1.000
0.999					
chr20q	loss	5> or <-5	0.000	0.042	0.917
1.000					
chr21q	gain	1.96> or <-1.96	0.048	1.000	1.000
0.970					
chr21q	gain	3> or <-3	0.000	0.979	1.000
1.000					
chr21q	gain	5> or <-5	0.000	0.201	1.000
1.000					
chr21q	loss	1.96> or <-1.96	0.086	1.000	1.000
0.970					
chr21q	loss	3> or <-3	0.000	1.000	1.000
1.000					
chr21q	loss	5> or <-5	0.000	0.354	1.000
1.000					
chr22q	gain	1.96> or <-1.96	0.016	0.736	1.000
0.962					
chr22q	gain	3> or <-3	0.000	0.250	1.000
1.000					
chr22q	gain	5> or <-5	0.000	0.000	0.660
1.000					
chr22q	loss	1.96> or <-1.96	0.075	0.896	1.000
0.962					
chr22q	loss	3> or <-3	0.000	0.653	1.000
1.000					
chr22q	loss	5> or <-5	0.000	0.014	0.847
1.000					

Table35.txt

Table 35. Primary Tumors

Name	Reads	Unique Molecular Barcodes	chr1p	chr1q	chr2p	chr2q
chr3p	chr3q	chr4p	chr4q	chr5p	chr5q	chr6p	chr6q
chr7p	chr7q	chr8p	chr8q	chr9p	chr9q	chr10p	
CRC 021 PT	16708297	11213670	-11.000	-3.113	-5.621	-11.000
-1.298	11.000	-6.679	11.000	11.000	-11.000	-3.698	-6.136
4.033	6.639	2.179	11.000	-3.727	-3.058	5.088	
CRC 022 PT	17587490	12270483	0.433	11.000	-1.800	-1.685
-0.983	-0.189	-0.564	-0.850	-1.339	0.148	0.064	1.241
-0.961	-0.464	-0.714	0.671	-0.741	1.744	0.120	
CRC 023 PT	15988025	11469279	-1.896	-1.475	-3.395	-3.400
-2.471	-2.232	-5.002	-5.592	-3.190	-4.410	11.000	11.000
-1.607	-1.204	-11.000	11.000	-1.317	0.024	-1.381	
CRC 024 PT	16404227	11386936	-11.000	11.000	-11.000	4.665
-3.550	4.012	-11.000	-11.000	11.000	-11.000	11.000	1.485
11.000	11.000	-11.000	4.472	11.000	4.557	0.182	
CRC 025 PT	15380099	10625296	-5.500	5.653	-5.306	7.565
5.423	6.563	-11.000	3.856	2.957	-11.000	-4.296	-11.000
4.485	5.938	-3.627	11.000	7.687	11.000	-4.059	
CRC 026 PT	16227636	11564792	0.089	-0.464	2.830	6.062
-1.932	-0.150	-1.357	-0.029	-1.555	-1.091	3.211	5.284
-1.858	0.766	-1.021	0.123	-1.569	0.630	-0.385	
CRC 027 PT	18143946	12252901	-1.458	5.224	-0.546	-0.786
-1.726	-5.988	1.041	-11.000	-5.176	3.139	1.201	-1.985
4.292	5.847	-6.059	11.000	-0.582	0.246	-0.186	
CRC 028 PT	18967094	14730425	-11.000	-0.140	4.504	5.705
4.539	5.208	1.596	-11.000	-11.000	-11.000	4.230	5.807
3.757	5.130	-6.315	11.000	3.046	4.186	2.436	
CRC 029 PT	17147427	11677839	-11.000	11.000	11.000	11.000
-11.000	-11.000	-11.000	-11.000	-1.350	11.000	4.777	7.343
11.000	11.000	-1.011	-1.890	-1.348	-1.167	-2.459	
CRC 032 PT	13828648	10205411	-1.116	-0.416	-1.098	0.778
-0.090	1.658	0.602	5.648	1.139	-11.000	-0.391	3.968
-0.782	1.412	-0.702	0.650	0.716	-0.578	0.030	
CRC 033 PT	18138542	11833489	0.575	0.545	-2.766	-0.550
-0.522	-0.162	-0.749	0.282	-0.855	1.362	0.563	0.630
-0.223	1.014	-0.297	1.072	-0.205	1.143	0.535	
CRC 034 PT	19394135	13789229	3.770	3.590	1.990	4.478
2.637	3.868	0.906	-11.000	1.749	5.129	2.800	4.188
1.666	3.208	2.081	3.597	2.395	3.519	2.131	
LCR 571 PT1	12771040	5224072	0.614	1.807	-1.983	11.000
-0.608	1.440	-11.000	-11.000	-1.071	-1.524	1.157	1.762
1.063	3.661	-11.000	11.000	2.045	1.718	-0.929	
LCR 572 PT1	11303441	2702099	2.744	1.078	0.392	1.146
-0.010	1.099	-1.483	-0.239	-1.360	-3.149	1.550	0.813

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0.858     1.009     -11.000   11.000    1.908     0.622     -0.933
CRC 246 PT     7945568        7005657       -2.662    -2.133    0.005     0.632
2.825     3.937     -0.167    -0.019    -3.116    -2.908    0.658     -0.222
0.604     0.450     -11.000   11.000    -1.524    0.950     -1.488
CRC 247 PT     8149006        7219190       -4.943    11.000    -5.442    -6.549
3.748     11.000    -4.116    -11.000   7.870     -6.036    1.791     -5.925
8.126     11.000    -11.000   11.000    11.000    -2.213    -3.557
CRC 249 PT     7918365        7083923       -1.115    1.038     -0.134    -4.804
0.566     2.027     1.193     1.744     -4.581    -11.000   1.125     -0.060
0.309     2.746     -11.000   11.000    -0.003    1.120     1.353
CRC 255 PT     7644469        6859875       3.538     2.647     2.864     4.530
3.302     3.301     -6.061    -11.000   -7.034    -11.000   2.404     3.168
8.210     3.366     -11.000   11.000    11.000    -6.018    1.638
CRC 256 PT     7597143        6755137       -11.000   -6.405    0.147     -1.047
0.294     0.950     -11.000   1.964     -4.366    -7.034    4.705     11.000
11.000    11.000    -11.000   11.000    11.000    1.456     0.683
CRC 259 PT     7508712        6626819       0.554     0.214     11.000    11.000
-11.000   -1.358    -11.000   -11.000   -1.490    0.099     -0.056    -0.494
11.000    11.000    0.730     1.391     -11.000   11.000    0.062
CRC 260 PT     7293084        6482426       -4.536    2.179     -2.103    0.933
-4.450    0.225     3.407     3.883     5.112     -1.783    1.897     -2.268
11.000    11.000    -2.181    -0.812    -4.654    -4.280    0.191
CRC 261 PT     7740467        6862237       -1.634    -1.384    -1.623    11.000
1.564     1.421     -2.000    -3.566    2.339     -6.758    -1.337    -2.669
11.000    11.000    -5.028    11.000    -11.000   -0.414    -5.437
CRC 264 PT     8976722        7716627       0.270     0.733     0.317     -4.965
-0.650    1.363     -0.322    -0.725    -3.413    7.564     -0.822    -2.697
6.249     0.312     -3.097    -0.103    1.970     6.971     -0.216
CRC 267 PT     8043631        6996244       -11.000   -2.836    -2.204    -2.747
-2.243    -1.766    -1.818    -2.450    -2.440    -4.387    11.000    11.000
11.000    11.000    -1.463    11.000    -1.682    -1.587    -2.301
CRC 270 PT     7728958        6873460       -7.034    11.000    0.589     -4.227
-0.029    2.552     -11.000   -11.000   1.268     4.011     1.015     -11.000
11.000    11.000    -11.000   8.126     -11.000   1.665     -0.141
CRC 274 PT     8916248        7373436       -4.118    -3.807    4.828     7.544
2.885     5.484     2.377     -11.000   2.766     -4.811    -2.883    -4.572
11.000    11.000    2.900     11.000    5.800     4.391     2.193
CRC 275 PT     8493369        6684169       -11.000   -11.000   2.497     4.005
1.656     3.205     1.476     3.049     -11.000   -11.000   1.687     2.268
11.000    11.000    -5.901    11.000    0.493     0.680     -11.000
CRC 276 PT     7703201        6528000       2.471     1.715     1.473     0.206
1.828     3.061     -11.000   -3.946    11.000    3.982     -2.057    -11.000
1.883     1.885     -3.438    2.216     -1.624    2.065     1.526
CRC 277 PT     8415773        6747467       -11.000   11.000    11.000    -3.924
-3.037    -2.662    -1.817    -3.648    -3.066    -3.668    -2.364    -4.024
11.000    11.000    -2.827    11.000    -2.299    -2.483    -2.301
CRC 279 PT     8495478        6909822       -0.633    0.580     0.890     1.473
-3.275    1.611     -1.016    -1.948    -0.107    1.167     -0.451    -1.834
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11.000    11.000    -3.618    11.000    -11.000   -11.000   -1.563
CRC 281 PT     9030236       7113466      -11.000   5.124     5.631     7.163
5.769     6.941     -11.000   -11.000   3.389     6.035     4.454     2.764
11.000    11.000    -11.000   5.142     3.286     4.138     -6.559
CRC 283 PT     8982949       7338328      -1.665    0.217     -0.621    -0.817
-0.966    -0.375    -1.023    -1.868    -1.451    -0.681    -0.476    -1.322
-1.856    -1.058    -0.970    -0.342    -0.155    0.243     -1.084
CRC 286 PT     7795806       6750658      -1.277    -0.806    -1.283    -0.336
-3.399    -0.370    0.204     -1.068    -0.589    -0.306    -0.315    -1.986
11.000    11.000    -0.860    -0.367    -7.034    -6.351    -1.148
CRC 289 PT     7790146       6852814      -11.000   5.554     4.465     5.564
4.561     5.630     -11.000   -11.000   11.000    2.496     2.294     -11.000
11.000    4.562     -11.000   4.658     3.373     4.349     3.009
CRC 290 PT     8306505       7408201      -0.288    -0.325    -0.222    0.178
-11.000   11.000    -11.000   -11.000   11.000    -1.529    0.569     0.101
11.000    11.000    -5.839    8.210     2.797     0.633     0.256
CRC 291 PT     7619290       6652596      -1.513    -1.039    -1.791    -1.081
-1.286    -1.255    -1.888    -11.000   -2.011    -5.307    0.518     8.210
11.000    11.000    -0.591    11.000    -11.000   -0.886    -1.475
CRC 295 PT     7821021       6823690      -1.523    -2.004    0.889     1.208
0.607     3.050     -2.761    -5.903    4.108     -11.000   4.264     -0.310
11.000    11.000    -4.670    11.000    -3.412    -3.633    -2.325
CRC 300 PT     8541249       7485468      -1.208    4.425     -6.190    3.773
6.941     5.144     -4.592    -11.000   3.519     -11.000   2.201     2.610
5.816     7.102     -11.000   -2.103    3.384     4.450     -1.518
LCR 007 PT1    16688322      2010170      -6.758    11.000    1.232     1.007
0.681     1.188     -6.224    -11.000   3.018     -6.254    2.202     0.848
11.000    11.000    3.805     11.000    -0.828    -11.000   -6.807
LCR 022 PT1    6106225       4076503      -3.984    -2.867    -4.880    -4.837
-3.867    -3.448    -3.003    -4.288    7.878     11.000    -2.208    -2.478
11.000    11.000    5.796     11.000    7.603     11.000    -2.394
LCR 023 PT1    24102823      2454734      -11.000   11.000    0.946     0.986
-2.941    -0.695    -11.000   -11.000   -5.280    -11.000   11.000    3.899
11.000    11.000    -11.000   11.000    1.222     1.726     -5.481
LCR 025 PT1    10088499      579885       0.845     0.642     0.448     0.819
-1.694    2.761     -2.044    0.474     -1.095    0.671     2.160     2.416
2.390     2.852     -2.581    2.181     0.089     0.934     -0.881
LCR 026 PT1    26520622      3042182      -2.566    -2.226    5.009     6.724
-2.936    -3.170    -3.205    -4.743    -2.211    -1.864    0.808     -1.575
11.000    11.000    -1.348    1.157     -2.290    0.171     -1.742
LCR 032 PT2    21956805      1379661      -11.000   2.385     0.910     2.495
0.659     2.479     -11.000   -11.000   -0.103    -1.594    2.034     3.900
3.167     1.441     -0.952    2.098     2.541     2.399     -0.172
LCR 036 PT1    23950909      1905415      -4.293    -4.300    -4.167    -6.209
3.955     4.158     -6.501    -11.000   11.000    -0.454    3.642     4.345
11.000    11.000    -11.000   11.000    -2.712    -2.440    0.022
LCR 037 PT1    21188227      1734274      -1.624    11.000    1.139     1.202
-2.702    -4.123    -4.254    -6.880    -3.321    -3.771    1.332     -0.430
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Table35.txt

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0.131     -0.262    -1.826    0.676     -0.325    2.139     1.650
LCR 040 PT1    25976551      1131985      -6.516    -0.984    -0.426    0.029
0.509     11.000    -6.195    -11.000   -1.572    0.572     -4.300    -11.000
4.540     7.124     -5.650    11.000    3.597     4.545     -1.317
LCR 041 PT1    23974638      2543351      0.523     1.186     0.679     0.813
1.868     1.026     -0.668    -11.000   1.100     -1.177    1.920     1.931
11.000    2.630     -11.000   11.000    -11.000   -11.000   -11.000
LCR 059 PT1    23777249      3707000      1.392     1.299     -0.683    0.516
0.250     1.286     -1.406    -0.802    -2.907    -0.824    2.434     1.218
11.000    11.000    -0.585    1.334     0.409     2.123     0.739
LCR 060 PT1    8670451       1506485      -6.679    -6.235    2.758     3.015
3.067     4.225     0.141     1.861     -6.692    -11.000   4.229     -2.927
11.000    11.000    6.030     11.000    1.013     3.424     -4.943
LCR 063 PT1    22653840      3180931      -0.773    -0.028    -0.522    -1.149
-0.612    -0.416    -1.809    -1.808    -1.593    1.053     2.023     0.355
1.349     3.028     -11.000   11.000    0.493     1.214     -0.461
LCR 064 PT2    27662758      2747689      -0.159    -1.124    -2.709    -2.364
-1.173    -1.711    -1.903    -5.366    -2.325    -1.899    2.374     -0.240
-0.068    -1.193    11.000    11.000    -1.034    0.506     -0.591
LCR 133 PT1    22133801      830859       -0.790    2.807     -1.740    -2.050
-3.315    -0.353    -2.971    -1.718    4.197     11.000    2.100     0.018
7.041     11.000    -3.181    -1.599    -1.018    2.128     -0.623
LCR 136 PT1    23576400      3209972      -1.341    -6.439    0.188     11.000
-5.223    3.991     -11.000   -4.720    -11.000   -11.000   0.854     0.618
11.000    3.481     1.974     11.000    -0.235    1.028     -0.785
LCR 142 PT1    25428337      1840742      0.516     0.548     -0.963    -1.635
-1.362    -0.599    -2.490    -2.192    -2.174    -0.156    2.052     -0.651
0.731     0.410     -0.950    1.467     0.206     2.719     -0.288
LCR 145 PT1    12097080      569866       0.394     1.115     -1.245    0.047
-0.508    2.127     -1.862    0.023     -1.811    1.516     2.214     1.427
-0.449    2.343     -2.262    1.237     1.393     1.651     -0.350
LCR 146 PT1    30644993      13013442     1.502     0.924     -0.499    -2.209
-1.945    -3.784    -2.525    -6.138    -2.510    -0.782    0.977     -1.613
-0.177    0.352     -11.000   4.464     0.359     3.011     1.691
LCR 147 PT1    22155006      2393328      0.997     1.000     0.145     0.698
-1.101    2.909     -1.510    -0.274    -2.466    1.419     4.013     2.629
-0.528    -0.144    -1.438    1.786     -0.387    1.336     -0.374
LCR 149 PT1    24042192      4930445      6.929     6.526     6.040     8.041
5.925     6.999     -11.000   -11.000   11.000    -11.000   -2.998    7.034
4.891     7.606     -6.271    7.560     3.866     6.515     -11.000
LCR 152 PT1    23436114      1068620      0.186     1.626     -0.408    0.498
-0.334    2.710     -2.347    0.988     -3.604    2.239     2.769     2.908
0.405     0.699     -3.154    1.610     -0.039    1.567     -0.526
LCR 153 PT1    14407930      1380663      -2.866    -1.822    0.956     0.496
-3.187    -2.904    -2.453    -3.815    -3.240    -2.261    5.542     11.000
4.288     7.194     0.898     6.760     -1.325    -0.819    -1.987
LCR 154 PT1    22945626      1426834      2.286     1.641     0.327     0.390
0.585     2.023     -6.692    -11.000   -11.000   -11.000   -2.691    -6.390
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Table35.txt

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LCR 155 PT1    19866621      2474730      -11.000   4.748     0.557     1.381
-0.501    0.978     -11.000   -11.000   11.000    0.597     2.173     1.130
5.454     7.683     -11.000   11.000    0.758     1.281     -2.534
LCR 156 PT1    31444399      2983777      1.117     1.165     -1.786    -0.634
-1.772    0.183     -2.338    -1.122    -3.632    0.466     2.314     0.840
-0.366    0.816     -0.148    0.350     0.911     2.229     0.729
LCR 157 PT1    28389922      5383661      -11.000   -11.000   4.042     6.804
-11.000   -11.000   -11.000   -11.000   2.250     7.714     0.496     -0.359
11.000    11.000    2.394     5.604     4.046     5.737     -5.074
LCR 158 PT1    28787065      1233692      -0.282    0.902     0.837     -0.777
-0.229    -0.097    -2.474    0.173     -0.452    2.083     2.889     2.253
0.923     0.997     -2.495    2.417     0.375     2.516     -0.024
LCR 160 PT1    25894468      3069845      0.697     0.575     -1.142    -0.879
0.252     0.481     -1.315    -11.000   -1.479    0.415     1.440     1.613
1.017     1.189     -6.143    11.000    -0.042    1.748     -0.315
LCR 186 PT1    31143753      3797580      -5.552    -4.414    1.017     1.826
0.014     3.118     -3.223    -11.000   1.803     -11.000   11.000    11.000
11.000    11.000    -11.000   11.000    2.760     3.673     -3.662
LCR 187 PT1    28341194      1684311      11.000    11.000    -4.051    -4.346
-4.001    -3.200    -3.826    -4.606    -4.594    -3.253    -0.119    -3.084
7.878     11.000    6.238     11.000    -1.971    -0.400    -2.250
LCR 190 PT1    22853948      2522593      0.159     0.625     -1.542    -1.107
-0.439    -1.130    -2.284    -2.053    -1.989    -0.334    1.243     0.533
-0.647    -0.854    -1.680    0.322     0.153     2.005     -0.170
LCR 193 PT1    20581563      2020598      1.283     0.508     -1.220    0.341
-0.812    0.615     -0.893    -0.130    -2.150    2.043     2.274     1.750
-0.239    0.453     -1.333    1.339     0.255     1.727     -0.605
LCR 206 PT1    26706511      1813778      -0.731    11.000    -2.264    -1.696
-1.868    -0.346    -2.068    -1.607    -6.668    11.000    0.914     0.611
11.000    0.091     -2.101    -0.041    0.041     0.523     -1.370
LCR 207 PT1    2701074       1885793      -1.287    1.510     4.426     -3.432
-2.408    -1.089    -2.297    -11.000   3.841     0.876     0.056     3.553
3.926     5.133     -11.000   11.000    0.943     2.741     -1.469
LCR 208 PT1    14336454      8015166      -4.448    8.210     -4.493    4.374
-5.915    -2.466    -11.000   -6.937    -1.720    1.960     3.861     -1.285
4.360     11.000    -5.037    11.000    2.987     4.699     1.534
LCR 209 PT1    14082755      7988977      0.108     1.034     -0.842    -0.605
-1.421    0.517     -1.595    -0.232    -2.026    0.770     0.566     1.279
0.622     -0.256    -2.510    0.518     0.596     1.434     -1.396
LCR 210 PT1    2338166       1084120      -2.088    -1.288    4.057     -0.288
-1.983    5.411     -6.839    -11.000   -1.122    -0.405    3.802     5.725
7.081     11.000    -5.754    3.641     -2.465    3.431     -2.584
LCR 210 PT2    2603952       1437742      -2.004    -1.374    3.951     -0.210
-2.191    4.884     -11.000   -11.000   -1.530    -1.109    4.039     4.372
7.393     11.000    -5.314    3.220     -3.050    4.547     -1.487
LCR 211 PT1    36367299      12790173     1.157     0.320     -2.182    -1.356
-1.902    0.220     -3.200    -1.522    -2.819    0.362     1.619     0.899
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Table35.txt

0.226	0.820	-0.900	0.693	0.172	1.499	0.686	
LCR 213 PT1	31384255	3131156	4.371	3.734	-1.375	-0.331	
-1.291	-0.068	-2.048	-1.468	-2.080	-0.008	1.935	-0.291
0.342	1.260	-1.475	0.672	11.000	11.000	0.897	
LCR 217 PT1	27176225	1747667	0.075	-1.046	-3.412	-2.760	
-1.989	-0.815	-3.242	-2.703	-3.317	-0.680	1.480	-0.953
-1.251	-0.783	5.142	11.000	11.000	11.000	-1.523	
LCR 248 PT2	2846210	1510122	-1.948	-2.022	-2.334	-2.847	
4.616	6.803	-2.533	-4.237	-2.136	-1.631	2.178	2.992
11.000	11.000	-11.000	11.000	-2.591	-11.000	-2.688	
LCR 284 PT2	2978062	2162444	-11.000	-3.063	-4.999	-4.303	
1.464	-0.938	-1.624	-0.571	0.067	4.015	4.236	3.285
6.312	11.000	-0.960	3.046	-3.447	-3.269	-1.308	
LCR 290 PT2	14389964	10661849	-4.575	0.378	-2.734	-1.470	
1.553	4.426	-2.548	-3.057	2.314	-3.697	1.425	6.063
11.000	11.000	-5.762	11.000	-1.789	-2.970	-4.217	
LCR 290 PT3	15122649	9796251	-1.549	0.202	0.061	3.462	
-1.635	2.172	-2.707	0.646	1.470	1.365	-0.047	5.737
2.436	2.670	-4.544	2.815	-0.366	-1.326	-2.942	
LCR 312 PT1	13553659	9605229	-1.982	-0.387	-0.301	-0.139	
-0.850	-0.114	-0.317	-1.445	-0.710	0.751	-0.442	0.774
11.000	11.000	-11.000	11.000	0.402	0.160	-1.584	
LCR 312 PT2	13498908	6775889	-2.630	-0.773	-1.214	-1.282	
-1.526	-0.417	-1.652	-0.893	-1.511	-0.094	-0.541	0.089
11.000	11.000	-11.000	11.000	-0.132	-0.499	-2.078	
LCR 313 PT1	13464201	7650064	0.145	1.623	-0.780	0.938	
-1.051	1.037	-1.626	-0.453	11.000	-11.000	0.185	1.930
1.606	0.885	-5.898	11.000	0.244	0.244	-0.731	
LCR 313 PT2	13420554	4443701	0.273	1.985	-0.305	0.935	
-0.108	1.532	-1.679	-1.487	11.000	-11.000	0.831	2.044
3.398	3.230	-11.000	11.000	0.500	1.072	-0.816	
LCR 315 PT2	2944895	1332744	0.458	1.530	0.986	0.611	
-1.979	1.116	-0.759	0.504	-1.037	2.541	0.838	2.434
1.166	0.746	-2.357	1.298	-1.443	1.377	-0.493	
LCR 317 PT1	14497047	9582218	-0.930	-0.734	-0.208	0.187	
-1.408	-0.244	-11.000	-11.000	11.000	-11.000	7.081	0.473
11.000	11.000	-11.000	11.000	-6.807	-11.000	-2.186	
LCR 332 PT1	14266452	6567648	-0.255	3.234	1.930	3.349	
2.163	3.052	-1.207	-2.309	-1.065	3.233	0.805	1.713
11.000	3.616	-5.032	11.000	1.772	2.313	-2.868	
LCR 333 PT1	2608375	1143305	0.377	0.833	1.347	0.386	
-0.307	1.755	-0.826	-0.250	-0.923	1.893	1.628	1.469
0.357	0.128	-2.783	-0.026	0.664	2.246	-0.598	
LCR 336 PT1	13964600	8032239	-0.707	0.719	-0.127	0.353	
-1.409	1.644	-0.683	1.575	-0.376	2.469	0.098	2.940
-0.044	1.569	-2.682	0.903	0.587	0.754	-1.669	
LCR 336 PT2	13995339	7547354	-0.923	0.932	-1.260	-0.273	
-1.487	0.538	-0.867	0.894	-0.959	1.721	-0.137	2.338

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LCR 336 PT3    14416497      6637448      -0.955    0.515     -0.876    1.843
-0.563    2.771     0.242     6.195     1.104     3.224     -1.283    5.022
0.366     3.492     -2.509    4.417     0.500     -0.973    -3.038
LCR 336 PT4    14401765      5862849      -0.631    0.841     -0.994    0.120
-1.445    1.712     -0.578    2.092     -0.144    2.188     0.212     3.239
0.999     2.935     -2.238    3.622     0.418     0.125     -1.632
LCR 336 PT5    13179864      9928761      -0.305    0.298     -0.589    1.032
-1.664    0.898     -0.891    -0.283    -1.845    0.447     -0.035    1.169
0.410     1.257     -1.582    -0.267    -0.983    1.031     -0.988
LCR 337 PT1    2054066       856006       -0.291    11.000    -0.594    -1.500
-1.985    -0.598    -1.081    -1.368    -1.723    0.920     -0.280    0.492
-0.399    -0.318    6.112     11.000    -0.529    0.260     -2.550
LCR 352 PT1    2852074       1563583      0.252     1.364     -2.402    0.950
-1.983    2.207     -0.958    3.091     -2.192    1.988     -0.381    4.236
6.824     11.000    -2.816    0.959     1.362     -0.166    -2.443
LCR 354 PT1    3047681       1739473      -3.090    -1.496    -2.801    -3.180
5.515     8.041     -1.565    -0.424    -1.909    -0.140    -2.407    -0.104
4.698     6.577     0.096     6.636     -0.527    -1.913    -3.616
LCR 356 PT1    3001059       2013930      0.213     1.549     0.061     0.472
-1.116    1.267     -0.681    1.059     -1.409    2.938     0.699     1.913
1.448     1.932     -3.287    0.849     1.026     2.274     -1.140
LCR 357 PT1    14113889      4981671      -1.509    -0.565    -0.836    0.129
-2.310    -2.800    -0.863    0.004     -2.201    -0.811    0.172     0.645
11.000    11.000    -3.801    11.000    -5.354    -6.116    -3.018
LCR 380 PT1    13952062      8726405      0.549     11.000    -1.551    -11.000
0.282     3.398     -11.000   -11.000   2.222     3.750     3.108     3.798
2.966     4.072     -6.937    11.000    11.000    3.018     -4.510
LCR 383 PT1    12704926      5031099      1.418     3.346     0.309     -0.137
-0.158    1.279     -0.963    -0.660    -0.856    1.217     1.576     0.759
11.000    11.000    -7.034    11.000    -11.000   -11.000   -1.301
LCR 383 PT2    15272933      8610325      -5.497    -5.260    5.822     6.885
0.690     1.500     -1.207    -1.194    -1.298    0.038     2.272     1.071
11.000    11.000    -11.000   11.000    -5.685    -5.010    0.976
LCR 384 PT1    3072560       2166429      -1.799    -1.330    0.734     1.895
-3.246    3.325     -2.412    -6.371    -0.378    -0.259    -0.620    1.268
0.950     3.258     -4.386    7.518     1.602     4.498     0.679
LCR 384 PT2    14406203      7472373      -5.452    11.000    0.286     0.017
-2.714    1.027     -4.199    -11.000   -1.728    -3.728    1.394     1.091
0.438     2.396     -11.000   11.000    0.221     1.715     0.071
LCR 390 PT1    13700957      6411140      -0.893    1.275     -0.352    0.381
-0.890    -0.250    -3.238    -2.679    -1.138    1.283     0.611     1.006
0.617     2.030     -11.000   11.000    -0.133    1.088     0.028
LCR 391 PT1    3312470       2181029      1.503     1.356     -0.972    -2.539
-1.120    0.189     -11.000   11.000    -1.992    -0.317    1.705     -11.000
0.497     0.411     -11.000   0.965     0.305     2.076     0.401
LCR 392 PT1    13475073      7987123      3.354     2.538     1.342     2.531
-11.000   1.806     -11.000   -11.000   5.801     3.194     3.149     1.500
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LCR 393 PT1    3072724       1792664       -4.825    -4.419    4.160     4.362
-6.291    -6.173    1.415     3.615     0.738     5.735     -2.992    -5.217
2.415     3.484     -0.642    3.902     -2.978    -2.478    1.291
LCR 395 PT1    14165337      11410882      -2.652    -2.734    -4.548    -2.518
-4.133    -3.209    -1.280    -2.603    -2.894    -3.382    -2.502    -1.611
11.000    11.000    -3.390    -1.923    -2.069    -1.323    -2.473
LCR 395 PT2    13468226      10251345      -5.806    -5.815    2.740     5.731
2.972     4.552     -3.873    -11.000   1.659     6.087     -4.097    -6.073
11.000    11.000    1.541     5.606     -2.578    -1.935    -4.375
LCR 396 PT1    13765524      10365500      -11.000   11.000    6.160     11.000
-3.479    -3.781    -5.278    -11.000   -3.683    -3.957    4.750     11.000
11.000    11.000    2.897     5.890     -2.433    -1.961    3.672
LCR 397 PT1    13668125      10884481      -5.920    4.491     4.232     11.000
-6.620    -6.839    -4.635    -7.034    -5.094    -6.880    3.158     8.041
6.016     7.481     -11.000   7.289     4.138     5.243     1.905
LCR 398 PT1    14048036      7957267       -11.000   1.288     1.339     2.187
0.888     1.894     -0.045    1.767     11.000    2.937     1.676     -11.000
1.385     2.732     -1.005    2.695     1.151     2.383     0.225
LCR 401 PT1    13935807      10756246      -2.587    -2.396    -4.323    -11.000
-3.067    -3.027    -2.220    -3.066    -2.890    -2.554    -2.003    -1.671
11.000    11.000    -3.191    -2.341    -1.709    -1.230    -2.237
LCR 403 PT1    15138287      7494030       0.364     0.443     -1.084    -0.271
-11.000   -3.815    -1.216    -0.201    -0.903    0.115     -1.865    -11.000
11.000    11.000    -11.000   11.000    0.057     0.680     -0.844
LCR 404 PT1    14391645      8837237       -1.694    -1.519    -2.520    -2.429
-2.701    -2.107    11.000    11.000    -2.726    -0.901    -1.013    -1.439
-1.460    -0.935    -6.483    11.000    -1.087    -0.490    -1.510
LCR 405 PT1    15085430      10321860      -11.000   -11.000   -0.307    1.120
-0.743    1.751     -5.442    -3.136    5.006     0.694     -0.480    0.102
11.000    11.000    -11.000   11.000    1.539     2.315     -1.669
LCR 406 PT1    12913800      7172980       1.429     2.419     1.269     1.096
6.090     11.000    0.009     0.686     -0.615    2.411     0.162     1.428
8.210     2.660     -0.775    2.265     0.377     2.853     0.321
LCR 407 PT1    13927527      8869296       -1.457    -0.873    -2.695    -1.122
-2.680    0.504     -2.013    0.894     -1.959    0.073     -0.354    2.064
-1.511    0.373     7.105     11.000    -1.472    -0.947    -2.507
LCR 408 PT1    1839975       969087        1.202     0.617     1.543     1.227
-0.220    1.487     -0.877    0.651     -2.320    1.738     2.431     2.979
0.563     1.194     -1.882    -0.674    0.172     -5.519    0.413
LCR 409 PT1    14150911      9361267       -11.000   -11.000   2.292     4.456
2.476     11.000    -4.317    -6.647    -4.336    -4.239    -3.230    -3.631
11.000    11.000    -11.000   11.000    -2.209    -2.450    -1.062
LCR 415 PT1    13224648      10880096      1.159     0.366     -0.994    0.180
-1.381    -0.477    -1.416    -1.371    -3.040    -0.760    0.576     0.664
0.253     1.034     -0.392    5.809     -0.714    1.367     0.728
LCR 416 PT1    13514923      10508807      -0.313    -0.321    -1.148    7.771
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-1.305    -1.002    -0.786    -0.159    -2.704    -2.489    -0.950    0.144
11.000    11.000    -11.000   11.000    0.077     -0.136    -3.021
LCR 419 PT1    13265807      5332733      0.976     11.000    0.218     -0.299
-0.785    0.263     -1.693    -0.829    -1.669    1.676     1.038     0.213
1.387     11.000    -11.000   11.000    0.545     0.596     -0.741
LCR 422 PT1    14924756      10831405     -3.170    -2.950    -4.651    -3.919
6.321     7.594     -3.023    -6.692    4.739     11.000    -11.000   -11.000
6.005     11.000    -11.000   11.000    -2.160    -1.869    -2.390
LCR 423 PT1    14305203      9251120      -1.282    4.860     1.943     2.591
2.783     4.721     -11.000   -11.000   11.000    11.000    1.614     2.869
11.000    11.000    -11.000   7.229     -11.000   -11.000   -11.000
LCR 424 PT1    2577289       1709537      -0.757    0.530     0.138     -0.370
-0.754    -0.463    -1.899    -2.651    -1.778    -0.691    1.882     -0.401
0.953     0.947     -6.620    11.000    5.498     8.077     -0.141
LCR 425 PT1    12888369      5385421      11.000    11.000    0.742     -11.000
1.208     1.846     -6.277    0.667     0.035     3.045     0.802     0.632
5.684     3.148     -11.000   5.560     1.281     2.088     -5.936
LCR 426 PT1    12616359      6972629      -1.524    0.738     0.085     0.691
0.055     1.567     2.833     -4.338    4.370     -5.818    -5.489    1.413
11.000    3.038     -11.000   11.000    0.153     1.728     -0.984
LCR 427 PT1    14019710      6476523      0.246     1.594     -0.181    -0.175
-1.747    0.668     -1.481    -0.593    -1.278    1.552     1.539     2.111
0.993     0.973     -2.186    1.356     0.977     1.466     -0.918
LCR 428 PT1    14372829      7089141      -1.796    -0.782    -2.262    -2.011
-2.321    -0.704    -1.430    -1.170    -2.403    3.185     -0.688    -0.182
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LCR 429 PT1    13473216      6757853      0.439     3.259     4.064     2.997
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LCR 430 PT1    2888950       1629251      -0.169    0.058     -1.199    -1.419
-1.097    0.498     -1.681    -0.518    -2.735    0.813     -0.646    2.295
0.237     0.629     -2.692    0.082     -0.248    1.255     -1.483
LCR 431 PT1    12837715      9616179      2.844     2.181     2.577     5.339
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LCR 432 PT1    13775349      6208899      -3.537    11.000    -5.866    7.878
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LCR 433 PT1    14580141      10731059     0.379     1.127     -1.769    -0.186
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LCR 445 PT1    3053606       2247033      -0.670    1.560     -0.473    1.429
-0.713    1.803     -0.426    2.758     -0.462    2.509     0.109     4.737
-0.570    1.458     -3.026    0.789     0.545     0.553     -1.709
LCR 446 PT1    2956157       1978934      -11.000   -0.052    -11.000   -6.668
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CRC 528 PT1    2550385        773391        1.488     6.015     0.150     -2.878
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-0.613    -0.153    3.348     -4.411    -11.000   2.192     4.188
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-2.770    1.175     -0.284    6.027     -11.000   1.503     5.245
G024 PT        14782107       7367831       -0.986    -0.385    4.625     3.095
2.463     3.552     -11.000   -11.000   -2.833    -3.258    3.766     -1.589
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G048 PT        12151250       6665874       -3.749    11.000    11.000    6.441
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G055 PT        9177751        3707291       -2.139    -1.232    3.186     -3.494
-3.332    6.967     -3.231    -11.000   11.000    -2.650    1.314     -3.832
7.795     -2.553    3.004     3.617     2.819     -1.580    -0.811
G079 PT        8611183        1425036       0.935     -0.252    -0.243    -3.811
-0.040    -2.459    -0.473    -1.394    0.666     -0.387    -0.059    -0.469
0.454     -2.031    4.611     11.000    1.064     -1.118    -0.160
G101 PT        11788765       5498150       -6.068    11.000    1.970     2.623
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2.811     0.613     7.442     11.000    -3.072    1.502     1.757
G110 PT        10110115       4258553       3.464     1.704     1.777     0.829
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7.114     7.081     -3.775    0.295     -3.031    1.597     1.676
G110 PT        12323000       8617984       2.825     1.961     1.474     1.432
-6.839    7.906     -5.665    -1.238    -0.969    -1.144    -2.415    -11.000
8.210     7.244     -3.736    -0.384    -3.322    1.092     0.741
G113 PT        13776295       8664903       -0.274    -0.457    11.000    5.102
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1.647	-0.561	4.002	2.830	2.707	3.247	2.274	
G115 PT	12506043	6782101	1.674	4.660	1.717	0.868	
-1.912	3.047	-4.626	-11.000	-2.281	-5.564	5.128	-4.114
7.032	-0.745	1.946	5.492	-5.329	-4.441	1.057	
G144 PT	11215765	5372319	-6.590	1.463	1.392	0.888	
0.038	0.912	-11.000	-11.000	0.140	0.703	-0.630	-11.000
11.000	11.000	-11.000	4.045	8.126	11.000	-0.546	
G144 PT	8781993	5891776	-3.225	1.383	0.760	1.233	
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6.992	-2.883	-4.410	1.616	5.653	5.997	1.161	
G147 PT	15759271	8908613	-1.956	11.000	-2.115	-11.000	
-2.240	7.326	-11.000	-11.000	5.633	-11.000	11.000	-2.413
11.000	7.676	-6.386	3.049	3.233	-0.724	2.125	
G212 PT	14008010	6962500	-5.517	0.169	4.381	6.437	
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G270 PT	8738517	6022056	1.730	-0.714	3.086	0.432	
-3.042	0.992	-1.911	-11.000	0.585	-3.001	5.161	-5.688
3.371	-4.452	2.874	11.000	-4.641	4.099	-0.101	
G332 PT	12120616	7796988	4.347	3.054	-11.000	2.162	
1.574	1.613	0.591	0.637	-0.496	-5.725	-3.847	3.170
1.468	-11.000	1.435	4.277	1.334	3.539	1.066	
G407 PT	12799488	9083421	-0.747	7.941	-0.145	-2.232	
-4.160	4.143	-3.129	-3.510	4.183	-3.429	0.079	-4.635
5.452	6.263	4.580	4.631	3.098	0.788	4.489	
G409 PT	4557590	1629459	1.045	3.555	1.626	-2.016	
-2.479	1.601	-3.069	-5.315	-0.311	0.946	1.564	1.418
3.070	-0.127	-0.683	0.499	2.169	-0.306	1.355	
G553 PT	14525593	9783444	-0.024	-2.130	0.335	-3.437	
-0.970	0.132	-0.522	-1.226	-1.499	-0.279	0.937	0.536
-1.288	-1.256	3.649	11.000	-6.839	-6.384	-1.762	
G801 PT	20713009	17274275	-0.780	-0.319	-2.233	-2.321	
-1.815	-0.418	-11.000	-6.096	-2.551	-2.254	0.922	-1.500
-0.700	-1.199	11.000	11.000	-1.406	2.591	0.686	
G803 PT	16783905	13235349	-2.822	0.194	0.501	7.620	
-0.067	4.498	-11.000	-11.000	0.274	-11.000	11.000	11.000
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HCC 003PT	10620449	7799300	2.346	11.000	0.937	0.939	
0.090	0.645	-0.607	-2.812	0.030	0.670	11.000	-11.000
2.226	-0.310	-11.000	-4.275	0.058	0.703	0.651	
HCC 007PT	12175789	8377395	1.459	11.000	0.176	-0.933	
-1.688	-1.777	-2.117	-3.082	-0.347	-1.809	11.000	0.266
0.988	-1.443	-11.000	6.733	-0.307	-0.114	0.927	
HCC 008PT	10020676	6966282	2.326	11.000	1.268	1.492	
-0.463	0.508	-5.300	-11.000	-0.067	0.095	6.945	-11.000

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-0.434	0.066	-1.962	-6.189	4.240	6.559	2.123	0.199
-0.107	-1.441	-3.689	2.663	-0.427	0.085	1.963	
HCC 013PT	8550273	5954673	5.534	11.000	4.213	4.239	
-11.000	3.339	11.000	-11.000	11.000	-11.000	4.034	4.988
4.010	2.961	-3.673	2.771	-6.270	3.588	2.887	
HN 001 PT2	11104903	7938655	-0.898	0.732	-1.419	-2.254	
-11.000	11.000	-3.065	-5.915	-1.085	-6.880	6.687	5.539
2.136	0.127	-0.287	11.000	1.046	-0.072	1.653	
HN 374 PT	12421987	11573909	-3.920	-4.324	0.356	0.349	
-11.000	11.000	-1.667	-2.255	5.424	3.366	-5.609	-3.405
-0.235	2.589	3.157	11.000	2.971	6.178	-3.435	
HN 375 PT	11634489	10169518	1.828	4.006	-11.000	-3.303	
-11.000	7.992	-11.000	11.000	5.225	-11.000	7.259	6.007
5.812	11.000	5.006	11.000	-11.000	1.153	4.727	
HN 376 PT	11911941	11037731	-1.894	0.359	1.162	6.491	
-11.000	11.000	-11.000	-11.000	2.034	-11.000	-2.250	-11.000
5.648	4.770	11.000	11.000	-6.361	11.000	-0.265	
HN 377 PT	12275817	11375660	1.819	1.733	-0.525	1.673	
0.376	-1.531	-0.267	0.825	-0.716	1.274	1.334	1.918
-0.165	1.455	-1.214	2.354	1.459	11.000	-0.376	
HN 378 PT	12256333	10722428	-5.754	4.787	2.909	-4.229	
-2.455	11.000	-5.215	-11.000	3.716	1.769	6.870	4.587
11.000	3.058	-5.618	11.000	-4.989	-2.093	-11.000	
HN 378 PT	10789811	8687829	-2.392	4.428	2.260	-2.000	
-3.446	8.210	-4.405	-11.000	-2.651	-2.673	6.593	4.390
6.290	1.076	-2.760	11.000	-2.807	-1.155	-11.000	
HN 379 PT	7787949	6757178	0.919	0.311	-0.800	-1.857	
0.693	0.915	-0.241	-1.320	-1.109	0.774	0.482	0.254
-2.010	1.612	-0.489	1.214	0.651	1.592	-1.119	
HN 381 PT	11286806	9630031	1.351	-4.268	0.656	-1.948	
0.105	11.000	-1.008	-11.000	-0.314	-11.000	2.264	2.285
11.000	-5.679	-6.046	1.625	6.905	11.000	4.774	
HN 383 PT	7955710	6939712	-0.683	-1.119	-2.541	2.626	
-4.740	11.000	-2.124	-0.224	11.000	-1.047	-0.842	-0.717
0.597	-5.189	-4.605	3.257	-0.734	11.000	-1.736	
HN 384 PT	12132969	11049656	11.000	11.000	-6.739	-11.000	
11.000	11.000	11.000	11.000	-5.393	-11.000	-4.505	-11.000
-5.467	-11.000	11.000	11.000	-4.273	-4.498	-4.488	
HN 387 PT	11493370	9964103	2.995	11.000	0.333	-1.232	
-11.000	-0.442	-11.000	-6.104	11.000	2.103	1.860	11.000
6.493	3.464	-2.095	2.619	4.549	11.000	-0.082	
HN 389 PT	8274638	7158680	1.374	1.043	0.057	-0.273	
-0.631	0.187	-1.900	-0.851	-1.116	1.647	1.972	-11.000
-0.470	1.021	-0.919	11.000	7.149	2.439	1.246	
HN 396 PT	12007771	10904316	2.755	2.254	-7.034	-11.000	
4.601	11.000	1.046	3.075	0.595	-6.628	-2.662	-5.626

Table35.txt

0.796	3.819	0.247	4.079	0.354	2.804	1.921	
HN 403 PT	8094839	5176315	-2.570	4.383	2.645	2.046	
-3.300	2.942	-3.903	-4.877	-4.894	-3.655	-1.381	-3.687
2.936	4.786	1.018	11.000	11.000	11.000	-2.675	
HN 404 PT	8473417	6098524	0.593	0.466	-0.819	-1.813	
-0.795	0.684	11.000	-1.515	11.000	3.531	-11.000	-11.000
0.044	1.051	3.615	11.000	7.127	1.284	-0.462	
HN 405 PT	9352645	8886082	-0.263	1.237	-0.593	-0.820	
-3.865	2.277	-0.822	-3.021	-0.810	-3.051	0.158	-3.805
0.892	-0.705	-1.532	-1.335	-2.081	3.725	-0.255	
HN 406 PT	8284842	5966765	-0.903	0.603	-1.870	2.642	
-11.000	6.856	-11.000	-0.683	11.000	-11.000	-3.786	-5.278
5.840	8.210	3.722	11.000	-11.000	11.000	-6.937	
HN 407 PT	8371882	5545774	-0.367	0.647	-1.001	-0.446	
-1.710	-0.251	-0.896	-1.070	-2.329	0.045	-1.652	0.435
-0.880	0.148	-6.571	11.000	4.532	5.622	-1.500	
HN 408 PT	8578312	6689356	-4.836	6.890	7.714	11.000	
-6.126	11.000	-5.272	-11.000	11.000	-6.425	-0.240	-11.000
11.000	-6.159	-11.000	11.000	-11.000	-3.109	-3.924	
HN 410 PT1	8149984	5132268	0.895	11.000	-1.359	-1.913	
-1.657	11.000	-4.281	-1.866	11.000	0.593	0.887	0.730
-0.360	3.580	-1.773	0.006	-0.100	0.938	-1.147	
HN 411 PT	8851401	7020515	2.914	3.514	0.430	-11.000	
2.886	11.000	0.417	-5.676	1.000	3.024	1.068	-11.000
2.206	2.546	0.221	3.032	2.770	4.283	1.250	
HN 412 PT	11408282	7359686	-2.624	5.392	4.768	0.503	
-6.110	4.877	-0.881	1.554	2.160	-11.000	1.096	0.334
2.772	-0.497	-2.213	3.418	-3.631	-2.644	-0.208	
HN 414 PT	6873532	5732182	3.481	1.902	-0.007	0.587	
-11.000	11.000	-5.244	11.000	-0.961	0.939	1.473	-11.000
0.624	-1.999	-1.196	1.179	-6.252	1.935	-4.018	
HN 424 PT	12017154	11600186	-3.679	11.000	4.041	1.376	
-11.000	11.000	-11.000	-7.034	11.000	-5.342	-1.154	3.376
11.000	-11.000	6.996	-4.330	-2.942	11.000	-1.855	
HN 426 PT	4807064	3567373	-2.219	-1.737	-1.521	-5.231	
-4.674	7.195	0.434	2.150	0.998	-0.548	1.111	5.131
11.000	-11.000	-11.000	3.615	11.000	1.008	-11.000	
HN 432 PT	12119772	11625518	-5.106	4.633	7.836	11.000	
-11.000	11.000	-11.000	-11.000	2.533	-11.000	1.648	3.206
3.962	4.261	-11.000	7.079	-11.000	-0.175	1.339	
HN 433 PT	11533126	11258743	5.765	5.102	3.044	-1.811	
-11.000	5.825	-0.130	-11.000	2.308	2.808	3.213	4.245
11.000	4.246	-11.000	11.000	1.662	3.325	-2.312	
HN 435 PT	12474957	11675078	-0.757	11.000	-1.267	-1.100	
-11.000	11.000	-0.689	-0.563	4.383	11.000	-11.000	-11.000
11.000	11.000	-11.000	6.189	-11.000	6.229	-11.000	
HN 437 PT	12541478	12204564	-1.302	-1.658	-2.399	-3.559	
-2.133	-2.241	-1.573	-4.139	-2.229	-1.595	-1.027	-2.526

Table35.txt

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11.000    11.000    -11.000   11.000    -3.164    -1.014    -1.469
HN 452 PT      7940958       7026812      -1.272    -1.096    -1.805    -2.379
-1.593    -1.987    -2.486    -4.426    -1.845    -1.761    0.026     -2.468
-2.310    -1.472    11.000    11.000    -1.384    -0.314    -1.627
HN 453 PT      12133923      10710407     0.616     0.540     -0.652    0.094
-1.682    0.792     -0.349    -0.132    -0.097    0.372     1.255     0.987
-0.545    0.065     -1.690    1.721     -0.064    1.446     -0.145
HN 455 PT      7828217       6953794      0.926     0.792     -0.048    1.785
-11.000   4.594     0.631     -6.405    0.325     -11.000   0.567     2.231
2.079     0.994     -11.000   11.000    -11.000   11.000    -11.000
HN 456 PT      8836597       7457950      0.212     -0.848    11.000    6.299
-11.000   11.000    -11.000   -11.000   11.000    -11.000   -0.269    -4.048
5.435     -0.870    -0.522    11.000    11.000    0.226     -1.482
HN 313 PT      1298426       947891       0.936     0.544     -0.050    1.292
-1.979    0.079     -0.477    -0.058    -0.778    1.329     0.213     0.996
0.157     0.761     -1.404    0.602     -1.177    0.914     2.641
HN 318 PT      1418581       1003186      -5.481    11.000    8.126     11.000
11.000    11.000    -2.610    -6.780    11.000    -5.515    5.468     -2.877
-3.499    -1.766    -4.080    4.913     6.354     0.668     -1.518
HN 321 PT      655337        476459       -11.000   3.923     4.754     -11.000
4.856     -3.674    -2.773    -5.843    -2.603    -2.101    -1.424    0.800
7.037     -3.583    -0.812    2.948     -2.661    -0.018    11.000
HN 322 PT      2460537       1575686      -0.066    0.862     1.679     1.853
-1.003    0.209     2.866     -1.347    0.043     1.300     2.364     2.290
0.287     3.061     0.672     1.243     -1.406    4.121     4.991
HN 325 PT      1666924       1150598      -1.017    -0.992    -1.574    -0.626
-0.860    -0.098    0.592     -2.321    -1.502    -0.173    11.000    11.000
11.000    2.790     -0.582    0.055     -2.400    0.689     1.330
HN 332 PT      2212440       1548823      -2.321    -2.778    11.000    11.000
-2.965    -0.866    -1.733    -3.626    -3.571    -1.906    11.000    -1.158
-1.846    -0.823    -3.028    11.000    11.000    11.000    11.000
HN 333 PT      3387631       2143476      -0.043    -1.682    -0.960    5.880
-2.131    -0.469    0.974     -1.329    -1.659    -0.937    0.850     -0.401
-0.733    1.727     -0.731    0.839     11.000    0.193     2.850
HN 334 PT      3378625       2142478      0.697     -1.403    -0.324    0.894
-0.021    0.776     1.054     -11.000   0.308     0.941     1.194     0.787
0.444     0.512     -1.978    1.060     -1.355    1.468     0.639
HN 335 PT      2155058       1502685      -6.679    -0.554    -0.579    -0.145
0.118     0.437     0.776     -0.573    -0.546    1.676     0.525     -1.230
-0.338    0.445     -2.483    0.137     -0.576    -0.134    1.438
HN 336 PT      1175350       801569       1.217     0.469     2.124     1.756
-2.312    0.482     1.478     -0.335    -0.841    1.169     -0.845    1.798
0.879     1.541     -0.654    -0.247    -2.144    0.846     2.622
HN 337 PT      1759164       1314337      0.914     2.058     1.719     1.066
-1.630    -0.211    1.878     -2.022    0.320     0.828     0.638     -0.322
0.577     1.543     -1.796    2.270     -0.650    1.936     1.399
HN 338 PT      1475114       1091908      0.712     -0.269    -0.310    1.123
-2.390    0.350     0.754     -1.501    -0.406    -4.087    -0.280    5.931
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Table35.txt

7.207 -0.069 -0.591 0.875 -0.298 1.309 -0.154
HN 339 PT 2104315 1560725 0.190 0.025 1.641 0.836
-0.804 0.719 0.442 -0.087 -0.671 -0.130 -0.669 0.520
-0.350 2.240 0.550 1.082 -0.271 2.285 0.994
HN 341 PT 1676635 1231075 -0.124 0.562 1.421 1.240
-1.057 -3.369 0.727 -1.452 -0.137 0.473 0.686 -0.080
-0.991 -11.000 11.000 2.089 -0.207 0.983 0.593
HN 342 PT 2908339 1929105 -0.257 0.807 2.103 11.000
-0.518 1.006 0.960 -1.069 -1.216 -6.461 0.903 2.374
1.348 1.601 -1.121 1.601 -0.672 1.427 3.940
HN 343 PT 2115651 1516327 -1.164 -6.839 -0.157 -5.246
-3.098 0.054 0.912 0.570 -0.227 -0.313 -0.135 -0.758
-6.363 -0.683 -2.184 0.451 -0.120 0.703 1.124
HN 344 PT 2062548 1446680 0.648 0.251 -0.402 -1.628
-0.348 -0.347 0.258 -0.634 -0.008 0.068 -0.649 0.209
-1.358 0.982 -0.922 0.671 -1.096 0.897 0.493
HN 345 PT 2306843 1559093 1.593 1.219 -0.294 0.452
-1.634 1.530 0.137 -0.314 -0.566 1.404 -0.186 0.485
0.276 0.120 -1.001 0.542 -0.925 1.524 0.294
HN 346 PT 2500849 1605624 0.823 -0.143 0.151 0.932
-0.135 1.364 1.428 -0.778 -0.539 -0.030 1.122 2.224
0.246 2.929 -0.577 2.860 -2.133 1.280 1.629
HN 348 PT 2923749 1962240 0.517 0.018 0.189 1.377
-1.992 1.116 0.872 -11.000 -1.367 0.379 0.062 -0.304
-1.696 0.373 -1.623 1.497 -0.367 0.793 0.277
HN 349 PT 1530656 1111505 -0.604 -0.560 1.305 0.165
-1.258 -1.002 1.637 -1.610 0.571 0.251 -0.313 -0.424
-0.158 -0.693 -2.512 2.251 -0.085 0.387 -0.123
HN 350 PT 1718905 1188330 -0.223 -1.100 -0.437 -0.959
-1.272 -0.091 -0.477 -2.042 -0.904 -1.284 -11.000 11.000
11.000 11.000 11.000 0.661 -0.719 1.269 -0.394
HN 353 PT 2276192 1578400 0.063 0.993 -0.197 1.296
-2.782 0.225 2.233 -0.819 -0.223 0.260 1.347 0.286
-0.726 2.012 -0.782 1.074 -0.687 2.422 2.508
HN 363 PT 3453281 2273733 -0.547 -0.834 -3.603 -4.129
-4.554 -1.499 2.305 -1.774 -1.948 11.000 5.931 0.220
-1.645 11.000 2.032 4.046 1.329 -1.292 0.380
HN 364 PT 14297934 10269705 -1.053 -0.614 0.301 -2.416
-5.746 11.000 1.527 -11.000 2.782 4.072 3.956 -0.973
11.000 -2.655 -6.880 11.000 1.806 0.483 1.581
HN 364 PT 1832822 1243550 -2.916 -1.554 1.127 -1.387
4.335 11.000 5.124 -2.487 4.198 -1.808 -1.249 -0.193
-1.961 0.391 2.237 3.338 -3.718 0.079 -1.694
HN 367 PT 1980684 1394686 2.288 2.024 -0.332 -0.474
-0.919 -3.388 1.768 1.321 -6.211 -11.000 -0.873 1.516
0.757 1.161 0.726 11.000 11.000 0.727 -1.656
HN 368 PT 2037824 1428887 -1.770 -1.258 -2.203 -0.117
11.000 -11.000 0.447 -1.737 11.000 11.000 6.469 3.828

Table35.txt

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5.343     0.546     1.622     3.184     -11.000   0.051     5.422
HN 371 PT      3507189       2462704       2.207     4.700     -0.111    2.980
-0.744    1.097     2.707     -1.173    -0.299    1.514     4.236     3.386
1.122     4.596     1.732     1.142     -2.914    4.052     5.433
HN 380 PT      2109952       1408192       -5.682    -5.304    -3.074    -5.143
-4.303    11.000    -3.342    -5.105    -5.431    11.000    1.393     3.214
3.288     -1.937    3.560     3.026     -11.000   -1.601    -2.584
HN 409 PT      3636496       2436160       11.000    8.126     -5.131    1.436
-1.081    -1.040    4.953     1.836     -5.155    5.571     -2.448    -1.756
-2.740    0.649     2.754     -6.401    -6.937    2.763     3.016
HN 415 PT      6819279       4437793       1.208     0.399     0.841     1.137
-1.463    0.712     1.293     -0.214    -0.571    -0.688    -0.402    -0.331
-1.443    2.093     -0.723    -3.273    7.244     1.625     1.701
HN 416 PT      7063932       4573276       -1.601    -1.212    -1.990    -4.332
-1.606    -1.004    -0.209    1.899     -11.000   4.833     6.356     -0.162
-0.876    2.916     -1.085    -2.814    0.805     0.087     4.403
HN 417 PT      4849435       3347138       1.158     11.000    -11.000   4.817
0.666     5.261     0.737     0.657     -2.209    1.032     0.668     0.102
0.547     -4.949    0.570     -3.881    -6.098    0.434     1.364
HN 418 PT      3960621       2829768       -1.390    2.071     -1.109    11.000
-1.740    -6.405    11.000    7.157     -11.000   -1.841    -3.381    -0.300
-1.541    0.168     -1.454    0.718     -2.305    -1.939    4.168
HN 419 PT      7130296       5211595       5.988     -4.538    -2.494    0.662
0.642     0.771     3.348     2.661     -3.973    5.578     -0.587    2.325
1.531     3.080     -0.098    2.117     -11.000   3.513     3.065
HN 420 PT      5790119       3959400       0.392     3.928     -1.075    4.522
2.151     -4.785    2.764     2.496     0.703     6.016     -1.921    0.901
2.073     -0.230    0.701     -4.325    -11.000   0.630     -0.715
HN 421 PT      21127707      18316187      2.445     1.697     0.331     1.364
-11.000   11.000    -0.908    -2.038    -0.562    -0.596    1.811     0.040
1.972     -0.526    -11.000   4.179     0.410     5.451     1.125
HN 421 PT      7338869       5446483       2.637     2.249     1.039     0.873
-1.225    -11.000   1.401     -0.697    -0.240    11.000    0.638     0.532
0.698     2.815     -0.763    1.004     -1.812    1.350     2.850
HN 422 PT      6157923       4523545       0.294     1.810     -0.687    1.272
-1.742    2.343     1.914     -0.969    -1.031    0.127     0.014     0.158
0.473     1.903     -0.374    1.800     -2.721    2.422     2.081
HN 425 PT      17587084      14376776      1.449     0.683     -0.020    0.439
-11.000   11.000    -2.110    -4.843    -2.716    -2.005    1.714     -1.965
4.743     -1.201    -5.899    11.000    0.281     0.039     0.630
HN 425 PT      2588132       1759411       -0.184    0.030     0.170     0.676
-1.119    3.943     0.498     -0.406    -1.442    11.000    0.138     -0.905
-0.380    0.155     -0.551    2.954     -6.029    11.000    0.923
HN 427 PT      8854898       6064853       7.669     4.175     -5.165    -6.880
-2.987    -4.380    11.000    -11.000   -11.000   11.000    -3.900    4.622
6.082     -1.403    0.745     -3.355    -1.206    0.477     7.454
HN 428 PT      6395396       4339204       -0.909    1.410     0.971     1.666
-1.395    0.023     1.983     -1.023    -1.699    3.802     -0.465    1.611
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Table35.txt

0.514	1.781	-0.857	-0.222	-3.263	2.626	1.171	
HN 429 PT	8541256	5668564	1.887	-2.537	-11.000	0.869	
0.350	11.000	2.017	-3.649	-0.318	2.611	1.235	0.862
1.282	2.010	3.074	1.654	-6.590	1.251	1.952	
HN 430 PT	11036695	7440912	-6.668	11.000	-3.795	-5.643	
-11.000	7.132	2.353	-7.034	-11.000	2.220	2.150	3.720
4.539	-0.037	3.773	-0.600	-1.036	0.917	5.285	
HN 431 PT	3030783	1897553	-6.758	-6.583	0.619	1.035	
-3.572	-3.179	5.896	7.707	-11.000	11.000	-3.221	2.760
2.196	0.155	1.373	-2.399	-11.000	-0.623	-1.529	
HN 436 PT	11190624	7681784	11.000	11.000	-6.159	5.071	
-2.134	11.000	2.294	5.084	-3.949	7.519	3.450	-3.858
4.626	-3.238	4.015	3.430	-6.612	0.788	-0.582	
HN 438 PT	6923162	4893335	-1.049	0.217	0.805	1.144	
-1.777	-0.683	2.254	-0.261	1.065	0.933	-0.732	-0.026
-0.259	0.683	-0.609	0.098	-0.502	1.179	0.473	
HN 464 PT1	181124	129707	0.696	0.827	0.630	-1.664	
0.900	1.056	1.073	0.649	0.723	-2.462	0.393	-1.503
-0.788	0.173	-1.811	2.021	-2.609	2.096	0.007	
HN 465 PT2	5298034	3898742	-0.042	-0.092	-1.601	4.193	
-0.253	1.508	3.667	-0.935	-4.238	0.456	-0.564	0.601
-1.192	3.791	0.579	0.789	-11.000	2.662	3.830	
HN 466 PT1	1295313	913263	0.524	0.466	0.198	0.185	
-1.654	-0.380	1.759	-1.641	0.318	2.997	0.128	1.530
0.600	1.506	-0.103	2.522	-3.966	0.746	3.354	
HN 467 PT1	288058	207220	-1.918	5.978	4.522	4.189	
0.642	-3.655	11.000	-1.952	-11.000	5.797	-2.873	2.729
0.994	-4.064	7.896	11.000	-11.000	-0.404	-0.944	
HN 468 PT2	410196	289396	0.960	-0.828	1.028	0.982	
4.545	-0.004	5.982	-1.023	-1.964	2.735	0.381	-0.144
0.869	1.418	-2.015	0.423	-2.533	1.747	1.380	
HN 469 PT1	695505	486706	-0.171	11.000	-1.430	-0.827	
-3.056	-11.000	-0.648	-3.246	-4.922	11.000	11.000	0.400
-0.445	1.654	-0.334	0.463	-3.446	2.258	0.528	
HN 470 PT1	1108576	754255	0.295	-2.927	-1.128	2.644	
-2.414	-0.529	3.359	-1.133	-5.599	2.545	3.852	2.096
2.028	2.594	-0.597	1.755	-5.089	1.750	2.035	
HN 471 PT1	927013	611692	0.862	4.664	-0.361	2.083	
-1.749	-11.000	2.587	0.160	4.343	3.300	11.000	2.183
1.285	2.421	3.538	3.511	-11.000	2.769	3.333	
HN 472 PT1	2338264	1451763	1.449	0.913	-3.565	-5.547	
-5.842	-6.107	5.796	11.000	-11.000	-11.000	1.827	-2.261
-11.000	-0.895	1.648	4.982	5.807	2.952	3.051	
HN 473 PT1	1494519	954988	1.904	2.230	-1.273	1.222	
0.662	-4.717	1.751	2.260	-5.396	-0.173	2.057	2.026
-2.651	3.271	1.175	2.106	0.347	2.504	2.640	
HN 474 PT1	2769541	1671022	1.165	1.453	1.207	2.376	
-1.801	-11.000	1.643	0.586	-1.001	-4.550	1.621	2.637

Table35.txt

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-11.000   4.558     2.275     7.251     -3.953    4.016     4.302
HN 475 PT2     1326521       877432       -1.718    -1.473    -1.188    -1.142
-1.639    0.271     -0.697    -2.390    11.000    -0.789    -1.520    0.229
-0.324    0.491     -1.186    0.385     -3.420    -0.256    -1.404
HN 476 PT1     1175737       906658       0.434     0.977     0.595     2.875
-1.550    -0.310    2.497     -1.045    1.177     1.775     1.780     0.014
-1.448    1.025     -0.827    1.438     -0.743    1.781     0.697
INDI 027       4187039       1515721      -0.233    -0.491    11.000    11.000
-3.268    11.000    -1.881    -2.352    -11.000   -3.249    11.000    11.000
-1.702    -1.986    -11.000   11.000    -0.969    -0.359    -2.403
INDI 028       3451999       1306365      -11.000   11.000    -1.376    -0.737
-2.768    -0.049    -2.419    -4.790    -1.628    -4.916    11.000    -11.000
11.000    0.172     -0.950    11.000    7.618     7.255     -1.508
INDI 029       4190595       1501240      -1.476    -0.369    -1.740    0.278
-2.023    -0.073    -2.220    -1.064    -3.115    -0.357    0.803     -11.000
11.000    11.000    -11.000   11.000    -0.531    0.191     -1.886
INDI 030       4837354       1643067      -5.644    11.000    2.715     4.058
-11.000   8.210     -11.000   -11.000   -11.000   -11.000   11.000    11.000
11.000    11.000    -11.000   11.000    -1.705    -1.870    -5.255
INDI 031       4570586       1701315      0.306     0.533     -1.194    -0.113
-1.121    2.643     -1.553    -0.797    -11.000   -11.000   2.061     0.668
11.000    11.000    -11.000   0.236     -2.463    -2.367    -1.183
INDI 032       2961505       1049241      0.918     3.008     -0.005    -0.196
0.494     4.563     -0.123    3.587     -0.472    -11.000   2.779     4.234
0.946     3.603     -11.000   11.000    1.667     0.653     -1.519
INDI 033       4105284       1433310      -4.254    -3.088    5.045     11.000
-3.829    -2.171    -3.030    -4.001    3.091     7.587     -1.879    -2.875
11.000    11.000    -1.934    -0.486    11.000    11.000    -11.000
INDI 034       4602791       1473141      -5.685    -2.352    2.646     7.286
5.121     7.257     -11.000   -11.000   -2.245    -11.000   6.522     11.000
11.000    11.000    -4.761    -11.000   1.722     0.618     5.285
INDI 035       4428442       1454542      1.828     2.231     -3.130    2.590
1.125     2.777     0.372     3.629     0.025     2.672     3.039     2.342
1.000     2.670     -1.456    0.630     0.990     0.612     -5.643
INDI 036       1305904       391281       -1.722    -0.291    -1.899    -1.198
-1.995    0.381     -1.763    1.791     -2.493    0.124     -1.479    -0.568
3.570     4.954     -2.303    0.661     3.472     3.058     -0.957
INDI 037       3085448       1023446      2.199     1.880     0.327     2.704
-0.394    2.535     -0.478    3.443     -0.995    1.533     1.666     3.281
-0.198    1.467     -2.089    1.744     1.121     2.085     -1.293
INDI 038       4431893       1479290      1.437     1.555     -2.381    2.230
-1.177    3.883     -0.904    1.399     -2.080    2.524     4.003     2.297
0.221     0.397     -3.279    -0.121    -0.074    0.742     0.145
INDI 039       1559243       565092       11.000    11.000    -2.244    -1.349
-0.904    1.584     -11.000   -11.000   11.000    3.738     -0.207    0.792
-0.109    0.262     -0.797    2.614     -1.248    -1.321    -0.455
INDI 040       1015496       359976       -11.000   0.208     0.280     0.499
-1.048    1.240     -0.635    2.098     7.026     -0.240    -0.037    0.655
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Table35.txt

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11.000    1.517     -11.000   11.000    -1.007    -11.000   -0.230
INDI 041       1475920       452268       -2.361    -1.588    -2.072    7.425
-11.000   -2.396    -2.106    -1.849    -2.437    -0.765    -1.452    -0.835
6.781     11.000    -11.000   11.000    -0.051    -0.941    -2.250
INDI 042       1944607       555206       -0.287    0.602     -1.559    -0.412
-2.081    11.000    -2.100    -1.029    -6.052    -1.355    0.632     2.162
11.000    11.000    -3.118    -0.543    -0.807    -0.901    -2.068
INDI 043       3051247       1105842      1.884     6.947     -1.220    -0.267
0.196     1.353     -0.916    0.293     -0.931    1.561     1.794     1.031
11.000    11.000    -11.000   1.486     0.759     1.412     -0.713
INDI 044       3126183       1123747      0.351     0.991     -0.400    0.475
-0.786    2.031     -0.821    -0.495    -0.012    1.447     0.456     1.532
0.399     1.461     -2.262    0.252     1.521     0.384     -1.016
INDI 045       724920        274483       0.972     1.456     -1.589    -0.539
-2.047    -0.069    -0.576    0.953     -1.634    0.007     -0.257    -0.627
4.922     7.147     -1.666    -0.066    -1.831    1.553     -1.198
INDI 046       2341279       885695       0.367     0.912     -1.432    -0.407
-6.220    0.914     -0.564    -0.278    11.000    -11.000   4.013     -0.385
6.997     6.266     -11.000   11.000    4.421     1.386     -3.606
INDI 047       2075664       796285       -2.610    3.160     -1.131    4.855
3.638     11.000    -11.000   -11.000   11.000    -11.000   0.638     2.580
3.115     5.394     -7.034    -2.549    11.000    -1.725    1.306
INDI 076       933612        324856       -1.512    0.839     0.119     -0.139
-5.449    11.000    -4.750    -11.000   0.767     0.984     -4.481    -11.000
0.888     -1.912    -1.245    11.000    -5.112    -3.039    2.485
INDI 077       316611        111816       0.872     3.688     0.679     0.545
-1.350    0.082     0.724     -1.037    1.961     1.276     2.220     -0.130
0.082     -0.581    0.510     4.884     -1.758    1.298     0.191
INDI 078       6193396       2205850      11.000    11.000    -4.581    -11.000
-0.394    0.677     1.041     -11.000   -1.796    -1.798    11.000    11.000
-1.169    -1.445    -11.000   -11.000   -3.943    -5.193    3.360
INDI 079       4091714       1365949      11.000    11.000    -5.839    -11.000
-5.975    -6.111    -4.095    -6.612    6.625     11.000    -4.161    -5.501
5.109     11.000    11.000    11.000    7.886     7.878     -4.825
INDI 080       1021882       352511       0.940     0.696     -0.189    0.451
-0.792    2.718     0.054     1.122     11.000    -2.413    0.686     3.155
0.293     0.880     -2.741    1.221     1.047     0.481     -1.848
INDI 081       3557059       1291450      -4.789    1.300     1.351     2.639
2.475     5.544     -4.760    -5.188    -2.812    -4.771    3.917     5.679
11.000    2.088     -0.991    3.313     2.977     2.286     -0.294
INDI 088       2032564       718776       1.684     4.160     3.501     7.570
0.496     1.738     0.026     7.941     0.519     3.479     -11.000   -11.000
11.000    11.000    -11.000   -11.000   0.119     6.371     -11.000
INDI 089       1564997       549509       -6.044    0.539     2.883     7.941
6.063     11.000    -11.000   -5.347    -2.994    -4.948    2.654     11.000
11.000    11.000    -11.000   -4.354    5.167     4.176     -0.929
INDI 090       2405759       782432       -4.968    -4.691    1.978     3.883
-0.831    3.326     -11.000   -2.886    -4.057    -4.737    2.779     6.142
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Table35.txt

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11.000    11.000    -4.542    -0.028    5.621     5.367     -0.073
INDI 093       1418585        513125        -3.215    -0.424    -2.875    -3.799
11.000    11.000    -2.322    -4.522    -3.003    5.190     5.979     0.149
11.000    -0.988    -11.000   11.000    -1.061    -1.237    -2.408
INDI 094       3135536        1108471       -0.071    -0.246    -1.075    5.662
-1.155    0.413     -11.000   -11.000   -1.104    -2.154    0.862     0.593
11.000    11.000    -6.880    11.000    2.321     2.094     -1.183
INDI 096       3304649        1234768       -2.063    -0.791    -2.181    -1.612
-1.998    -0.565    -1.979    -0.781    -0.947    -1.375    -0.572    0.248
11.000    11.000    -3.586    -1.061    -0.941    -1.490    5.213
INDI 097       1618035        505846        -0.912    0.836     -0.003    0.167
-1.445    1.327     0.108     1.712     -0.629    1.582     -0.150    1.767
-0.889    0.075     -2.174    0.919     -0.066    -0.349    0.043
INDI 098       918360         332831        -6.839    -0.220    -2.160    -3.027
-3.175    -2.910    -4.378    -6.628    -0.150    1.249     5.568     7.569
5.274     7.503     -3.707    0.984     -1.546    -0.447    -1.267
INDI 100       3776328        1326776       -0.588    11.000    -1.574    -1.311
-11.000   0.722     -11.000   -11.000   -0.078    -0.294    0.875     0.677
7.321     11.000    -11.000   11.000    0.436     -1.393    -1.020
INDI 101       3387653        1238380       -5.122    -1.578    1.620     1.395
2.499     5.333     -2.563    -3.544    -4.756    -0.734    3.240     5.588
6.540     11.000    -7.034    11.000    -1.655    -1.082    -3.055
INDI 102       2410759        822043        -0.268    0.486     -0.464    -0.693
-1.177    4.550     -11.000   -4.894    -2.130    -11.000   -0.077    0.448
11.000    11.000    -4.321    11.000    -0.878    11.000    -0.162
INDI 106       494328         180081        -1.036    1.791     -0.945    -0.838
-2.254    3.292     -1.477    -3.457    -1.465    -0.464    -0.050    2.858
6.155     -1.497    -3.181    2.920     -0.730    -0.472    -0.541
INDI 107       796998         293176        -0.895    0.489     -1.731    -0.972
-0.402    0.178     -0.824    0.537     -0.747    -0.642    0.678     0.616
-1.636    -0.042    3.253     11.000    0.713     0.688     -3.012
INDI 108       1743293        630944        -0.306    1.764     0.223     0.041
-11.000   0.987     0.991     1.038     -1.049    0.966     0.298     0.406
0.131     0.799     -1.370    -0.063    1.462     0.414     -1.301
INDI 109       2663650        874502        1.272     1.744     0.897     1.029
-0.690    1.592     0.174     -3.739    1.540     -11.000   0.594     1.841
0.442     0.951     -11.000   11.000    0.592     0.700     0.289
INDI 112       274579         106068        0.364     3.035     -0.263    -1.732
-0.574    1.438     1.001     0.060     0.638     -1.903    1.588     1.822
4.020     0.200     0.149     1.452     -2.336    0.590     0.396
INDI 113       3173101        993130        -1.227    -0.265    2.223     11.000
1.469     -0.161    -2.526    -0.897    6.202     -11.000   2.103     0.172
3.357     0.344     -11.000   8.210     4.231     4.861     -2.784
INDI 118       3679185        1195172       -11.000   11.000    -3.264    -3.909
7.550     11.000    6.250     11.000    4.318     -2.917    4.916     -11.000
-2.172    -3.498    -3.068    -3.130    -11.000   -2.056    3.832
INDI 119       1135731        381254        6.508     4.500     1.282     2.948
-4.522    -5.803    0.052     -11.000   1.424     -3.842    -1.039    -6.058
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Table35.txt

-0.505	7.201	1.270	11.000	-2.508	-1.198	1.442	
INDI 122	846447	270756	-0.665	2.353	-0.230	1.070	
-1.072	0.626	0.150	0.373	-1.804	0.590	0.119	0.274
1.433	0.132	-1.978	0.681	0.333	1.294	-1.824	
INDI 123	1908566	639081	-0.168	11.000	0.286	0.414	
-0.939	0.793	-1.699	-11.000	-2.794	0.137	0.816	2.195
4.537	1.898	-11.000	11.000	1.513	2.202	-0.842	
INDI 124	1083990	466075	-0.009	1.409	0.482	0.446	
-2.117	-1.329	0.525	1.777	-0.334	0.216	-0.159	1.582
-1.670	0.941	-1.098	1.750	1.265	1.848	-2.050	
INDI 125	1536716	491452	2.252	6.456	4.718	-4.378	
-3.742	11.000	-2.964	-11.000	5.163	-3.264	-3.462	-3.651
7.537	11.000	5.200	11.000	-2.339	-2.693	2.977	
INDI 127	4766512	1559471	0.860	1.886	-0.845	0.862	
-1.566	1.509	-0.536	1.277	-1.487	2.410	0.233	1.860
0.166	1.491	-2.660	0.238	1.249	0.413	-0.721	
INDI 128	880071	310083	1.178	5.684	-0.944	0.061	
-1.369	0.522	-0.291	0.220	-1.024	1.168	0.483	1.738
0.413	0.422	-2.895	1.052	-0.645	1.584	-1.583	
INDI 129	1227012	431949	-11.000	11.000	-1.362	-0.884	
0.072	0.258	-11.000	-11.000	-0.437	0.360	11.000	-0.825
4.637	0.209	-3.840	11.000	-1.439	-0.101	2.935	
INDI 132	4107941	1308789	-1.330	4.365	0.107	5.735	
-11.000	6.707	-6.030	-11.000	-1.253	-11.000	-0.410	0.114
7.973	-0.546	-5.742	11.000	-4.835	4.282	-5.850	
INDI 136	4345078	1560509	-0.191	2.326	-0.157	1.248	
-1.667	0.735	0.026	3.112	0.314	1.164	-0.276	1.762
0.678	1.310	-2.224	0.926	1.441	-0.057	-2.395	
INDI 142	4757655	1721916	6.846	4.589	-11.000	-11.000	
4.266	6.749	-11.000	-11.000	11.000	-11.000	4.216	11.000
5.285	11.000	4.472	11.000	5.787	7.005	-2.630	
INDI 143	4933139	1570979	-3.113	-1.831	-4.155	-3.475	
-3.379	-1.688	-2.088	-1.425	-1.351	-1.103	11.000	11.000
-1.552	-1.379	11.000	11.000	11.000	11.000	-2.974	
INDI 144	2206258	741750	-2.373	-2.102	3.094	4.998	
3.601	5.379	-11.000	-11.000	-2.829	-3.977	2.019	5.595
1.815	4.219	-11.000	11.000	3.417	3.899	-3.497	
INDI 145	5352651	2018923	-3.101	-2.475	-2.403	-2.416	
-3.900	-1.995	6.972	11.000	-2.774	-1.770	-1.636	-1.210
-1.600	-1.278	11.000	11.000	-2.545	-1.953	-3.123	
INDI 146 PT1	4845415	1771639	-1.565	-2.436	-0.453	-0.577	
1.985	11.000	-0.255	-11.000	11.000	-0.334	-11.000	-0.630
-1.211	-6.347	6.053	-6.327	-11.000	-0.030	-0.757	
INDI 148 PT1	2662096	1071426	-11.000	-3.020	0.182	-2.936	
-0.223	0.947	-1.203	-11.000	11.000	0.099	-3.813	-0.325
-0.391	-2.497	1.124	-4.220	-11.000	1.383	-1.693	
INDI 150	2254008	669312	-3.223	1.953	0.193	0.298	
-0.315	1.227	0.556	-1.703	0.449	0.976	-6.692	1.000

Table35.txt

11.000	11.000	-5.122	7.917	0.716	11.000	-1.232	
INDI 152	3601576	1188182	-6.167	2.971	3.674	4.742	
-7.034	-5.939	0.169	-11.000	-5.525	-6.780	7.642	-4.517
2.066	3.240	-11.000	11.000	-4.495	1.421	3.221	
INDI 155	2472761	877033	-0.202	0.503	0.604	1.709	
-0.358	0.666	2.049	1.639	0.408	0.330	-0.729	1.570
1.362	1.067	-3.134	0.314	1.448	0.239	-0.851	
INDI 156	3087589	1104447	-1.357	-0.407	-1.931	-2.106	
-2.325	-1.834	-3.227	-4.928	7.262	-11.000	1.749	-1.828
11.000	11.000	-11.000	11.000	11.000	4.449	-3.873	
INDI 157	1444600	437403	-0.963	-1.732	-2.593	-3.431	
-3.462	-3.504	-6.880	11.000	-3.552	-2.684	-0.364	-1.348
11.000	11.000	-6.739	11.000	-0.926	-1.875	-2.415	
INDI 158 PT1	2129708	1016155	-3.281	-1.233	-4.826	-6.270	
0.367	0.403	4.863	5.429	11.000	-5.302	-6.176	1.399
11.000	0.918	2.729	-2.280	-6.657	0.351	0.092	
INDI 159 PT1	840955	325310	0.397	11.000	-2.141	1.793	
1.498	-0.443	2.363	-0.216	-0.426	0.928	-0.681	-2.330
-1.468	-0.505	2.247	-1.755	-2.855	0.445	11.000	
INDI 160 PT1	1650103	762657	-2.105	0.333	-1.090	0.000	
-1.095	-0.276	1.476	0.226	11.000	-11.000	0.157	-0.990
-2.118	-6.326	-1.336	-11.000	-11.000	0.460	-1.536	
INDI 163 PT1	2851218	1143243	-2.003	-0.120	-2.169	-0.304	
-2.547	-1.056	0.605	-0.990	-0.254	-2.569	-2.577	-3.502
-4.214	-2.182	-0.897	-0.305	-4.580	-1.430	-3.090	
INDI 164 PT1	836745	410569	-11.000	6.510	-4.909	-0.132	
-1.072	1.185	1.290	-0.600	11.000	-11.000	-1.422	3.257
4.736	-2.191	5.694	-1.217	-11.000	-0.728	7.295	
INDI 165 PT1	2337275	950460	-2.874	-1.483	-3.332	-3.026	
-3.187	-3.394	6.574	-3.967	11.000	-2.875	-1.929	0.314
1.749	-4.869	4.563	-5.574	-11.000	1.562	1.327	
INDI 166 PT1	2457843	1203256	5.289	5.259	-0.411	-11.000	
-1.896	-1.358	-2.619	-4.283	11.000	-11.000	-11.000	-1.581
-11.000	-4.244	4.908	-4.711	-11.000	-0.982	-0.903	
INDI 169 PT1	2429418	1042798	-2.082	-0.131	-1.259	-0.726	
-1.436	-1.147	0.247	-1.118	11.000	-1.852	-11.000	-2.273
-1.925	-3.959	-1.106	-3.109	-11.000	-0.429	-1.982	
INDI 170 PT1	2571683	1271362	-4.251	-4.294	-3.533	-3.132	
-1.200	-0.641	0.795	-0.246	5.533	7.006	-3.599	1.133
-0.464	-3.283	-1.599	-2.640	0.504	-0.034	0.036	
INDI 174 PT1	2769517	1089067	-11.000	-6.192	-4.297	-3.481	
-1.128	0.330	-1.219	2.071	11.000	-11.000	-5.689	-0.307
0.078	-4.159	3.246	-4.649	-11.000	-2.740	-1.096	
INDI 175 PT1	1808028	702092	-2.955	-2.019	-3.101	0.050	
3.185	2.899	4.147	5.118	4.952	-1.707	-2.830	2.140
0.215	-3.482	-2.031	-3.142	-11.000	-0.904	3.271	
INDI 175 PT2	2016172	773573	-2.284	-1.550	-2.215	1.730	
0.818	2.086	3.261	0.280	6.135	-0.427	-0.805	-1.031

Table35.txt

-1.757 -1.487 0.532 -1.072 -2.518 -0.732 -1.306
INDI 177 PT1 2228854 1057352 -11.000 11.000 2.115 3.915
2.608 3.538 -0.770 -3.070 -11.000 -2.489 -5.081 0.624
-6.260 -3.060 1.730 -1.351 -6.206 0.779 1.937
INDI 178 PT1 3301545 1286747 0.083 -0.799 -0.533 1.018
-0.371 -0.595 1.426 0.538 1.676 0.850 -0.976 -1.027
-1.113 0.305 0.343 -0.272 -1.651 0.286 -0.586
INDI 179 PT1 2756596 1140013 -5.862 0.143 5.580 11.000
0.130 1.602 2.578 0.328 0.746 -0.860 6.950 1.180
1.945 -0.803 1.343 -1.772 -5.829 -0.786 0.597
INDI 180 PT1 3394231 1404859 -0.041 1.464 -0.329 1.334
-2.127 -0.528 2.324 0.761 -0.180 -0.543 0.631 -0.587
-1.815 1.038 1.162 0.337 -4.165 0.446 0.093
INDI 181 PT1 3544553 1418912 -4.189 11.000 5.915 -3.882
-11.000 -4.264 6.401 1.169 -4.153 11.000 3.335 -1.714
2.444 2.467 11.000 0.793 -6.839 0.963 0.521
INDI 182 PT1 3251937 1153023 -0.125 4.694 -0.561 0.748
-0.078 0.427 1.122 -0.613 -0.751 -4.034 -0.800 0.546
-0.173 -4.148 1.702 -1.119 -3.236 0.295 -0.389
INDI 184 PT1 3266717 1330588 11.000 -0.218 -0.952 -0.689
-1.846 -0.908 -0.021 3.968 -11.000 11.000 -0.432 -1.142
-0.758 -0.638 6.900 3.641 -1.977 -0.420 4.901
INDI 189 PT1 1658517 665175 0.009 11.000 -1.734 3.533
-2.363 -4.656 0.465 -2.278 11.000 -1.311 -2.961 4.421
0.442 -0.375 -0.772 -5.265 -4.703 1.856 1.191
INDI 190 PT1 5473965 2278366 0.274 11.000 2.134 0.286
-11.000 -11.000 1.518 2.486 -11.000 -11.000 0.338 1.729
-3.445 -1.212 1.070 0.280 -0.374 -2.155 5.823
INDI 191 PT1 3928674 1509077 1.977 0.819 0.585 1.154
0.624 0.714 1.891 -0.090 11.000 -11.000 -11.000 2.294
11.000 -2.104 2.050 -3.440 -11.000 0.443 0.983
INDI 192 PT1 7107700 2945655 -11.000 1.095 -2.058 -1.255
-3.018 -3.659 2.311 1.795 11.000 -4.247 -11.000 -1.563
-2.921 0.475 11.000 -5.904 -11.000 2.750 2.733
INDI 193 PT1 1831471 714519 -11.000 -1.483 -0.600 6.197
-1.367 -2.089 4.771 -0.265 7.830 0.104 2.156 1.020
-6.097 -2.828 2.959 -1.408 -2.764 2.113 0.668
INDI 194 PT1 5575985 2392841 -0.907 -1.213 -0.263 1.403
-1.299 -0.533 11.000 11.000 0.001 0.643 0.042 0.118
-1.796 0.343 0.528 -1.019 -3.276 -0.309 0.582
INDI 195 PT1 4468150 1549393 1.031 1.608 -1.318 -2.474
-0.249 -0.196 3.578 0.280 4.905 -1.916 -1.451 -2.187
4.723 -1.474 0.500 -0.379 -11.000 0.949 -0.933
INDI 196 PT1 3394778 1526505 0.636 0.438 -0.889 1.231
0.377 1.155 1.460 -0.256 -11.000 0.554 -11.000 0.370
-0.799 0.629 -0.220 0.265 -1.437 1.166 -0.098
INDI 201 PT1 2309638 1042679 -6.590 -11.000 -4.689 -5.705
2.899 3.406 5.362 7.048 11.000 -6.003 3.667 -2.479

Table35.txt

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-4.431    -2.704    3.803     -2.792    -6.088    2.042     2.605
INDI 202 PT1   672811        377890       -0.022    0.888     -0.231    1.092
-0.549    -0.389    2.251     -0.553    1.746     2.741     1.430     -1.788
-2.132    -0.267    -2.079    -0.721    -0.635    0.272     -1.941
INDI 204 PT1   1479728       845293       0.500     -0.141    -0.530    1.544
-1.410    0.396     2.070     0.244     1.598     0.435     -0.540    -0.116
-1.053    -1.360    -1.412    11.000    -0.132    -0.144    -1.110
INDI 207 PT1   2469966       1204683      0.500     0.793     -1.067    0.697
-1.063    -0.635    1.762     -1.606    11.000    -0.248    1.097     -1.461
-2.688    0.442     1.073     -0.635    -3.991    0.221     -0.555
INDI 208 PT1   3253423       1436330      -11.000   3.138     -1.401    1.398
-2.628    -1.100    1.119     -0.331    -11.000   0.090     -0.612    0.551
-11.000   -5.552    0.517     1.161     0.450     -1.188    -0.276
INDI 209 PT1   926224        600778       1.347     0.276     -1.623    0.949
-0.350    0.034     1.350     -1.941    0.268     0.569     0.503     -0.791
-4.521    0.046     -0.954    -4.610    -11.000   2.761     -0.386
INDI 211 PT1   2378259       1283450      -11.000   11.000    -2.296    0.875
1.938     -11.000   0.917     -2.668    11.000    -11.000   0.054     11.000
-0.420    -4.776    -5.699    -4.245    -11.000   0.269     0.019
INDI 212 PT1   2148247       867190       -2.146    6.199     -0.350    5.223
2.737     2.331     3.750     2.031     0.655     -5.875    4.986     -0.242
-0.700    -4.146    -5.981    -3.347    -2.968    0.664     -1.813
INDI 213 PT1   2702020       1026725      0.440     7.992     -0.837    -0.888
0.728     3.389     1.362     -0.051    11.000    -11.000   -11.000   1.993
3.820     -2.854    0.352     -4.150    -11.000   2.476     4.214
INDI 215 PT1   2048239       888030       -4.765    11.000    4.681     -11.000
-5.494    -11.000   -0.654    -2.758    11.000    11.000    -0.368    5.195
-5.609    -3.161    2.222     1.150     2.875     -4.434    -3.526
INDI 216 PT1   660801        309391       -3.747    -3.701    -0.602    2.320
-0.347    1.299     -0.175    -2.952    11.000    0.552     -0.377    -0.155
-0.967    -2.272    5.101     -1.753    -6.529    -0.213    -1.048
INDI 217 PT1   546326        277156       -2.287    2.381     1.222     -3.058
11.000    -2.712    0.213     -2.478    11.000    -11.000   -5.404    2.701
4.417     -3.593    -3.092    -5.017    -11.000   -0.862    -0.387
INDI 219 PT1   772245        309644       -11.000   11.000    2.072     4.028
2.232     2.837     3.002     -1.786    -11.000   -11.000   2.788     -1.385
0.437     0.728     1.874     5.605     3.079     -2.018    -1.414
INDI 221       2482688       862287       -2.159    11.000    7.941     11.000
-5.081    -3.060    -4.740    -5.096    -5.125    -4.668    -0.868    -3.898
11.000    11.000    -4.458    -4.087    -2.893    -3.303    -3.736
INDI 222       2837360       1030344      -1.944    4.758     -2.512    -1.946
0.824     7.714     -2.296    -0.883    1.857     -0.203    4.021     1.672
0.998     1.037     -3.449    5.124     1.538     6.105     -2.441
INDI 223       2806499       960807       -2.496    6.841     0.295     1.088
-6.152    6.214     -6.069    -11.000   -0.792    -3.329    3.107     3.700
11.000    11.000    -4.853    -4.222    8.210     5.416     2.115
INDI 225       5327743       1749316      0.780     1.492     -1.828    1.105
-0.447    2.047     -1.571    1.218     -3.063    0.920     3.413     0.767
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Table35.txt

-0.287	0.299	-2.731	0.645	-1.015	1.535	-1.023	
INDI 229	3853345	1345506	-11.000	0.647	1.700	4.006	
1.503	3.817	-0.016	1.113	-2.308	0.666	1.229	-0.392
1.710	2.347	11.000	11.000	1.228	2.293	1.553	
INDI 230	4720652	1558522	0.219	-0.360	-1.313	1.271	
0.514	4.311	-1.359	0.273	-2.853	2.927	2.654	1.615
0.367	1.930	-1.152	1.723	-0.098	1.612	-1.256	
INDI 232	1821602	658899	-4.794	5.128	-3.169	1.184	
4.816	-1.669	-5.238	-4.834	-1.520	1.340	3.310	2.495
3.325	11.000	-3.830	-2.872	-2.930	4.455	-1.969	
INDI 233	3671832	1292485	-5.994	4.801	3.148	5.739	
2.594	3.537	-2.948	-11.000	-11.000	-11.000	11.000	0.966
11.000	11.000	-6.559	11.000	-4.420	-4.657	-5.471	
INDI 234	3099760	1100527	5.417	4.691	2.534	4.769	
3.028	4.892	-11.000	-11.000	-1.566	-11.000	11.000	7.259
11.000	-11.000	0.900	4.682	1.977	-6.064	-6.202	
INDI 240	4941026	1677072	-11.000	8.041	7.819	11.000	
-0.517	0.228	-6.780	-11.000	-0.729	-0.638	2.982	4.591
11.000	11.000	-2.439	0.848	0.500	0.011	-1.516	
INDI 243	4304219	1288455	-2.327	-1.555	-2.329	-1.193	
-1.508	11.000	-4.951	-4.111	-4.153	-3.551	7.292	11.000
3.985	6.405	-11.000	11.000	-1.417	-1.305	-2.132	
INDI 244	3554930	1115259	-3.536	-3.293	2.651	3.766	
-2.548	0.907	-1.620	1.388	-4.073	-11.000	-1.103	-3.034
11.000	11.000	-4.300	1.223	2.166	2.214	1.123	
INDI 245	3876778	1339088	-1.805	3.179	-2.114	-2.537	
-3.114	-0.166	-2.775	-1.470	-3.919	-1.924	0.673	5.656
7.448	-1.203	-1.576	11.000	-0.977	-1.351	-1.501	
INDI 248	2419133	881893	-0.246	0.733	-0.329	0.881	
-0.858	1.262	-0.520	1.753	-0.893	2.469	0.488	2.135
-0.177	0.840	-1.934	0.724	1.124	-0.988	-1.526	
INDI 249	3907080	1213337	1.048	11.000	-1.682	-6.839	
-1.381	0.981	-2.317	-1.737	-1.229	-1.239	7.211	-11.000
11.000	11.000	-11.000	11.000	-0.651	-0.297	-1.798	
INDI 255	2089394	675363	-0.783	6.026	-2.264	-0.282	
-2.996	-0.191	-2.524	0.425	-3.008	-1.752	0.112	1.080
11.000	11.000	-3.049	-0.576	-0.747	-0.923	-1.715	
INDI 256	1962468	625357	1.727	2.174	-1.411	-1.197	
0.546	4.534	-1.632	-1.166	-0.154	6.653	0.357	0.416
-0.880	-0.310	-6.612	11.000	2.393	1.237	-2.049	
INDI 258	4216959	1496682	0.439	0.316	0.343	0.523	
-1.764	1.638	-1.851	-0.311	-3.230	0.381	3.052	1.393
0.208	-0.175	6.982	11.000	-0.295	0.542	-0.383	
INDI 259	1654296	857741	-11.000	11.000	-0.549	1.827	
-11.000	2.244	6.806	-11.000	6.556	3.195	-4.434	-5.487
4.729	11.000	4.770	11.000	4.548	2.524	-1.006	
INDI 263	5772346	1992716	1.315	2.058	-6.392	-11.000	
-0.741	11.000	-11.000	-11.000	0.375	4.317	3.317	11.000

Table35.txt

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5.678     11.000    -11.000   -5.548    5.325     6.213     4.360
INDI 268       4683490       1575229       2.213     4.798     0.062     0.621
0.965     2.525     -1.358    -0.425    -1.341    1.101     3.236     0.401
0.552     -0.204    -11.000   11.000    0.022     0.911     1.011
INDI 271       5176896       1801276       -1.406    0.454     -0.027    0.876
-1.011    11.000    -0.166    3.126     -1.105    1.778     2.121     1.928
0.272     -0.436    -11.000   0.690     0.561     0.784     -1.654
INDI 279       5384986       1914655       -0.286    -0.131    -2.444    -0.099
-0.957    1.688     -1.329    2.413     -1.850    1.071     -5.532    2.003
-0.775    0.611     -11.000   11.000    -0.190    2.050     0.279
INDI 281       7117655       2621642       -0.926    1.216     -0.919    1.641
-1.094    1.566     -1.760    0.792     -1.076    1.666     3.607     11.000
-0.394    0.142     -2.485    0.812     0.535     -0.708    -1.319
INDI 282       2082208       732548        -2.829    -1.737    -2.850    -2.797
4.828     7.520     -11.000   -11.000   -1.055    1.450     5.424     -11.000
3.720     11.000    -4.394    11.000    2.577     3.685     1.352
INDI 284       4252130       1399575       -2.327    -1.178    6.556     11.000
-3.079    -1.429    -11.000   -3.291    -5.517    -5.703    11.000    6.630
6.318     11.000    -7.034    2.721     5.440     -1.968    -2.056
INDI 290       5337770       1680159       -11.000   0.014     -0.866    -1.339
-4.478    -11.000   -1.360    -11.000   -0.754    -11.000   11.000    11.000
7.917     11.000    -6.612    11.000    3.873     4.548     0.034
INDI 294       4325684       1485902       -4.828    4.194     2.374     5.787
3.182     5.766     -4.688    -11.000   1.286     -11.000   4.028     6.047
11.000    -3.348    -11.000   11.000    11.000    11.000    -5.070
INDI 295 PT1   3307050       1241015       -2.222    1.362     -1.697    -0.912
-1.903    -11.000   11.000    11.000    11.000    -0.830    1.350     -3.866
-2.761    -5.021    -0.039    -0.999    -11.000   3.305     5.031
INDI 296 PT1   2285611       972971        0.934     5.687     2.554     -1.250
2.857     -5.452    6.067     4.586     3.727     -4.414    2.601     -1.994
0.198     -1.089    -0.788    -6.937    -11.000   0.299     11.000
INDI 298 PT1   2591221       1044392       -11.000   11.000    4.101     7.992
-3.539    -3.020    -0.061    -3.101    11.000    -2.842    1.343     -2.501
-3.476    -4.092    7.928     -6.197    -11.000   2.528     3.884
INDI 299 PT1   2782859       1098115       -0.882    -0.915    -11.000   -11.000
5.397     5.584     -4.143    -6.396    7.956     -11.000   -0.779    7.679
-3.162    -5.349    0.502     -6.022    -11.000   -0.762    4.650
INDI 302 PT1   2317855       993323        3.341     4.664     -2.474    -3.213
-3.708    -3.653    3.663     2.265     11.000    -11.000   -2.625    -1.857
-3.038    -4.951    3.962     -5.550    -11.000   0.450     0.328
INDI 303 PT1   2727624       1217981       1.606     1.534     0.132     0.967
-0.247    0.572     3.126     1.071     -0.333    -0.983    -1.116    -4.044
-3.235    -0.849    0.129     -0.384    -1.637    -0.315    -1.511
INDI 304 PT1   3016938       1185750       -5.893    3.526     1.095     3.957
11.000    11.000    11.000    3.527     11.000    -11.000   -1.326    5.674
5.818     -3.247    11.000    -0.190    -0.060    -1.951    4.715
INDI 305 PT1   2441146       1051751       0.252     6.317     6.841     -11.000
-11.000   -11.000   -1.556    -4.769    11.000    4.833     -6.758    -2.628
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Table35.txt

-4.457	-2.524	-6.036	-3.616	-11.000	-0.717	0.090	
INDI 306 PT1	4517264	2065205	-5.934	11.000	1.833	-3.917	
-1.048	-0.890	-2.278	-6.396	5.062	-4.683	-4.610	0.627
0.836	-4.882	1.815	-5.451	-11.000	1.559	1.543	
INDI 307 PT1	677606	238404	-11.000	6.434	-2.615	-2.787	
-2.628	-2.842	4.853	0.105	11.000	3.396	-11.000	2.109
3.178	-4.322	2.911	-4.673	-11.000	-0.624	4.310	
INDI 308 PT1	3024680	1202575	-11.000	11.000	0.468	2.940	
0.796	1.488	2.524	1.447	-2.419	0.340	0.030	-7.034
-11.000	1.304	0.778	0.343	0.661	-4.479	7.472	
INDI 309 PT1	3346969	1930480	-2.745	2.227	-3.843	-2.497	
0.083	-5.187	2.348	3.065	11.000	2.455	-5.724	-2.976
-4.950	-1.914	0.403	0.731	-6.030	5.271	6.944	
INDI 310 PT1	2206508	1262127	-1.457	-0.312	-0.130	0.232	
-1.292	-0.584	1.250	-0.192	1.323	-0.290	-0.020	-1.992
-1.677	-0.474	-0.514	-1.436	-0.245	0.352	0.171	
INDI 311 PT1	2711593	1478598	-11.000	3.147	2.259	-3.015	
2.256	3.491	1.015	0.590	11.000	3.226	-11.000	2.347
1.358	-1.857	3.556	-5.532	-11.000	1.293	2.341	
INDI 313 PT1	2342154	1346587	-3.923	2.257	0.794	-5.171	
-1.144	11.000	11.000	0.387	-6.244	-0.777	-3.613	3.113
3.337	-1.853	1.300	-1.362	-11.000	1.747	2.232	
INDI 320 PT1	2012667	939465	3.069	-5.450	-0.161	2.038	
-2.020	0.282	2.684	0.235	0.493	-0.163	2.622	-1.189
-1.129	1.215	3.047	-0.136	-2.588	-0.201	-1.496	
INDI 321 PT1	2593644	1179455	0.594	1.354	1.035	-0.034	
-2.034	-0.063	1.987	-2.563	1.463	3.976	0.519	-3.776
-5.724	-0.295	0.102	0.413	-2.100	-0.723	-1.282	
INDI 322 PT1	2950095	1247437	2.297	5.292	-2.946	-1.375	
-1.706	-1.128	11.000	3.635	11.000	-1.362	-3.344	0.728
0.308	-4.343	-0.012	0.513	-6.721	4.175	4.419	
INDI 325 PT1	3393141	1375752	-0.657	0.143	-1.116	-4.080	
-1.494	-0.911	2.161	-1.189	11.000	0.025	-11.000	-2.537
-1.712	-0.983	-0.224	-5.399	-11.000	-1.259	-1.409	
INDI 327 PT1	4685654	1968132	-1.134	11.000	6.911	-0.850	
0.049	0.692	11.000	-5.612	11.000	-11.000	-11.000	-1.948
-0.609	6.305	1.120	-11.000	-11.000	-0.344	-0.281	
INDI 328 PT1	1550079	580420	-11.000	1.448	-2.465	-2.729	
-3.301	-3.300	4.530	3.617	11.000	-11.000	-0.828	-0.240
-3.870	-5.767	3.369	-4.919	-11.000	-0.272	0.452	
INDI 329 PT1	3292349	1413588	0.327	-0.821	-0.057	0.313	
-1.006	-0.121	4.242	1.625	-0.579	-0.975	0.760	-0.515
-1.046	1.548	-0.036	1.798	-2.541	2.244	1.540	
INDI 337 PT1	1758483	773203	-3.790	11.000	3.670	4.419	
1.754	3.956	1.580	-5.038	2.575	-3.551	-4.396	4.852
-5.058	-2.855	-0.895	-3.304	-11.000	-1.701	5.453	
INDI 338 PT1	1258784	557452	0.030	11.000	-1.743	-0.235	
-1.046	0.171	3.044	-0.882	-0.300	-0.240	-0.327	-3.876

Table35.txt

-3.492 -3.408 -0.623 -1.856 -3.368 -2.756 -3.792
INDI 340 PT1 2682158 1121974 -7.034 -11.000 11.000 -3.336
3.973 11.000 2.286 0.275 11.000 2.421 -11.000 1.351
2.401 -3.840 11.000 -5.902 -11.000 -2.123 -3.894
INDI 341 PT1 1506627 601241 -2.693 11.000 2.081 2.783
-5.226 0.904 1.796 -2.470 -2.205 -2.422 2.692 -4.628
-4.860 -0.553 1.638 1.172 -1.966 -1.285 -1.829
INDI 343 PT1 3268139 1412748 0.989 2.919 0.532 0.545
-0.993 0.484 3.073 -2.529 1.112 0.221 2.878 -3.129
-2.454 1.039 1.703 -3.803 -11.000 -0.377 -0.642
INDI 344 PT1 4307371 1716247 -1.652 -0.143 -0.961 -0.515
-1.753 -0.830 11.000 0.506 -0.291 11.000 -0.504 -2.776
-1.999 -0.144 4.046 -11.000 -11.000 -0.956 -1.002
INDI 345 PT1 2805402 1146417 -5.418 11.000 4.684 3.105
-1.598 1.655 1.252 -0.001 7.783 -5.323 6.438 -1.677
-1.628 -1.627 -1.312 1.919 0.913 1.001 0.744
INDI 347 PT1 3532328 1477006 -0.096 7.842 -5.556 -1.222
0.242 -5.178 7.973 1.949 -6.880 11.000 -2.993 -0.090
-0.433 0.927 1.727 11.000 0.285 1.138 -0.793
INDI 349 PT1 3216721 1479273 0.617 6.660 -1.970 -3.242
-3.760 -3.525 1.418 -1.412 3.495 -0.966 -1.072 -2.417
-1.536 -2.494 1.580 -0.493 -11.000 -0.216 -0.853
INDI 351 PT1 1730652 659445 -6.554 11.000 -0.262 0.456
-6.470 -11.000 2.124 0.490 11.000 -1.111 0.817 -2.995
-3.618 -3.412 -1.993 -4.086 -11.000 -1.308 -2.205
INDI 356 PT1 2973421 1223124 -0.714 -0.759 0.272 -2.331
-1.823 -3.238 0.897 -1.225 11.000 -2.830 -0.919 -2.088
-3.005 -0.288 -0.235 -1.193 -3.064 -1.004 -1.043
INDI 365 PT1 3249096 1284215 -4.245 11.000 3.556 4.505
-1.352 -1.417 1.256 -1.178 11.000 -5.904 -6.628 -1.851
-1.132 -3.882 1.125 -1.958 -11.000 -0.058 0.968
INDI 367 PT1 5332497 2023561 -0.851 11.000 -0.675 1.703
-1.694 -1.727 0.201 -1.002 -0.971 -1.213 -0.425 -1.074
-2.089 2.958 3.015 -0.554 -2.498 -1.466 -0.099
INDI 370 PT1 3548555 1401861 -1.383 5.797 -0.415 0.976
-2.680 -3.284 3.528 -1.060 1.916 -2.621 0.409 -2.615
-0.111 -1.775 -0.100 -1.404 -4.577 -0.392 -1.710
INDI 374 PT1 2298610 1171565 -6.544 -3.082 -1.488 -5.983
3.862 6.879 -1.600 -4.290 11.000 -11.000 -11.000 11.000
7.388 -2.475 -3.289 -5.029 -11.000 -0.379 -3.381
INDI 375 PT1 1251912 535035 0.134 1.047 -0.528 -0.503
0.240 -0.792 -2.282 11.000 0.797 -0.115 0.310 -2.449
-1.993 -2.925 4.295 -0.021 -2.782 -0.807 -2.621
INDI 376 PT1 3411107 1440893 -0.057 0.119 -0.163 -0.253
-1.235 -0.403 1.935 -1.171 2.220 -2.589 -3.994 -0.997
-0.717 -5.375 11.000 -6.403 -11.000 -0.503 0.510
INDI 377 PT1 2524430 1157296 -6.706 11.000 -1.287 2.266
1.460 1.978 2.098 -0.912 -0.229 -4.090 -2.153 -3.087

Table35.txt

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0.057     -3.620    2.713     2.214     2.488     3.804     11.000
INDI 378 PT1   2864304       1320021       1.859     2.102     0.905     3.023
-3.256    0.089     2.910     1.502     11.000    -11.000   2.634     0.186
-0.327    -3.995    1.724     -1.581    -11.000   0.231     0.434
INDI 379 PT1   3121802       1369298       -3.408    -3.718    -2.375    -2.958
-3.629    -4.002    -1.009    -4.125    11.000    -3.432    -2.427    -2.766
-3.059    -11.000   -5.356    -5.052    -11.000   -1.206    -1.567
INDI 380 PT1   2738204       1238995       -0.737    0.273     -1.320    -1.054
-1.396    -1.896    0.979     -2.014    4.239     -11.000   -1.114    -1.602
-1.866    -7.034    6.984     -5.992    -11.000   -1.127    -1.528
INDI 385 PT1   2599304       1079577       -3.282    -1.415    -1.612    -1.334
-2.956    -2.474    0.251     -3.387    11.000    -2.271    -0.289    -2.734
-3.205    -11.000   8.077     -6.692    -11.000   -2.086    -2.105
INDI 386 PT1   3147908       1317358       -0.396    0.501     -1.099    -1.131
-2.528    -1.515    2.061     -1.904    -1.875    -1.123    0.211     -2.537
-3.066    -0.558    0.773     -1.349    -4.008    -1.088    -1.216
INDI 387 PT1   3653306       1477191       5.404     6.441     11.000    -11.000
-4.028    -3.497    -0.118    -3.347    5.944     5.231     4.916     -6.668
-11.000   -4.866    2.591     -4.969    -11.000   1.511     1.917
INDI 391 PT1   5192519       2237431       5.036     11.000    -2.344    -1.915
-2.646    -2.785    7.431     5.943     -11.000   -11.000   -2.914    -1.559
-2.781    0.050     11.000    5.515     -11.000   2.352     3.895
INDI 393 PT1   3238064       1342468       -0.621    5.828     0.560     0.043
-1.595    6.306     4.425     3.151     -3.116    -1.948    -6.807    -4.078
-5.388    -3.960    0.473     1.216     -5.632    -1.189    -2.211
INDI 396 PT1   2970975       1328481       4.951     4.803     2.247     7.351
2.108     3.326     3.339     3.945     11.000    -0.607    -11.000   -4.177
11.000    -4.808    -6.361    -5.096    -11.000   1.219     2.211
INDI 397 PT1   3571442       1581846       0.999     1.903     -0.893    -0.873
-1.981    1.619     3.155     -0.277    -0.971    1.577     -0.094    -1.111
-0.856    -0.120    0.001     0.112     -2.047    0.814     -0.205
INDI 398 PT1   1777603       1069884       -6.839    11.000    -0.108    0.376
-0.922    -5.537    11.000    7.751     -0.632    -11.000   -5.835    3.072
-5.363    -2.814    -0.078    -2.426    -11.000   1.844     2.118
INDI 400 PT1   1853766       778401        -0.289    -1.506    -3.707    -1.083
6.921     7.289     0.285     -1.121    11.000    -11.000   -11.000   -2.267
-2.211    -4.331    5.548     -5.566    -11.000   -3.299    -3.151
INDI 418 PT1   2741215       1489758       1.030     1.639     0.179     0.568
-0.317    0.915     -2.653    0.982     11.000    -11.000   0.328     1.855
0.718     -11.000   0.372     -11.000   -11.000   0.827     0.004
INDI 419 PT1   1527757       919744        2.790     2.910     1.227     2.574
2.197     3.484     2.908     2.516     2.057     -11.000   2.688     0.752
0.149     -5.877    11.000    -6.273    -11.000   0.770     0.992
INDI 420 PT1   1936997       1196080       -11.000   -11.000   -0.254    -1.228
11.000    11.000    1.050     -0.875    1.993     4.776     -2.540    0.821
0.430     -2.825    3.615     -3.048    -11.000   -0.017    1.068
INDI 421 PT1   2557381       1459342       -2.325    11.000    -5.672    -2.869
3.989     -11.000   6.056     -5.159    11.000    4.953     -11.000   0.772
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Table35.txt

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6.467     -4.031    -4.545    2.700     -11.000   -3.354    -2.148
INDI 422 PT1   1989893       1127810      -2.798    5.909     4.303     1.712
-3.658    -5.184    -1.268    -4.720    11.000    -3.894    -3.722    0.833
-2.167    -4.402    -1.520    -4.364    -11.000   0.661     2.021
INDI 423 PT1   2395176       1422844      -4.018    -4.068    -2.766    -11.000
3.962     5.710     -2.127    -5.085    11.000    -4.633    -3.428    6.398
11.000    -4.104    3.770     -5.276    -11.000   -0.366    -1.589
INDI 427 PT1   2782411       1659894      -11.000   11.000    -6.839    -11.000
-11.000   -11.000   2.912     2.050     11.000    -11.000   -11.000   0.209
0.606     -2.122    -2.818    0.001     -3.582    1.641     1.461
INDI 428 PT1   1522569       900985       -4.965    11.000    -3.271    -4.934
5.048     -2.224    -1.842    -5.188    5.471     -3.707    -2.614    1.983
1.728     -1.217    -2.779    -1.325    -11.000   1.057     11.000
INDI 430 PT1   6127787       3399426      -5.730    11.000    3.364     7.804
-4.513    -5.132    -0.649    5.728     -5.215    -4.203    -4.482    -4.031
-4.494    -11.000   -4.966    -1.726    -5.312    2.755     3.435
INDI 431 PT1   1619461       747894       -3.186    2.237     0.071     -1.368
0.374     2.410     4.074     -1.282    1.559     -4.030    0.391     -1.817
0.414     0.286     1.407     -1.011    -11.000   0.634     0.679
INDI 432 PT1   1924934       1120625      -5.567    6.062     4.874     -11.000
-3.244    -3.416    -2.031    -5.239    11.000    -11.000   -11.000   1.449
2.017     -4.886    -2.071    -2.149    -11.000   -1.799    -2.573
INDI 433 PT1   1674501       982279       1.489     1.515     0.343     1.282
-11.000   -11.000   1.210     0.038     11.000    -11.000   -2.258    -1.105
-1.009    -6.839    0.261     -7.034    -11.000   -0.435    -5.203
INDI 434 PT1   1727737       991203       -11.000   -0.857    1.473     -11.000
-11.000   4.522     3.751     3.434     4.302     4.042     -1.466    -0.266
1.558     -4.922    -5.252    -5.244    -11.000   -0.032    0.658
INDI 435 PT1   2100748       1272223      -0.389    0.258     -0.786    -0.075
-1.501    -0.789    -5.020    -2.287    11.000    -11.000   -11.000   1.966
2.601     -4.734    -5.126    -5.177    -11.000   -0.278    -0.206
INDI 436 PT1   2856079       1193982      0.104     11.000    2.300     -4.578
-2.660    -1.424    11.000    11.000    -2.025    -3.146    -1.098    -1.482
-1.697    -1.341    -0.045    -4.232    -3.612    -0.596    -0.744
INDI 437 PT1   3089196       1310486      -2.152    -1.543    -1.277    -1.726
-1.010    -1.602    0.744     -2.171    11.000    -3.367    -11.000   -2.455
-3.094    -0.403    -1.405    -6.187    -11.000   0.523     2.641
INDI 438 PT1   2267574       927579       -11.000   11.000    0.342     0.957
-6.880    -4.041    2.128     -0.355    11.000    0.025     -5.715    -3.622
2.460     -4.110    2.122     -1.933    -11.000   0.896     0.848
INDI 439 PT1   2057628       1057149      1.448     0.576     0.431     1.195
-0.166    0.142     1.213     0.128     11.000    -1.150    11.000    -1.712
-11.000   -3.621    2.468     -5.222    -11.000   0.589     1.304
INDI 440 PT1   1336663       759669       2.320     1.936     -3.240    2.977
-0.136    -6.839    1.601     0.806     -11.000   11.000    1.524     0.452
0.333     0.966     1.082     11.000    -11.000   0.859     -5.802
INDI 441 PT1   2173108       1220845      -0.730    0.367     -1.127    -4.364
-6.276    -1.960    4.941     4.529     -11.000   -0.332    2.913     2.430
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Table35.txt

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1.712     1.576     -1.964    -1.717    4.722     1.424     2.800
INDI 444 PT1   2733617       1513187      -11.000   11.000    -0.108    1.363
0.208     3.190     1.847     -3.729    11.000    -11.000   1.191     -1.379
0.634     0.176     0.253     -11.000   -11.000   0.553     -0.614
INDI 456 PT1   1298455       749905       1.208     1.212     -0.509    2.019
-1.619    0.611     1.933     -1.880    0.180     0.578     -11.000   -1.686
-1.393    -4.225    0.615     -1.038    -3.203    -0.284    -0.893
INDI 461 PT1   739663        420719       -3.085    -2.746    -2.314    -1.583
2.171     3.214     0.332     -4.462    11.000    -4.615    -0.495    2.023
3.193     -1.749    0.781     -3.016    -11.000   -0.059    -1.749
INDI 463 PT1   2085658       1208506      1.793     2.908     -2.284    -2.332
1.728     2.605     0.762     -2.007    11.000    -5.408    -11.000   3.441
0.240     -1.308    4.127     -6.409    -11.000   3.169     4.547
INDI 464 PT1   1666037       989577       -1.331    11.000    1.677     -1.223
-2.336    -1.595    5.262     0.652     11.000    -2.159    -11.000   3.717
3.719     -4.997    2.523     -5.688    -11.000   -3.290    3.782
INDI 465 PT1   2032735       1174826      -4.153    8.014     -4.091    -4.301
-4.609    -11.000   -1.436    -4.194    1.484     6.453     6.878     -1.551
-3.731    3.937     4.662     2.653     -5.409    -0.915    -0.668
INDI 466 PT1   1212960       672953       2.622     4.994     -11.000   -11.000
1.821     7.504     11.000    -11.000   5.305     4.734     -11.000   2.335
-3.991    -3.549    -2.469    -4.366    -11.000   1.822     6.189
INDI 467 PT1   3319979       1974532      3.492     3.868     4.971     -6.280
1.679     -11.000   6.944     3.490     -5.495    -1.765    3.584     2.002
2.518     2.066     -6.692    0.278     -11.000   0.900     1.978
INDI 468 PT1   723962        425378       -2.805    3.693     -2.138    -2.303
3.410     5.512     1.242     -1.742    11.000    -2.573    11.000    -1.601
-3.646    1.292     -0.790    -0.799    -11.000   3.483     4.909
INDI 470 PT1   3222263       1858576      -1.890    1.411     0.766     1.373
0.723     1.927     -3.590    -6.559    11.000    -2.628    -4.036    2.698
2.138     -4.263    2.138     -5.812    -11.000   1.194     2.065
INDI 472 PT1   2947379       1692824      3.003     2.288     1.463     11.000
1.095     1.914     -11.000   0.928     2.275     -0.477    -1.026    2.106
0.527     -11.000   -11.000   -11.000   -11.000   0.586     2.324
INDI 475 PT1   2100419       1120622      -11.000   2.517     0.602     3.831
2.497     2.946     -11.000   1.832     -11.000   -11.000   2.371     0.893
11.000    1.459     1.276     0.307     1.461     0.697     -6.937
INDI 476 PT1   3271056       1780362      1.754     6.153     -3.309    -3.313
-11.000   3.241     1.859     0.284     -0.751    4.761     -6.739    1.286
-0.240    4.240     2.920     0.583     -4.717    1.173     -5.181
INDI 477 PT1   2043623       1139925      -3.614    11.000    -3.825    4.007
-1.112    0.754     1.787     1.565     3.806     -0.450    -1.697    1.085
0.807     -1.203    -2.763    -2.042    -2.456    1.821     0.825
INDI 481 PT1   3435686       1911098      -0.175    11.000    -0.394    -4.211
-0.562    5.562     11.000    -1.409    -11.000   0.106     -1.711    4.490
2.060     0.021     5.144     6.789     -11.000   0.656     5.059
INDI 482 PT1   2988432       1783463      -11.000   11.000    0.580     1.342
0.462     2.329     2.295     0.073     -0.683    11.000    -1.490    1.229
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Table35.txt

-1.445	1.089	4.105	0.409	-11.000	0.669	1.516	
INDI 483 PT1	2944167	1768025	-2.978	-1.856	-1.310	-0.915	
-1.168	-0.896	-0.498	-2.793	11.000	-2.439	-1.342	2.696
1.562	0.682	-0.475	-0.528	-11.000	-0.027	1.632	
INDI 484 PT1	2698825	1471131	-7.034	-11.000	0.976	-11.000	
11.000	11.000	-0.155	-3.301	11.000	-11.000	-6.508	3.642
3.190	-3.633	-5.154	-3.636	-11.000	0.902	0.949	
INDI 485 PT1	2330936	1388816	6.103	5.887	-1.061	0.449	
-0.777	-11.000	-3.380	-5.023	-0.306	11.000	2.263	-6.739
1.593	-0.170	1.461	-0.578	-2.691	0.471	-0.452	
INDI 498 PT1	1614307	903312	0.663	1.360	0.843	1.897	
0.803	1.351	2.336	1.218	11.000	-11.000	2.520	4.372
-0.997	-5.580	2.731	-6.213	-11.000	-0.093	-0.400	
INDI 500 PT1	2221945	1254066	-2.645	-2.446	-2.692	-2.069	
-3.248	-2.643	11.000	7.073	7.992	-2.879	5.175	-1.247
-2.978	0.165	-1.638	-0.908	-4.665	-0.396	0.191	
INDI 501 PT1	1854509	1114441	-5.653	11.000	-4.474	-6.127	
2.806	3.236	-3.296	-6.937	11.000	-6.065	-4.844	1.281
1.387	-2.417	11.000	1.627	-11.000	1.667	1.955	
INDI 502 PT1	2469250	1450685	-0.158	-0.692	-0.910	-0.079	
-0.873	-0.682	1.069	-1.463	11.000	-1.099	0.017	-0.749
-0.267	1.862	3.501	-11.000	-11.000	0.386	0.073	
INDI 506 PT1	3231558	1887479	-0.048	-1.157	-1.213	-0.399	
-2.004	-1.144	1.743	-1.536	-1.987	-1.315	-0.275	-1.097
-2.467	0.883	-0.037	-0.193	-3.952	0.799	0.596	
INDI 508 PT1	1841164	1042572	-0.052	-0.364	4.100	4.588	
5.403	-11.000	6.484	-1.024	11.000	-11.000	-11.000	3.005
2.504	-4.051	3.006	-4.797	-11.000	2.155	2.759	
INDI 511 PT1	3179020	1891774	-6.091	-11.000	-3.343	-3.727	
0.754	0.852	-1.985	-5.249	11.000	-4.603	-0.726	6.600
2.991	-5.428	11.000	0.163	-11.000	-0.454	-1.285	
INDI 515 PT1	7869916	4770173	-4.454	-2.656	-11.000	-2.740	
3.094	3.925	-2.349	-4.821	11.000	-6.880	-5.316	0.648
1.672	-1.015	-1.485	-4.089	-11.000	1.122	1.413	
INDI 518 PT1	1165438	676243	-3.240	-3.227	-2.190	-11.000	
-3.867	-2.935	0.633	-3.078	11.000	-3.254	-3.897	-3.431
-1.494	-11.000	5.004	-2.444	-3.739	-1.575	-2.783	
INDI 520 PT1	1566269	892654	-11.000	4.077	-1.834	-2.697	
0.223	0.551	3.081	-0.358	11.000	-0.846	-1.214	-1.560
-1.226	-4.960	0.785	-5.831	-11.000	0.811	0.095	
INDI 521 PT1	3641493	2164335	-1.529	-3.245	-1.089	-1.400	
5.579	5.413	-0.169	-3.659	11.000	-2.575	-4.332	3.625
3.160	-0.309	4.230	-3.656	-11.000	4.011	4.551	
INDI 523 PT1	3133928	1917411	0.417	1.281	0.436	0.166	
-0.639	-0.566	11.000	11.000	-0.555	-0.295	-11.000	-0.759
-0.451	1.117	0.500	-3.755	-11.000	5.286	6.303	
INDI 525 PT1	4047328	2205598	1.705	11.000	-0.587	-0.155	
-1.170	-0.107	1.408	-0.558	-1.153	-0.676	0.776	0.128

Table35.txt

-1.446	1.606	1.152	0.963	-3.335	1.498	11.000	
INDI 526	7669226	2141429	-4.202	0.315	3.245	-4.702	
-4.229	-0.642	-3.772	1.076	11.000	-11.000	-2.056	-2.474
11.000	1.882	3.201	11.000	-0.980	0.730	2.125	
INDI 527 PT1	8547464	4824818	1.951	0.703	0.598	1.414	
0.658	0.035	1.446	0.061	11.000	-1.689	-11.000	-0.655
0.023	-11.000	1.424	-11.000	-11.000	0.919	0.888	
INDI 529 PT1	3650991	2042350	-0.761	-0.231	5.192	0.472	
-7.034	-5.949	2.159	-1.495	11.000	-11.000	-1.198	0.202
-1.207	3.296	-0.415	-2.874	-11.000	1.756	1.352	
INDI 539	3754502	1006740	1.783	0.000	-1.314	-0.494	
-1.620	0.868	-1.750	-0.652	-1.920	-0.482	1.429	11.000
-1.102	-0.239	-11.000	11.000	-2.645	2.072	-0.320	
INDI 542 PT1	4130683	2492991	-7.034	11.000	-2.979	-0.711	
-5.793	-6.565	4.585	11.000	-2.729	-5.157	2.201	0.894
2.008	1.984	3.294	-2.995	-11.000	2.712	8.014	
INDI 544 PT1	8051329	4559181	-4.098	-3.586	-2.448	-3.394	
-3.747	-4.302	-2.966	-4.343	11.000	-1.942	-1.701	3.251
3.299	-5.338	5.388	-5.907	-11.000	-0.983	-0.744	
INDI 551 PT1	3502431	2031755	0.518	-0.205	-0.747	-0.364	
-1.551	3.491	0.934	-1.395	11.000	-1.644	0.892	-3.141
-1.563	0.350	0.545	-1.090	-3.490	-0.157	-0.092	
INDI 555 PT1	2782840	1731758	-11.000	11.000	-1.001	-1.619	
-0.992	-0.790	-0.403	-3.024	11.000	2.473	-11.000	2.134
2.075	-1.610	-0.799	2.104	-11.000	1.359	0.392	
INDI 558 PT1	347823	229548	4.007	4.333	2.902	1.048	
-2.429	-1.628	4.919	1.664	5.040	0.276	-3.990	0.553
-1.003	2.506	0.677	0.553	-6.839	3.083	0.745	
INDI 560 PT1	4579501	2626408	-3.860	4.988	-3.399	-3.958	
-3.951	-4.692	0.958	-1.851	11.000	-11.000	-4.006	-2.402
-3.940	-3.603	1.787	-4.469	-11.000	0.033	1.566	
INDI 562 PT1	7310576	4200727	-4.399	-4.350	-3.845	-2.094	
1.561	2.812	-1.623	-5.257	11.000	2.941	-3.234	-0.920
0.642	-3.621	11.000	-6.033	-11.000	1.874	2.962	
INDI 563 PT1	2960054	1769868	3.356	3.303	-2.863	-4.109	
0.821	1.958	-5.685	-11.000	11.000	-11.000	-11.000	3.028
3.604	-3.422	6.225	-11.000	-11.000	0.131	-0.582	
INDI 564 PT1	1927649	1150899	0.832	6.001	-3.904	-2.985	
1.833	-11.000	2.454	1.743	11.000	-0.777	-1.748	-0.723
1.358	-4.523	0.123	-4.775	-11.000	0.388	-0.503	
INDI 567 PT1	2014677	1166051	-11.000	11.000	1.651	-2.598	
-5.941	-6.311	11.000	11.000	11.000	3.736	-6.739	-2.193
0.700	-11.000	2.305	-11.000	-11.000	-0.376	0.370	
INDI 569 PT1	1903342	1052437	0.151	11.000	-1.314	0.366	
-0.540	0.372	0.910	-0.993	0.593	-0.727	0.922	0.603
-6.156	-0.275	-0.773	-0.506	-2.643	0.540	1.185	
INDI 570 PT1	1293078	766832	2.355	0.831	-0.478	0.446	
-0.332	-0.177	3.258	-0.287	0.567	-0.468	0.616	-1.124

Table35.txt

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-2.420    0.716     1.635     -0.546    -3.578    0.126     11.000
INDI 571 PT1   1535845       898262       -3.061    11.000    -7.034    -11.000
-3.865    -6.265    2.442     3.933     -5.970    -4.746    -5.068    11.000
-11.000   3.823     6.240     -3.437    -5.226    -1.422    -2.483
INDI 572 PT1   1896897       1077514      0.352     1.433     -0.022    1.435
-1.282    0.328     0.863     -0.642    0.183     0.233     2.134     0.094
-1.909    2.233     1.422     -0.345    -1.518    -0.592    1.640
INDI 573 PT1   2038760       1193351      1.632     4.611     -1.032    -1.189
7.252     -6.437    -4.595    0.846     11.000    -11.000   -4.611    -0.732
-0.326    -11.000   -0.434    -3.132    -11.000   0.169     -0.083
INDI 574 PT1   1706159       1019875      -2.605    11.000    -2.690    11.000
-2.913    -2.141    -0.096    -3.800    -3.678    -3.793    -3.644    -4.193
-3.153    -1.888    -1.816    -2.783    -5.011    -2.211    -2.247
INDI 575 PT1   1899645       1130112      7.361     11.000    3.474     -1.143
-5.717    8.126     0.081     2.034     11.000    -1.588    -0.810    -1.529
-11.000   -5.629    7.155     -0.058    -2.824    -0.245    -3.599
INDI 577 PT1   2389479       1261191      -2.580    11.000    -5.389    -1.775
-1.776    11.000    -1.694    -1.584    -6.158    -2.358    -1.703    -2.231
-2.713    -4.370    4.292     -5.048    -11.000   -0.414    -2.109
INDI 578 PT1   1176115       668454       -5.227    8.210     -0.684    1.124
0.464     1.040     1.004     -3.968    4.650     1.668     -0.892    3.942
-11.000   -3.515    11.000    -2.360    -4.149    -4.140    -4.319
INDI 579 PT1   1362308       719273       1.121     11.000    -0.214    2.996
0.388     -11.000   2.224     0.639     8.041     -4.187    0.171     -1.574
-1.611    -5.768    11.000    -1.203    0.023     -0.391    -0.579
INDI 580 PT1   1932449       1100869      -1.520    -1.542    -2.048    -1.069
-2.518    -2.214    7.973     11.000    11.000    -0.959    -4.522    -1.415
-1.861    -4.778    -1.027    -5.963    -11.000   0.172     0.283
INDI 582 PT1   1875149       1112006      -3.592    -5.202    4.071     -3.456
2.320     11.000    -0.646    -4.332    4.104     3.070     -0.224    0.503
-0.360    -5.039    1.304     -5.748    -11.000   4.047     1.508
INDI 583 PT1   1711042       1003836      -2.878    -2.873    -3.232    -1.496
-2.300    -1.819    2.136     -2.770    -1.490    -2.528    -0.458    -1.973
-3.102    -0.415    -1.915    -0.562    -4.683    -0.020    0.786
INDI 585 PT1   486953        282656       -0.624    4.529     -0.813    -3.571
-2.244    -5.134    2.519     -2.064    -4.543    7.237     -1.233    -3.540
-0.953    -0.441    -0.187    11.000    -7.034    1.886     1.147
INDI 586       2289886       602790       5.575     11.000    0.359     3.512
1.004     2.081     0.167     1.376     1.156     -5.207    1.393     3.654
0.941     2.894     -2.221    2.302     1.390     1.768     -2.201
INDI 587       2658493       659324       -1.171    1.060     0.928     0.475
0.768     1.819     2.376     5.351     0.539     -11.000   -0.398    2.265
-2.663    -4.196    -11.000   11.000    0.470     0.541     -1.281
INDI 588       3211367       843122       -2.245    11.000    3.181     -3.558
4.391     11.000    -4.112    -7.034    -11.000   2.834     3.131     2.012
3.210     -1.638    -11.000   5.286     -2.805    -2.206    -3.498
INDI 589       2761769       662384       -1.882    4.113     -3.148    4.045
1.475     4.019     -11.000   2.088     0.770     -3.077    2.670     1.416
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Table35.txt

2.004 3.605 -5.531 11.000 -1.225 11.000 0.141
INDI 590 4370724 1166588 0.606 2.192 2.615 1.995
1.473 2.107 -11.000 -11.000 0.467 2.602 1.052 3.616
1.116 3.424 -1.431 2.513 1.286 1.984 -0.105
INDI 591 728503 165109 1.177 2.537 -0.391 0.305
1.008 0.984 0.350 -1.159 -0.832 0.116 0.636 -0.076
1.064 0.481 0.117 2.341 0.194 0.794 0.504
INDI 592 556623 185308 -1.014 5.636 -1.372 -2.211
-3.352 -2.326 1.606 -0.440 -0.483 -2.312 -1.307 -2.081
-0.443 -0.199 -1.643 11.000 2.202 3.013 -0.187
INDI 593 1453684 385252 0.138 2.558 0.050 1.345
0.149 1.366 -0.334 1.098 -1.188 1.564 -0.710 1.330
1.105 -0.090 -2.724 1.126 0.070 0.492 -0.182
INDI 594 364603 109446 -0.764 0.200 0.479 0.695
-1.180 1.177 2.255 0.249 -1.138 -1.495 -0.620 -0.975
0.865 1.511 0.725 11.000 -0.314 -1.651 0.735
INDI 595 1452665 348959 -0.128 6.837 2.869 3.381
-11.000 4.733 -6.305 -11.000 -0.018 -6.044 -0.350 2.957
6.398 5.789 -3.395 1.907 3.053 3.174 -1.790
INDI 596 988245 271118 0.876 8.210 1.273 4.932
-2.911 -2.670 -5.617 0.006 -0.246 -1.053 -1.509 -3.274
-0.607 -1.010 -4.176 11.000 -4.525 1.017 2.051
INDI 597 3303845 860944 -2.236 11.000 3.860 -0.360
2.321 7.237 0.305 -11.000 -4.184 -1.899 2.088 -2.129
11.000 0.645 -11.000 11.000 5.115 2.176 0.903
INDI 598 3094308 799317 -0.253 0.720 0.812 0.622
-0.371 0.357 -1.199 -0.973 -0.745 3.079 0.509 2.035
0.458 1.054 -2.555 1.783 0.689 0.098 -1.478
INDI 599 1126844 285742 -0.985 4.236 0.646 -2.378
-3.780 -2.430 1.557 2.885 3.845 2.026 0.591 1.409
-2.938 -3.549 0.870 7.270 -2.631 -0.027 -0.888
INDI 600 3371527 850776 -3.109 -3.314 2.457 4.298
-3.915 -4.039 -2.789 -4.995 -2.487 -3.006 1.147 4.011
11.000 11.000 -6.130 11.000 -4.887 -5.806 -3.520
INDI 601 3355446 913454 -1.704 11.000 -2.778 -3.295
-2.889 -1.741 -2.125 -2.472 -1.732 -2.563 -1.980 -1.520
11.000 11.000 -3.071 -2.768 -0.644 -1.384 -2.035
INDI 602 385840 120952 2.867 2.277 -1.360 0.437
0.789 3.718 -0.321 2.319 1.376 -1.135 -0.885 -0.579
-1.632 -0.013 0.564 2.100 -1.002 0.649 1.807
INDI 603 569542 172186 -3.565 7.289 -0.370 0.609
-1.655 0.421 2.173 -0.790 -2.150 0.238 -0.552 -3.161
5.167 11.000 -0.593 0.782 -1.730 2.088 -0.246
INDI 604 350724 115605 2.718 3.323 1.539 -1.281
-1.229 -1.641 -0.057 -0.637 2.267 -1.701 0.584 0.743
-0.605 -0.420 -1.183 11.000 -0.584 -0.795 -0.720
INDI 605 1381320 359030 0.911 1.217 0.763 1.018
0.683 1.412 -4.350 -6.937 -1.391 5.031 0.487 0.756

Table35.txt

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0.120     -0.107    -1.314    0.799     -6.807    -4.966    0.771
INDI 606       3821250       965239       6.138     11.000    4.692     -1.412
-0.777    1.792     -4.288    -11.000   1.554     -11.000   3.376     3.199
7.460     4.612     -11.000   11.000    11.000    11.000    0.570
INDI 607 PT1   1228498       741830       -3.371    11.000    -0.886    -1.448
-3.692    -2.014    3.778     -11.000   0.651     0.052     -2.020    -0.439
-3.955    -1.447    -0.480    -1.891    -6.420    -0.243    -0.663
INDI 608 PT1   2194499       1258957      1.014     2.502     1.286     3.623
3.186     2.565     -5.787    0.554     11.000    -11.000   -11.000   -2.646
-1.774    -3.868    3.006     -5.478    -11.000   1.249     1.182
INDI 609 PT1   1770834       1019154      -2.445    -3.523    -2.721    -2.555
1.861     2.513     -0.649    -4.842    11.000    -11.000   -1.670    11.000
-3.555    -2.724    3.555     -5.112    -11.000   1.083     2.997
INDI 610 PT1   1527343       856850       -2.019    -1.169    -1.830    -0.233
5.143     7.112     0.435     -3.020    7.973     -1.387    0.169     -1.618
-2.717    -3.293    5.031     -4.787    -11.000   3.426     2.512
INDI 611       1916233       575615       -0.207    0.201     -1.827    -1.869
-1.890    0.146     -1.928    -1.882    -1.866    -0.157    0.059     -0.559
-1.504    2.218     -2.445    -0.090    0.490     1.452     -1.656
INDI 612       3159154       842084       -0.789    11.000    5.661     11.000
-0.859    5.545     -6.331    -11.000   11.000    -11.000   7.416     -1.576
11.000    0.548     -11.000   -1.350    -4.608    -5.244    -1.863
INDI 613       6288961       2059769      3.986     2.727     3.630     3.362
-4.688    -0.273    0.792     -11.000   1.897     4.167     3.460     -11.000
2.096     7.034     -11.000   3.752     -0.579    5.018     1.708
INDI 614       1091100       289221       -3.877    -2.369    1.509     3.283
-1.766    3.865     -1.751    -5.257    1.344     2.364     1.004     0.146
3.614     3.704     -0.491    2.084     1.901     3.601     -2.992
INDI 615       1515293       425141       -4.387    11.000    2.988     3.085
4.536     5.438     -6.679    -2.674    0.735     4.689     -2.256    -1.516
-4.135    -3.337    -4.829    -2.148    1.136     2.586     -0.797
INDI 616       2217507       572076       -2.337    -0.073    -0.914    -1.327
-1.248    -0.211    -0.516    -0.095    11.000    11.000    -1.982    -5.428
-1.432    -0.268    -0.740    0.973     -0.499    -1.076    -2.256
INDI 617       1738377       440677       7.517     11.000    -11.000   -11.000
-1.685    0.056     -5.264    -11.000   -2.120    -3.749    3.579     -3.374
3.764     6.855     11.000    11.000    11.000    7.493     -5.581
INDI 618       3848857       1235622      -1.877    -1.088    -2.267    -1.411
-1.048    4.795     -1.768    -1.577    -1.405    -0.149    -0.978    1.841
0.196     0.945     -4.020    11.000    1.802     0.516     -2.239
INDI 619       5045579       1389511      2.502     3.859     1.396     2.548
2.674     4.753     1.860     3.801     2.178     -11.000   1.581     -11.000
1.824     2.528     -5.567    3.469     -3.290    -2.514    2.940
INDI 621       961154        281201       -3.382    -1.956    1.222     -2.759
-3.131    -4.846    -1.741    -4.407    6.387     -2.775    2.070     2.867
2.049     3.840     -4.660    3.847     3.151     4.304     0.636
INDI 622       5198556       1351700      0.514     11.000    -11.000   -0.005
0.342     0.805     0.601     -1.616    -5.154    1.609     11.000    11.000
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Table35.txt

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4.615     0.558     -11.000   11.000    -11.000   -2.437    -0.213
INDI 623       1172895        360224        11.000    8.210     3.394     0.147
-2.142    7.663     -6.109    -11.000   -2.685    -11.000   1.555     7.973
4.497     1.167     -5.352    11.000    -4.458    -0.856    2.994
INDI 624       1163065        328385        -3.032    -2.703    5.002     7.322
-2.977    -3.198    -6.143    -11.000   -4.183    -7.034    2.882     6.172
3.458     4.664     -1.332    11.000    -6.807    -5.399    -3.622
INDI 625       1905756        511270        -11.000   1.379     1.525     2.812
-0.608    0.930     -6.807    -11.000   2.229     -2.270    -0.642    1.605
5.454     11.000    -3.359    1.409     11.000    -6.193    -2.006
INDI 626       1615802        495328        -11.000   -2.329    -1.039    -1.370
-2.150    0.378     -11.000   -11.000   -11.000   -4.170    4.813     11.000
5.571     7.169     2.566     6.396     5.599     -1.457    -1.772
INDI 627       1243555        412472        -1.933    11.000    -3.627    -4.310
6.964     11.000    -5.089    -4.562    -3.148    -3.273    -1.062    -2.145
-2.853    -2.406    -11.000   11.000    4.514     5.663     -2.268
INDI 628       1255461        367847        0.278     0.590     0.670     0.744
-1.630    1.218     -0.673    2.871     -0.174    2.784     0.461     2.133
-0.910    0.010     -1.920    -0.101    0.776     2.393     -0.735
INDI 629       1614745        416147        1.322     1.548     -11.000   -11.000
7.721     11.000    -1.990    0.325     -5.842    2.347     5.974     -5.359
-0.192    0.453     -7.034    11.000    3.580     6.037     -0.094
INDI 630       1142607        351776        -0.167    11.000    -1.530    -0.949
-0.594    1.055     -1.448    -0.098    0.076     -1.096    -5.558    -7.034
11.000    11.000    -3.209    -0.282    -0.509    0.243     -1.225
INDI 631       2972001        894403        0.620     -3.729    -0.133    -0.442
-0.125    0.415     7.658     11.000    -1.034    -0.391    -11.000   -11.000
11.000    11.000    -2.843    11.000    0.470     0.174     -0.498
INDI 634       804740         225850        0.086     0.602     5.461     2.404
-1.759    4.065     -2.248    -1.209    3.818     0.735     -1.190    -3.138
1.188     0.655     -3.042    4.668     -2.130    -1.879    1.551
INDI 635       369678         131635        1.640     1.189     0.712     2.222
3.398     1.108     -0.911    0.672     1.058     0.993     -0.287    2.119
-0.429    -1.056    -0.386    0.204     -0.335    -0.648    -0.386
INDI 637       2179063        608103        -11.000   11.000    6.512     -11.000
-4.831    -5.561    4.021     11.000    11.000    -11.000   5.106     11.000
-0.759    11.000    -11.000   11.000    -6.200    4.545     -6.521
INDI 638       332113         101401        2.341     3.267     2.743     4.115
1.400     2.768     0.805     1.221     -0.321    0.531     0.614     -1.083
-0.024    3.161     2.019     2.301     -0.584    -0.039    1.517
INDI 639       2024839        547561        0.798     11.000    2.850     5.091
-3.160    1.227     0.439     -11.000   11.000    -11.000   0.649     1.720
2.826     5.241     -4.415    11.000    -1.735    0.075     1.022
INDI 641       611793         170687        1.213     3.243     0.537     0.593
0.329     2.559     0.275     0.722     0.054     0.289     -0.427    -1.620
2.739     2.000     0.187     -0.143    2.123     3.883     1.079
INDI 643       1448141        395238        -3.516    -5.739    -5.182    0.797
1.592     2.245     -0.427    -0.790    -5.584    -11.000   5.850     -5.781
```

Table35.txt

11.000	11.000	-2.256	11.000	1.928	1.923	-4.373	
INDI 644	2852885	871101	-0.225	11.000	-0.787	-2.142	
-1.167	-1.022	-0.049	-1.112	-1.558	-0.374	2.000	1.260
-1.451	-0.986	-1.779	0.951	-0.585	1.989	-0.227	
INDI 646	4480988	1271100	-0.497	2.370	-0.301	2.063	
-3.864	2.756	-11.000	0.992	0.980	3.818	3.380	-0.596
2.022	7.270	-11.000	11.000	2.371	3.946	1.392	
INDI 647	889340	309199	-4.075	2.525	0.981	1.177	
-2.136	0.639	-3.934	-6.232	4.325	-6.108	-0.191	-4.150
11.000	11.000	-3.658	11.000	-0.252	1.858	0.400	
INDI 648	375372	127215	0.564	3.734	0.152	1.253	
1.265	0.470	0.181	0.174	0.504	0.156	1.679	-0.209
0.721	0.897	-2.264	0.485	0.054	2.469	2.036	
INDI 651	4305891	1234967	-0.014	0.607	1.185	0.021	
0.497	0.826	-0.844	0.313	-1.676	0.340	1.323	1.687
-0.272	0.889	-2.095	1.806	1.284	1.199	0.216	
INDI 654	5944832	1669723	0.123	0.730	-0.521	0.227	
-0.934	1.061	0.190	0.434	-1.127	1.661	11.000	1.258
0.209	0.931	-11.000	0.550	0.364	1.141	-0.883	
INDI 655	2856070	800164	1.042	1.580	-0.125	0.680	
-1.206	0.324	-0.084	1.291	-1.345	0.755	-0.406	1.564
-0.623	-0.112	-2.075	0.290	1.373	2.078	-0.901	
INDI 656	2077562	607796	-0.686	11.000	-1.756	-0.894	
-2.691	-0.599	-1.203	-0.345	-0.913	0.441	-0.795	-0.638
-0.837	0.729	1.763	7.555	-0.482	0.972	-1.671	
INDI 657	835562	269259	-3.310	6.716	0.451	-0.197	
-3.820	6.820	-3.511	-11.000	7.279	0.264	-2.530	-0.335
3.375	5.054	-1.786	5.632	-3.889	-2.893	-2.562	
INDI 658	2761896	783010	-4.618	3.389	2.141	0.700	
-5.094	1.897	-1.161	-3.429	-1.557	-0.066	3.914	7.809
3.668	6.218	-11.000	11.000	2.359	-0.602	-4.164	
INDI 659	1736025	524931	2.566	11.000	-0.557	-0.166	
1.395	4.794	-6.937	-1.826	0.995	-11.000	5.626	5.500
1.154	-0.706	-11.000	4.479	6.997	2.695	1.486	
INDI 660	2441741	782205	-11.000	-1.047	3.775	6.200	
3.438	6.180	-11.000	-11.000	1.563	5.786	-3.263	5.874
3.463	4.795	0.774	11.000	3.453	3.982	2.738	
INDI 661	2972224	924736	1.257	3.962	1.487	2.637	
-11.000	-0.798	0.330	-6.437	1.240	-0.740	0.082	-4.484
0.180	3.443	-1.308	2.311	2.455	1.625	-0.278	
INDI 662	1820634	471970	-6.937	1.385	-3.999	-4.590	
-3.780	-4.092	-0.084	2.210	2.668	-2.170	4.721	6.800
11.000	4.484	0.653	11.000	-4.984	0.684	5.453	
INDI 664	1173776	360611	-0.238	11.000	0.034	-1.117	
-0.028	-0.494	-0.951	0.017	7.418	-0.859	0.130	0.852
-0.078	-0.962	-6.266	11.000	1.208	1.534	-0.126	
INDI 665	2762155	837866	-11.000	11.000	7.973	11.000	
-11.000	-11.000	-11.000	-11.000	0.012	0.755	0.098	11.000

Table35.txt

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11.000    3.106     3.118     11.000    -6.706    0.146     -11.000
INDI 666       3308568        965684        -2.352    1.004     5.119     1.640
-11.000   -11.000   -2.474    11.000    11.000    -5.350    3.481     5.937
4.214     5.607     -11.000   11.000    2.354     4.230     1.960
INDI 667       4325095        1163996       -11.000   11.000    3.991     4.940
1.004     4.809     -11.000   -6.152    3.117     5.889     3.371     -3.845
2.964     4.766     -1.491    5.327     -0.966    2.936     1.495
INDI 668       3821909        1108648       6.022     11.000    3.388     -5.810
4.813     4.578     -3.568    4.326     3.140     7.761     3.491     -11.000
3.614     4.846     1.988     6.421     -11.000   -11.000   11.000
INDI 669       3752777        939495        2.190     3.636     -1.436    -2.709
-4.367    -5.015    0.536     1.017     4.674     2.561     1.111     -11.000
1.622     11.000    3.187     11.000    2.152     -4.556    0.153
INDI 670       13451930       3429960       4.826     5.231     1.305     1.407
-3.170    1.885     -4.322    -11.000   -2.893    -3.024    4.270     3.354
2.515     2.508     -11.000   11.000    1.686     3.655     -0.932
INDI 672       671610         215305        1.204     0.791     -0.072    -1.421
-0.561    0.085     -1.966    1.011     -0.069    1.117     1.384     -1.705
0.078     -1.143    -0.592    11.000    -0.743    0.868     0.393
INDI 673       2668290        795306        0.784     11.000    -0.550    -0.619
-2.608    -1.617    -1.351    0.036     -1.961    -1.074    2.652     0.429
11.000    11.000    -6.442    11.000    -0.420    0.618     5.912
INDI 675       2728280        793070        0.313     -0.152    11.000    11.000
-0.714    -0.194    -11.000   -11.000   -6.937    -11.000   11.000    4.157
6.795     11.000    -2.285    -0.181    5.625     7.078     11.000
INDI 677       2608103        778512        -3.314    11.000    1.044     -4.581
-4.988    -3.436    -3.471    -11.000   -4.174    -4.786    2.095     -1.907
11.000    11.000    -11.000   11.000    -2.633    -2.558    -2.350
INDI 678       4382305        1259455       4.481     4.927     2.467     2.952
-4.269    5.410     -11.000   -11.000   2.446     4.588     11.000    -11.000
2.834     4.982     -11.000   5.456     3.719     4.288     2.543
INDI 679       2889075        882222        -1.451    -0.086    -1.487    -1.408
-1.637    -0.391    -2.279    -1.920    2.652     -1.711    1.215     -0.258
-1.323    -1.944    -3.246    11.000    -0.649    -0.522    2.614
INDI 680       4283014        1345212       -2.460    -2.710    -3.359    7.121
-2.802    -3.732    -3.522    -11.000   11.000    -2.230    -0.951    -3.708
11.000    6.829     -5.397    11.000    2.736     1.525     -2.953
INDI 683       3972034        1039960       -11.000   7.278     -1.355    -2.445
2.465     3.263     -11.000   -11.000   -0.132    -11.000   4.812     -2.608
11.000    11.000    -7.034    1.503     1.740     2.628     7.666
INDI 685       3102975        804701        -0.607    -0.573    -1.613    -0.277
-0.333    0.131     -2.223    -2.455    -1.883    -1.805    0.413     0.329
11.000    11.000    -11.000   11.000    0.068     -0.527    -1.758
INDI 688       8734930        2347674       -2.779    -2.886    -2.324    -3.532
-2.743    -2.547    -2.736    -4.303    -2.756    -2.936    0.114     -2.057
11.000    11.000    -11.000   11.000    -2.090    -1.773    -2.316
INDI 689       3034333        947807        2.180     2.849     0.870     2.591
2.045     3.856     1.396     -11.000   -0.145    3.046     0.344     -11.000
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Table35.txt

8.041 2.092 -11.000 6.614 1.362 2.708 0.694
INDI 692 1479961 527017 -1.633 2.047 -0.224 2.951
-0.476 2.943 -1.547 2.511 -2.723 0.347 3.288 3.714
-0.353 -0.255 -3.146 1.509 0.475 -0.613 -1.150
INDI 697 4104203 1129938 -11.000 11.000 2.215 3.504
3.191 3.395 -6.554 -11.000 2.480 3.665 5.119 4.515
0.467 1.428 -0.039 3.877 1.110 0.758 -3.329
INDI 701 3259067 930739 0.284 0.207 0.853 -0.242
-1.592 -0.227 0.197 -0.526 -0.121 -0.295 0.837 1.904
-1.914 -0.435 -1.471 1.568 -0.297 -0.430 -1.478
INDI 704 2263746 679490 -0.222 11.000 -4.327 -4.364
2.211 3.219 -0.419 3.042 0.881 5.318 5.083 -11.000
1.224 3.428 -11.000 3.456 0.083 0.363 3.073
INDI 708 6823828 1350760 -0.560 1.006 0.577 1.791
-0.473 -0.682 -5.757 -11.000 -1.679 -0.401 2.735 3.299
11.000 11.000 -11.000 11.000 1.171 1.434 1.343
INDI 709 3099891 873120 0.974 2.171 -0.633 1.474
-0.976 2.929 -0.483 1.025 -1.372 2.691 1.463 2.858
0.187 -0.450 -1.683 0.898 0.122 -0.266 -2.400
INDI 710 4003716 1170308 -3.184 -3.021 -2.994 -4.181
-2.809 -1.986 -2.851 -4.307 -3.210 -3.246 -0.179 -2.047
11.000 11.000 -0.013 11.000 11.000 11.000 -2.659
INDI 711 3051766 876608 -3.072 5.269 5.509 11.000
-11.000 2.250 -4.265 -2.307 11.000 -2.117 5.842 7.405
-1.580 -4.883 -11.000 11.000 -1.635 -2.774 7.587
INDI 712 2780537 803829 3.002 5.974 -1.422 -3.035
-3.941 2.771 -4.763 -4.927 1.521 -3.164 4.956 4.773
-0.998 1.021 -3.104 11.000 3.710 -2.008 7.036
INDI 713 4378752 1175485 -1.183 11.000 0.502 1.075
-3.109 7.906 -5.878 1.374 0.134 -11.000 1.743 0.450
0.254 0.280 -2.474 11.000 -4.911 -4.528 6.113
INDI 714 3611545 1016126 11.000 11.000 6.737 -3.562
2.458 3.799 -11.000 -11.000 11.000 -11.000 4.429 2.632
-0.873 11.000 0.176 11.000 1.372 -6.368 11.000
INDI 715 2548043 786339 -2.718 7.215 -3.152 -2.551
-3.953 1.883 -0.082 2.621 0.390 3.560 -2.597 -11.000
3.201 6.645 -3.962 11.000 -4.504 3.976 -11.000
INDI 716 4589698 1382464 0.988 0.994 -0.817 1.114
-0.849 -3.132 -0.967 0.234 -2.121 0.639 1.728 1.660
0.433 0.110 -1.249 11.000 0.520 -0.103 -1.336
INDI 717 3708202 1048878 1.335 0.046 -1.001 0.335
-1.875 -0.187 -0.833 -0.161 11.000 11.000 11.000 -11.000
-1.369 0.078 -1.769 0.424 -1.569 -0.034 -5.933
INDI 719 3758665 1127767 0.791 11.000 -0.918 -0.050
-6.405 -6.227 -1.705 -1.336 2.781 7.134 6.250 6.899
-0.962 -1.375 0.010 5.621 0.508 -0.492 -0.063
INDI 720 3499424 1162433 1.294 1.333 -0.633 1.489
-1.341 1.495 -2.453 2.141 -2.970 1.980 2.756 1.821

Table35.txt

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4.129     5.033     -2.404    1.832     -2.515    0.900     -0.994
INDI 721       3277844       939619       6.479     4.018     -11.000   -11.000
4.894     5.448     1.254     4.474     2.989     5.339     -2.744    -11.000
5.245     2.443     11.000    11.000    -2.669    -2.292    -0.261
INDI 722       4154424       1168766      -2.664    11.000    -3.472    -2.718
6.427     11.000    -3.877    -3.439    2.500     4.476     5.629     -11.000
4.457     8.077     -6.371    8.210     -0.163    -0.602    0.965
INDI 724       2179089       581530       -11.000   0.363     -0.470    -3.584
-6.559    0.429     -1.018    1.788     -2.129    0.930     0.831     -2.278
7.297     6.302     -11.000   11.000    0.213     0.579     -1.267
INDI 725       2921768       721727       -5.971    5.014     1.347     11.000
-3.305    -2.739    -3.119    -3.059    4.322     -11.000   -4.250    -2.536
11.000    11.000    7.087     11.000    -1.710    -2.662    -2.477
INDI 726       3091396       958099       1.188     -1.539    -0.140    0.861
11.000    11.000    -11.000   -11.000   -0.964    0.777     7.168     7.399
11.000    11.000    -11.000   0.429     0.112     1.142     -0.909
INDI 728PT1    3338568       889520       0.599     11.000    -0.280    1.206
-0.134    1.610     -1.077    1.572     -0.246    2.638     1.680     2.344
-0.434    0.909     -11.000   11.000    1.143     0.208     -0.487
INDI 729       2554609       714328       1.201     2.146     -1.836    1.537
-0.308    3.101     -2.221    2.202     -3.552    1.312     3.174     6.613
0.678     0.407     -2.394    0.931     0.587     0.385     -0.496
INDI 746       5130582       1379469      0.031     0.108     -2.610    0.538
-0.444    -0.619    -1.919    0.195     0.532     0.161     2.636     1.870
-0.010    1.194     -1.100    2.482     1.368     1.284     -0.158
INDI 747       545518        172901       -1.583    -0.231    0.064     -1.074
0.628     0.848     0.441     -1.038    -1.226    -3.034    1.461     1.432
2.462     4.382     -1.580    6.298     -1.498    2.439     0.144
INDI 748       1385719       463061       -3.383    -4.229    -0.453    -1.777
-0.791    -0.047    -6.937    -11.000   11.000    -11.000   3.159     3.884
6.449     4.025     -11.000   11.000    -0.719    -1.968    2.103
INDI 750       1245264       372488       1.409     8.041     0.488     0.014
-1.434    -1.182    -6.529    -11.000   2.703     -0.321    -0.571    -0.646
5.841     7.572     0.917     5.790     5.132     -3.529    -2.259
INDI 751       743098        188812       0.314     1.104     1.153     -0.209
0.038     -1.557    0.525     3.291     0.311     1.297     0.430     1.242
-0.062    1.033     -0.509    1.202     -0.664    0.803     -1.003
INDI 752       6559345       1842520      1.024     0.865     0.824     0.767
2.111     11.000    -0.314    -11.000   11.000    -11.000   0.880     1.219
-0.096    0.609     -11.000   11.000    1.318     0.604     -0.151
INDI 753       372603        134277       -0.360    4.572     1.720     -0.663
-0.910    11.000    -1.109    -3.189    -1.131    -1.192    -0.675    -1.510
0.613     0.065     -2.513    -2.046    1.784     5.559     -1.182
INDI 754       4866423       1263189      -0.252    8.041     7.928     7.754
0.162     11.000    -11.000   -11.000   6.823     -6.004    1.812     -1.838
11.000    0.595     -4.105    11.000    -5.371    -6.233    11.000
INDI 755       1243553       357358       0.739     1.751     3.075     7.249
-5.086    5.182     -3.737    -6.937    3.526     -5.542    0.432     -2.910
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Table35.txt

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Table35.txt

1.223	1.573	-4.140	0.872	-6.679	-5.541	-0.068	
INDI 772	551199	161533	2.490	1.909	0.443	1.434	
1.599	-0.511	-0.170	2.699	-0.857	2.491	-0.200	0.253
-0.061	-1.561	-0.912	1.098	5.092	0.078	0.268	
INDI 773	1643795	402237	-0.525	1.830	0.310	0.902	
-2.269	-1.960	-3.830	-11.000	-1.836	-2.416	-1.861	-2.048
11.000	4.983	-11.000	11.000	-2.517	-2.861	2.745	
INDI 774 PT1	1125671	518846	-11.000	6.099	-3.639	-4.278	
-4.135	-4.435	-1.649	-3.675	11.000	-4.810	-4.707	-4.606
-4.441	-2.701	-3.146	-2.111	-4.358	-1.738	-4.335	
INDI 775 PT1	615157	384207	-3.848	11.000	-4.562	-5.219	
-11.000	-1.800	4.886	3.967	3.208	4.918	1.221	-5.364
-6.780	-5.348	-5.220	0.095	-0.168	-3.274	11.000	
INDI 776 PT1	2237013	855617	-11.000	5.528	-4.383	-11.000	
-1.209	1.597	6.453	1.694	11.000	-0.582	0.650	-0.360
-6.467	-1.448	2.111	-1.638	-4.946	-1.593	-2.528	
INDI 777 PT1	3191909	1194962	-3.880	-0.799	1.570	4.297	
3.146	3.261	2.884	3.467	11.000	-5.180	-11.000	1.033
1.302	-1.572	-2.219	-5.330	-11.000	-0.955	-5.227	
INDI 778 PT1	2203681	917270	-4.038	-1.550	-4.279	-4.344	
-3.986	-4.794	-0.509	-3.499	-11.000	-2.991	11.000	-4.169
-3.671	-2.230	2.117	3.216	7.082	1.717	1.458	
INDI 779 PT1	1427718	577488	-11.000	-2.150	-1.155	0.028	
3.992	5.081	1.835	-2.041	6.651	-3.038	-5.996	-0.448
2.151	-5.512	4.697	-6.114	-11.000	-0.537	0.650	
INDI 780 PT1	2151019	857080	0.719	3.737	-1.209	-0.162	
7.036	11.000	4.110	1.931	11.000	-11.000	-0.855	-1.100
-4.591	-5.750	-3.064	-5.844	-11.000	-2.535	-4.596	
INDI 781 PT1	2783706	1148806	-0.134	-0.198	-1.391	-0.316	
-1.421	-1.117	0.233	-0.606	-0.078	1.109	-0.456	-0.988
-2.297	0.338	0.069	-1.925	-3.106	0.051	0.245	
INDI 782	3723532	1106220	-0.853	1.218	5.386	0.116	
-1.833	0.924	-2.038	0.614	11.000	0.913	-11.000	0.985
-0.466	-0.006	-2.413	6.850	0.241	0.150	-1.342	
INDI 783	4625770	1291325	-4.205	7.855	1.098	1.863	
-3.712	-2.936	-4.660	-6.739	1.562	-11.000	2.109	1.634
11.000	11.000	-0.027	3.401	5.865	4.704	0.231	
INDI 785	3546277	1192274	-0.966	1.693	0.537	-0.369	
0.844	2.285	0.239	2.047	0.586	-3.775	1.959	1.975
-0.312	0.433	-1.493	2.381	1.320	1.118	-1.316	
INDI 786	2169684	658155	-0.898	3.652	0.864	3.983	
0.287	5.736	-3.945	-2.680	-0.894	3.625	1.091	2.743
-0.450	2.497	-1.837	7.666	-0.037	1.095	-1.774	
INDI 787	1854929	582183	-5.722	11.000	-5.574	-6.758	
4.383	6.230	0.277	3.786	2.857	5.603	-1.856	-5.513
2.637	4.189	1.760	6.742	-4.614	-4.399	2.301	
INDI 788	3205025	872938	-1.984	11.000	-5.314	-1.809	
-1.894	-0.098	-2.260	-1.976	-2.837	-1.502	0.696	1.002

Table35.txt

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11.000    11.000    -5.180    11.000    -2.662    -0.140    -1.602
INDI 789       2497541       777245       -6.004    7.524     -11.000   6.969
-11.000   11.000    -0.704    6.801     -2.433    -4.375    -11.000   -3.165
4.618     6.526     -0.970    11.000    2.336     -2.388    -2.854
INDI 790       2373262       735594       0.711     11.000    -0.984    -1.034
-2.994    -2.522    0.807     8.210     -1.408    -4.821    1.994     -1.356
2.557     3.695     0.810     6.878     2.744     2.341     5.073
INDI 791       2735447       925298       -1.539    11.000    -3.363    -3.609
11.000    11.000    -2.397    -3.196    -2.635    -3.540    0.423     -2.146
-2.645    -3.882    -11.000   6.831     -1.017    -1.478    -1.455
INDI 796       4369382       1348263      -3.550    11.000    -4.573    -7.034
-4.445    -5.049    -4.063    -5.035    11.000    11.000    11.000    -4.591
11.000    11.000    2.342     8.210     -2.646    -2.760    -4.194
INDI 800       5436171       1481511      -0.658    11.000    1.649     3.268
3.756     11.000    0.617     -11.000   1.182     -3.969    2.631     -11.000
2.314     2.435     0.861     3.910     -11.000   -11.000   0.674
INDI 803       2283725       698888       0.395     2.211     -0.926    1.958
-5.527    -3.102    -1.119    1.293     0.789     -11.000   11.000    11.000
-0.570    0.356     -4.048    -2.581    3.870     1.516     -4.696
INDI 804       1958361       689005       -3.215    -0.407    4.559     7.110
-3.410    -2.212    -2.590    -3.337    -3.293    3.963     0.517     -1.494
2.706     7.709     -11.000   8.126     -0.681    -2.314    -11.000
INDI 806       2457015       736695       -11.000   6.920     -1.982    1.889
-2.122    -4.618    1.426     1.184     7.553     -4.754    7.367     -11.000
11.000    7.056     -3.701    11.000    -0.039    4.309     3.432
INDI 806       7329415       1944366      -1.960    4.630     8.210     -0.341
6.474     11.000    -5.788    -6.739    11.000    -11.000   -2.417    -3.112
5.250     1.758     -0.421    7.941     0.437     4.933     -0.646
INDI 808       4056656       1257947      -11.000   1.615     0.587     0.884
0.084     1.762     -0.061    2.281     0.691     1.331     2.074     2.120
11.000    11.000    -0.420    1.985     7.117     0.547     -0.789
INDI 809       3382158       1053235      -0.124    0.887     -0.714    0.270
0.152     1.680     -0.132    0.664     -0.130    0.994     1.170     0.879
0.999     2.339     -11.000   11.000    1.579     0.312     -0.711
INDI 810       3015877       769601       0.313     0.789     -0.564    -0.884
-2.212    0.796     -2.317    1.738     -2.675    -0.491    1.060     1.333
-1.058    0.454     -2.174    1.033     11.000    11.000    -0.509
INDI 811       981109        272920       -1.120    0.053     -1.488    -2.128
0.705     2.149     -2.199    -1.967    -3.830    -5.666    2.412     3.682
0.438     4.112     0.858     5.620     3.448     3.016     -4.274
INDI 813       2599996       690494       -1.865    11.000    0.241     0.502
1.243     2.720     -0.845    1.737     0.426     2.480     0.981     2.658
1.179     1.773     -0.834    11.000    11.000    1.098     0.271
INDI 815       3851176       1140078      0.219     1.042     -0.512    0.701
-1.598    0.603     -1.388    -0.050    0.222     2.520     2.200     2.695
0.266     -0.410    -0.169    1.373     0.119     0.939     -0.822
INDI 816       1680957       429872       -1.216    -1.274    -2.649    -2.626
-2.758    -1.475    -1.016    -0.342    -3.358    -2.285    -3.704    -1.577
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Table35.txt

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7.149     11.000    -4.368    11.000    -0.498    -1.476    -1.911
INDI 817       4282574       1129065       0.661     3.499     -0.721    -1.222
-1.402    0.859     -1.228    0.898     1.039     -1.039    3.093     3.613
-0.707    0.124     -3.215    11.000    -0.564    0.425     -1.140
INDI 819       4230325       1399586       2.753     11.000    -2.495    0.788
-0.716    -0.276    -3.443    -1.605    -3.004    -0.633    2.418     -0.979
11.000    11.000    -3.420    -0.418    -1.137    0.400     -0.150
INDI 820       3787486       1052425       -2.196    -0.395    0.170     1.507
0.293     6.010     -6.458    -11.000   -2.012    6.471     3.066     0.804
0.760     0.913     -2.707    4.025     -0.321    1.063     -0.188
INDI 821       3413892       1111215       1.749     0.123     0.541     1.769
-6.244    2.914     -11.000   1.028     -11.000   -6.054    2.125     -3.586
11.000    2.270     -7.034    11.000    -6.065    1.020     1.444
INDI 823       1638487       494088        4.154     11.000    2.597     3.304
-2.837    4.648     0.313     -11.000   2.473     4.137     3.202     4.191
1.288     -11.000   -11.000   2.902     -6.302    -11.000   1.513
INDI 825       3032120       806357        -11.000   -1.315    -1.483    -2.154
-2.261    -2.089    11.000    11.000    -2.188    -3.327    0.666     -1.189
11.000    11.000    -2.453    -0.753    -11.000   0.709     -0.891
INDI 826       3548686       1072023       -11.000   1.225     0.989     1.518
1.382     2.552     -0.741    -5.457    1.654     -1.865    2.013     2.195
11.000    2.676     -5.673    11.000    0.761     1.642     0.155
INDI 827       5012795       1434311       0.145     0.752     -1.746    -0.293
-0.164    1.524     -1.223    0.030     -1.180    0.969     1.878     0.718
0.536     0.004     -2.651    0.168     -0.169    -0.961    -1.071
INDI 829       3655531       1076046       1.817     2.795     -0.210    1.674
0.056     2.280     -11.000   -11.000   -0.074    2.090     1.402     3.559
1.593     1.328     -11.000   11.000    1.040     0.499     -0.474
INDI 830       2940219       888030        -6.032    11.000    0.963     3.125
-0.370    7.737     0.106     0.013     0.192     -11.000   6.664     2.398
3.635     11.000    -4.794    11.000    -5.417    -4.563    -5.934
INDI 831       5359953       1466640       4.890     11.000    11.000    -0.540
-5.277    6.153     -5.233    -4.819    2.648     -5.572    2.304     -0.189
3.021     4.297     -4.905    11.000    3.547     -2.526    3.074
INDI 832       3376820       975116        3.189     11.000    0.467     0.719
1.526     0.630     -0.430    1.477     -0.825    0.363     3.472     0.484
0.132     -0.301    -2.163    2.383     0.083     0.621     1.445
INDI 833       2978493       1040482       -1.951    11.000    -2.381    -5.207
-3.348    -3.686    -3.563    -5.849    3.173     4.904     0.527     -6.297
11.000    11.000    1.160     4.772     -2.184    -1.863    -0.868
INDI 835       1094348       360886        -1.080    1.112     0.137     1.041
-1.070    0.231     -3.220    -3.453    0.778     -4.457    0.671     2.495
3.747     5.611     -4.569    11.000    -3.753    -2.530    -3.493
INDI 837       5768391       1461231       0.003     2.102     -1.334    0.315
0.384     0.763     -1.855    1.633     -2.540    0.959     3.637     3.998
-0.383    0.032     -3.332    1.818     0.335     1.361     0.372
INDI 838       5759868       1435661       -4.087    4.888     3.547     3.154
4.875     1.069     -11.000   3.450     6.883     -11.000   -1.965    -3.182
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Table35.txt

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11.000    -3.991    -11.000   11.000    11.000    -1.984    -0.898
INDI 841       3457710       1008369      2.882     0.575     2.948     4.582
-4.520    4.895     -11.000   -11.000   7.247     -6.807    3.864     4.821
11.000    -4.776    -11.000   11.000    1.984     2.218     1.393
INDI 843       4169706       1306062      -4.512    6.495     4.096     6.582
-11.000   5.806     -5.372    -6.366    4.299     -4.146    3.863     6.786
3.552     5.467     -4.331    11.000    -11.000   -1.364    -1.478
INDI 845       2463713       588739       -3.558    1.560     -0.707    -0.500
-3.597    3.222     -6.839    -11.000   -2.886    -3.407    0.633     -0.498
7.304     11.000    0.579     7.315     -0.023    -0.571    0.747
INDI 846 PT1   4243554       1601460      0.670     2.234     1.143     -0.066
4.956     2.020     -5.843    -2.803    11.000    -1.601    11.000    -2.531
-2.272    -6.620    -6.326    -6.156    -11.000   -0.702    -2.818
INDI 847 PT1   2941483       1221631      -11.000   11.000    4.169     7.791
-3.673    -4.611    3.567     4.902     -11.000   4.544     -4.070    -2.868
-0.977    1.736     1.906     0.942     2.344     0.727     0.168
INDI 848 PT1   3919175       1501095      -0.175    1.333     -0.799    0.315
-1.864    1.399     1.766     -0.321    1.224     0.057     0.944     -0.423
-1.576    -0.112    0.448     -0.947    -2.212    -0.412    0.138
INDI 849 PT1   2431726       898942       -11.000   -2.076    1.776     0.933
-7.034    -2.424    6.113     6.455     11.000    -11.000   -0.377    -1.427
-2.201    -4.373    3.811     -4.242    -11.000   -0.760    -0.580
INDI 850 PT1   2403925       1136427      6.365     6.081     0.363     -11.000
3.914     4.081     -5.842    -11.000   -11.000   4.867     -11.000   1.777
-5.729    -3.714    -5.088    4.297     11.000    2.291     -1.781
INDI 852 PT1   4499091       1787034      0.664     1.813     -0.356    1.356
-1.862    -1.065    1.079     -1.001    -1.263    -0.831    1.021     -0.362
-1.793    0.538     0.732     0.798     -2.602    0.475     0.242
INDI 853 PT1   3346975       1427862      -3.677    11.000    -1.801    -3.828
-3.898    -4.759    3.313     1.581     -2.900    -3.927    1.585     -1.229
-2.197    1.567     7.654     3.471     -11.000   0.306     -2.167
INDI 854 PT1   6754665       2300244      0.885     -0.159    -0.199    0.639
-0.638    -0.062    2.761     -0.043    -11.000   0.344     1.317     -0.569
-0.894    0.808     -0.184    0.919     -1.786    0.820     0.390
INDI 855 PT1   3533136       1499327      -11.000   6.412     -0.415    -0.045
-0.486    1.895     6.858     6.753     1.889     -11.000   -2.416    0.148
1.144     -4.003    4.176     -5.284    -11.000   1.085     1.049
INDI 856 PT1   1782245       845800       3.625     2.485     1.118     -3.884
1.879     -6.721    -3.090    2.886     -3.972    -2.482    2.937     0.161
-11.000   -5.680    1.623     -0.667    -11.000   0.322     -0.489
INDI 857 PT1   3012683       1146872      2.458     11.000    3.457     6.087
11.000    11.000    5.693     11.000    -11.000   -1.233    -2.906    -1.529
-5.493    -5.212    7.956     0.659     -0.656    0.870     -3.564
INDI 858 PT1   3795395       1666203      7.992     6.920     1.280     -4.365
4.930     5.940     5.026     4.947     -11.000   1.088     2.408     4.731
-11.000   -5.697    -2.212    1.041     -3.460    2.373     -1.214
INDI 859 PT1   2020053       711694       2.509     -1.901    -5.675    -2.906
-2.397    -6.483    6.925     -4.098    -11.000   11.000    -1.770    0.579
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Table35.txt

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-3.973    -1.300    0.846     -1.228    -5.850    -2.729    0.046
INDI 860 PT1   2499975       1049814      -6.758    11.000    1.178     -3.166
-2.640    -3.922    5.796     2.629     -2.159    -3.013    -6.423    -0.761
-6.739    -5.213    11.000    -0.787    -6.004    -2.582    -3.671
INDI 861 PT1   1954118       820090       1.530     11.000    -0.404    -11.000
1.035     2.365     1.280     3.257     2.754     1.682     0.682     -0.314
0.081     -5.229    0.386     -0.015    0.947     -0.920    -1.625
INDI 864 PT1   1351106       619042       11.000    7.681     1.921     -2.387
1.844     -11.000   4.653     11.000    6.315     4.343     7.188     1.859
-2.944    -5.170    -1.964    -3.062    -6.577    1.022     -0.230
INDI 865 PT1   1143518       710118       -6.153    11.000    -4.437    -3.980
2.374     -6.880    3.276     3.574     -11.000   -2.595    1.701     1.835
-1.737    -2.115    1.476     -3.711    -7.034    -0.299    -1.043
INDI 866 PT1   2076049       883328       -4.370    8.210     -0.415    5.838
1.064     -11.000   11.000    11.000    2.993     5.699     6.339     2.575
-4.533    -4.295    11.000    1.758     11.000    -3.073    -3.847
INDI 867 PT1   2479038       1075141      -6.205    4.334     -4.112    -4.904
-2.214    3.686     0.226     -1.102    1.806     11.000    4.402     -3.043
5.074     0.759     1.584     -11.000   -11.000   0.094     -4.338
INDI 868 PT1   3496434       1527707      2.098     11.000    1.218     -1.690
-2.274    -11.000   3.168     3.077     -11.000   -3.322    -11.000   0.926
-11.000   -3.772    1.476     1.400     11.000    0.878     -1.384
INDI 869 PT1   3423706       1527633      -11.000   1.745     1.181     1.414
-5.702    -6.807    1.476     -0.212    11.000    -1.179    -5.091    -0.460
-0.757    -2.539    7.455     -1.543    -7.034    0.987     0.625
INDI 870       2465649       605983       0.254     11.000    -2.067    -2.949
-1.990    -2.028    -1.346    -0.254    0.371     -3.978    -1.541    1.705
6.126     1.655     -11.000   11.000    -4.039    -1.897    -1.814
INDI 871       1080074       305581       -1.734    11.000    -0.502    -0.965
-1.974    -0.859    -3.298    -1.505    -3.095    -0.302    4.365     0.789
-0.908    -0.750    -1.319    -0.035    -1.185    1.719     2.138
INDI 872       10573155      2667776      5.445     11.000    5.170     5.315
-11.000   11.000    -11.000   -11.000   -3.630    -5.452    11.000    -1.673
1.924     2.066     -5.624    11.000    -11.000   -11.000   -4.890
INDI 873 PT1   2132953       920294       -11.000   11.000    -0.780    -0.774
2.557     0.380     2.096     1.789     0.014     1.968     -4.549    2.015
-6.739    -3.277    3.938     -4.184    -11.000   0.719     -0.147
INDI 875 PT1   4745176       1903785      3.878     6.397     3.794     5.705
3.394     4.437     4.882     5.891     -11.000   -11.000   4.471     11.000
-0.506    -11.000   2.177     1.527     2.847     0.632     2.555
INDI 876 PT1   2811501       1131871      -0.984    4.871     5.154     -11.000
-11.000   -11.000   4.958     6.035     -11.000   0.470     4.512     2.340
2.548     -5.154    4.227     -4.925    5.069     1.513     -0.525
INDI 877 PT1   2679379       1123388      4.523     11.000    5.635     -1.337
3.177     -3.954    7.353     7.630     11.000    -7.034    0.496     0.418
-3.963    -2.451    11.000    -1.005    -11.000   0.102     -1.153
INDI 878 PT1   960840        419607       3.597     11.000    11.000    2.606
6.441     0.142     5.477     -3.342    11.000    0.592     -5.167    -3.730
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Table35.txt

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0.412     -1.229    -2.768    1.751     -11.000   4.881     11.000
INDI 879 PT1   2420799       1042203      -4.364    4.517     7.941     -4.549
-1.663    -11.000   1.371     1.382     -11.000   5.748     6.985     2.009
1.852     -4.706    6.342     0.014     -2.648    0.118     -0.823
INDI 880 PT1   2012121       833319       -11.000   11.000    1.422     0.339
1.188     -3.213    1.906     2.544     1.257     0.439     -11.000   -1.052
-4.517    0.068     1.075     -1.733    -3.641    -0.200    -0.734
INDI 881 PT1   1273392       457212       -4.634    11.000    -2.738    -3.485
-4.492    -5.463    5.818     5.717     -5.272    3.230     -3.569    11.000
-6.206    1.456     3.526     2.622     2.264     -1.405    -3.812
INDI 882 PT1   3066911       1529902      -11.000   11.000    -6.390    -11.000
-11.000   -11.000   -1.475    -3.821    -11.000   11.000    11.000    -0.930
0.661     -3.308    11.000    0.181     11.000    -2.394    -4.297
INDI 883 PT1   7340234       2874284      -11.000   11.000    2.419     -11.000
3.319     1.723     4.919     5.082     -11.000   -11.000   -11.000   2.356
-11.000   -3.412    2.002     3.183     3.073     2.074     2.720
INDI 884 PT1   1266846       635159       2.912     11.000    1.926     -1.735
-6.432    -4.092    11.000    11.000    -6.037    -5.793    -2.196    1.605
-0.701    -2.316    -0.738    -1.484    -5.944    0.979     -0.018
INDI 885 PT1   1156689       461475       0.419     5.520     11.000    5.488
-3.232    -5.798    3.019     2.057     7.188     -4.712    -0.307    1.826
3.204     -4.221    -2.871    -1.009    -3.259    0.012     -2.440
INDI 886 PT1   2402518       1071179      -0.557    -1.321    -4.591    -6.368
-1.128    11.000    2.388     0.669     11.000    -0.376    -4.115    -2.725
-3.313    -3.526    -0.309    -2.819    -11.000   3.229     5.803
INDI 887 PT1   631892        387673       2.373     11.000    -2.689    0.530
-1.786    -1.907    11.000    -11.000   5.879     5.363     6.074     -0.759
2.599     -4.383    5.487     -4.419    -11.000   -0.758    0.143
INDI 904 PT1   2305644       1022833      3.442     7.842     1.921     1.601
1.687     -11.000   3.196     0.906     -11.000   0.986     2.152     -5.193
0.077     -5.337    -0.401    0.910     11.000    -0.559    0.398
INDI 905 PT1   1467722       667776       -6.657    11.000    -6.214    -3.197
0.367     1.571     11.000    5.104     5.619     7.707     -0.051    -5.887
-5.559    -0.056    -0.670    -4.220    -11.000   -0.682    -4.649
INDI 906 PT1   2883345       1232792      -3.089    11.000    -11.000   -0.047
-0.410    -0.544    2.425     0.003     5.216     -0.913    -3.124    -2.270
-1.324    -2.994    0.615     -1.406    -11.000   -2.109    -1.219
INDI 907 PT1   3256825       1238291      -2.073    1.042     -5.129    3.920
-1.818    -3.251    3.485     -1.830    -11.000   11.000    5.224     0.998
2.214     0.006     -1.710    -0.287    -5.656    2.718     -5.045
INDI 908 PT1   2104947       807359       -0.601    4.542     1.629     11.000
3.368     -2.669    -4.676    -6.241    -3.614    -7.034    6.532     -1.446
0.646     -3.504    -2.630    -3.726    -11.000   -3.300    -0.711
INDI 909 PT1   2371684       897121       1.385     1.846     11.000    0.773
3.864     -2.245    3.490     4.574     -7.034    -0.249    1.443     -4.312
-4.588    -2.558    2.889     -3.138    -6.565    -0.635    1.397
INDI 910 PT1   2473507       1077165      7.528     4.030     -2.264    -5.551
7.129     -0.967    2.772     -3.914    2.163     11.000    0.080     -0.440
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INDI 911 PT1	2216312	1064374	4.843	6.260	1.458	-1.272													
3.218	6.375	4.979	5.916	0.364	-4.244	-11.000	-2.291												
-4.284	1.103	2.088	-4.318	-11.000	-0.313	-2.518													
INDI 912 PT1	4197248	1861396	-5.333	-1.911	-2.510	-11.000													
-5.071	1.258	11.000	6.678	-11.000	11.000	-4.506	0.555												
2.948	1.727	0.371	4.151	-11.000	1.160	0.286													
INDI 913 PT1	1692344	799159	4.099	4.966	-1.066	-3.545													
-2.234	1.032	3.227	3.601	-11.000	2.995	6.838	-4.312												
-3.614	-2.166	5.867	-0.740	-11.000	0.812	1.782													
INDI 914 PT1	2974879	1171131	-11.000	11.000	-6.121	-11.000													
-7.034	-11.000	5.167	7.057	-11.000	-3.133	11.000	0.108												
-5.284	-0.388	7.047	-2.394	1.831	3.798	11.000													
INDI 915 PT1	3736720	1681371	0.467	11.000	1.201	0.527													
11.000	11.000	2.551	-0.170	0.687	-0.096	1.462	-3.668												
-2.810	-1.624	11.000	0.279	-2.660	0.994	-0.753													
INDI 916 PT1	2046419	912914	0.890	3.101	-1.769	-0.357													
-2.753	3.373	1.249	-1.785	-1.543	-5.808	-7.034	-11.000												
-11.000	4.216	-0.469	5.411	8.077	0.650	2.193													
INDI 921 PT1	3978167	1683761	-2.499	11.000	-2.607	-3.339													
-3.201	-3.470	-2.299	-4.159	-3.551	-2.782	-3.805	3.080												
4.429	-2.516	11.000	-0.872	-3.793	4.322	6.282													
INDI 925 PT1	2658195	1376217	6.027	6.451	-11.000	-1.955													
11.000	5.061	2.775	0.528	-3.076	4.075	2.580	0.008												
-2.031	-2.985	1.578	-1.172	-3.629	-3.667	11.000													
INDI 928 PT1	2329976	1292620	2.172	-0.905	11.000	3.578													
-1.176	-1.909	5.202	6.569	6.556	-2.128	-2.216	-5.002												
-6.188	3.540	4.366	-0.470	-5.822	-3.078	11.000													
INDI 929 PT1	3627862	1709291	-11.000	11.000	2.574	-1.390													
-1.665	-2.086	11.000	11.000	-1.588	-1.164	3.320	2.234												
-2.044	-5.942	11.000	0.540	-1.040	-4.523	-0.371													
INDI 930 PT1	3301024	1792846	-1.791	2.586	-4.285	1.953													
2.894	2.091	11.000	-2.044	3.393	-2.744	-0.079	1.673												
-0.802	-2.604	-0.954	3.775	-6.516	2.137	2.157													
INDI 932 PT1	2329376	1525966	1.225	11.000	6.380	-4.582													
3.667	-1.320	11.000	5.400	-6.434	1.080	-11.000	5.398												
1.484	-11.000	-1.822	0.035	-2.203	0.128	11.000													
INDI 933 PT1	3249035	1537940	-1.535	-1.193	11.000	7.097													
4.538	5.726	11.000	-11.000	3.719	-2.995	-11.000	-6.807												
-11.000	-5.678	-0.127	1.206	-3.270	-0.977	-1.512													
INDI 934 PT1	4324907	1656899	3.957	3.395	11.000	2.775													
-11.000	-4.312	11.000	-4.073	-4.895	3.356	-11.000	-2.679												
-3.206	-5.850	-1.799	-4.342	-11.000	7.814	-2.086													
INDI 937 PT1	2980914	1399706	-11.000	7.696	-2.169	-2.994													
4.403	6.558	7.320	-4.138	0.307	-2.597	-2.748	-2.722												
11.000	-6.554	4.079	-3.120	0.136	-2.416	-3.121													
LCR 808 PT1	1165237	548940	-7.034	-0.148	2.015	4.593													
-5.829	1.907	4.406	4.275	4.160	-5.958	-3.148	3.432												

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LCR 811 PT1 1646592 674552 -11.000 5.227 -0.963 2.567
1.100 0.495 -11.000 -11.000 3.050 2.524 0.853 1.099
-0.070 -5.467 1.881 -6.721 -11.000 0.955 0.515
LCR 812 PT1 690889 233180 1.009 1.834 -1.653 -0.492
-1.393 -0.484 1.014 -0.298 2.908 -6.325 -0.043 -0.904
-4.637 -2.011 0.577 0.536 -0.737 -0.234 -0.986
LCR 814 PT1 860545 310953 -1.646 -2.056 -1.677 -0.154
2.121 2.322 -2.036 -4.847 3.176 -2.489 0.819 -1.333
-1.382 1.530 4.317 -1.910 -11.000 -0.010 -0.682
HCC 046 PT 14188498 9793394 3.024 11.000 2.572 1.521
-6.780 -11.000 -5.877 -11.000 11.000 11.000 0.232 -11.000
3.750 3.238 1.599 11.000 1.456 1.521 1.468
HCC 047 PT 13132742 8823389 -11.000 11.000 3.782 4.431
3.158 3.389 -2.988 -5.520 1.833 1.967 11.000 -11.000
6.171 11.000 -11.000 7.301 -11.000 1.304 3.309
HCC 048 PT 16676167 10985419 -11.000 11.000 2.146 2.822
2.305 2.621 11.000 -11.000 0.978 2.109 2.575 4.086
-1.983 2.015 -11.000 2.946 -5.700 3.463 4.752
HCC 102 PT 13801977 9584353 -1.712 11.000 -6.937 8.210
-11.000 -11.000 -2.179 -4.509 3.605 6.045 3.133 4.616
4.539 7.716 5.261 8.126 1.839 3.790 2.844
PANC 317 1161592 626822 -3.754 0.924 -0.332 0.127
-2.822 1.122 0.700 1.793 -1.632 2.218 -0.064 -3.733
-0.031 1.483 -0.488 2.769 -2.179 0.604 -1.534
PANC 333 871250 519090 2.190 1.001 -0.113 1.452
-11.000 2.562 0.657 1.882 -1.104 3.190 2.319 -6.880
-0.535 2.335 -6.758 11.000 -6.839 1.417 0.696
PANC 335 1308428 684807 0.617 2.242 0.875 1.161
-11.000 0.438 0.911 3.953 0.759 3.438 -5.247 -0.220
1.422 4.491 -0.347 0.779 -11.000 1.429 2.358
PANC 336 820194 457895 -0.435 11.000 -0.098 0.274
-1.013 3.423 -2.116 -0.166 -1.237 -0.052 -0.569 -1.531
-0.309 1.635 -0.106 11.000 -6.571 -4.089 -3.104
PANC 339 1250181 744654 -0.671 1.444 -0.802 1.292
1.064 2.936 1.027 1.284 -1.689 2.361 -0.089 -11.000
1.462 2.068 1.055 1.595 -0.245 0.796 -11.000
PANC 344 313408 171198 1.492 -3.676 -2.088 -4.998
0.599 3.168 -3.309 -4.438 3.168 -3.254 -1.534 -2.454
2.161 2.870 -4.184 5.361 -3.129 -0.156 -2.464
PANC 345 592020 220063 0.567 1.745 -0.280 -1.126
0.009 0.361 0.374 0.443 -0.644 1.305 1.645 -0.277
0.376 0.792 -1.782 1.773 0.544 1.803 0.013
PANC 346 403865 197061 0.114 2.232 -0.980 2.742
-0.944 1.519 0.305 0.042 -0.513 3.570 0.259 -1.652
0.662 0.153 0.658 2.247 -3.095 -1.373 0.636
PANC 348 1376634 665859 4.086 4.484 5.513 7.374
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PANC 350       530719         233396        0.355     6.919     -0.605    -0.660
0.486     2.079     -1.024    -1.659    -1.438    -0.393    -0.508    -6.668
2.134     0.129     0.257     2.526     0.250     0.773     -0.128
PANC 352       824363         404389        0.213     5.425     0.181     -0.039
-1.556    0.848     -0.391    -1.529    -2.668    0.126     0.976     0.149
-0.156    -2.760    0.974     1.038     -1.546    -0.062    2.115
PANC 353       1016762        465299        0.227     1.007     -0.840    -0.768
-11.000   11.000    -1.293    -11.000   -1.892    -0.254    4.209     6.828
-0.331    -0.096    -2.742    6.675     -0.161    -3.828    0.759
PANC 355       1384352        611721        0.264     0.969     4.214     4.639
0.722     4.193     -0.968    3.909     1.094     3.158     -5.506    -11.000
3.052     1.804     -11.000   -3.646    -11.000   7.804     -3.724
PANC 356       1753806        792705        -2.081    5.035     -1.708    2.187
-5.861    6.120     -1.771    6.557     -1.530    0.259     1.438     -0.651
4.004     2.893     -1.567    8.210     -11.000   -5.368    -0.397
PANC 357       1775288        817661        1.150     1.117     -0.454    1.750
-5.192    2.048     0.035     -1.788    -0.214    1.375     2.461     4.661
0.141     0.008     -3.088    5.766     -4.069    -2.272    -0.331
PANC 358       1660638        746846        0.843     6.126     -2.093    -2.033
-3.645    6.114     -5.034    0.187     -2.778    -0.805    0.386     0.511
2.423     3.844     -0.857    -0.067    -3.332    0.518     2.304
PANC 359       1940030        897178        -5.510    4.079     3.452     11.000
-6.937    6.703     -2.197    -0.962    -6.937    -11.000   -3.474    -11.000
3.170     -1.266    -0.357    11.000    3.275     4.859     -0.411
PANC 362       898694         389354        2.437     4.957     4.292     4.894
-2.232    1.244     -5.313    -2.124    -2.629    -2.315    -2.838    -5.116
4.707     -0.836    -2.006    11.000    -1.887    0.004     -2.356
PANC 363       2057588        923386        0.452     5.670     1.118     0.125
-0.907    1.392     -2.065    -0.911    -0.835    1.761     2.979     1.155
0.225     -0.178    -3.120    0.053     -0.079    0.741     -1.001
PANC 387       1477560        695334        -6.937    7.809     1.378     -5.997
-11.000   2.430     -1.585    -2.070    -0.329    -11.000   2.974     2.660
4.723     8.077     -2.251    11.000    -6.414    -6.416    0.631
PANC 388       508894         221889        0.963     1.455     -0.429    2.125
-3.056    1.011     -2.664    0.434     0.989     0.712     0.361     -0.059
1.225     -0.712    -4.636    4.615     -4.028    -3.631    1.043
PANC 389       1461686        633559        1.954     3.231     1.872     2.476
1.695     3.221     4.102     -6.937    -0.572    3.185     -11.000   -11.000
5.271     11.000    -0.435    3.173     -4.723    7.524     1.009
PANC 391       347426         164371        0.128     4.790     1.933     1.137
-2.366    -0.082    1.912     -1.485    -2.711    1.600     -0.157    -1.683
0.311     -0.161    -0.863    1.866     -2.651    0.185     3.017
PANC 393       1712308        896274        0.585     1.441     0.856     0.581
-1.157    0.796     -2.906    0.280     -1.375    -0.578    1.520     0.837
-0.876    -0.039    -0.820    1.230     0.748     1.343     0.383
PANC 394       1204635        523743        2.741     2.950     0.738     2.335
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-11.000   -11.000   -5.485    -11.000   6.173     11.000    -5.234
PANC 396       2213153       1144122       -4.541    4.410     -1.837    4.333
-11.000   8.210     -4.622    -11.000   1.653     4.423     -3.986    -6.070
2.254     3.905     -11.000   4.278     -11.000   0.776     1.581
PANC 397       945820        473034        -11.000   11.000    -0.253    1.415
-4.357    5.069     -11.000   -11.000   -2.773    0.978     1.807     -0.480
11.000    2.695     -11.000   6.398     -11.000   -6.368    1.164
PANC 398       2105036       1020504       1.574     2.098     1.301     3.256
-11.000   1.688     1.263     -0.753    0.482     3.492     1.566     2.361
1.511     11.000    -11.000   7.340     -11.000   11.000    1.657
PANC 399       2511255       1255400       -11.000   11.000    4.773     11.000
2.831     11.000    -11.000   -11.000   -0.249    -11.000   2.042     2.431
2.322     1.702     -11.000   1.636     11.000    11.000    1.572
PANC 400       1808361       881995        -0.312    0.795     0.141     -1.624
0.387     2.402     0.431     -2.561    -0.456    -1.257    -1.885    0.901
2.140     -1.787    0.191     3.953     3.347     3.571     -0.852
PANC 401       13720179      7046825       -3.891    4.955     -2.335    -1.732
-4.461    -3.028    3.538     11.000    -2.383    0.718     -11.000   -11.000
7.310     4.679     3.230     11.000    -11.000   -11.000   -0.764
PANC 402       1768560       932566        -7.034    11.000    2.452     4.338
2.820     3.951     1.767     3.641     -7.034    -11.000   -5.863    -11.000
7.628     11.000    -2.733    11.000    -5.766    -6.351    2.133
PANC 403       1886890       1014826       2.574     3.504     -2.644    4.404
-11.000   6.819     -1.202    -0.200    3.800     1.995     2.143     4.503
1.978     4.592     -11.000   4.545     2.109     2.904     -0.426
PANC 404       17160164      8114214       -11.000   11.000    0.512     0.862
-0.321    2.496     -0.596    1.642     -1.375    2.314     0.133     -11.000
-0.603    2.234     -0.917    1.242     -6.191    -3.754    1.093
PANC 405       1893736       897232        0.550     0.116     1.632     2.918
-2.845    -11.000   0.193     0.029     0.099     0.825     -5.572    0.912
2.806     3.450     2.158     11.000    -11.000   0.861     0.153
PANC 406       2792078       1344492       -11.000   11.000    6.065     11.000
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-1.474    -2.071    -2.119    -1.473    -11.000   4.065     3.372
PANC 406       12591001      5768356       -11.000   11.000    -0.197    1.367
-2.691    8.077     -4.608    -3.224    -2.080    -1.588    -0.695    -0.015
6.972     11.000    -2.903    -1.090    -11.000   1.803     0.455
PANC 407       3446614       1749918       -3.325    11.000    0.630     5.750
-6.414    -0.928    -4.958    -6.758    -0.721    -0.069    4.163     7.089
3.140     6.196     -3.262    0.876     -4.323    -3.660    -1.404
PANC 408       7922837       4226113       -1.269    -1.890    -6.285    3.357
-5.231    6.132     1.918     4.428     -0.420    1.465     1.969     1.048
-0.510    1.136     -11.000   11.000    -3.585    -3.420    -2.222
PANC 408       3802115       1924549       4.644     5.695     -4.566    -5.162
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1.814     2.072     -4.073    -6.612    4.970     -11.000   0.004     -2.654
-0.952    0.492     -2.317    11.000    -4.874    1.860     -0.261
PANC 409       12345620       6575140       -5.700    11.000    1.278     2.276
1.816     2.400     -5.163    -11.000   5.769     -11.000   1.283     -2.282
0.323     2.523     0.102     11.000    -11.000   3.333     0.935
PANC 417       2315430        922795        0.067     1.683     -0.385    5.604
-2.655    3.691     1.537     7.291     2.123     -0.498    -1.539    3.270
0.846     3.320     -2.798    2.982     -1.726    -1.889    -2.813
PANC 418       2138523        922303        1.683     3.511     1.957     3.943
-4.394    0.351     2.244     4.445     1.469     -1.549    -3.771    -11.000
3.210     2.628     -6.679    4.995     -6.493    -0.973    0.001
PANC 419       663345         274111        1.883     -0.525    0.513     0.494
-0.129    0.700     0.007     1.848     2.964     -2.726    -0.681    0.047
0.558     -0.096    -2.437    0.717     -0.409    1.634     -1.268
PANC 420       2206740        965992        -2.768    8.210     0.845     3.437
-4.835    11.000    -6.450    0.644     -0.362    -11.000   -2.290    -5.500
0.793     1.199     0.672     4.664     -6.583    1.143     -0.123
PANC 421       2361201        1022814       -4.649    0.528     0.511     1.442
-2.069    -3.547    -2.536    -4.703    4.528     -1.248    -1.424    -0.540
4.034     5.638     -6.268    11.000    -2.098    -0.512    -1.000
PANC 422       718661         256041        -0.429    2.195     -0.068    0.169
-0.906    2.880     -1.262    1.849     -0.408    0.323     -2.190    0.227
1.607     0.298     -0.200    1.507     -1.151    -0.794    1.073
PANC 423       193165         150670        -1.479    1.792     -0.224    1.535
-1.964    -2.915    -1.110    0.460     -1.895    -1.216    -0.513    3.249
0.513     -0.195    -2.528    4.807     -2.581    -0.574    4.431
PANC 424       2133518        924806        1.299     2.715     0.727     0.567
-11.000   -3.535    -0.546    0.043     5.252     1.925     0.320     0.948
11.000    11.000    -0.654    7.444     -6.839    1.816     -1.163
PANC 425       2076463        857006        1.080     2.327     0.868     1.493
0.998     1.023     0.845     0.279     0.651     2.958     -4.469    -6.501
0.533     2.205     -5.762    3.244     -4.272    -3.114    -0.888
PANC 426       3831728        1786763       -4.212    -0.984    2.632     4.596
-11.000   3.709     -4.739    -11.000   -0.068    3.284     0.247     3.446
3.590     4.183     1.837     4.044     -4.763    -0.256    -0.374
PANC 427       4797977        2169571       1.405     0.918     -0.451    0.002
-6.171    0.138     -0.680    -0.477    2.996     -6.112    -3.504    -5.242
3.663     5.338     2.952     8.077     -4.194    -2.996    0.882
PANC 428       1399547        616343        -2.726    3.030     -1.870    -0.794
-3.418    4.079     -1.481    0.986     -1.041    4.457     -1.387    0.155
0.591     -0.920    -0.984    1.636     -0.778    0.194     0.046
PANC 430       1271448        536121        -2.269    4.647     0.831     4.859
-1.604    1.097     -0.822    -0.927    -0.796    0.355     -0.065    -1.479
2.941     3.999     -5.867    -1.316    -1.504    -0.927    -2.925
PANC 431       2400349        1152649       1.180     0.381     -0.444    1.127
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Table35.txt

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PANC 432       759441         439827       1.923     2.469     1.749     2.332
-1.398    -1.563    -4.132    -6.388    3.945     -3.515    0.765     4.366
0.366     2.830     -4.707    3.069     -0.276    3.045     -1.893
PANC 433       1465459        486536       -0.345    0.351     0.621     0.347
-3.569    0.074     -0.268    2.407     -0.747    2.301     -0.751    1.997
0.240     -0.577    -1.037    0.531     -1.887    -1.574    -0.497
PANC 434       4575465        1530985      -2.994    -2.013    0.470     2.792
0.975     2.829     -0.508    0.686     -3.046    -0.843    -3.492    -1.468
4.882     0.207     2.055     11.000    0.649     3.091     -1.602
PANC 436       1612460        544340       1.963     2.773     1.947     1.834
-5.718    2.604     0.274     0.850     1.189     -1.438    -3.188    -5.684
0.533     1.214     -3.999    2.038     -2.762    2.874     -0.789
PANC 437       2726701        1014927      0.396     4.027     1.765     3.734
-4.632    3.518     -6.321    5.714     2.057     6.198     2.010     -11.000
3.454     4.149     -11.000   11.000    -11.000   -11.000   -2.385
PANC 438       4075607        1350092      -1.826    8.210     -2.101    -2.909
-2.952    -2.852    0.492     0.669     -1.189    -1.006    -0.952    -11.000
5.757     11.000    -5.798    2.108     -1.264    3.162     2.802
PANC 439       1954073        591012       -1.137    3.489     -0.997    -0.823
1.460     4.490     -1.476    0.124     0.982     -1.266    -0.164    0.573
1.937     -0.070    -0.665    2.751     -1.152    -0.486    -1.559
PANC 440       7184761        2457364      0.506     7.842     -0.880    0.339
-0.663    -0.545    -0.069    1.580     -0.580    1.556     -0.518    1.344
1.018     0.239     -1.626    1.184     -0.175    -0.335    -1.123
PANC 442       5627135        1867910      -0.790    4.229     0.110     2.866
-3.471    3.534     2.554     4.413     2.584     0.139     -3.246    -1.727
1.804     0.996     -3.393    1.962     -3.129    -0.620    -4.203
PANC 444       4375617        1577165      -11.000   2.785     2.157     3.910
-11.000   2.906     -1.386    4.403     1.447     4.723     3.294     -0.187
7.731     1.689     1.238     3.379     -11.000   -11.000   0.660
PANC 445       2648490        936059       -1.670    2.439     0.670     1.713
-0.079    0.973     -0.268    -0.176    -0.693    2.486     1.229     -2.546
1.483     -0.240    -0.749    7.332     -2.156    1.568     0.154
PANC 446       3766774        1303955      -4.652    11.000    5.531     11.000
0.215     2.380     -4.973    -11.000   0.279     0.271     -3.008    -4.935
11.000    11.000    11.000    11.000    -4.168    -2.907    -4.146
PANC 447       2976381        1169222      -2.653    2.518     0.628     1.389
-4.859    3.650     -1.959    -1.743    -1.728    -1.906    0.039     0.779
0.560     0.468     -0.157    5.566     0.917     1.470     1.137
PANC 448       3510949        1069029      2.098     4.079     -4.305    4.536
-4.619    -4.633    1.646     2.803     -3.176    -2.825    -2.170    -1.148
8.126     4.736     -6.094    5.707     -2.404    0.959     -3.591
PANC 449       9362656        3143095      -2.369    2.198     -1.968    -3.554
-2.791    -2.082    -3.456    -7.034    5.197     11.000    -1.896    -4.479
11.000    11.000    6.896     8.210     -1.239    0.505     -3.323
PANC 450       1394345        567637       0.211     -0.249    0.766     -1.869
-0.112    0.569     -1.072    -0.688    -2.051    0.211     0.569     0.860
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4.074	4.714	-11.000	3.028	-5.352	-5.508	2.558	
PANC 452	649860	214274	0.795	5.049	0.309	1.527	
-1.192	4.471	0.410	0.725	1.565	1.861	1.036	-4.390
-0.589	-3.821	-1.171	2.635	-3.909	-1.358	-0.204	
PANC 454	2865855	832954	4.889	5.286	0.025	5.206	
3.087	4.529	2.857	-3.556	11.000	-3.570	2.693	-11.000
3.829	3.388	-5.239	4.227	-5.049	0.320	-6.174	
PANC 455	8850992	3031029	1.281	1.669	-0.506	0.046	
-1.675	-0.542	-2.366	-4.222	-1.292	-1.620	1.331	-1.181
1.050	-0.557	-4.603	3.456	-0.429	1.027	0.669	
PANC 456	2576683	940581	2.043	11.000	-0.902	1.409	
-3.614	-1.263	-1.852	-1.183	0.731	2.752	-1.202	3.309
6.472	-0.967	-0.510	0.737	-3.767	-4.287	-0.774	
PANC 457	2748592	896787	-4.797	11.000	-0.371	-0.768	
-3.058	0.303	-0.665	-0.229	-1.428	1.343	0.354	0.795
-0.007	-0.635	-11.000	4.468	-3.160	3.618	-1.992	
PANC 458	4514931	1435426	1.290	7.296	0.983	1.603	
-0.869	0.762	0.789	1.412	-0.728	4.797	-2.667	-5.228
1.800	0.383	-1.449	0.979	-4.079	2.700	-3.477	
PANC 459	12222544	5615924	-11.000	11.000	-1.245	-1.754	
-1.450	-0.037	-1.882	-0.477	-2.095	0.281	-0.319	0.588
-1.115	-0.281	11.000	11.000	-6.758	11.000	-0.224	
PANC 462	3113776	1487438	-1.264	11.000	-5.170	-2.944	
7.696	11.000	-1.561	-2.688	-3.348	-2.556	-4.781	-2.412
11.000	4.169	-3.075	11.000	-11.000	-11.000	-1.160	
PANC 463	2829589	1394037	-0.783	-0.021	2.860	5.363	
6.114	11.000	-6.144	-11.000	11.000	3.094	1.372	3.752
11.000	1.972	-0.442	4.896	-11.000	-11.000	-2.483	
PANC 464	18381220	9375803	4.237	4.631	2.459	4.301	
2.361	4.381	1.015	3.280	-0.227	3.879	-2.889	-11.000
1.723	1.277	0.076	4.031	-11.000	-5.273	-5.224	
PANC 465	1297824	655940	-11.000	7.158	-2.202	-2.954	
-11.000	-4.472	-5.536	-11.000	-4.902	3.973	-0.362	6.271
2.112	3.535	-0.512	11.000	-5.889	-11.000	4.034	
PANC 466	4022060	2104650	0.672	1.030	-0.351	0.210	
-0.004	1.511	0.249	2.547	-0.837	1.197	0.915	-2.734
-1.057	1.899	-3.970	2.571	-1.842	3.679	-2.008	
PANC 467	1400388	694534	1.710	2.630	1.869	1.313	
-11.000	4.343	0.958	2.612	1.208	7.928	-2.095	-4.766
1.154	2.139	-7.034	0.050	-11.000	1.472	0.800	
PANC 468	1776803	865281	1.265	2.576	0.756	2.089	
-4.195	2.701	0.031	0.147	-0.189	2.221	1.073	1.235
-0.625	0.050	-4.369	11.000	-5.000	0.459	-1.910	
PANC 469	1829880	865581	4.269	3.348	3.120	4.589	
3.464	5.188	-0.139	-2.281	2.362	1.132	3.507	-11.000

Table35.txt

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PANC 469	1911386	912889	4.851	3.818	1.535	3.566	
2.581	4.325	0.437	4.279	0.555	3.918	3.485	-11.000
2.685	2.934	0.579	5.037	-11.000	-6.721	2.204	
PANC 470	3757151	1879185	-0.388	11.000	-0.261	-1.144	
-0.300	11.000	-2.956	5.838	-1.202	-3.946	1.198	-11.000
5.764	6.145	-5.970	11.000	-2.346	-3.728	-1.068	
PANC 471	13243255	6447385	1.000	0.921	0.091	0.182	
-0.155	1.940	-0.713	0.464	-1.800	1.733	-4.651	0.648
-1.223	1.023	-4.200	4.535	-3.703	1.909	0.776	
PANC 472	2404258	767900	1.375	11.000	-1.255	2.354	
-11.000	11.000	-11.000	-11.000	-1.988	0.801	1.777	-3.428
7.018	11.000	-11.000	7.133	0.690	0.455	-0.099	
PANC 482	1444850	548115	2.011	2.283	1.093	0.416	
-0.442	1.009	-1.871	-0.281	-1.934	1.458	1.570	2.284
1.342	1.977	-2.880	-0.092	0.262	-0.106	-0.136	
PANC 482	2123777	771174	-5.251	0.801	-0.315	0.420	
-11.000	7.030	0.178	1.299	11.000	-1.073	1.108	7.454
1.673	0.846	-4.574	11.000	-4.701	0.661	-1.729	
PANC 483	1272416	428921	-1.426	-0.235	-0.982	2.581	
-2.084	2.351	0.933	3.321	2.197	2.354	1.035	-0.206
1.943	1.777	-2.343	1.789	-1.605	0.290	-0.330	
PANC 484	1294497	414553	-1.456	-0.560	-1.696	-0.606	
-0.248	2.433	-0.100	4.237	1.362	1.681	-0.240	4.224
-0.429	0.999	-2.492	3.426	0.421	0.059	-1.793	
PANC 484	1758329	597918	-0.509	3.261	-0.909	-1.098	
-0.888	3.408	-1.460	1.197	0.257	1.749	0.209	2.430
-0.546	1.560	-1.066	2.764	-0.532	-0.538	-1.588	
PANC 485	377168	119863	2.092	3.006	0.851	1.646	
1.297	1.705	1.280	4.261	-2.066	0.589	1.112	2.155
2.020	0.214	1.229	1.263	2.338	1.203	-0.760	
PANC 488	1495079	454509	-0.827	-0.734	-1.175	-0.931	
-1.014	1.739	-0.804	0.352	-1.009	0.784	0.718	0.175
-1.309	-0.549	-1.735	1.066	-0.235	0.962	-1.269	
PANC 489	1508466	465508	2.205	11.000	0.735	-2.721	
0.145	11.000	-5.630	-11.000	0.299	0.808	2.409	0.767
-4.255	1.070	-0.495	0.065	1.721	-2.759	0.384	
PANC 490	1598244	478253	4.791	5.294	4.409	5.094	
-2.519	11.000	2.092	3.308	1.525	4.275	3.019	-2.512
1.747	2.588	-1.857	5.175	-5.344	-6.213	-3.983	
PANC 491	2231357	567199	0.387	11.000	0.002	1.208	
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0.073	1.307	-5.547	11.000	-11.000	-6.807	0.072	
PANC 492	2190919	612598	2.421	2.965	-0.508	1.110	
0.510	3.186	-1.615	3.218	-0.688	2.552	0.223	3.313
-1.222	2.703	-1.356	0.721	-0.619	-0.177	-2.528	
PANC 493	2081702	629759	-11.000	11.000	1.213	2.895	
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Table35.txt

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0.259     1.826     -2.077    2.887     -0.767    0.605     -1.932
PANC 495       3317892        933370        6.018     7.015     -2.708    2.184
0.301     1.798     0.632     2.655     0.447     1.806     -5.751    -11.000
-0.194    2.022     0.709     11.000    -2.895    -4.467    -0.894
PANC 496       2300558        690666        -11.000   3.866     1.350     2.223
1.256     8.126     -6.839    -11.000   2.013     3.056     0.288     2.849
0.440     2.224     -5.517    11.000    1.849     1.712     -1.304
PANC 497       2334862        726810        -0.017    0.716     0.542     0.700
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1.714     2.439     -11.000   2.688     2.101     0.630     -1.123
PANC 498       2303141        660169        -0.651    1.921     -0.499    2.009
1.645     7.153     -0.296    3.566     1.019     2.017     -6.647    -11.000
0.875     2.028     -3.465    1.301     2.640     1.231     -1.231
PANC 499       2132593        687513        -6.839    -3.498    1.177     3.031
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11.000    2.756     -0.817    11.000    -3.324    -1.482    -5.156
PANC 500       2586323        873926        0.340     0.419     -0.667    0.842
-0.914    1.129     -2.696    6.559     2.487     1.859     0.648     3.146
0.814     2.269     -2.694    3.459     1.269     -2.529    -2.953
PANC 501       1819958        525625        3.757     11.000    3.486     5.138
-2.242    11.000    1.179     -11.000   1.805     -5.450    2.923     -11.000
11.000    -6.450    -11.000   4.356     -11.000   -11.000   -11.000
PANC 502       2700323        867452        0.032     2.525     1.204     4.524
-2.690    11.000    -0.087    3.842     1.068     2.603     -2.940    -3.394
2.345     3.078     -5.091    4.186     -5.868    -6.219    -0.276
PANC 503       3205857        930438        1.234     -0.023    1.998     1.029
5.565     4.553     1.404     -0.395    1.551     0.258     -11.000   -11.000
11.000    2.573     -6.303    3.749     -5.374    1.583     11.000
PANC 504       2102970        686305        1.469     2.197     -0.898    2.235
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1.688     11.000    0.310     2.892     -3.507    -6.549    -0.832
PANC 505       2104822        666882        0.469     3.558     0.831     2.095
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PANC 506       2473598        802241        1.043     3.936     0.645     2.978
0.931     3.623     1.755     5.311     0.364     2.327     -6.880    -11.000
1.296     2.404     -11.000   4.367     -11.000   1.846     -0.596
PANC 507       1372355        396590        1.056     0.057     0.456     -1.464
-3.598    3.011     1.615     2.032     11.000    -1.159    0.524     1.100
1.576     0.507     -5.174    -1.148    -2.283    4.559     -0.129
PANC 508       3596485        1158879       0.740     0.868     -0.292    0.344
0.020     0.631     -0.468    1.495     -0.174    -0.864    1.612     2.301
-0.801    0.845     -1.052    0.844     0.163     0.459     -0.369
PANC 509       2402784        688127        -11.000   5.028     4.195     7.080
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7.047     11.000    4.572     11.000    -1.577    -3.130    -1.885
PANC 511       2842953        825135        -1.930    3.229     3.628     5.384
2.439     5.579     -4.240    4.037     0.569     0.915     0.882     1.419
-1.567    -2.682    -6.368    6.022     -4.952    -2.292    1.220
PANC 512       1601954        474172        -3.917    4.059     2.524     2.280
-0.143    2.402     2.028     2.222     0.893     -11.000   -3.766    -6.340
0.679     3.291     -2.853    7.795     -5.957    2.896     -4.544
PANC 513       2652513        773693        -0.249    1.241     2.988     0.963
2.971     6.032     -1.818    -4.761    0.978     -4.225    1.782     5.385
2.208     11.000    -3.540    11.000    -2.521    -5.443    -1.653
PANC 514       2198033        654286        -4.474    2.217     0.700     2.818
1.529     3.096     -0.431    3.097     6.351     -0.051    -0.460    -1.718
1.673     3.205     -4.820    4.757     -4.505    4.817     -5.249
PANC 515       2155673        698462        -11.000   5.971     11.000    11.000
-11.000   0.605     -2.905    -3.509    -2.632    -2.833    3.265     -11.000
3.702     -5.464    3.327     11.000    -11.000   -11.000   -2.708
PANC 516       3105271        913066        -5.169    7.599     -0.424    -1.883
-11.000   2.188     -0.057    3.042     6.662     11.000    -0.856    -3.828
11.000    11.000    -11.000   -3.473    -11.000   -11.000   -5.804
PANC 517       2876191        820046        -1.807    0.208     -0.391    0.913
-0.724    0.693     0.614     2.760     -0.673    1.085     1.103     2.651
-1.276    1.036     -2.201    5.840     -0.490    -0.594    -2.423
PANC 518       5277476        1753500       -11.000   -4.356    0.268     11.000
0.565     3.159     -11.000   -11.000   11.000    -4.431    11.000    -5.022
11.000    0.772     -3.442    11.000    -11.000   1.708     -5.640
PANC 519       2823690        804708        -1.807    6.089     -0.523    2.319
-11.000   11.000    -3.523    -2.330    1.850     3.207     -1.652    -1.713
0.896     3.280     -3.342    6.475     0.315     -1.480    -3.690
PANC 520       1623055        532617        -6.529    2.725     1.608     3.839
2.276     4.525     -6.937    -11.000   2.284     2.664     1.877     -3.337
1.209     3.107     -2.993    2.380     1.389     1.519     -0.485
PANC 522       246062         114523        0.452     1.692     3.761     1.962
0.746     2.384     0.063     1.696     0.167     -0.236    2.421     -0.371
0.674     0.684     -0.160    3.724     -0.808    3.457     0.954
PANC 525       648288         244083        -0.736    -0.966    1.126     0.873
0.471     3.731     -1.259    -2.114    -0.511    1.052     -0.060    -4.891
7.191     0.377     -1.560    4.431     -3.798    0.955     0.077
PANC 526       592014         255175        -0.362    0.237     0.490     0.175
1.034     1.464     0.165     2.283     -1.453    1.851     -0.620    -1.699
-0.353    0.690     -3.172    2.806     -2.871    -1.516    1.414
PANC 527       364107         192623        1.148     2.272     -1.513    0.487
0.156     0.073     1.877     1.447     -1.847    -0.314    -1.711    -3.794
0.820     1.353     -1.765    7.535     2.039     -0.642    -1.554
PANC 528       454859         214696        0.835     1.075     -0.966    2.209
1.525     0.808     -0.935    -3.064    -1.365    0.742     -1.481    -0.530
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Table35.txt

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3.652	3.602	0.214	4.579	1.545	2.809	1.416	2.513
1.556	0.995	0.865	3.293	2.219	1.774	-1.562	
PANC 530	653913	240124	0.325	3.505	-0.373	1.186	
-1.274	-0.725	1.425	-1.289	-2.106	1.862	-1.042	2.827
-0.006	1.708	-0.640	2.058	-3.067	-1.268	-0.334	
PANC 531	756813	325064	-11.000	0.996	11.000	11.000	
1.581	7.148	-6.577	-11.000	-0.006	2.625	-2.720	-11.000
1.971	-3.178	-3.347	6.828	-5.172	-4.421	1.495	
PANC 532	2131045	709876	-11.000	-0.140	0.355	2.859	
-5.276	3.257	-0.310	3.685	0.012	1.523	1.339	5.026
1.988	2.422	-3.601	11.000	-2.768	-2.966	-0.548	
PANC 533	2020527	697400	-0.563	0.929	-0.499	1.131	
0.430	2.603	-0.412	3.092	-0.463	2.004	1.067	3.241
-0.089	1.983	-0.886	1.853	0.999	-0.290	-1.092	
PANC 534	2681299	847236	-3.120	-1.663	3.212	-3.576	
-2.034	11.000	3.647	-3.966	2.573	4.019	-4.531	-11.000
11.000	2.584	-4.406	11.000	-11.000	-4.898	0.305	
PANC 535	2454703	693908	-3.421	3.396	1.315	3.069	
3.182	4.894	1.871	5.474	2.298	4.371	-7.034	-11.000
0.901	-1.916	-5.861	11.000	-5.887	1.506	-2.675	
PANC 536	2194949	597417	0.908	1.724	-0.024	1.925	
0.570	3.120	-1.035	4.183	1.918	1.602	-3.805	-5.430
1.229	2.723	0.217	3.772	2.331	0.379	-5.379	
PANC 537	1922053	601233	-3.286	-2.895	7.328	11.000	
-11.000	3.951	-3.302	-3.593	-0.297	0.654	-3.735	-5.264
11.000	3.094	-0.176	2.168	-11.000	-3.488	-11.000	
PANC 538	2001699	650387	-0.381	11.000	-6.011	1.001	
-1.433	1.314	0.132	1.861	-0.858	0.845	2.493	4.434
-0.370	1.466	-0.971	2.208	-6.637	0.160	-1.537	
PANC 539	2644877	817006	-0.036	0.360	-0.944	-1.921	
0.213	1.460	-0.621	3.174	1.073	1.262	0.778	2.027
0.079	1.530	-0.883	1.082	2.126	-0.844	-2.283	
PANC 540	2068020	660441	-1.130	3.704	-0.724	-1.522	
-1.427	0.049	-2.993	-1.053	-0.680	-1.933	-0.741	-0.030
4.976	5.305	0.367	3.777	-0.566	-0.927	-0.447	
PANC 541	2320898	722960	-1.040	-2.771	-2.450	11.000	
-6.706	-11.000	6.222	11.000	-11.000	0.155	-0.020	-0.137
-0.855	-0.177	4.324	11.000	-7.034	-11.000	-6.015	
PANC 542	3694518	1125446	0.212	1.015	-0.322	5.142	
1.231	2.096	0.544	5.992	0.858	3.763	1.020	-1.757
0.033	2.777	-0.218	2.559	-3.130	-4.693	-3.862	
PANC 543	3137031	944491	3.322	4.500	2.018	3.369	
0.801	4.167	-0.500	0.311	2.315	4.585	-3.799	-11.000
7.490	1.898	0.242	3.383	-6.273	-11.000	0.323	
PANC 544	3009522	914076	1.044	0.676	0.554	1.497	
-11.000	1.270	0.813	3.342	1.370	2.133	1.574	3.762

Table35.txt

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2.399     3.559     5.668     11.000    -1.087    -2.766    -0.022
PANC 546       2880084       791647       0.378     2.493     -0.919    2.278
-5.648    3.271     -3.405    -11.000   0.679     1.897     1.341     0.200
0.534     3.662     0.929     5.161     -2.354    -5.346    0.583
PANC 547       3637195       1097590      -2.890    -1.850    4.084     8.210
5.383     11.000    -3.996    -3.471    -2.566    -3.128    -4.020    -11.000
11.000    -2.262    3.521     7.128     -4.529    -5.430    -3.096
PANC 548       2516708       818103       1.339     3.014     0.790     2.265
1.473     2.683     0.709     4.518     1.581     3.927     3.212     -5.620
0.611     2.726     -4.815    3.916     -5.456    2.727     -6.657
PANC 549       1775997       577173       -11.000   11.000    1.344     3.043
1.275     3.604     -6.758    -11.000   -6.263    -2.976    2.414     -4.430
7.298     3.684     -0.505    2.746     -2.333    0.680     -0.160
PANC 550       6208643       2057627      1.513     0.461     3.695     5.073
0.782     1.391     -1.415    -1.605    -6.214    -11.000   -4.211    -11.000
3.500     0.183     2.632     5.938     -5.183    -4.161    -3.955
PANC 551       4136824       1194261      -0.469    0.180     -0.198    0.234
-0.512    0.555     -1.109    0.938     0.063     1.170     2.745     -1.183
-0.339    0.133     -1.715    5.633     1.144     0.345     0.347
PANC 552       2521494       822546       -0.810    -0.104    2.800     5.910
3.115     5.037     -2.424    -0.688    -1.444    0.810     0.342     2.945
2.093     3.552     -2.029    5.658     1.159     0.012     -1.644
PANC 601 PT1   1531388       300345       -1.908    5.000     -1.475    1.893
-1.580    -3.527    -0.096    -3.020    1.186     2.674     -1.207    -1.604
-1.325    -4.177    -1.154    -2.699    -7.034    -2.399    -2.258
PANC 602 PT1   1715738       392335       -0.496    0.385     1.104     1.893
-0.163    1.012     1.432     1.367     0.514     0.448     1.601     1.348
-0.559    0.907     1.531     0.455     -5.599    0.059     2.337
PANC 603 PT1   2212707       414814       0.833     1.104     -2.111    2.278
-0.079    0.870     4.391     -0.984    0.164     1.913     0.040     -1.473
-1.528    -1.927    -0.823    -1.915    -5.217    0.968     -0.991
PANC 604 PT1   1183578       290473       -3.644    11.000    -4.736    -5.200
-2.065    -1.535    3.048     -0.779    6.582     -4.432    -1.252    1.133
-0.660    -2.886    1.015     1.629     -11.000   -0.376    0.650
PANC 605 PT1   2582836       591070       -2.969    0.497     -0.180    0.309
-1.262    1.263     2.364     -2.329    4.852     0.858     -2.814    -2.820
-2.983    -2.655    -0.993    -0.531    -2.838    -1.653    -0.953
PANC 607 PT1   2229883       521960       -4.789    11.000    -0.592    1.306
-1.149    -1.303    1.831     -1.472    1.578     1.701     7.499     0.892
-0.402    -2.384    -3.874    2.686     -11.000   0.380     1.395
PANC 609 PT1   2103512       469847       2.128     8.210     -2.631    -2.138
-2.622    -2.344    11.000    -0.275    11.000    -1.866    -1.292    0.684
1.156     -0.545    -0.150    -0.175    -11.000   -0.315    6.483
PANC 610 PT1   1711729       372937       0.990     2.728     -4.052    -3.839
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Table35.txt

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PANC 613 PT1   1217526       343096       0.480     -0.110    -0.870    0.263
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-0.692    -1.826    1.071     -0.860    -3.266    -0.185    -0.234
PANC 615 PT1   2114389       482768       -0.505    1.192     -0.765    2.874
0.464     -0.562    1.556     0.109     5.484     -2.470    -0.217    0.748
-2.155    -2.294    0.672     -2.021    -6.392    0.021     3.528
PANC 616 PT1   2099141       370223       -6.839    7.236     0.157     3.750
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3.577     -1.444    1.107     1.815     -6.706    -0.299    1.873
PANC 617 PT1   960805        220160       -0.708    -0.891    -1.829    2.677
0.040     -1.346    -0.814    0.167     8.210     1.987     -2.293    -0.646
-1.616    -2.270    1.493     1.889     -2.558    -1.224    -0.296
PANC 618 PT1   1516301       373004       0.157     1.257     -1.976    1.253
-0.720    -2.100    2.653     -0.135    1.048     0.073     -0.688    -1.957
-0.401    -1.785    -0.544    -2.152    -4.655    -0.786    -2.591
PANC 619 PT1   1687773       387568       -2.739    7.213     0.364     6.216
1.949     1.803     -0.046    -1.931    0.424     -1.694    -3.321    0.683
2.005     -2.235    -2.283    -2.010    -11.000   -1.873    -2.610
PANC 621 PT1   1129282       290595       -5.705    11.000    2.145     4.073
-0.654    -1.443    -0.013    0.119     4.355     0.260     -5.033    -4.865
2.406     -3.157    -1.020    -1.190    -11.000   -1.795    -0.915
PANC 622 PT1   2203140       438205       1.182     2.652     -0.506    2.278
1.152     0.579     2.317     -2.279    3.651     2.902     -0.758    -1.213
-0.775    -4.450    -0.766    -1.180    -5.834    -1.089    -2.068
PANC 623 PT1   1385306       288105       -0.173    11.000    -1.961    -0.850
2.314     -5.861    0.991     -0.923    0.158     1.299     -0.858    0.474
7.862     -3.557    -1.552    -1.239    -1.114    -0.457    -2.238
PANC 625 PT1   2426948       466406       -11.000   2.737     1.396     4.295
0.719     0.640     1.730     -4.021    4.044     2.344     0.566     -0.231
-0.889    -1.665    -1.071    -0.403    -5.739    -0.796    -0.080
PANC 626 PT1   1108281       315850       -2.452    1.976     -0.600    -0.640
0.704     4.906     -1.771    -3.986    4.604     1.402     0.113     -1.104
-1.638    -3.569    0.083     -0.565    -5.347    -1.328    0.101
PANC 627 PT1   984276        239366       -2.812    4.067     0.098     1.625
-0.924    1.158     0.090     -1.323    3.457     -1.759    -0.016    -0.903
-1.114    -0.838    0.575     1.025     -1.507    -0.409    -0.870
PANC 628 PT1   2752923       767452       -1.199    11.000    -3.062    0.291
0.449     -1.496    1.128     -3.405    -0.724    -0.674    0.483     0.285
-2.091    2.022     -0.771    -1.233    -11.000   -0.476    11.000
PANC 630 PT1   520663        110217       0.017     1.572     -0.771    -2.450
-0.144    -0.946    0.512     -1.449    0.672     1.231     -4.419    -1.580
-0.122    -2.179    0.749     3.634     -1.851    -1.959    -2.369
PANC 631 PT1   1379182       316170       -0.881    11.000    -0.128    -6.464
-11.000   -1.252    1.527     -5.516    2.010     11.000    0.091     3.332
-0.892    0.560     0.488     -0.367    -6.170    -0.287    -4.039
PANC 632 PT1   1355097       299819       -3.380    11.000    -1.854    -1.636
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Table35.txt

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PANC 637 PT1 682547 152279 -0.132 2.583 -4.953 -0.093
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PANC 638 PT1 851956 167682 -2.385 4.840 -1.378 1.832
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PANC 639 PT1 2727540 509440 -0.785 1.055 -1.279 2.250
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PANC 640 PT1 1390089 316897 -0.918 2.204 -0.335 0.673
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PANC 641 PT1 4063812 1081017 -2.706 3.370 1.311 4.172
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0.422 -3.302 1.940 -4.539 -1.371 1.203 3.019
PANC 642 PT1 1803527 394499 1.835 3.520 -5.151 -6.384
-1.037 0.328 3.724 1.293 -6.178 1.719 0.640 -0.956
-5.331 -2.620 1.666 -2.291 -11.000 0.294 -0.885
PANC 643 PT1 3369716 717335 0.662 2.443 -0.690 0.664
-1.007 -0.267 1.479 -0.035 3.321 2.423 -1.783 -1.247
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PANC 645 PT1 1843912 370102 2.725 4.672 -4.481 -0.901
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PANC 646 PT1 5051009 1141815 1.463 2.091 0.248 2.331
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PANC 647 PT1 1791181 431073 -0.312 5.179 -5.360 -5.799
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PANC 650 PT1 1664857 311988 0.150 0.930 -3.534 -0.036
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PANC 651 PT1 1594084 320634 -0.266 1.303 -0.688 1.747
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PANC 652 PT1 2747279 641541 -2.081 6.717 -0.105 0.391
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PANC 653 PT1 1496358 294332 -0.084 2.056 -1.411 -0.176
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PANC 654 PT1 2429639 526486 -1.258 2.088 -2.898 0.181
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Table35.txt

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PANC 656 PT1 2474802 603229 0.929 4.339 -4.883 6.617
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PANC 657 PT1 2445008 489288 0.706 3.172 -0.288 1.522
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PANC 658 PT1 2669657 557557 -3.089 4.848 2.160 2.736
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PANC 660 PT1 4241187 823685 -7.034 11.000 -3.899 1.249
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PANC 661 PT1 4257715 924137 0.117 2.065 -1.263 -0.205
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-0.552 0.910 1.689 1.794 -4.536 0.356 2.768
PANC 662 PT1 3192643 691338 1.957 2.032 -11.000 -11.000
1.267 0.803 8.014 -11.000 1.557 2.408 -0.252 0.855
-0.151 -3.140 0.041 -3.361 -11.000 -0.023 -0.639
PANC 664 PT1 456525 101210 -0.471 1.471 -3.049 -2.617
0.352 -0.466 1.744 -1.270 -1.138 0.866 -0.953 -3.010
-0.575 -0.569 -0.291 -1.192 -2.458 -1.144 -0.221
PANC 665 PT1 1284490 250453 -3.914 2.298 -2.905 0.404
0.553 -0.385 4.519 1.226 1.418 1.178 -1.499 -0.816
-1.524 -2.499 -0.825 -0.290 -3.723 -0.611 -1.841
PANC 666 PT1 1097018 338947 -1.331 0.544 0.238 0.594
-0.580 -0.258 1.998 -0.521 2.167 0.376 0.220 -1.126
-1.283 -1.638 -1.949 -0.785 -2.010 -0.486 -1.551
PANC 667 PT1 1489658 483714 -5.191 3.035 1.794 3.583
1.910 1.622 2.676 -11.000 2.987 2.581 2.872 0.220
0.124 -3.349 0.137 0.643 -11.000 0.509 -0.062
PANC 668 PT1 2191039 455699 -0.230 4.827 -1.517 -1.001
1.117 -1.325 2.083 0.404 2.649 1.994 -2.660 -0.602
-2.247 -1.493 -2.258 0.507 -4.338 1.290 11.000
PANC 681 3233109 1044823 0.425 1.833 -2.533 0.569
1.043 3.815 -1.872 -0.469 0.149 0.605 0.723 -0.028
0.749 3.792 -1.411 2.246 -0.401 1.402 -0.240
PANC 682 3335979 970396 -7.034 6.750 -1.129 11.000
-11.000 2.108 -5.045 0.422 3.728 6.804 5.568 -4.145
4.561 7.617 -3.838 4.187 -11.000 0.295 0.251
PANC 683 2327800 755596 1.359 0.506 0.319 1.413
1.184 1.367 -0.457 1.794 0.709 0.457 2.045 -11.000

Table35.txt

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0.167     2.083     -5.569    6.806     -6.366    0.802     -1.470
PANC 684       4476915        1278427       0.904     0.934     0.420     2.738
0.324     2.153     2.199     6.749     1.470     3.304     0.680     -11.000
0.078     2.477     -11.000   11.000    -6.839    -2.169    -0.854
PANC 685       3282007        925613        1.273     2.352     2.515     1.517
1.764     2.987     -11.000   4.928     1.147     3.326     -2.650    4.935
0.366     2.838     -11.000   -11.000   -5.592    1.146     0.432
PANC 686       2719024        904903        -6.780    5.841     3.340     4.986
-3.435    -0.469    0.374     5.527     -1.268    3.188     1.052     2.542
3.611     3.507     -11.000   11.000    -11.000   -5.663    -2.423
PANC 687       2342145        808562        -0.471    0.491     0.197     1.845
-5.223    3.742     -0.142    5.334     0.426     1.711     3.244     -3.388
0.272     3.961     -4.237    11.000    -2.048    0.380     -4.241
PANC 688       2647326        830983        -2.952    11.000    1.394     7.696
-11.000   11.000    -2.144    -2.595    3.362     11.000    -11.000   -11.000
4.875     -2.894    -2.138    2.344     -11.000   -11.000   2.853
PANC 689       3774580        1206429       -4.671    6.180     -0.471    0.234
-2.010    6.633     -1.030    -1.018    -0.831    -0.206    -3.433    -6.010
4.473     6.175     2.013     5.735     -3.113    0.518     -5.308
PANC 690       2988708        832290        2.075     3.350     2.525     2.957
2.726     3.336     2.740     5.721     2.765     3.650     -5.432    -11.000
2.523     4.241     -2.990    4.878     -6.880    1.766     0.037
PANC 691       2991571        825369        1.971     3.703     0.082     2.744
-5.186    -2.796    -0.030    2.829     4.288     -5.330    -1.027    0.155
3.574     6.231     -1.395    2.238     -2.388    -3.647    0.191
PANC 692       1342787        386629        -11.000   11.000    -1.827    -0.059
-11.000   3.197     0.482     -2.605    -6.204    0.674     1.431     5.076
3.376     -11.000   -4.842    11.000    -3.370    -3.743    -4.335
PANC 693       3232330        980880        1.185     0.725     1.682     1.068
2.069     2.628     -0.179    2.628     1.152     11.000    2.969     3.613
0.846     1.267     -0.215    3.024     -11.000   -11.000   1.175

PANC 694       2880814        777909        -1.936    4.094     0.150     11.000
-6.937    3.879     -0.133    -1.349    1.740     5.254     -1.505    -0.655
5.163     4.949     -11.000   3.463     -3.980    -1.924    -2.897
PANC 695       3033319        984920        -4.622    -4.915    -0.032    2.643
3.545     7.122     -5.780    -11.000   11.000    -11.000   2.707     4.070
0.263     11.000    -2.090    7.242     -11.000   4.021     -0.855
PANC 696       3340633        992687        -2.293    11.000    -2.622    -3.545
-2.787    -2.299    -2.744    -1.906    2.612     7.941     -2.947    -0.493
3.903     -2.703    -2.323    6.294     -11.000   3.788     -1.731
PANC 697       8032581        2585217       -5.875    -4.889    7.520     6.832
3.868     -0.156    5.850     3.115     -1.179    -2.709    -11.000   -11.000
11.000    6.052     -5.153    11.000    -11.000   -11.000   3.599
PANC 698       3431197        988712        -5.395    2.557     0.137     1.912
-11.000   2.698     0.381     2.836     1.285     1.109     2.467     2.970
1.020     2.363     -0.204    4.110     -11.000   -11.000   0.018
PANC 699       2938251        816781        -1.143    6.565     2.227     3.988
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Table35.txt

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PANC 700	3182669	970884	1.782	4.233	-0.986	3.965	
-3.858	-2.329	1.401	4.660	0.314	-0.565	0.175	1.444
1.219	3.167	0.360	5.482	-2.518	-1.873	-5.767	
PANC 701	2915570	852067	-1.925	2.159	-2.737	0.360	
-3.806	0.862	-0.869	3.087	-0.248	0.382	-1.046	1.085
1.551	2.693	0.312	1.873	-1.087	-2.783	-1.583	
PANC 702	3265485	1043106	-0.811	0.958	-0.139	1.314	
-0.457	-1.251	0.360	3.691	0.666	2.016	0.932	0.594
0.382	2.425	-1.950	-0.071	0.219	-0.644	-1.621	
PANC 703	2736411	831883	1.077	11.000	-3.820	-4.235	
-0.464	2.259	-1.272	2.520	-0.283	1.385	5.413	11.000
-0.274	-0.044	-0.345	6.891	-4.525	-0.573	-1.430	
PANC 704	4574895	1306931	7.344	7.487	-1.001	0.206	
0.033	0.725	-1.342	1.825	0.099	0.569	0.949	1.902
0.865	1.047	-0.028	2.973	-1.129	0.720	-11.000	
PANC 705	4458892	1430466	1.882	11.000	0.418	1.040	
1.908	6.552	-5.838	-11.000	2.945	5.289	3.622	1.537
5.321	4.974	-11.000	-3.897	0.820	5.883	-1.953	
PANC 706	2983788	925418	-11.000	0.867	-0.305	2.431	
-11.000	1.200	0.232	2.741	0.141	2.748	1.114	2.724
1.864	1.232	-3.123	7.556	-7.034	0.661	-1.080	
PANC 707	2910635	792496	0.822	1.902	1.493	2.483	
0.958	1.437	0.214	1.031	1.516	2.828	1.669	2.471
1.300	-4.645	-0.611	2.138	-1.164	-0.187	-0.918	
PANC 708	2784740	1046321	3.091	5.447	2.842	3.103	
-1.591	4.690	-0.809	2.523	-1.824	0.249	-4.358	-11.000
2.106	4.661	-3.214	11.000	-2.599	-3.684	2.733	
PANC 709	3726954	1072481	-11.000	8.077	7.443	11.000	
-11.000	6.752	3.255	-11.000	1.858	5.397	-6.464	-11.000
5.773	7.479	-4.230	8.041	-11.000	-11.000	3.705	
PANC 710	2556386	754235	0.159	-3.357	5.166	1.795	
-0.326	8.126	-0.123	-4.683	11.000	1.625	0.762	3.216
2.613	-3.358	-4.766	7.610	-3.135	-0.504	-5.365	
PANC 712	2726482	881194	-11.000	2.424	-0.793	0.727	
0.008	0.795	-4.513	2.089	2.301	2.285	0.182	2.833
-0.392	4.122	-2.677	3.227	1.105	0.747	-0.801	
PANC 713	3328758	978780	-5.161	8.210	0.280	1.712	
0.544	2.784	-4.700	-5.571	0.153	2.158	1.298	-5.174
1.680	0.962	0.058	3.446	1.917	1.852	-0.338	
PANC 714	4745878	1500803	-0.382	7.003	-11.000	6.252	
-11.000	7.941	2.451	4.039	5.783	5.057	0.526	-11.000
0.634	11.000	-5.754	6.943	-5.762	1.469	2.104	
PANC 715	2600623	1004683	-0.671	-0.027	0.945	1.068	
-0.462	0.352	-0.449	1.319	-1.005	0.959	2.192	2.229
-4.274	-0.149	-1.704	1.948	0.640	0.289	0.703	
PANC 716	2025075	776796	0.586	1.478	0.391	0.030	

Table35.txt

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-0.183	1.920	-0.946	2.038	1.699	0.661	-0.240	
PANC 717	2245879	921045	-11.000	5.892	0.919	1.280	
-6.189	3.631	-6.153	5.000	-6.880	-11.000	2.470	1.842
2.907	0.898	-5.230	11.000	-2.272	1.306	1.330	
PANC 718	4670888	1603115	3.239	11.000	2.445	2.663	
-11.000	3.298	1.375	3.843	1.607	4.654	-11.000	-11.000
2.360	2.930	-6.544	4.505	-11.000	2.390	-6.739	
PANC 719	4887478	1738972	-0.854	-0.502	3.692	5.528	
-2.610	-0.350	0.792	3.206	-3.545	-3.125	-3.923	-11.000
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PANC 720	3487131	1162610	-2.920	-2.902	-1.917	7.096	
4.936	7.108	-2.634	-4.008	11.000	-11.000	-3.747	-6.668
4.604	7.069	3.673	4.074	-11.000	-11.000	1.873	
PANC 721	4635041	1423205	0.352	2.161	2.589	4.369	
-3.911	11.000	-0.572	1.432	0.071	4.991	-0.459	-6.525
1.948	3.802	-6.504	2.866	-5.812	1.430	-0.789	
PANC 722	3771047	1307167	1.566	11.000	1.268	3.060	
-3.053	2.134	1.273	4.317	0.787	4.975	1.859	-11.000
1.570	2.877	0.308	4.324	-11.000	-0.129	1.840	
PANC 723	2525965	956114	-1.119	6.072	0.781	5.476	
-11.000	2.997	-1.536	0.996	-0.138	2.082	-5.095	-11.000
11.000	4.238	1.409	1.698	-6.366	-5.807	-5.796	
PANC 724	3410581	1107773	-0.480	3.095	4.900	4.886	
1.460	4.298	-2.750	-0.286	-1.053	-2.794	-1.849	-0.015
2.435	3.168	0.327	3.511	1.659	3.468	-4.434	
PANC 725	2637552	1022288	0.285	0.800	0.523	0.170	
0.772	2.101	1.611	-2.216	-0.488	1.818	-6.637	-6.807
1.385	2.781	0.007	11.000	0.535	1.516	-0.034	
PANC 726	2194673	702648	-1.040	-0.208	-1.639	-0.520	
-1.894	-0.535	-3.284	-0.164	-0.883	1.618	2.683	2.435
4.731	7.721	-1.141	1.543	-0.451	0.582	1.626	
PANC 727	3833261	1298933	0.096	1.852	-0.357	-2.081	
-0.643	-1.748	0.233	-0.608	-0.733	-0.873	1.457	1.154
-0.823	0.127	-0.241	1.532	-0.022	2.050	-0.682	
PANC 728	3761518	1170474	-11.000	11.000	1.074	5.900	
0.873	2.837	-11.000	-11.000	-0.176	2.789	2.055	3.295
1.626	1.611	-11.000	2.790	-11.000	-2.307	1.041	
PANC 728	3514629	978537	-11.000	11.000	1.177	2.395	
0.521	2.647	-11.000	-11.000	0.337	2.702	2.641	2.486
1.236	1.369	-11.000	1.457	-6.758	0.976	0.897	
PANC 729	843281	302797	-0.864	-0.202	-1.410	-0.601	
0.578	0.265	-2.880	0.501	-0.882	1.316	1.954	1.730
1.346	-1.090	-0.388	2.421	-0.940	0.560	1.310	
PANC 730	3618249	1281027	2.058	11.000	0.064	-0.852	
-2.701	7.221	-1.368	-3.235	-2.286	-0.268	1.394	0.049
3.591	-0.306	0.516	0.386	-3.496	-0.670	0.383	
PANC 731	2555772	958284	3.823	3.183	1.682	3.810	

Table35.txt

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-0.876	-2.570	6.983	11.000	-6.780	3.038	2.024	
PANC 732	4240407	1308868	1.735	5.030	5.366	6.830	
-11.000	6.353	3.637	5.941	-11.000	-2.243	4.355	-11.000
4.276	0.084	-11.000	-0.024	-6.780	4.792	-5.704	
PANC 733	3288398	1144583	-3.225	-3.122	6.230	11.000	
-4.145	-2.371	3.212	6.425	-1.733	-4.689	-0.151	-4.739
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PANC 734	3367269	1083522	-3.473	3.089	-3.456	-4.682	
-11.000	7.582	-4.613	-11.000	11.000	-11.000	-0.362	2.946
4.750	5.696	-5.743	11.000	3.509	5.352	3.984	
PANC 735	3360614	1085088	0.995	11.000	-0.390	0.717	
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PANC 736	2807258	910717	0.486	11.000	-1.238	0.227	
-2.294	0.109	-1.449	-0.324	-3.170	0.400	-4.106	0.470
0.091	0.293	-1.937	11.000	0.283	-0.188	11.000	
PANC 737	3552099	1068459	-2.690	4.576	-1.453	11.000	
1.633	3.432	-11.000	-11.000	0.640	3.220	-4.946	3.908
5.226	4.307	-11.000	11.000	-4.887	1.339	-2.683	
PANC 738	3214123	995213	1.315	1.692	1.618	1.566	
1.087	3.193	0.824	3.271	-0.057	1.990	1.501	-11.000
1.281	2.443	0.162	2.203	0.739	-0.353	-0.035	
PANC 739	2738851	978068	1.254	7.956	-3.112	1.628	
-0.661	2.164	-2.462	-0.431	-1.176	0.168	2.439	-1.910
0.651	-0.130	-0.103	1.100	-5.692	0.580	0.070	
PANC 757	787091	339046	1.353	0.700	-1.602	7.660	
-1.407	0.172	-0.141	3.656	0.459	4.181	0.790	-2.930
1.787	5.159	-4.513	1.359	-3.423	-2.823	-4.182	
PANC 759	1164443	515258	-1.185	-1.022	-4.681	6.201	
-6.260	6.089	-0.499	1.814	-0.295	-1.522	-4.988	-0.681
1.374	5.086	-1.949	3.447	-3.754	-5.283	-5.994	
PANC 760	806908	315292	-1.480	2.869	0.120	1.771	
-3.021	2.934	1.741	4.726	-0.600	1.923	-2.697	-3.034
-0.495	-2.486	-0.356	2.427	-2.841	2.005	-0.216	
PANC 761	964936	359047	-6.219	5.074	-3.994	4.505	
-1.401	3.436	2.572	4.031	1.492	2.618	-0.968	-11.000
0.361	2.101	-4.056	5.017	-3.847	1.210	0.154	
PANC 762	749737	318499	-2.331	5.729	2.295	3.538	
-2.582	-1.838	-2.354	-1.132	-2.413	2.749	-2.798	0.167
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PANC 763	2079400	917889	-0.450	-0.466	-0.063	11.000	
-3.004	0.184	-11.000	-6.554	-0.954	-11.000	-0.087	0.886
3.586	11.000	-0.486	-0.407	-5.935	-4.044	-11.000	
PANC 764	1144363	530868	-0.024	0.425	0.130	0.622	
0.633	2.366	0.161	1.118	0.705	2.808	-0.464	0.729
-1.749	-0.593	-1.255	1.219	-0.498	1.383	-1.518	
PANC 765	1334231	553071	3.715	11.000	-1.854	-3.049	

Table35.txt

-1.372 6.751 -2.011 -2.105 0.248 1.301 -4.128 -5.494
-2.621 -1.916 0.751 7.537 -1.949 -1.774 -5.323
PANC 766 1221566 589692 1.631 1.944 -0.002 -0.501
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-1.579 -0.198 -1.952 0.136 0.752 1.322 -1.998
PANC 767 547367 248546 0.313 0.786 -0.765 1.443
-1.327 -0.478 -0.416 2.457 0.857 0.267 -1.977 0.546
2.490 1.376 -3.222 1.304 -1.763 -0.875 -0.544
PANC 768 838689 361399 -0.142 7.235 -2.325 0.728
-1.323 0.981 -1.379 1.370 -1.340 -0.117 -0.429 0.823
3.844 8.126 -1.783 1.131 0.272 0.953 -2.058
PANC 769 1212791 533022 -1.581 -1.466 -2.016 -1.657
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7.679 11.000 -1.902 0.427 -4.782 -0.417 -2.431
PANCA 1103 2644830 963627 -1.004 0.639 2.019 3.349
-5.449 2.581 -1.180 -1.855 0.800 3.614 -1.108 -3.918
1.144 0.946 0.922 2.396 -0.359 -0.232 -1.681
PANCA 1104 3866896 1391426 -6.807 6.294 0.483 1.673
-11.000 -1.524 0.678 2.060 -0.109 3.128 0.707 -1.135
1.496 1.917 0.302 11.000 -5.382 -0.711 -0.865
PANCA 1105 1293295 391631 0.570 -0.006 -2.523 1.174
-2.304 3.296 -0.338 0.544 4.629 -1.541 -1.704 2.293
0.542 2.059 -2.378 1.833 0.162 -0.584 -1.273
PANCA 1106 1531734 550983 -0.320 11.000 0.863 1.428
-11.000 0.604 -0.512 1.323 -1.112 2.945 -0.215 -0.222
-0.200 0.153 -1.354 0.023 -0.102 0.761 -1.184
PANCA 1107 1463000 517331 -1.082 0.841 -1.691 0.152
-0.631 2.081 -0.155 -0.696 0.200 1.118 -1.293 -0.779
0.877 2.644 -1.889 0.614 0.044 -1.775 -1.167
PANCA 1108 2744958 1063985 0.719 0.919 0.812 1.146
-4.042 3.115 -0.635 -1.084 1.400 3.347 -1.888 1.134
2.138 2.661 -2.163 2.423 -3.477 0.652 -3.569
PANCA 1109 470728 149369 1.606 1.940 0.875 0.851
-1.005 -1.615 1.128 0.523 1.517 2.135 0.491 -1.615
-0.751 0.026 0.181 0.828 1.002 1.737 -1.689
PANCA 1110 2233039 787028 -4.944 3.420 -4.490 2.062
0.931 2.711 1.780 6.492 -3.519 -0.538 0.966 6.222
1.359 3.123 -6.937 3.806 -6.807 1.338 0.348
PANCA 1111 1819478 639540 0.953 11.000 1.461 3.040
-2.095 3.369 -2.745 -4.894 0.597 -0.538 0.137 -5.791
0.564 1.248 -1.403 2.965 -4.493 2.031 -1.185
PANCA 1112 1031556 413449 -1.995 7.341 0.245 1.395
-2.036 6.653 -6.839 6.364 1.224 2.868 -3.276 -0.934
5.463 0.009 -6.053 4.844 -5.825 1.145 -0.474
PANCA 1114 444493 166117 -2.085 3.780 -3.934 0.462
-1.453 -0.306 0.667 11.000 -1.398 -2.184 -2.460 -1.694
0.285 1.761 -0.005 7.414 -2.329 -0.913 -1.300
PANCA 1115 537528 199474 2.454 4.326 0.498 -0.088

Table35.txt

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0.351     7.152     -0.256    -0.327    1.911     3.178     -2.428    -0.084
1.987     -0.147    -0.276    2.601     -1.277    -1.539    -0.926
PANCA 1116     456921        149099       2.353     2.089     -1.132    1.140
-0.615    -0.937    1.471     1.911     1.032     2.320     -0.172    -0.624
2.347     2.827     0.375     2.720     -1.228    2.250     -1.445
PANCA 1117     1574933       561151       -5.923    2.517     1.481     3.530
1.353     3.608     0.437     2.240     1.791     3.346     -2.267    -1.325
-3.197    -11.000   0.249     3.774     -3.508    -5.947    0.143
PANCA 1118     2503087       929869       -1.541    -0.137    1.605     4.971
0.511     11.000    -0.807    -0.251    -0.358    0.418     -2.315    -0.458
0.918     -1.462    1.210     4.293     1.130     3.213     -5.492
PANCA 1119     834568        183781       -1.069    1.969     1.601     0.842
-1.337    -1.461    0.791     0.343     0.210     1.055     -1.889    -1.030
1.545     1.521     -0.728    5.899     -1.069    2.455     -3.178
PANCA 1120     6774538       2214694      -5.487    11.000    1.921     11.000
-2.634    1.457     1.006     5.293     0.472     -2.888    -1.249    3.502
4.663     6.001     -2.457    7.836     -2.237    -4.811    -3.934
PANCA 1121     2543639       957389       1.117     3.114     -11.000   5.687
0.205     2.431     0.223     1.822     0.125     -4.108    0.328     2.519
0.758     1.968     0.023     2.319     -0.641    2.189     -0.376
PANCA 1122     2636515       898659       1.012     0.731     0.577     2.312
1.198     2.548     -11.000   -11.000   -0.249    2.438     -5.579    -2.510
4.561     5.714     -3.068    3.863     1.573     0.635     0.112
PANCA 1123     978590        390123       0.356     6.048     0.035     1.230
-1.506    0.271     -1.698    0.067     -0.830    1.027     -2.569    -5.553
2.798     5.525     -0.652    0.849     3.532     0.560     -0.690
PANCA 1124     3349163       1317484      1.729     1.707     1.781     2.268
-6.679    3.215     1.411     4.266     1.893     4.058     -3.211    -11.000
0.733     2.088     -0.305    2.642     -3.315    0.254     -0.818
PANCA 1125     875830        300296       1.658     0.362     -1.234    0.340
0.039     1.005     0.373     2.271     -0.007    0.455     -1.056    -2.934
3.252     4.537     -3.316    -1.127    -0.076    1.336     -1.909
PANCA 1126     2563666       847095       -6.476    11.000    0.472     0.464
-11.000   -11.000   4.256     -6.336    -0.214    2.102     -2.760    -0.813
11.000    1.354     -5.364    11.000    -5.133    -4.726    3.259
PANCA 1127     5471603       1759697      0.326     3.670     1.572     3.826
1.181     3.758     -3.161    -2.799    1.314     2.624     -0.637    -11.000
1.842     2.018     -5.122    11.000    -6.325    0.759     -0.424
PANCA 1128     455373        156096       1.992     1.028     -0.849    -1.206
-0.179    0.803     -0.627    0.614     -0.265    0.816     0.726     1.001
1.944     0.000     -2.051    2.507     -1.202    2.156     -0.755
PANCA 1129     3277488       1101402      -1.847    3.443     1.009     0.546
-3.558    2.088     0.410     0.765     -0.427    4.871     1.494     1.268
-0.845    0.515     -4.106    1.722     -0.170    0.901     -0.837
PANCA 1130     2325404       930864       0.732     1.172     0.480     1.897
0.471     1.901     -1.071    0.743     -0.687    1.885     -2.404    3.080
0.297     1.816     -1.655    1.007     -0.548    2.105     -1.370
PANCA 1135     1467514       497649       -3.894    3.558     2.163     4.772
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Table35.txt

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PANCA 1149 PT1 414327 164629 1.573 5.862 -3.502 -1.264
-1.574 -2.506 0.493 -1.314 0.824 -0.730 -0.431 -0.135
-0.009 0.217 2.129 0.641 -6.016 -1.468 6.883
PANCA 1151 PT1 1981853 827855 1.258 6.754 11.000 1.569
0.981 1.627 1.496 0.814 -0.408 0.614 -1.333 1.948
0.927 -2.380 0.561 -0.536 -11.000 1.527 3.249
PANCA 1152 PT1 1168509 423743 1.200 11.000 0.862 0.761
-0.655 1.017 1.817 -11.000 1.511 0.317 -3.601 3.731
-1.172 -1.407 0.881 6.185 -6.647 -0.528 1.031
PANCA 1153 PT1 788690 342044 -3.748 3.278 -1.980 0.399
0.681 -1.075 0.731 -1.592 1.872 0.683 -1.487 -0.589
-1.625 -0.075 -2.420 -0.352 -5.056 -0.940 -2.016
PANCA 1155 PT1 722570 324694 2.804 2.241 0.295 -1.866
2.088 2.645 2.270 -3.625 2.080 0.454 -11.000 1.560
0.261 -3.856 0.752 0.798 -11.000 0.993 1.537
PANCA 1163 PT1 890476 163397 -0.310 0.708 -6.168 11.000
-1.688 -1.963 11.000 -0.359 0.528 1.111 -1.289 -1.936
-0.261 -1.764 1.462 -4.009 -6.668 -0.979 -1.034
PANCA 1164 PT1 7076282 1383722 0.057 6.142 0.192 2.167
-0.460 0.309 3.200 -2.629 1.900 3.305 -4.012 1.909
1.835 -0.138 3.274 0.494 -11.000 2.232 11.000
PANCA 1165 PT1 927683 169937 -5.104 3.899 -1.090 3.072
0.150 1.109 3.400 3.758 4.319 -2.877 1.480 2.818
0.958 -3.357 -0.806 -1.811 -4.078 -2.649 -2.113
PANCA 1166 PT1 576268 106898 -4.302 7.768 -0.921 2.310
1.022 0.253 -1.110 0.472 3.030 1.529 1.445 0.221
-0.746 -2.927 -0.962 -0.012 -4.963 -0.707 -1.231
PANCA 1167 PT1 922574 190928 -2.328 -2.945 0.602 -3.667
1.594 4.323 -1.607 1.517 3.638 0.235 2.244 -0.308
-1.206 -3.746 4.216 6.857 -6.839 0.768 0.995
PANCA 1168 PT1 6596656 1500081 -11.000 11.000 0.425 2.828
-4.607 -4.681 3.315 1.239 3.074 2.498 -2.842 1.911
-0.208 2.677 3.540 -3.478 -11.000 0.483 0.310
PANCA 1169 PT1 5911662 1345166 -2.203 11.000 -4.495 -1.126
-1.835 -0.933 11.000 -1.187 -1.233 -6.534 -2.009 -1.017
-1.964 -1.013 1.852 0.947 -11.000 -1.658 11.000
PANCA 1170 PT1 590327 126225 -0.669 0.664 0.591 0.683
-0.075 -1.954 2.962 0.817 0.583 0.448 0.431 -1.108
-0.476 -0.176 0.173 0.353 -2.671 -0.845 -1.109
PANCA 1172 PT1 3955042 1066427 -0.008 11.000 2.089 -3.597
-1.872 0.089 1.778 -5.602 -2.895 -4.513 -1.824 1.461
-0.910 1.512 0.553 2.741 -6.807 -0.747 3.162
PANCA 1173 PT1 2616471 607723 -1.453 7.560 -1.433 -2.069
4.428 -5.214 4.793 -0.141 7.113 3.879 -0.564 0.801
0.422 -2.131 -0.645 6.265 -11.000 -0.652 11.000
PANCA 1175 PT1 9062585 2048926 1.185 2.340 0.154 2.302

Table35.txt

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1.816 -2.851 -1.514 0.848 -11.000 0.831 1.047
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0.114 0.086 3.343 1.336 1.714 -0.980 1.228 1.447
-0.471 -2.278 0.269 0.286 -11.000 -0.751 -0.852
PANCA 1177 PT1 6087736 1158277 -11.000 2.662 0.061 2.724
-0.166 0.991 2.909 2.430 1.695 2.430 1.755 2.246
-0.311 -2.736 7.836 -3.668 -11.000 1.611 2.027
PANCA 1178 PT1 9738825 2148423 -0.136 2.374 0.019 2.195
-1.116 1.089 3.134 0.497 0.402 2.042 2.499 3.373
0.704 2.296 0.500 -0.070 -4.616 3.452 3.441
PANCA 1179 PT1 2537061 788044 1.087 11.000 0.365 0.752
-2.513 -0.140 0.700 -0.739 0.514 0.415 1.222 2.648
-0.900 2.436 0.568 0.838 -1.811 2.249 3.337
PANCA 1181 PT1 3756610 971015 2.552 2.001 0.245 2.219
-1.348 1.624 0.386 -6.657 -11.000 2.405 1.734 1.236
-0.031 0.666 0.986 4.747 0.821 1.010 11.000
PANCA 1184 PT1 7064495 1485821 1.243 2.663 0.019 2.561
-4.299 -1.835 0.829 -2.043 3.865 5.287 -1.878 4.043
2.533 0.405 1.520 -0.350 -4.912 0.735 4.830
PANCA 1185 PT1 1295583 225187 1.085 1.707 0.026 2.709
-3.386 1.210 1.871 0.942 3.400 1.810 1.053 -0.020
-1.128 -1.873 -2.323 -2.911 -4.818 -2.005 -0.817
PANCA 1186 PT1 5475017 1484401 -0.689 0.379 -0.833 0.752
-2.296 -0.660 0.525 -0.735 -0.201 0.690 -1.930 0.170
-1.229 0.742 -1.154 1.071 -1.080 0.806 0.989
PANCA 1188 PT1 6076139 1284480 -5.173 1.493 0.570 2.963
0.039 -11.000 4.698 1.957 0.510 -0.387 2.849 1.655
0.237 -3.621 2.216 -4.361 -11.000 0.927 3.705
PANCA 1189 PT1 703301 131363 -3.062 2.410 -2.531 3.449
0.300 0.965 2.648 -3.990 3.502 2.289 -1.165 -0.096
2.072 -1.879 -0.494 -0.809 -4.555 1.461 -0.459
PANCA 1191 PT1 4377618 1079686 1.658 2.705 0.152 1.941
-1.349 0.648 -1.663 -11.000 2.254 2.587 1.422 -3.732
-1.435 -1.408 -1.600 1.044 -5.163 1.141 0.527
PAP 119 PT1 646092 473312 -2.522 11.000 -2.037 -2.230
0.601 0.940 -1.041 -1.455 -2.373 -0.521 -2.410 -1.469
-0.449 0.748 -3.528 1.282 -0.437 0.489 -1.249
PAP 120 PT1 2174045 1596922 -0.331 11.000 -1.137 -0.397
-0.049 0.881 0.426 2.213 -0.889 -0.184 -1.028 -0.597
0.457 0.463 0.257 0.742 0.105 0.091 -2.053
PAP 121 PT1 2350934 1618060 -0.380 -0.397 1.717 0.941
-0.682 -0.965 6.292 7.928 -1.287 -0.537 0.012 -0.626
0.357 1.078 -1.168 0.642 -0.264 -0.334 -0.309
PAP 122 PT1 2250031 1706745 -0.235 -0.089 0.111 -0.800
0.685 1.074 0.200 -0.845 -1.409 0.727 0.025 0.648
0.496 0.697 0.629 0.093 -0.110 0.401 0.409
PAP 123 PT1 3139530 2375253 -1.916 -2.045 11.000 11.000

Table35.txt

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PAP 124 PT1    1297652       945567       -0.188    11.000    -1.665    -0.834
-1.772    0.205     -0.368    -0.080    -1.387    0.543     0.256     -3.014
0.169     -0.377    -1.343    0.714     -0.481    -0.152    -0.593
PAP 125 PT1    1757619       1308110      -0.423    -0.250    11.000    11.000
0.764     0.300     0.031     -0.128    -1.577    -1.871    -1.108    -1.971
-0.095    -1.296    -0.719    -0.984    -0.472    -2.004    -0.999
PAP 126 PT1    1248193       939294       -4.434    11.000    11.000    11.000
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-1.881    -1.254    -2.553    -1.101    -4.102    -1.749    -1.806
PAP 127 PT1    2209023       1518222      0.319     11.000    0.348     1.715
-0.924    -0.212    1.333     -1.353    -3.223    0.209     -0.839    0.197
-1.884    0.778     0.910     -0.458    -1.400    1.956     -0.727
PAP 128 PT1    2596324       1779126      0.507     1.568     0.383     0.447
-0.030    -0.272    -0.297    -0.932    -1.716    1.560     0.742     -0.728
0.297     0.553     -0.394    1.199     -0.576    1.342     1.506
PAP 129 PT1    1431005       1010818      -0.098    -0.287    2.230     0.488
0.054     0.807     -0.533    0.102     -0.776    0.374     -1.604    0.044
-1.477    0.113     -0.098    -0.217    -0.526    1.188     -0.045
PAP 130 PT1    2087985       1344357      0.482     0.284     1.580     1.537
-0.483    -0.228    2.156     -1.242    -1.862    1.656     0.482     -0.704
0.604     -0.850    -0.503    0.551     -1.486    1.123     -0.317
PAP 131 PT1    1395848       1079212      1.453     0.657     -1.145    -0.767
-0.276    0.945     1.270     0.498     -0.684    1.559     0.062     0.100
-0.583    0.662     -0.781    0.693     -1.061    -0.011    0.533
PAP 132 PT1    2314957       1592566      0.818     1.506     1.420     0.447
-0.003    -1.536    0.233     -1.015    -1.423    0.260     0.820     0.776
-0.309    2.354     0.614     0.525     -0.793    1.112     1.637
PAP 168 PT1    1856598       1193184      1.964     2.316     -11.000   1.394
-4.061    11.000    -5.483    2.707     -11.000   2.360     2.380     1.532
2.141     -3.078    -11.000   -6.807    -11.000   -0.172    -3.161
PAP 169 PT1    2277891       1632885      0.408     0.886     -0.644    -2.650
0.420     -0.229    2.536     1.385     -0.673    0.412     -0.493    -1.280
-0.919    -11.000   1.108     -0.580    0.234     -1.451    -1.094
PAP 170 PT1    2258971       1441823      -0.899    3.310     -2.815    -2.092
-11.000   -11.000   6.803     7.037     -11.000   -3.220    7.355     -1.455
-2.670    -0.770    -2.052    -0.904    -2.947    -0.135    -0.486
PAP 172 PT1    1171450       876704       4.913     -0.557    -1.442    2.478
0.010     3.886     1.960     3.173     -2.026    -0.883    -3.211    -0.690
-11.000   -1.165    3.881     11.000    11.000    1.627     -2.231
PAP 173 PT1    1854526       1345719      -0.313    -0.029    0.958     0.150
-2.160    0.073     2.435     0.245     -11.000   0.321     0.520     -1.304
-1.464    -2.022    6.197     0.420     -1.434    1.275     1.798
PAP 174 PT1    5710957       3327133      -0.287    0.489     0.387     2.106
-1.355    0.220     1.838     -1.959    -1.873    -0.093    0.632     -3.275
-2.043    1.039     -1.212    -0.875    -2.359    1.164     -0.328
PAP 175 PT1    1929377       1423378      -1.271    -1.556    -0.072    -0.567
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Table35.txt

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-1.519 -0.052 2.938 -1.552 -0.502 0.100 1.426 0.572
-0.013 2.119 1.173 1.232 -1.589 3.379 2.066
PAP 177 PT1 2120742 1400319 0.822 -0.873 -0.476 -0.282
-0.723 -0.604 1.045 -1.205 -1.754 -2.050 1.049 -0.888
0.036 1.859 -0.829 -0.250 -1.612 0.661 1.101
PAP 178 PT1 4358944 3040821 -1.011 -0.732 6.172 11.000
-0.363 0.854 2.025 -2.739 -0.649 -0.596 -0.582 0.262
-0.240 0.305 -1.841 0.062 -1.641 2.080 1.494
PAP 179 PT1 1864784 1310529 -0.609 11.000 4.151 0.083
-6.544 -11.000 11.000 2.749 -5.057 -4.355 -4.696 -3.016
-1.480 -0.346 4.647 -1.177 -6.807 2.150 11.000
PAP 180 PT1 2561582 1791449 2.218 0.908 -0.752 1.046
-0.724 1.133 1.541 -0.973 -1.189 0.349 1.974 0.130
0.782 1.730 -0.086 1.365 -0.245 1.906 2.669
PAP 181 PT1 1910404 1344554 -1.658 -1.864 -1.916 -1.521
7.196 -2.501 -1.373 -3.961 4.648 -11.000 -2.593 2.653
-2.397 -3.210 2.040 4.525 6.155 -0.164 11.000
PAP 182 PT1 2046987 1482256 -0.102 2.772 1.947 2.018
1.147 6.753 -11.000 -11.000 -11.000 1.281 3.292 2.668
1.750 -5.352 -11.000 1.602 0.333 1.062 -1.657
PAP 183 PT1 2137068 1558456 -3.621 -0.071 -1.734 -6.937
-6.807 2.112 11.000 5.760 5.540 2.701 -2.704 -4.598
-6.647 -3.764 1.907 3.256 -0.669 1.719 2.628
PAP 184 PT1 470125 345880 -2.461 11.000 5.959 11.000
-3.254 -2.924 -2.178 -4.693 -4.457 11.000 -2.205 -3.044
-3.274 -0.797 -2.089 -2.381 -3.013 -0.726 -1.478
PAP 185 PT1 2958039 2176083 3.696 11.000 -5.315 -1.506
0.104 -0.606 4.939 3.211 11.000 -11.000 1.535 2.174
-11.000 -4.880 -3.869 -3.516 -4.954 0.583 -5.135
PAP 186 PT1 3217035 2389694 -11.000 11.000 5.110 4.801
0.669 1.202 1.517 -4.650 -11.000 2.404 2.448 -1.310
1.730 -5.043 -11.000 1.547 -6.647 1.016 1.687
PAP 187 PT1 1748386 1199600 2.029 1.394 0.466 1.878
0.712 0.502 11.000 0.211 0.253 -11.000 1.972 -2.193
-11.000 -11.000 7.351 1.982 0.167 0.047 0.743
PAP 190 PT1 2119266 1592823 -3.219 11.000 0.455 2.811
-2.538 -2.854 11.000 7.302 -11.000 -0.414 -2.463 -1.886
-11.000 3.672 5.601 5.120 2.231 -0.265 6.107
PAP 191 PT1 1458661 1060849 1.791 3.962 1.905 3.879
2.569 3.555 3.388 2.363 -0.412 3.521 2.936 2.070
2.144 2.142 0.062 1.728 1.677 -2.893 3.910
PAP 193 PT1 1908059 1352795 -2.194 0.623 -4.528 3.793
-3.323 0.623 1.202 -6.277 0.459 -1.406 -0.642 1.947
-4.887 -4.736 -4.654 1.421 -11.000 0.960 -4.776
PAP 194 PT1 1981115 1452819 5.722 -1.258 2.579 -11.000

Table35.txt

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PAP 195 PT1    932058        650206       -3.948    -5.988    -3.010    1.841
0.400     11.000    5.107     2.165     0.724     -3.205    -6.364    2.246
-4.501    0.439     -2.419    2.100     -4.314    2.190     3.370
PAP 196 PT1    2449111       1654788      -3.200    0.692     -0.646    6.624
3.673     11.000    2.423     1.096     -11.000   2.279     -1.927    0.032
-0.770    -2.239    0.360     3.806     -11.000   0.748     2.656
PAP 197 PT1    1321401       997045       0.418     11.000    -2.432    -0.114
7.742     -6.544    11.000    -2.400    2.111     1.369     1.462     -3.187
-11.000   1.602     5.257     11.000    -5.886    5.690     3.656
PAP 198 PT1    9604866       7126039      0.952     11.000    3.081     0.495
-5.719    11.000    0.584     -1.308    -5.160    -0.697    2.304     0.228
0.032     -6.374    -2.878    -0.092    -11.000   0.198     -2.132
PAP 199 PT1    1982162       1430361      4.017     -2.173    0.855     0.546
-1.539    11.000    11.000    1.054     -11.000   0.948     4.000     1.196
-11.000   -0.696    2.320     0.833     -11.000   -2.842    -2.556
PAP 200 PT1    3293107       2162487      1.116     0.333     1.875     0.571
-1.176    -0.161    2.033     -1.832    -1.856    -0.055    1.651     2.033
0.777     1.264     1.258     1.048     -1.078    1.744     1.292
PAP 201 PT1    3286413       2304998      -1.236    -2.782    11.000    11.000
-1.413    -1.078    -0.375    -2.656    -3.654    -2.579    -0.613    0.471
-0.561    0.029     -2.235    -0.671    -2.706    -0.230    -0.358
PAP 202 PT1    12806632      9060584      0.505     -0.174    0.843     0.501
0.430     0.416     1.202     0.707     -11.000   0.055     -0.895    0.630
0.043     2.038     0.195     0.791     -1.174    0.279     -0.227
PAP 203 PT1    4580961       3261861      -2.115    11.000    11.000    11.000
-1.288    -1.042    0.212     -3.117    -1.616    -2.739    -1.692    -0.347
-1.141    0.228     -0.873    -0.605    -2.463    1.012     1.738
PAP 204 PT1    9673509       7030230      -0.918    -3.510    1.945     1.391
-2.640    -1.179    1.450     -2.064    -4.368    -1.772    -1.012    -0.861
-1.384    -0.776    -0.395    1.410     -2.367    0.807     -0.613
PAP 205 PT1    2497266       1723233      1.202     -0.740    0.115     0.786
0.212     0.442     1.514     -1.659    -1.210    0.652     2.492     0.337
0.375     1.407     0.806     0.779     -1.162    1.022     2.605
PAP 206 PT1    3153836       2268334      -0.673    -1.040    0.089     -1.383
-0.958    -0.199    -1.543    -1.708    -2.585    -1.656    -0.581    -1.140
-0.783    0.236     -1.600    0.202     -2.230    1.169     0.321
PAP 207 PT1    3501775       2544800      -1.913    -1.729    11.000    11.000
-1.429    -1.019    -0.748    -2.470    -2.615    -1.555    -1.457    0.414
0.365     0.659     -2.650    0.413     -2.870    2.386     2.320
PAP 208 PT1    2226262       1626445      -0.731    -0.685    0.503     -1.605
0.919     -0.856    -1.234    0.142     -1.092    -0.465    0.022     0.708
0.108     -0.545    -0.941    -0.204    1.629     -1.746    -0.055
PAP 209 PT1    3177246       1891854      -1.710    -0.186    11.000    11.000
-3.385    -1.496    0.475     -1.849    -2.250    1.043     -1.971    -1.210
-0.228    0.035     -0.614    -1.007    -2.829    -1.505    -0.427
PAP 210 PT1    1519366       1141397      -2.312    1.572     0.475     -0.389
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Table35.txt

0.752	0.269	-1.042	1.897	-0.500	-2.133	-1.769	1.185
0.692	1.043	1.186	-0.529	-0.045	0.820	1.220	
PAP 212 PT1	1408709	1067230	1.229	-0.791	-0.332	-0.878	
0.336	1.009	-0.034	-1.300	-0.057	0.201	-0.650	-0.770
0.635	1.232	-1.426	-0.478	1.377	-1.155	1.525	
PAP 214 PT1	2578615	1874234	-1.137	11.000	-0.161	-2.125	
-0.229	0.103	1.198	0.619	-2.522	0.489	-1.737	-0.786
-0.633	0.307	-0.760	0.326	-0.203	-1.986	0.407	
PAP 215 PT1	6585115	4750258	-6.298	11.000	11.000	-1.918	
-5.474	1.490	-1.600	-5.940	-1.796	-11.000	-3.697	-1.044
-2.461	-4.221	-4.981	2.644	-11.000	1.955	5.852	
PAP 216 PT1	1337604	992393	-0.735	-0.142	-0.602	-0.137	
-0.430	-0.266	-1.097	1.775	-1.214	-0.791	-1.394	-0.712
0.016	-0.869	-0.601	0.026	1.791	-0.827	-0.140	
PAP 217 PT1	1585138	1143294	0.801	-0.116	-0.589	-1.554	
-0.488	0.569	-0.093	0.720	-1.368	0.698	-0.907	1.251
2.106	0.920	1.520	0.235	1.202	-0.978	-0.220	
PAP 218 PT1	1975096	1268368	-3.849	3.990	-3.241	6.868	
-1.075	7.015	0.154	-0.851	1.652	3.353	-11.000	0.054
-11.000	0.667	-3.294	-0.924	-3.182	-4.279	11.000	
PAP 219 PT1	11159799	8389172	-0.232	-0.136	1.830	-1.533	
0.385	1.037	-0.103	1.281	-1.077	-0.260	-0.395	0.601
0.133	0.012	0.761	-0.798	0.183	-0.508	-1.412	
PAP 221 PT1	1446432	1060370	-1.022	-2.169	0.522	-1.451	
0.760	-0.213	1.160	1.767	-1.360	2.099	-0.813	0.450
-1.601	1.138	-0.498	0.259	0.690	0.787	-0.523	
PAP 222 PT1	1498078	1073460	-1.205	1.474	-0.018	-0.116	
2.420	0.129	0.013	-0.240	-0.598	1.079	-0.077	-1.289
-1.054	0.408	-0.819	0.162	0.586	1.737	0.045	
PAP 224 PT1	1649039	1216391	-2.330	0.610	-1.106	-3.113	
0.948	1.297	0.268	0.521	1.149	-0.380	-1.698	-1.041
-1.796	-0.666	0.530	-0.283	1.834	0.351	1.150	
PAP 225 PT1	421200	320489	-1.748	1.884	0.726	-1.381	
-0.268	-1.185	0.934	0.890	-1.477	-0.277	-2.085	-1.574
0.376	0.211	-0.697	-1.746	-1.010	-1.600	-0.984	
PAP 226 PT1	1325633	981142	-0.764	1.461	2.346	-1.673	
0.562	1.149	1.071	0.092	-0.428	1.322	-0.227	-0.079
0.223	0.025	-0.097	1.096	-0.873	-1.536	1.134	
PAP 227 PT1	1638209	1210919	-2.426	11.000	0.550	-1.902	
-1.739	-2.879	3.632	6.384	3.567	-1.916	-2.140	-1.282
-1.263	-1.765	-1.396	-1.542	-0.460	-2.123	-1.877	
PAP 228 PT1	1740655	1291191	-0.600	11.000	-0.773	-0.887	
0.342	0.874	-0.323	0.648	0.559	0.133	-1.083	0.579
-0.680	0.705	0.600	0.033	0.335	-0.483	-1.096	
PAP 229 PT1	1235469	905628	-3.343	-2.158	-0.558	-3.249	
2.535	3.720	-0.125	0.727	-3.065	-1.701	-2.305	-2.092
-1.475	-1.035	1.025	-2.796	-2.898	-1.865	-0.634	
PAP 230 PT1	1550691	1144478	-1.200	-1.984	-0.243	-0.985	

Table35.txt

0.076	0.804	-1.800	-0.569	-1.107	-2.113	0.896	0.033
1.740	0.426	0.248	-1.485	-0.469	-0.134	1.585	
PAP 231 PT1	1354068		1029357	0.866	5.411	6.753	-11.000
-6.017	4.467	-0.587	-7.034	6.922	1.370	-6.559	0.678
-6.880	0.996	-3.782	-1.123	-0.845	5.087	5.466	
PAP 232 PT1	1673003		1244477	-0.226	11.000	-0.803	-2.124
0.779	1.471	-1.693	1.417	0.617	0.495	-1.303	-2.428
-0.828	-1.225	-0.560	-0.113	1.907	-0.813	-5.199	
PAP 233 PT1	1547142		1139417	-2.246	0.914	-0.536	-2.009
1.627	1.310	-0.886	0.617	-0.929	0.461	-1.140	-0.451
0.943	-0.221	0.058	0.426	-0.814	0.226	-0.557	
PAP 234 PT1	1234794		888989	-1.706	0.046	0.582	-0.114
0.234	0.065	-0.426	1.002	0.085	0.246	0.126	-0.096
0.585	1.118	-0.519	-0.038	0.099	-0.234	-0.092	
PAP 235 PT1	2742240		1695004	0.412	11.000	0.411	0.644
-0.998	-0.349	11.000	11.000	-0.330	-1.056	1.008	-0.138
-1.556	7.956	11.000	-4.689	-11.000	0.149	-0.594	
PAP 236 PT1	2664621		1631840	0.127	0.812	0.163	0.885
-2.081	-1.007	1.419	-0.814	0.782	-0.216	0.711	-2.864
-1.104	-0.259	-0.850	-1.168	-0.159	0.286	0.487	
PAP 237 PT1	3061860		1879511	-3.909	11.000	11.000	11.000
-1.810	-4.272	-3.524	-3.451	-2.864	-2.118	-3.464	-2.956
-1.936	-1.704	-1.956	-0.840	-1.444	-2.981	-2.554	
PAP 238 PT1	2973646		1838190	-0.161	1.280	-1.444	0.389
-2.887	0.404	1.055	-0.779	-0.021	-1.175	-0.697	-1.174
-1.563	0.688	0.306	0.617	-0.199	-1.145	-0.551	
PAP 239 PT1	3381649		2059706	-0.766	2.544	0.815	-11.000
-11.000	-11.000	3.374	11.000	0.262	3.522	5.066	1.238
-5.464	-5.046	-4.136	1.819	3.110	0.499	0.816	
PAP 240 PT1	4367628		2476988	5.529	7.332	5.167	-4.735
-11.000	-11.000	11.000	-2.997	-4.271	8.210	-11.000	0.441
-5.743	3.573	4.769	3.956	7.992	6.942	11.000	
PAP 241 PT1	2787761		1796337	3.051	11.000	5.019	0.118
-3.910	-2.069	11.000	-0.556	-11.000	-2.018	-3.449	0.260
-2.710	-6.418	-3.006	0.594	-0.599	-0.695	0.231	
PAP 242 PT1	2792427		1759400	-0.477	11.000	-1.027	-0.313
-2.742	-0.292	0.024	1.588	1.309	1.179	-1.488	-1.147
-1.063	-0.621	-0.483	0.248	-0.635	0.124	0.290	
PAP 243 PT1	2874482		1787400	1.611	11.000	1.000	-0.046
-2.534	-0.393	1.125	-1.269	-0.781	1.031	0.896	-1.333
-11.000	0.922	-1.232	1.006	-1.193	-1.669	0.906	
PAP 244 PT1	1736236		1228241	2.901	3.354	-2.813	-5.335
-2.867	-3.883	-11.000	-11.000	11.000	3.566	-5.214	6.113
-2.819	1.517	-0.570	2.422	-1.472	-1.287	1.738	
PAP 245 PT1	2564915		1628775	-0.618	11.000	0.187	0.052
-2.220	0.353	-0.361	0.143	0.148	0.374	0.185	-0.733
-1.486	-0.703	0.943	1.003	-0.871	0.108	-1.289	
PAP 246 PT1	1368891		1012617	-0.536	0.648	-0.224	-0.396

Table35.txt

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0.235     1.473     -0.115    0.152     -1.890    0.503     -0.722    -1.193
-1.506    -0.923    -1.229    -0.045    0.685     -2.234    0.592
PAP 247 PT1    2704809       1702131       -0.564    1.619     -0.477    -0.869
-1.201    -0.331    1.155     -2.338    -0.344    -0.173    -0.794    -0.503
-2.277    -0.952    -0.271    11.000    11.000    -0.057    -1.475
PAP 249 PT1    2530570       1753087       4.300     1.448     11.000    4.585
0.893     11.000    2.587     -11.000   -11.000   7.168     6.084     -0.106
-11.000   -5.742    -11.000   -6.038    -11.000   0.836     -4.945
PAP 250 PT1    3131311       2059023       5.426     2.066     2.308     -0.655
-2.954    2.904     2.966     -6.201    -11.000   -6.692    0.707     1.406
1.782     -0.685    -4.623    3.213     5.275     0.804     0.342
PAP 251 PT1    2974804       1883877       -4.325    11.000    -2.731    7.477
4.164     3.242     6.524     11.000    -4.632    11.000    -2.780    -0.687
-4.399    -0.370    11.000    -1.003    -11.000   -0.244    6.083
PAP 252 PT1    2133486       1435917       0.593     0.051     -2.022    1.470
0.023     0.119     0.651     -0.055    1.938     0.461     0.322     -2.215
-0.554    -2.832    -1.765    -1.562    1.586     -2.834    -2.826
PAP 253 PT1    2462377       1602774       -2.814    6.189     -2.593    2.677
-5.014    -4.741    2.535     -1.685    3.674     5.474     -2.944    -1.305
-3.123    -2.848    -4.071    0.880     -4.304    1.731     1.489
PAP 254 PT1    2911018       1946409       0.060     0.509     1.755     1.517
-0.983    -0.751    2.551     -1.338    -1.562    0.948     0.474     1.729
0.274     0.837     -0.382    1.290     -0.867    1.324     2.972
PAP 255 PT1    2089100       1423279       0.818     6.789     0.266     0.443
-5.902    1.445     11.000    -6.423    3.307     -2.461    0.225     0.186
-3.945    -3.121    0.901     -3.720    -11.000   -0.430    0.485
PAP 256 PT1    3058141       2075389       -3.888    11.000    1.065     1.167
7.109     11.000    11.000    11.000    -0.686    7.337     -6.597    0.331
0.933     1.168     0.298     1.196     0.054     -2.736    -2.973
PAP 257 PT1    2445552       1636539       1.078     0.691     0.491     1.120
0.071     -0.049    0.377     0.618     -0.426    -0.477    -0.177    -0.095
-0.858    0.459     -0.720    0.735     1.411     -1.414    -0.021
PAP 258 PT1    1552840       1019501       1.820     0.769     -2.792    0.134
-0.001    1.328     1.976     0.430     -1.454    -3.412    -0.074    -3.676
-0.495    -11.000   11.000    -0.699    -0.482    -4.106    -3.836
PAP 259 PT1    3013672       2014325       1.269     -0.217    0.716     0.933
-2.409    0.225     1.534     -0.751    -2.540    -0.405    1.111     0.821
-0.234    2.419     1.221     1.495     -2.559    1.233     1.535
PAP 261 PT1    2632164       1751886       2.285     2.768     -5.243    11.000
0.615     1.077     -2.381    2.115     -3.643    11.000    -7.034    1.640
1.459     -7.034    0.725     1.220     0.492     -4.916    1.720
PAP 262 PT1    2438890       1676531       5.527     4.812     0.324     0.308
-0.285    11.000    -5.132    -11.000   -11.000   -2.292    -1.761    0.112
-4.442    -5.536    0.568     -0.183    0.161     2.659     -0.347
PAP 263 PT1    2339275       1578068       1.947     2.859     2.395     1.866
0.472     -7.034    2.905     -11.000   -11.000   1.792     -3.371    5.003
0.023     -1.660    6.506     -11.000   -11.000   0.690     0.550
PAP 264 PT1    2568771       1669096       3.628     11.000    3.889     0.930
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Table35.txt

-11.000	-11.000	7.118	2.743	-11.000	-4.031	1.919	-1.677
-5.123	-1.667	0.240	-0.803	-11.000	2.120	1.527	
PAP 265 PT1	2811325	1946051	0.807	-0.109	11.000	11.000	
-2.360	-0.487	-0.478	-1.985	-2.205	0.606	-2.394	1.628
-0.101	3.033	0.037	1.238	-0.462	2.608	1.777	
PAP 266 PT1	2537365	1737091	1.389	0.634	-0.239	1.077	
-2.127	-0.519	2.137	-0.154	0.408	0.633	0.804	2.137
0.086	2.524	0.460	1.514	-1.151	2.097	2.793	
PAP 267 PT1	3147911	2041493	0.113	0.496	1.020	2.065	
-1.266	0.995	1.850	-0.119	0.159	-0.837	1.975	1.780
0.396	3.486	0.416	0.806	-1.971	2.114	3.248	
PAP 269 PT1	2954860	1995964	7.276	7.804	-11.000	-1.017	
-3.803	2.487	2.388	-2.444	-11.000	1.263	11.000	-0.026
-1.833	-3.864	-2.953	2.766	-6.215	2.580	1.170	
PAP 270 PT1	2970267	1959673	1.586	0.309	0.206	1.956	
-1.189	-0.434	0.747	-1.570	-0.838	0.975	1.863	3.126
0.665	2.618	1.033	0.940	-1.746	3.112	3.029	
PAP 272 PT1	2541922	1728670	11.000	11.000	-11.000	-11.000	
2.079	4.199	-0.743	-1.995	-2.532	11.000	-11.000	-0.289
-0.855	-0.207	-0.306	0.460	-1.800	3.304	5.955	
PAP 273 PT1	2031372	1297742	0.788	-0.991	0.925	0.176	
-0.498	1.479	1.293	-0.069	-1.734	0.815	1.515	0.624
0.313	0.626	-0.562	1.759	-0.864	0.406	1.804	
PAP 274 PT1	2076363	1470284	-0.218	11.000	0.345	0.657	
-1.619	-1.141	1.026	-2.019	-1.986	-0.365	-0.612	0.605
-11.000	1.537	-1.220	1.354	-0.160	1.621	2.886	
PAP 275 PT1	2591479	1768231	-0.358	0.594	0.433	0.874	
-0.781	0.328	1.330	-0.788	-0.270	0.097	0.758	1.442
-0.279	1.115	-0.069	1.312	0.143	0.845	2.924	
PAP 276 PT1	2628344	1768963	0.081	0.061	11.000	11.000	
-3.242	-0.159	4.980	2.392	-2.871	-0.755	0.438	0.679
0.193	1.963	-1.085	0.968	-0.975	1.381	2.384	
PAP 277 PT1	2963860	2006726	-0.757	-0.516	11.000	11.000	
-2.242	0.213	1.264	-1.057	-0.848	-0.155	0.828	1.452
0.057	2.093	-0.516	1.453	-0.146	0.525	2.269	
PAP 524 PT1	1784832	1238840	-6.314	2.703	3.852	1.657	
-2.103	11.000	11.000	-3.334	-11.000	-11.000	3.680	1.554
-2.483	-0.212	2.527	1.869	-11.000	1.728	2.063	
PAP 525 PT1	2083602	1453864	-2.595	-1.777	1.365	5.458	
-11.000	-0.195	0.651	6.242	3.915	-0.582	6.644	0.061
-1.353	-0.165	-1.083	11.000	11.000	4.770	6.479	
PAP 526 PT1	1723061	1213897	0.984	11.000	-2.403	0.977	
-1.982	11.000	4.223	-2.533	11.000	-1.896	2.394	-0.072
-5.162	-1.198	-1.989	2.124	1.006	5.167	1.605	
PAP 527 PT1	2132062	1461123	11.000	11.000	11.000	-0.781	
-0.273	-11.000	6.440	11.000	-11.000	-11.000	-11.000	-5.184
-6.194	-3.301	-3.620	4.151	7.632	-3.186	4.883	
PAP 528 PT1	2397436	1617555	0.497	4.688	-3.986	4.585	

Table35.txt

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-11.000   0.539     11.000    2.345     -11.000   4.412     -1.176    5.722
-6.758    -4.021    -5.740    11.000    5.630     3.443     5.083
PAP 529 PT1    2522725       1612880      5.957     -2.804    2.128     7.167
-5.331    4.877     11.000    -11.000   -11.000   4.149     4.390     2.812
-2.786    -1.759    -11.000   -4.706    -3.102    -3.483    -4.139
PAP 530 PT1    1200877       797254       11.000    4.738     2.744     0.013
-2.325    11.000    1.762     0.714     -11.000   2.459     7.520     0.412
-5.466    -4.458    1.461     1.062     -11.000   0.472     1.873
PAP 531 PT1    1754413       1115524      -0.840    1.092     11.000    0.124
-1.242    1.589     11.000    5.750     -11.000   -6.880    4.252     1.233
-4.959    -3.943    -4.472    1.395     -0.130    0.776     -0.938
PAP 532 PT1    1997768       1290854      6.677     5.399     5.723     1.350
-4.043    -2.340    11.000    -11.000   -11.000   0.688     7.073     3.631
1.547     -3.841    -2.271    3.427     -6.304    0.516     -0.559
PAP 533 PT1    1877533       1261056      11.000    11.000    -3.563    -2.811
-7.034    3.110     1.871     -3.950    -11.000   -3.934    -1.165    -0.318
0.030     3.549     -3.319    -0.268    -11.000   6.019     8.210
PAP 535 PT1    1649390       1158619      7.127     6.749     -0.399    -0.586
0.894     1.011     4.599     5.868     11.000    11.000    -11.000   4.535
4.463     -4.438    0.400     -6.067    -11.000   5.483     11.000
PAP 536 PT1    1961890       1327822      -0.492    11.000    2.683     3.408
-4.240    -6.256    11.000    5.407     4.834     -11.000   -11.000   -1.413
-11.000   -3.074    -0.363    2.646     4.162     2.997     11.000
PAP 537 PT1    1491976       993027       0.216     11.000    3.094     -11.000
-2.373    -0.421    -2.409    -11.000   -11.000   -4.959    0.646     -1.142
-11.000   -4.049    2.223     5.532     -4.137    3.163     -0.378
PAP 539 PT1    1914686       1302186      3.164     -4.571    5.836     -0.218
0.019     2.467     11.000    11.000    -11.000   0.160     1.326     -6.300
-11.000   0.558     0.124     -0.638    -11.000   2.736     -4.180
PAP 540 PT1    2090291       1362095      3.256     1.308     3.493     -4.680
5.392     -2.414    -11.000   -11.000   -11.000   0.659     -6.159    -2.384
-11.000   -4.127    -4.651    0.744     -3.251    5.681     11.000
PAP 541 PT1    1665811       1155260      -0.036    2.205     0.783     3.342
-2.172    2.915     11.000    -11.000   -3.777    -2.025    6.904     1.634
-6.171    -2.730    -5.682    0.446     -11.000   -0.485    2.883
PAP 542 PT1    1699240       1139912      2.440     4.447     7.941     3.796
-6.937    5.710     11.000    0.976     -11.000   2.571     -1.269    -0.260
-1.487    0.788     1.754     2.416     1.366     2.749     4.645
PAP 544 PT1    1786835       1249524      1.288     0.211     2.113     1.931
-1.171    -0.086    1.295     0.645     -3.182    0.869     0.753     3.226
2.735     3.788     2.876     0.427     -1.953    0.845     5.569
PAP 549 PT1    1975134       1297838      0.163     11.000    0.204     1.119
-0.289    -0.413    1.667     1.809     -11.000   -0.898    0.218     0.533
-0.134    0.831     -1.514    0.303     -0.675    0.405     11.000
PAP 550 PT1    2129593       1492781      -4.854    11.000    11.000    11.000
-4.333    -4.665    -2.184    -5.638    -6.447    11.000    -3.951    -1.749
-3.185    -1.661    -3.343    -1.661    -4.296    -1.074    -2.347
PAP 551 PT1    2281513       1529583      3.501     3.930     3.625     4.227
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Table35.txt

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0.042     7.672     11.000    2.455     -11.000   -2.295    -11.000   -4.018
2.849     0.125     -3.558    -2.585    -11.000   -0.230    -2.349
PAP 552 PT1    1657038        1112921       2.235     11.000    6.181     -11.000
5.770     3.415     11.000    7.505     -11.000   -11.000   -11.000   -2.096
-4.833    -2.549    -1.571    -1.942    -11.000   4.349     11.000
PAP 554 PT1    1213979        834685        1.257     0.499     4.469     1.961
-1.640    0.436     2.643     -1.435    -4.937    0.202     -2.582    3.082
2.992     4.673     6.704     0.084     -1.703    4.495     5.807
PAP 555 PT1    1982101        1317236       11.000    8.210     5.753     8.126
4.839     6.797     -11.000   -11.000   -11.000   7.630     -11.000   -5.476
-11.000   -4.080    -11.000   -5.385    -11.000   3.774     5.127
PAP 556 PT1    2104232        1360329       -1.730    -0.443    11.000    11.000
-2.949    0.098     0.128     -0.096    -2.816    -0.904    -1.588    1.505
-1.162    5.526     0.229     -0.277    -1.266    1.808     4.135
PAP 557 PT1    2632138        1704271       2.619     11.000    3.871     2.171
-7.034    0.037     1.876     -3.216    1.091     -11.000   -5.311    -3.631
-11.000   -2.222    0.013     4.652     3.518     1.188     6.160
PAP 558 PT1    1747358        1146818       1.437     11.000    11.000    3.408
-2.299    11.000    0.637     -1.837    -11.000   -11.000   0.282     -3.912
-4.970    -1.861    -0.688    -1.928    -1.936    0.298     -0.711
PAP 560 PT1    2317991        1491324       -0.169    0.917     1.532     0.293
-0.574    0.605     1.337     0.687     -0.962    0.962     0.628     2.938
1.602     2.122     1.039     1.238     -0.401    1.822     3.904
PAP 561 PT1    2681841        1734304       -11.000   11.000    6.625     11.000
-6.880    -11.000   5.989     11.000    -11.000   7.456     -6.098    -2.529
-3.657    -0.663    -3.375    -2.363    -6.432    4.031     8.126
PAP 562 PT1    1941540        1278701       0.557     11.000    -0.611    -3.107
-3.136    -6.493    11.000    11.000    -11.000   -6.217    -1.799    -0.176
-1.556    1.043     0.034     1.225     2.118     -0.840    0.552
PAP 563 PT1    1051927        690192        -0.032    11.000    0.476     -1.269
-0.614    1.143     0.848     -0.854    -0.217    -1.606    -0.180    1.860
1.121     0.058     0.750     -0.205    -2.030    -0.274    -0.428
PAP 564 PT1    1869943        1276469       0.650     11.000    11.000    3.762
-6.758    -5.382    0.033     -1.291    -2.694    -3.283    2.774     -1.033
3.282     -1.581    -1.527    0.120     2.840     -0.246    11.000
PAP 565 PT1    2082105        1407781       0.821     0.292     1.152     0.804
-2.047    0.697     1.836     -0.005    -1.829    -2.070    2.159     2.321
1.562     3.547     1.902     0.626     -2.815    0.341     3.648
PAP 566 PT1    1715027        1159595       6.891     6.875     3.585     11.000
-3.459    -3.110    4.974     -1.938    -11.000   -11.000   -2.688    0.893
-1.302    -3.067    -1.797    -1.612    -4.272    11.000    6.579
PAP 567 PT1    2033536        1340732       0.445     0.641     1.305     3.749
0.165     11.000    1.865     -11.000   3.555     2.134     -3.245    1.294
-4.079    -4.383    -6.458    2.213     0.129     0.896     1.703
PAP 568 PT1    1503091        996214        -5.799    11.000    -0.693    -11.000
-1.926    3.129     3.822     11.000    -2.545    -6.133    -11.000   -4.601
-4.998    -4.547    -3.772    1.187     1.778     7.076     2.614
PAP 569 PT1    2209334        1494475       -1.362    11.000    1.192     2.649
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Table35.txt

1.402 5.569 -6.583 -11.000 -11.000 -1.443 0.825 0.756
-4.635 -5.002 -0.977 0.519 -4.481 0.633 -1.286
PAP 570 PT1 1914311 1245166 1.164 11.000 1.637 3.722
-11.000 -4.426 11.000 -2.959 1.939 -3.565 -0.284 3.892
-4.580 0.505 -0.310 -0.753 -11.000 0.270 -2.344
PAP 572 PT1 1038656 698885 6.635 8.014 5.008 6.071
3.297 -11.000 -0.468 -4.065 -11.000 5.284 -11.000 -4.003
5.151 -3.574 3.806 3.974 5.470 0.677 5.758
PAP 573 PT1 1491163 994236 -1.025 2.650 11.000 -1.914
-1.525 11.000 7.638 -6.038 -4.524 -0.553 -3.807 2.843
-1.768 -3.533 1.380 -3.495 -11.000 0.023 -0.537
PAP 574 PT1 1860231 1249122 1.687 1.746 0.967 1.241
-2.454 -1.353 1.400 0.261 -2.087 0.231 0.774 2.764
1.488 3.948 3.108 0.218 -2.329 1.208 2.130
PAP 575 PT1 685056 433936 3.108 6.336 1.230 -1.821
-3.820 7.830 1.575 -3.806 -2.066 2.037 -1.688 1.728
0.240 1.226 -3.879 -3.004 -11.000 1.272 -0.782
PAP 576 PT1 211797 148371 3.540 -3.170 11.000 0.730
-0.521 11.000 11.000 11.000 -11.000 -5.736 3.092 0.408
-7.034 -2.557 -4.549 -0.070 -0.358 2.286 -0.957
PAP 579 PT1 1636984 1187560 4.511 -0.710 3.927 -1.374
-4.716 1.794 6.063 -1.255 -11.000 -0.825 -5.866 4.334
-2.837 -3.953 -3.419 1.050 -4.882 0.043 5.061
PAP 580 PT1 1500853 1119465 2.623 11.000 5.494 1.880
4.922 6.907 4.463 4.854 -6.188 -2.142 4.098 -1.741
-3.233 4.245 3.571 2.222 4.845 0.138 -2.118
PAP 581 PT1 916664 684286 1.921 0.194 1.419 0.498
-0.792 0.099 1.001 11.000 -0.998 -0.472 0.279 -1.020
0.000 0.774 -0.013 -0.524 -1.370 0.330 1.047
PAP 582 PT1 1420092 1049983 -0.205 -0.358 -0.117 -1.737
-1.414 0.829 1.149 0.944 -1.005 -1.084 0.046 1.431
-0.572 0.808 0.930 1.833 0.509 1.375 -0.431
PAP 583 PT1 1759216 1318568 -0.995 -1.231 -0.209 -0.940
-0.586 0.459 1.998 -0.821 -1.981 -0.221 -0.812 0.547
-0.427 1.174 -0.636 0.996 0.023 0.346 2.230
PAP 584 PT1 1570108 1135059 -0.547 -1.038 11.000 11.000
-0.696 -0.092 0.553 -0.135 -2.386 -1.573 -1.773 1.181
-0.117 1.088 -0.718 0.294 -1.726 0.014 -0.017
PAP 585 PT1 1483864 1034954 -0.495 -1.523 11.000 11.000
-0.512 -0.574 -0.391 -2.610 -1.439 -0.119 -0.258 0.661
1.081 -0.037 -0.802 0.580 -0.555 1.887 0.313
PAP 586 PT1 2244547 1579746 -0.004 11.000 0.216 -1.887
-1.027 -1.198 -0.554 -2.643 -4.653 -0.991 0.018 1.632
-0.613 1.174 -2.010 0.433 -0.835 1.641 2.028
PAP 587 PT1 1665773 1168441 0.546 -1.126 -0.487 1.270
-0.095 0.274 -0.052 -0.423 -0.979 0.687 1.113 1.883
0.019 1.629 -1.293 0.792 -1.076 2.745 2.405
PAP 588 PT1 1516652 1130602 -0.095 0.442 2.934 2.594

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PAP 589 PT1    1601925        1177083      0.591     5.525     3.093     1.366
-3.222    3.931     0.700     -1.898    -2.717    -0.721    -0.324    -0.921
-1.090    3.186     2.412     2.174     -1.860    1.030     7.040
PAP 590 PT1    1635408        1176406      -0.716    11.000    -0.623    1.059
-1.758    -0.712    -1.386    -2.381    -2.060    -1.984    -1.107    1.931
-0.812    0.916     -1.337    0.683     -2.010    0.516     2.383
PAP 591 PT1    2568825        1850118      -0.934    0.736     0.158     0.356
-0.029    -0.519    -0.589    -0.073    -1.602    0.533     0.189     1.655
-0.062    1.751     -0.588    0.954     -0.238    2.175     2.850
PAP 593 PT1    1815715        1265268      -0.316    0.259     0.440     1.113
-1.173    1.910     1.143     -1.828    -0.151    0.323     1.940     0.375
-0.007    1.812     -0.306    1.160     -0.963    0.739     2.344
PAP 594 PT1    2050335        1483601      -0.617    11.000    0.575     -0.062
-2.020    -1.861    -0.386    -1.941    -0.757    -1.187    -0.699    0.865
-11.000   1.872     -0.740    1.443     -1.907    1.590     2.852
PAP 595 PT1    1480194        1085064      -0.223    7.824     0.031     -0.477
0.093     0.083     -0.229    -0.838    1.200     -2.309    -11.000   -4.944
-11.000   0.103     -0.146    0.458     -5.828    1.097     6.822
PAP 596 PT1    667646         418130       -1.974    1.954     -2.018    -0.707
-0.470    -0.235    -1.257    -0.096    2.484     0.273     -5.182    -0.361
-2.193    -3.038    -4.854    0.897     3.093     -1.878    -3.424
PAP 597 PT1    1452115        894052       11.000    11.000    4.679     3.730
-2.384    -2.589    -2.784    1.049     1.752     -1.214    -7.034    -0.577
-0.425    -2.773    -5.318    -1.857    -5.301    3.040     -0.602
PAP 599 PT1    817784         484014       -1.699    0.091     6.889     11.000
-1.230    -2.108    2.118     0.132     0.090     0.355     -0.285    -0.206
-0.804    0.373     -0.610    -0.058    -1.337    0.393     -0.209
PAP 600 PT1    3474619        1856955      5.296     5.107     3.217     -1.607
-0.109    0.897     4.800     3.677     -11.000   6.065     -11.000   -4.622
-11.000   -4.278    3.192     3.231     0.627     1.668     0.702
PAP 601 PT1    805589         431319       -3.387    -3.715    -1.661    -0.113
-3.575    -4.361    2.532     6.810     -3.197    11.000    -2.497    -0.478
-1.614    0.433     6.963     -0.320    -0.057    11.000    -2.356
PAP 603 PT1    2219069        1183913      1.656     1.421     1.552     2.019
0.808     2.930     -0.072    4.587     -1.865    0.171     -2.006    0.836
0.255     0.924     1.051     2.430     -0.842    -0.877    -0.046
PAP 604 PT1    1095804        578044       -1.562    7.819     4.395     7.243
4.318     6.106     5.163     1.466     -11.000   11.000    -11.000   0.222
-4.805    -3.756    -6.937    1.243     3.339     3.095     -2.002
PAP 605 PT1    2467530        1408160      1.072     2.717     0.121     1.820
-1.027    0.357     2.180     -1.038    0.698     -0.996    -0.045    0.126
0.050     1.518     0.479     0.386     -1.070    1.270     0.310
PAP 606 PT1    791809         471574       -0.057    11.000    -1.599    -0.727
-1.907    11.000    -0.469    -3.596    -11.000   -0.133    1.790     -1.407
-1.043    -3.889    -11.000   2.507     -3.862    -0.185    -3.106
PAP 607 PT1    907520         490087       8.210     -0.598    3.523     5.372
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PAP 608 PT1    2428703        1397157       -4.893    0.735     11.000    -11.000
-1.752    -0.275    11.000    1.587     -11.000   1.101     -11.000   -4.066
-5.659    3.089     2.617     6.529     -3.483    5.492     4.331
PAP 609 PT1    983797         583804        0.031     -0.343    0.163     1.253
0.207     0.980     1.598     -1.673    1.695     1.805     0.219     0.553
-0.507    0.691     0.585     0.877     -0.886    0.818     1.127
PAP 616 PT1    448356         246239        -0.355    -0.368    7.241     11.000
-2.139    -0.903    1.480     -0.922    -0.380    -0.862    0.978     -1.985
-0.404    0.569     -0.914    -0.576    -2.825    0.440     2.209
PAP 617 PT1    1825112        1097243       5.302     11.000    -3.275    -1.514
-4.714    -3.885    1.517     2.285     2.022     -5.901    -4.515    0.784
-4.687    0.158     3.853     2.671     0.217     -1.542    0.362
PAP 619 PT1    2563874        1441297       0.271     -0.309    -0.401    0.051
-0.841    -0.046    2.459     -0.317    0.391     0.101     0.261     1.543
-1.731    0.273     0.303     0.074     -2.453    0.596     0.562
PAP 621 PT1    3616353        2025990       -1.566    0.496     -1.391    -1.712
-2.060    0.019     -0.270    -1.949    -1.528    -0.954    -1.576    -1.208
-1.577    0.684     -2.904    1.528     -3.243    -0.162    -0.199
PAP 622 PT1    2232501        1245445       -0.834    -1.790    -0.477    -0.186
-1.727    -1.779    0.601     -1.054    -0.556    -0.297    3.733     0.387
-2.178    0.470     -1.203    2.287     0.990     1.349     0.046
PAP 625 PT1    2115986        1162486       1.853     0.882     -1.515    0.295
-0.752    1.514     0.626     -0.432    0.847     1.099     -0.005    -1.649
-1.972    -0.139    -1.666    -0.087    -0.786    0.357     -1.603
PAP 626 PT1    1603376        861345        -0.624    -0.683    1.178     1.677
-0.722    0.013     2.378     -0.143    0.406     0.944     -1.706    0.475
-1.884    0.769     0.477     1.350     -0.920    2.604     0.515
PAP 627 PT1    559600         300756        0.645     0.873     -0.107    1.835
0.424     -0.209    0.380     -0.223    0.344     0.987     1.718     -1.004
-0.081    1.789     -0.741    -0.019    -1.329    0.572     0.111
PAP 628 PT1    1010045        533319        3.656     6.393     4.604     2.554
-11.000   2.743     1.971     -11.000   -11.000   4.197     1.574     3.084
-11.000   -4.594    -5.348    0.385     -11.000   4.686     0.466
PAP 629 PT1    2666988        1418878       -0.188    1.038     -0.272    1.668
-0.608    0.185     0.503     -1.115    -0.179    0.403     1.562     0.448
-0.893    0.798     -0.683    -0.555    -2.516    0.082     1.430
PAP 632 PT1    2733575        1467161       7.293     7.543     -2.494    -3.217
-11.000   -1.309    6.473     -0.177    11.000    -11.000   -1.815    -3.930
-2.822    -4.251    0.802     -0.293    -5.108    -1.777    8.210
PAP 633 PT1    1034915        557813        -0.691    -0.567    4.403     11.000
-2.040    -0.172    0.700     0.250     -0.199    0.956     1.332     -0.064
0.526     1.698     1.638     -0.140    -2.233    1.324     0.740
PAP 634 PT1    1416064        864860        1.418     1.194     0.424     0.859
-1.863    0.761     1.068     -0.464    -1.278    2.251     0.725     1.875
1.943     3.138     0.730     1.936     -2.153    4.042     3.744
PAP 635 PT1    2182067        1275069       2.273     11.000    3.114     7.304
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Table35.txt

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-6.423    -1.124    11.000    -1.977    -11.000   0.341     -5.045    -0.992
-4.560    -1.660    -3.181    0.804     0.804     1.742     1.170
PAP 636 PT1    550932        328109       1.361     0.604     1.019     2.937
-1.857    6.675     1.703     -1.690    -0.007    -1.680    -6.807    1.059
-3.497    -4.115    -0.301    2.340     -2.757    2.278     -2.287
PAP 637 PT1    2041570       1186537      2.162     2.106     -2.832    -4.027
-11.000   -11.000   7.836     4.058     -11.000   -4.159    -11.000   -0.276
-2.873    0.684     4.795     7.448     11.000    -0.069    11.000
PAP 638 PT1    2095631       1201335      -4.640    2.844     4.966     1.287
-11.000   -6.706    -0.151    -6.508    0.723     -2.335    -3.026    7.310
-5.264    -4.413    11.000    5.953     1.671     5.270     11.000
PAP 641 PT1    1261221       941404       -5.716    11.000    1.661     11.000
-11.000   -11.000   0.998     6.919     -6.937    11.000    -11.000   4.957
-11.000   0.181     0.347     -5.212    -11.000   -1.607    11.000
PAP 642 PT1    1189554       871740       -1.810    -1.514    0.669     -1.878
-1.500    0.662     0.028     -1.683    -2.216    -1.154    -1.373    0.797
0.365     -0.118    -0.932    0.718     1.665     -0.846    -0.941
PAP 643 PT1    1007057       747226       -3.529    2.704     1.137     1.667
0.536     2.949     -4.579    -6.739    11.000    -5.294    2.904     7.380
5.549     -2.502    1.480     -11.000   -11.000   -2.021    1.658
PAP 644 PT1    1158926       843543       -11.000   -5.280    1.295     -2.602
0.470     1.602     0.182     -2.998    -2.528    1.205     -4.614    -11.000
0.961     -1.592    -4.289    2.114     6.307     -3.722    -2.372
PAP 645 PT1    4017802       2422204      -11.000   11.000    1.209     1.614
0.477     -11.000   1.577     1.071     0.835     -11.000   0.941     -0.781
0.516     0.378     0.289     1.718     -0.670    -1.736    -1.054
PAP 646 PT1    1386136       1018989      1.077     -0.226    0.123     -0.488
-0.163    0.356     1.620     0.469     -2.018    0.795     0.875     -1.704
-1.530    0.429     -0.204    0.312     -0.458    2.020     0.879
PAP 647 PT1    1465205       1083028      -0.465    -0.956    11.000    11.000
-1.249    -1.530    -1.178    -2.141    -2.069    -1.118    -0.708    -0.428
-0.112    -0.113    -0.445    0.968     -2.372    -0.943    -1.369
PAP 649 PT1    4587204       2577984      11.000    11.000    3.476     11.000
-1.501    -1.375    6.929     0.270     -11.000   5.268     -4.564    -11.000
-11.000   2.167     -5.078    0.786     -11.000   6.411     5.778
PAP 650 PT1    768879        565462       -2.093    11.000    -1.026    -0.842
0.652     1.896     0.916     -0.286    0.552     -1.262    0.494     -0.860
-11.000   -0.395    0.119     -0.584    0.378     -1.258    0.181
PAP 651 PT1    1647566       1130473      0.551     -0.095    0.218     0.399
0.159     -0.044    -0.714    0.236     -2.633    0.008     0.174     -0.818
0.427     0.932     -0.009    0.248     -0.675    0.997     1.791
PAP 652 PT1    1760062       1260797      1.516     3.531     5.573     7.264
-1.474    -1.295    -11.000   11.000    -11.000   -11.000   -3.682    0.520
0.215     -1.681    6.258     0.316     -1.110    1.945     1.215
PAP 653 PT1    1057566       783948       0.389     11.000    -1.358    -1.239
-0.735    0.650     0.112     -0.357    -0.311    -1.090    -1.479    -1.351
-0.782    -0.423    0.853     1.878     -0.997    -1.746    -0.567
PAP 654 PT1    1249645       885167       -0.817    -0.322    8.210     11.000
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Table35.txt

-1.087 -0.289 11.000 11.000 -2.135 -1.050 -2.512 -1.173
-0.399 -0.331 -0.866 0.111 -1.091 -1.239 -1.795
PAP 655 PT1 1263873 932094 -0.004 11.000 -0.502 -1.085
-1.612 -0.212 -0.260 1.231 -1.809 -2.326 -0.908 -0.902
0.153 -0.013 -0.851 -0.843 0.614 -2.527 -2.781
PAP 663 PT1 2543372 1401123 1.329 2.065 -1.123 1.399
-1.411 -1.580 1.337 -1.685 -1.749 0.622 0.341 -0.613
-3.808 3.237 2.296 0.127 -3.577 1.230 0.961
PAP 665 PT1 647310 413554 -3.131 11.000 -2.469 -1.244
-2.732 -1.675 11.000 11.000 0.134 0.542 -2.327 -3.137
-2.916 -0.975 -1.114 -0.532 -2.910 -1.208 -1.270
PAP 667 PT1 303919 192806 -11.000 11.000 11.000 11.000
-2.450 -3.592 5.187 5.550 7.020 4.999 -11.000 -2.513
-2.350 -1.550 -1.113 -4.237 -11.000 -2.833 -4.461
PAP 668 PT1 2368009 1326227 -11.000 5.212 2.658 5.913
-11.000 -11.000 5.046 5.246 4.212 -1.209 5.338 0.721
-6.679 -1.667 2.984 1.240 0.437 2.582 4.468
PAP 669 PT1 1095526 712619 -0.093 7.223 -0.986 1.125
-0.492 0.935 0.542 -0.998 2.439 1.321 -0.494 -0.016
-4.580 0.498 -0.279 -0.088 -1.243 0.723 0.220
PAP 670 PT1 1372309 878382 11.000 -5.307 5.219 -4.369
-7.034 1.737 -0.913 -0.113 -2.781 -11.000 -6.512 -1.317
-11.000 -1.695 -2.119 -1.995 -5.748 1.182 6.422
PAP 671 PT1 1974657 1113060 -1.116 1.239 11.000 11.000
-2.013 -0.128 0.903 -0.590 -2.197 -0.241 1.285 0.334
-0.657 1.069 -0.966 -0.474 -3.287 0.704 0.683
PAP 672 PT1 2203767 1299511 -3.821 11.000 0.820 4.386
-3.575 -3.922 1.150 1.997 2.397 1.659 2.016 -1.883
-2.489 -1.708 -2.859 -0.528 -5.105 -0.168 -0.498
PAP 674 PT1 845087 536557 0.821 5.829 -3.133 1.223
-4.206 5.797 5.946 -11.000 -11.000 11.000 -4.213 2.466
-5.196 -3.464 0.960 -1.630 -0.555 0.716 2.061
PAP 675 PT1 1837615 1088749 -3.073 -4.007 -2.834 -2.101
7.748 11.000 0.206 -3.664 -4.555 -2.035 -2.568 -1.084
-2.827 -0.131 -1.812 -0.995 -4.764 -0.631 -0.409
PAP 676 PT1 1490241 860161 7.391 7.603 2.929 0.520
-3.814 -3.846 11.000 -1.310 -6.637 -11.000 -3.421 1.212
-11.000 -3.712 -2.833 3.705 6.530 11.000 5.217
PAP 678 PT1 3562346 2099727 3.409 4.762 -4.248 2.803
6.358 -3.699 4.951 -1.873 -11.000 1.168 -4.684 2.348
1.040 -5.569 0.261 3.594 -2.250 -3.277 11.000
PAP 679 PT1 2548498 1525805 -2.074 -0.022 -0.586 1.290
-1.425 -0.847 0.980 -0.984 1.027 0.481 -0.094 1.361
-0.413 1.357 -0.671 0.919 -1.738 2.742 2.420
PAP 681 PT1 5258091 3371300 0.214 0.437 1.560 4.960
-0.726 -1.278 2.538 0.682 -0.253 1.174 1.460 1.936
-0.812 5.271 1.772 0.954 -2.836 2.516 3.537
PAP 683 PT1 1019921 565850 0.520 -0.498 -2.266 1.406

Table35.txt

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-2.363    1.205     -1.237    0.406     -2.086    0.652     0.066
PAP 684 PT1    2837069       1542871       0.536     0.350     -0.598    1.251
-0.149    1.223     1.403     -0.760    0.239     0.090     0.737     0.376
-11.000   0.428     0.741     -0.833    -2.997    1.016     -0.131
PAP 685 PT1    1601077       898110        0.322     -0.874    -0.223    1.218
-0.901    -1.360    1.719     0.247     -2.293    0.732     1.944     3.002
0.134     4.013     2.523     1.587     -1.491    2.164     2.976
PAP 686 PT1    1053116       614256        1.543     -0.697    1.357     -0.153
-1.556    0.355     0.896     -0.594    0.319     -0.292    1.650     -1.887
-1.279    2.752     0.367     0.897     -1.843    2.267     2.908
PAP 687 PT1    1047302       588644        0.552     -4.292    1.959     3.745
-2.046    0.538     0.735     -2.513    -11.000   4.381     0.859     1.423
2.274     -6.169    -11.000   1.317     -1.558    0.699     11.000
PAP 688 PT1    1754850       923355        -1.266    -2.139    0.547     0.752
-3.778    -2.892    4.830     4.303     -3.545    -1.431    -0.189    1.107
-1.103    2.775     -0.697    0.596     -4.126    1.356     2.175
PAP 689 PT1    399031        309355        -3.693    -0.814    -2.462    -3.481
3.552     4.039     -1.269    -4.817    3.615     5.118     -11.000   0.099
1.355     -4.886    -0.430    1.180     2.727     6.421     3.208
PAP 694 PT1    22485829      8884675       -0.345    11.000    -3.140    -2.797
-1.577    -0.639    -2.770    -1.306    -2.556    -1.994    -0.840    -1.278
-1.516    -0.715    -0.627    0.540     -1.553    -0.221    11.000
PAP 696 PT1    11623491      8743593       -0.982    -0.187    -3.073    -3.148
-2.466    -1.987    -2.947    -2.924    -3.306    -1.791    -0.229    -0.262
11.000    11.000    -1.650    -0.647    -1.294    0.061     11.000
PAP 697 PT1    21759891      8795884       0.364     11.000    -1.481    -0.638
0.532     0.086     -1.222    -0.634    -2.077    -0.182    0.149     -0.273
-0.208    0.700     0.469     0.507     -0.229    -11.000   -0.089
PAP 698 PT1    12076904      9443794       1.334     0.900     -2.243    -1.662
0.413     0.756     -0.888    -0.780    -1.052    0.527     1.669     1.596
-1.269    1.159     -1.514    0.269     -0.478    1.926     1.063
PAP 699 PT1    21818919      8625634       1.008     0.370     -1.300    -1.387
-0.152    -0.579    -1.586    0.223     -1.311    0.595     1.187     1.385
-0.644    0.511     -0.154    1.293     -0.239    1.909     1.665
PAP 701 PT1    22065513      8755040       2.514     1.739     11.000    11.000
1.712     2.529     0.249     2.025     11.000    11.000    2.384     2.293
1.205     1.436     0.844     2.673     -11.000   2.181     1.972
PAP 702 PT1    11978157      8743199       0.910     -5.140    -0.636    11.000
11.000    11.000    -11.000   -11.000   0.290     6.032     0.775     -11.000
-11.000   5.103     -11.000   11.000    0.587     3.413     1.353
PAP 705 PT1    23193828      9270619       -11.000   11.000    -4.301    7.274
2.882     11.000    -11.000   -11.000   4.226     -5.423    4.838     -3.364
4.086     0.160     -11.000   11.000    3.143     -3.295    -2.155
PAP 707 PT1    22823572      8882225       -2.234    4.554     -6.657    3.338
-4.972    6.027     -11.000   -11.000   7.809     -4.888    11.000    11.000
-4.040    11.000    -11.000   11.000    -0.310    -1.756    -1.358
PAP 709 PT1    11561378      5894595       -0.837    -0.752    -1.838    -2.188
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Table35.txt

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PAP 710 PT1	23900454	9396198	3.658	1.206	2.391	1.589	
-5.752	11.000	-5.039	-11.000	-3.978	2.882	2.651	3.906
-3.084	-11.000	-5.891	7.464	-2.813	-1.781	0.489	
PAP 711 PT1	22757320	9050113	5.787	11.000	-11.000	-11.000	
3.009	11.000	-6.291	-11.000	5.785	4.794	3.920	5.541
-6.272	-6.880	-11.000	2.046	11.000	-11.000	2.204	
PAP 715 PT1	13918597	9722364	1.465	5.217	-0.429	2.635	
-7.034	4.612	-4.501	-11.000	0.027	-4.219	2.129	11.000
-2.958	4.025	-4.484	2.861	1.542	1.150	-1.813	
PAP 717 PT1	11733100	7145796	5.204	4.610	5.252	0.804	
-11.000	4.700	3.373	-2.365	-1.066	0.207	11.000	6.520
-2.047	-0.497	-11.000	11.000	2.270	-5.280	11.000	
PAP 719 PT1	2243477	1843061	0.115	11.000	-0.495	-0.961	
0.039	-1.022	-2.813	-2.771	-1.922	-0.903	0.479	-0.852
-0.705	-1.302	-2.877	-1.445	-0.842	-0.625	0.288	
PAP 721 PT1	2377718	2011494	-1.703	4.816	11.000	7.154	
-3.071	11.000	-5.397	-11.000	-4.347	-0.825	7.862	-11.000
-3.183	-3.696	-4.002	4.827	-1.553	-3.259	1.725	
PAP 726 PT1	11881027	6753576	0.363	0.542	0.358	0.044	
-0.965	-0.482	-1.227	-0.493	-2.627	1.326	2.014	1.447
0.531	1.007	-1.509	0.698	1.058	1.390	-0.482	
PAP 728 PT1	11565807	7624365	0.596	11.000	-0.643	1.396	
0.103	-0.436	-2.447	-2.239	-2.254	-0.059	2.094	0.012
-0.410	-0.326	-2.566	-0.597	0.421	1.975	0.073	
PAP 735 PT1	2125213	1783366	-0.572	11.000	-1.763	-2.255	
-1.594	-0.384	-2.560	-2.255	-2.853	-1.152	0.530	-0.964
-0.210	-0.583	-3.142	-0.785	-0.232	0.484	11.000	
PAP 744 PT1	2114707	991641	0.980	11.000	-1.864	-0.744	
-0.353	0.834	-1.890	-2.862	-1.755	-0.009	11.000	1.089
-1.584	-0.129	-0.188	-0.568	0.373	0.359	-0.329	
PAP 746 PT1	24063390	9080430	-0.596	2.898	-3.690	0.122	
0.200	11.000	-4.625	-11.000	0.365	-2.833	0.718	-2.637
1.202	4.315	-4.138	11.000	11.000	2.090	0.554	
PAP 749 PT2	11487082	7175804	-11.000	11.000	0.547	0.862	
0.854	1.886	-0.705	0.534	-0.312	1.991	1.687	2.221
1.327	1.051	-0.923	1.050	0.755	1.130	0.450	
PAP 751 PT1	10937334	6766446	2.597	2.866	1.076	2.943	
-0.095	11.000	5.189	-11.000	3.920	-5.135	11.000	-6.003
2.008	-0.958	-11.000	11.000	-6.839	-0.395	1.020	
PAP 753 PT1	2096896	1533309	4.630	4.507	11.000	4.394	
3.390	4.752	-5.600	-7.034	1.281	-5.645	11.000	-3.690
-11.000	-1.839	-3.370	11.000	1.432	-2.417	6.850	
PAP 757 PT1	2044955	1604556	-1.179	11.000	1.621	2.377	
-2.590	-1.660	-2.894	-2.602	-2.214	-2.524	-1.202	-1.600
-1.410	11.000	-2.601	-1.677	-2.170	0.045	1.664	
PAP 758 PT1	11622939	7919903	-1.170	1.056	-1.573	-0.968	

Table35.txt

1.765 2.137 -0.192 -1.371 -2.888 0.994 2.951 1.784
-1.095 0.620 -2.111 1.616 0.646 2.112 -0.360
PAP 761 PT1 11782258 7961324 7.404 11.000 -4.382 -5.589
7.562 11.000 -3.754 -6.317 -6.721 -11.000 6.666 7.814
5.687 -11.000 -11.000 11.000 4.640 4.252 3.193
PAP 761 PT2 11110174 7568611 6.701 11.000 3.247 -11.000
8.126 11.000 -4.581 -11.000 4.635 -1.020 7.066 3.582
6.058 -11.000 -3.570 11.000 -2.482 -3.533 -4.340
PAP 763 PT1 2048319 1471780 3.818 4.891 3.736 0.826
4.687 6.900 0.126 -11.000 1.866 4.729 3.801 -11.000
0.657 4.355 -11.000 3.109 1.663 3.846 -5.100
PAP 768 PT1 2064605 1390161 2.037 2.518 -11.000 -11.000
0.328 4.439 1.488 -2.349 -1.690 -0.789 0.180 -1.186
-5.585 1.760 -11.000 0.846 0.656 2.153 2.167
PAP 770 PT1 11402145 7755829 -0.544 -2.292 -3.217 -1.253
-0.804 -0.856 -1.424 -0.094 -1.141 -1.678 -0.130 0.938
-1.007 0.876 -2.903 0.196 0.247 1.932 11.000
PAP 775 PT1 2675453 1829303 -0.010 -0.053 -0.312 0.801
-1.307 0.438 0.624 -0.125 -0.634 -0.135 0.547 2.798
1.416 3.114 0.201 1.556 -2.372 3.655 4.864
PAP 777 PT1 10664948 5780987 11.000 4.021 5.535 1.882
-3.366 11.000 -1.391 -11.000 5.663 -11.000 11.000 5.501
1.198 0.474 -11.000 6.640 5.844 -1.779 -5.823
PAP 777 PT2 2107565 1872453 11.000 3.182 5.904 2.285
-3.361 11.000 -1.570 -11.000 7.597 -11.000 11.000 5.425
1.822 0.570 -11.000 6.712 7.236 -1.779 -6.207
PAP 791 PT1 11376310 7572298 0.347 1.113 -0.474 -0.215
-0.999 1.266 -2.920 -0.835 -3.020 1.134 1.325 1.119
-1.194 1.950 -0.835 0.885 0.259 1.291 0.967
PAP 791 PT2 12016008 7566211 -1.079 -0.187 -0.966 0.700
0.112 -0.338 -1.081 2.240 0.939 2.471 0.153 3.418
-1.368 1.726 -1.372 1.179 1.352 0.066 -0.662
PAP 799 PT1 2208491 1728027 0.178 -0.508 11.000 11.000
-0.858 -0.882 -2.709 -1.854 -4.811 -1.735 0.235 -1.264
-1.584 -1.474 -1.526 0.109 -0.332 0.107 -0.445
PAP 800 PT1 11968902 7169650 -1.029 -1.547 -1.258 -1.810
-1.662 -0.496 -2.701 -1.373 -2.852 -0.890 1.107 -0.212
6.728 11.000 -2.758 -0.637 -1.309 -0.194 11.000
PAP 802 PT1 11267840 7247762 1.355 0.201 0.488 0.058
0.550 0.035 -2.274 -0.357 -1.456 2.206 2.742 0.378
1.154 -0.149 -1.190 -0.510 -0.334 0.597 -0.010
PAP 802 PT2 11633292 7716353 0.898 0.069 0.097 -0.105
0.513 -0.088 -1.153 -0.331 -0.973 1.698 2.087 0.819
1.852 0.934 -2.319 -0.679 0.012 0.705 -0.290
PAP 804 PT1 10404144 5723034 -0.350 -0.051 5.780 11.000
-2.179 -1.016 -2.403 -3.461 -3.743 0.254 0.487 -0.478
-0.626 0.315 -1.716 -0.861 -0.613 1.015 0.123
PAP 805 PT1 2037995 1444484 11.000 11.000 1.172 -0.104

Table35.txt

-1.396	-6.758	1.011	3.046	-11.000	0.061	-0.659	2.905
-0.320	-2.790	-4.959	0.646	-5.958	-1.774	-3.549	
PAP 809 PT1	1996121	1402423	-6.284	11.000	2.135	11.000	
0.587	1.383	11.000	2.003	0.515	2.017	2.564	1.403
-3.130	3.214	2.214	-5.819	-6.444	-0.037	3.664	
PAP 812 PT1	1768075	1268001	-0.238	-1.188	11.000	11.000	
-1.399	-1.585	0.662	-1.307	-1.391	-0.340	-4.848	1.543
-1.312	1.261	1.096	-0.146	-3.515	1.667	3.437	
PAP 812 PT2	1397285	1016001	-0.270	-1.356	11.000	11.000	
-1.102	-1.443	1.632	-0.961	-1.578	-0.441	-3.719	1.356
-1.251	3.023	0.962	0.382	-2.170	2.396	4.480	
PAP 815 PT1	3723577	2613964	-0.171	-0.307	0.113	-0.093	
-1.524	2.525	0.772	-2.118	-0.757	-0.560	-0.295	-2.647
-2.279	0.848	-1.863	1.303	-1.270	1.064	2.251	
PAP 816 PT1	2818606	2043171	-0.692	11.000	0.602	1.140	
-2.978	-2.391	0.328	-3.126	-3.098	-1.687	-0.117	1.495
-0.614	3.619	1.358	0.124	-4.883	3.350	3.926	
PAP 817 PT1	1815564	1264248	11.000	11.000	1.372	0.271	
-1.031	-0.725	0.583	-1.416	-2.827	-0.155	1.599	1.382
0.762	3.418	1.448	0.946	-2.835	4.151	3.703	
PAP 817 PT1	1873537	1342583	2.797	11.000	0.905	0.871	
-0.623	-0.328	1.236	-0.691	-2.793	-0.362	0.877	1.220
0.362	2.603	1.181	0.883	-1.271	4.684	3.821	
PAP 829 PT1	1811539	1065249	0.592	0.491	0.983	1.966	
-0.335	0.813	2.416	-0.411	-1.275	-0.684	2.792	1.868
0.534	2.462	0.330	0.035	-2.081	2.824	4.469	
PAP 830 PT1	1164947	686000	-1.501	0.342	0.029	0.799	
-2.188	-1.030	2.459	-1.970	-1.328	0.099	-0.835	-0.517
-1.458	1.718	-0.235	0.622	-2.568	0.339	0.489	
PAP 831 PT1	12052587	8642062	-0.662	11.000	6.600	6.504	
-0.930	11.000	-11.000	1.410	2.782	-1.962	2.894	0.054
1.875	-3.081	-11.000	11.000	-1.511	-0.335	-1.847	
PAP 832 PT1	12003570	7459309	1.911	2.528	-2.023	-0.490	
-6.386	2.642	1.719	4.238	0.313	3.216	0.421	3.671
-0.332	1.071	-2.243	3.501	1.316	2.626	-3.472	
PAP 832 PT2	24036258	9385719	2.225	4.128	-11.000	3.430	
-6.807	-1.081	3.368	7.992	2.771	4.770	-0.276	7.083
2.502	5.643	5.996	6.499	-11.000	1.738	0.588	
PAP 833 PT1	1065501	661183	0.301	0.378	3.265	4.152	
1.561	3.361	3.324	3.382	-11.000	0.459	0.957	0.660
2.362	3.318	3.165	0.353	-2.728	4.962	5.031	
PAP 836 PT1	12356835	6444484	2.091	0.099	0.395	0.676	
0.074	0.086	-1.158	2.755	-1.771	3.697	3.293	3.073
0.155	-0.593	-4.428	0.160	0.427	1.244	-2.740	
PAP 837 PT1	2114213	1473813	1.254	-0.389	0.375	1.899	
-1.525	0.559	1.487	-1.243	-0.619	0.668	3.265	1.523
-0.012	4.126	2.022	1.117	-2.673	3.037	4.355	
PAP 839 PT1	19413521	8567442	-0.265	11.000	11.000	11.000	

Table35.txt

-3.122 -0.755 -2.608 -2.757 -3.657 -2.294 0.623 -1.768
-0.310 -3.416 -3.505 -0.096 -1.276 -0.587 -0.592
PAP 842 PT1 2191022 1820469 1.671 11.000 0.560 -0.475
-0.359 0.894 -2.024 0.194 -0.527 1.409 2.332 2.044
0.431 0.037 -3.155 -0.442 0.148 0.144 -1.191
PAP 851 PT1 2835479 2095438 2.498 1.210 1.038 -11.000
1.337 2.208 1.827 1.595 11.000 -11.000 -11.000 -11.000
-11.000 1.624 -1.312 1.868 -0.177 0.135 1.419
PAP 853 PT1 1469538 1020086 2.403 11.000 1.470 0.687
-1.639 0.412 1.086 -0.316 -1.331 0.216 2.167 -1.178
-1.307 2.406 1.671 -1.466 -3.149 1.630 1.605
PAP 860 PT1 1879552 1549932 2.525 11.000 -0.633 -0.312
-0.233 -0.063 -0.714 1.235 -0.827 0.915 0.944 1.996
-0.342 0.104 -2.375 0.916 0.608 0.047 -2.028
PAP 862 PT1 2397527 1775641 7.167 0.458 2.732 -2.229
-6.604 -4.925 6.579 -4.544 -3.214 -0.677 -11.000 -1.439
-2.864 -1.219 -4.896 5.398 5.091 -0.233 1.288
PAP 868 PT1 2144949 1659619 -0.631 11.000 -1.524 -1.150
-1.674 -1.232 -2.073 -1.486 -1.926 -0.517 0.968 1.325
-1.072 0.152 -2.368 0.169 0.430 -0.192 7.719
PAP 870 PT1 2216558 1142043 1.906 0.125 0.283 -0.611
-0.801 -1.334 -2.290 -3.750 -3.448 -0.565 1.840 -0.439
0.148 -0.236 0.296 -1.900 -0.408 3.229 0.371
PAP 872 PT1 1598441 860457 0.351 -0.676 -1.029 -1.443
-0.940 -0.571 -2.423 -1.833 -3.858 -1.595 1.720 0.297
-0.592 -0.242 -1.462 -1.325 -1.210 1.075 11.000
PAP 873 PT1 2404427 1581515 0.154 -1.333 -0.714 -1.970
-1.161 -0.795 -2.820 -2.578 -3.856 -1.018 1.742 -0.607
11.000 11.000 -2.051 1.161 -0.256 1.254 4.890
PAP 874 PT1 2372551 1380842 -4.610 -4.917 11.000 11.000
-4.997 -6.229 -4.343 -11.000 -5.874 -6.880 11.000 11.000
-3.781 -4.102 11.000 11.000 -2.620 -2.866 -3.944
PAP 875 PT1 2004073 1604953 0.478 11.000 -0.721 -1.279
-0.018 0.490 -1.206 -1.004 -2.868 0.284 1.376 -0.482
-0.459 0.153 -3.276 -0.878 0.212 1.508 -1.332
PAP 877 PT1 2194793 1281429 0.638 0.498 -1.062 -0.566
-0.326 0.029 -1.731 -0.283 -2.098 0.094 1.898 0.999
-1.006 0.622 -1.622 -0.016 -0.040 1.839 0.607
PAP 878 PT1 11675088 6494607 -0.181 11.000 -0.841 -1.570
-0.135 -1.169 -1.124 -2.769 -2.097 -0.618 2.130 0.268
0.034 -0.831 -0.549 11.000 -1.110 0.311 0.305
PAP 881 PT1 12217065 7974731 -1.833 11.000 6.627 5.887
-0.037 11.000 4.715 -6.018 4.652 -11.000 7.928 -1.904
-1.490 -4.613 -11.000 11.000 5.028 6.409 5.257
PAP 892 PT1 10704949 7110997 -0.691 -0.618 -2.139 -1.862
-1.192 -0.405 -2.029 -0.977 -2.437 -0.787 0.865 0.043
-1.385 -0.107 -1.574 -0.256 -0.903 1.375 11.000
PAP 897 PT1 12056628 8950332 -11.000 11.000 -0.506 -0.527

Table35.txt

-0.428 0.428 -1.773 -0.607 -0.393 2.209 1.628 0.734
-1.234 1.731 -0.761 1.988 0.201 1.970 0.986
PAP 900 PT1 11823530 8419830 -11.000 11.000 11.000 11.000
-11.000 11.000 -1.351 -0.731 7.112 5.546 8.210 -11.000
-0.416 0.331 -0.977 -11.000 -11.000 -11.000 7.061
PAP 901 PT1 11999659 8420035 -6.493 11.000 -1.999 -1.780
11.000 11.000 -3.851 -5.236 -2.035 -2.213 11.000 11.000
-3.798 -3.119 -3.705 -11.000 -5.294 -4.328 11.000
PAP 902 PT1 12415335 7695673 -1.643 11.000 -1.434 -3.178
-2.024 -1.981 -3.490 -4.463 -2.767 -2.071 11.000 11.000
-1.816 -2.359 -2.833 -1.541 -1.099 -1.364 11.000
PAP 904 PT1 12076345 7253807 5.265 5.577 3.506 3.933
4.964 7.059 -1.847 -11.000 2.255 -1.275 5.712 3.355
3.569 -1.575 -11.000 -0.231 0.367 0.881 3.731
PAP 907 PT1 11647516 7797479 1.110 11.000 -0.308 0.012
-1.586 -0.090 -3.124 -2.048 -1.731 0.740 1.862 -0.037
0.316 -1.018 6.425 -0.897 -0.456 -0.171 -0.997
PAP 910 PT1 12025900 7971747 0.772 -0.257 -1.456 -0.749
-1.243 0.614 -2.008 -0.482 -1.814 0.619 1.949 0.813
-0.327 1.666 -0.802 0.347 -0.045 0.809 1.103
PAP 925 PT1 934303 564407 1.284 3.493 0.602 -0.459
-1.410 11.000 1.527 0.298 -11.000 0.553 1.139 0.672
-3.477 -4.886 -0.250 1.505 -0.922 0.335 -0.960
PAP 926 PT1 853349 590520 0.972 0.725 0.051 1.681
-2.045 -0.597 0.861 -0.854 -0.652 0.410 1.335 2.131
0.406 3.129 0.137 0.623 -2.617 4.374 4.525
PAP 927 PT1 501375 304969 -0.618 11.000 -0.049 -0.058
-3.125 -1.792 1.338 -1.620 -1.960 0.059 0.283 -1.623
-1.657 2.292 0.826 0.430 -3.003 1.817 0.175
PAP 928 PT1 343456 190174 -3.285 11.000 3.155 3.918
-4.548 4.382 6.917 -2.589 -5.656 -11.000 6.679 0.625
0.601 -0.542 -1.372 -2.537 -11.000 2.733 11.000
PAP 931 PT1 290512 172560 0.006 11.000 0.357 0.217
-1.674 -0.156 2.278 0.630 -0.409 1.355 -0.285 -0.902
-0.520 1.855 1.138 0.705 -1.657 1.178 0.806
PAP 989 PT1 1499652 1104291 1.851 11.000 11.000 -6.807
-4.936 -2.492 -3.780 -4.874 1.423 -11.000 -11.000 -6.554
-11.000 -3.520 7.973 11.000 -0.226 3.243 11.000

PAP 990 PT1 1255771 885374 -0.177 11.000 0.418 -0.131
0.060 -0.213 1.781 -0.938 -2.180 1.389 1.384 -0.138
0.040 2.251 1.149 -0.647 -3.444 2.318 1.571
PAP 991 PT1 1719429 1230952 0.514 0.640 1.329 1.148
0.357 -0.032 2.142 -0.528 -0.029 -0.054 1.924 0.108
-0.727 1.831 0.911 2.659 -2.030 2.583 3.379
PAP 993 PT1 1750080 1278607 -6.350 2.624 4.086 3.981
-3.862 3.804 11.000 2.227 -1.950 -4.526 -6.464 -2.943
-6.303 -1.847 -2.228 -2.225 -6.216 4.856 4.047

Table35.txt

PAP 994 PT1	2745890	1858615	0.972	0.622	-1.114	1.491	
-1.423	1.151	1.843	0.008	-1.611	0.719	1.808	0.548
-0.064	3.268	1.906	0.174	-2.485	3.097	2.185	
PAP 995 PT1	2993540	2225203	-1.892	3.353	-3.094	-1.559	
4.457	5.247	2.900	1.633	-11.000	-2.448	-4.965	1.509
-0.550	2.000	0.105	3.865	3.018	2.279	1.512	
PAP 996 PT1	3929926	2714160	0.732	0.035	-0.168	0.805	
-0.321	1.728	1.500	0.632	-2.031	0.309	1.347	1.404
0.453	1.944	-0.191	1.262	-2.067	2.790	3.191	
PAP 998 PT1	1148398	836070	-5.012	-6.937	-3.879	-4.629	
-5.361	-6.154	-0.973	-4.562	-6.352	11.000	-4.547	4.937
6.589	-11.000	6.339	-1.494	-6.384	-1.197	-2.676	
PAP 999 PT1	2785065	2036304	-3.144	6.779	1.650	0.395	
0.544	1.733	11.000	0.914	-1.519	1.948	-1.396	3.140
1.318	-3.487	-4.473	4.044	4.947	1.798	11.000	
PAPA 1001 PT1	1914482	1358416	-0.488	0.573	3.131	4.659	
-1.943	-0.652	2.358	0.503	-0.779	-0.417	1.244	1.489
0.884	0.815	3.968	1.634	-2.767	2.214	2.926	
PAPA 1002 PT1	3064069	2141807	0.526	0.121	1.503	1.582	
-0.525	1.281	1.095	-1.320	-0.852	0.540	-0.150	1.083
-0.245	3.843	0.259	0.906	-2.298	1.545	3.365	
PAPA 1003 PT1	2298082	1660896	-0.403	11.000	-0.228	0.585	
-3.072	-1.247	0.214	-1.063	-3.441	11.000	-0.403	0.365
-0.479	1.649	0.018	0.948	-2.436	2.013	2.512	
PAPA 1005 PT1	2408400	1709018	1.465	5.849	-11.000	-11.000	
-6.407	5.291	2.291	-0.056	4.938	-11.000	-6.033	-1.451
-0.550	-4.188	-3.739	11.000	11.000	-4.184	-0.785	
PAPA 1011 PT1	2853339	1981248	1.270	-0.520	0.704	1.396	
-0.903	0.429	1.734	-0.325	-1.481	1.969	2.206	-0.313
0.261	2.630	2.070	0.968	-1.466	3.207	2.986	
PAPA 1012 PT1	3070922	2073245	1.081	11.000	-0.223	-0.178	
-1.033	-0.759	2.894	0.373	1.611	1.305	1.985	-1.151
-1.906	0.044	-1.293	1.638	-1.774	0.996	0.523	
PAPA 1013 PT1	2724308	1991823	3.357	4.936	-3.038	4.399	
0.386	-1.211	4.243	-5.748	4.825	2.417	6.325	-3.930
-11.000	3.180	-3.173	5.745	-2.248	0.887	3.052	
PAPA 1022 PT1	1154218	826824	1.705	0.585	-1.332	0.807	
-0.448	0.824	1.233	-0.185	1.455	2.647	0.774	-0.745
-2.247	1.098	-1.507	0.370	-2.151	-1.450	-0.301	
PAPA 1028 PT1	1225766	828765	1.167	1.087	-0.829	2.883	
0.053	0.271	1.894	-0.619	-0.823	-0.211	0.676	0.202
-2.350	2.439	-1.185	0.816	-2.447	0.719	1.612	
PAPA 1035 PT1	2474135	1668047	-0.480	5.926	11.000	11.000	
-0.719	-4.931	0.854	-2.610	11.000	-3.557	-3.493	-1.373
-5.003	-3.528	11.000	7.120	2.498	3.767	11.000	
PAPA 1037 PT1	3034908	2056206	11.000	5.296	11.000	6.273	
-2.000	11.000	7.992	2.670	-5.784	4.118	-4.365	-2.000
-5.394	-1.231	-3.099	-0.847	-4.854	4.610	11.000	

Table35.txt

PAPA 1044 PT1 2412273 1686056 3.065 3.734 -1.515 -11.000
1.655 1.174 2.499 0.020 -6.167 4.305 -2.414 -2.065
-6.758 -2.334 2.064 1.310 -1.761 1.491 3.078
PAPA 1048 PT1 942491 655603 -11.000 6.213 -4.306 -11.000
3.492 11.000 -1.200 -3.373 -4.809 4.109 -11.000 11.000
-3.779 4.683 1.339 5.900 2.828 11.000 6.589
PAPA 1057 PT1 1991552 1459881 2.196 11.000 1.229 1.270
-2.634 1.562 0.794 0.896 -0.576 0.320 -0.847 0.827
0.215 0.950 1.273 1.342 -0.817 2.081 2.294
PAPA 1059 PT1 2619403 1826228 -2.003 -0.383 0.476 1.490
-1.709 -0.581 4.702 5.735 -1.956 -0.349 0.633 2.050
0.509 2.954 1.931 0.959 -3.419 4.468 5.148
PAPA 1062 PT1 2504082 1822689 -5.032 7.262 2.389 3.278
3.390 4.190 0.924 1.450 -11.000 -1.662 -0.443 -1.016
-3.341 -3.410 -6.153 1.189 -2.173 -2.200 -2.005
PAPA 1066 PT1 1848106 1353357 1.143 -0.091 0.952 0.340
-1.027 1.991 2.295 -0.453 0.192 0.468 0.416 -1.280
-0.061 0.876 -0.313 2.055 -0.392 0.442 1.105
PAPA 1072 PT1 1672017 1223359 -11.000 11.000 0.376 0.828
-0.997 0.385 0.397 -0.841 -1.375 -0.533 0.819 1.474
0.579 1.062 0.943 -11.000 -11.000 1.482 2.690
PAPA 1074 PT1 3671368 2616727 5.115 7.830 -1.853 2.926
-3.697 3.468 7.613 0.185 5.740 -11.000 3.755 -1.726
4.824 -1.151 -2.846 3.000 -3.121 2.823 1.455
PAPA 1077 PT1 2848617 1970330 1.128 0.506 1.913 1.461
-1.367 0.225 0.651 -0.502 -0.216 0.490 0.470 1.561
2.378 3.580 0.296 1.645 -1.580 2.230 4.427
PAPA 1081 PT1 1510202 1086040 0.692 0.691 2.315 4.346
-1.024 1.216 2.282 0.971 -11.000 0.758 -2.644 1.170
1.599 4.170 1.990 1.086 -0.789 2.822 5.124
PAPA 1094 PT1 3513585 2507590 3.997 4.358 -2.460 -4.870
-0.568 6.852 3.091 3.166 -0.004 -11.000 2.584 2.012
-6.937 -4.612 -0.502 -4.784 -2.242 11.000 6.382
PAPA 1095 PT1 3560890 2518421 -0.981 11.000 1.543 2.286
-2.448 -0.514 0.981 -1.731 -2.160 0.101 1.096 1.047
-0.721 2.615 11.000 -0.164 -2.402 2.532 3.028
PAPA 1096 PT1 3958088 2813626 -3.593 7.461 -1.809 3.875
-4.334 -2.193 2.362 -4.399 -2.663 2.516 5.989 -0.843
-2.431 -5.074 1.655 3.043 -1.547 2.729 7.705
PAPA 1097 PT1 623832 427924 0.557 11.000 11.000 11.000
-2.909 -2.040 -0.625 -1.707 -4.928 -1.706 1.912 3.221
1.132 5.147 2.798 -0.356 -3.021 4.307 5.736
PAPA 1099 PT1 1677255 1222562 0.280 0.739 1.046 1.677
0.187 1.047 1.892 -0.560 -1.252 -0.084 1.636 0.459
0.031 2.422 -0.312 1.031 -2.169 3.666 3.749
PAPA 1100 PT1 3796100 2730660 0.301 11.000 0.578 1.140
-1.108 -0.643 -0.383 -0.676 -2.294 0.224 -0.217 11.000
-11.000 2.442 -1.530 0.909 -3.011 2.406 3.602

Table35.txt

PAPA 1103 PT1 2995934 2231085 0.788 -0.006 2.361 2.280
-1.113 1.623 2.842 -0.620 -0.541 0.529 -11.000 1.062
0.591 2.476 0.293 2.426 -0.814 2.917 5.321
PAPA 1109 PT1 1964835 1393879 11.000 4.135 -0.534 0.890
0.962 2.718 11.000 4.190 -11.000 7.262 4.233 -5.227
-11.000 -0.342 -0.647 1.956 -11.000 1.714 -0.306
PAPA 1110 PT1 1168554 850384 2.381 11.000 5.024 1.146
0.106 4.189 6.223 -2.609 -1.370 -0.655 -0.231 -0.233
-0.579 1.089 0.261 1.811 -2.034 1.929 3.067
PAPA 1112 PT1 645068 455990 1.017 -0.161 0.229 2.751
0.748 -0.394 1.695 -0.279 -1.327 -0.765 3.578 -0.529
-1.427 -6.229 11.000 -0.318 -2.700 -0.323 0.901
PAPA 1113 PT1 545241 378323 6.074 1.267 -4.834 -11.000
8.210 6.074 4.100 0.102 -11.000 0.461 3.669 -5.179
-6.721 -4.511 -5.897 4.300 -3.826 2.650 0.302
PAPA 1114 PT1 1010270 731328 -11.000 11.000 11.000 11.000
-0.539 1.105 1.314 0.198 -11.000 1.362 11.000 0.845
-1.647 1.586 1.807 -0.009 -1.730 1.787 1.953
PAPA 1115 PT1 658520 472314 -1.349 0.400 7.848 -5.780
1.208 -0.242 5.450 0.880 -3.952 11.000 -11.000 4.384
2.693 2.813 -1.625 1.218 2.193 1.340 11.000
PAPA 1116 PT1 2498108 1775319 -1.146 0.720 -11.000 1.768
0.097 1.653 2.117 2.084 -1.127 -0.695 1.297 -0.493
-4.795 2.131 11.000 0.926 -1.467 0.077 2.631
PAPA 1117 PT1 950972 664666 -2.406 3.639 4.564 11.000
-5.661 -0.853 -2.707 -5.014 -5.159 -0.743 -4.977 5.390
-3.185 -0.710 3.901 -2.961 -11.000 4.483 7.973
PAPA 1118 PT1 535966 389544 4.055 6.961 11.000 -2.534
-3.572 -2.675 3.835 -4.475 -3.386 -1.073 -4.709 -1.882
-3.691 -1.120 -0.946 3.147 -4.844 0.913 -0.024
PAPA 1120 PT1 881893 616046 -1.701 1.483 3.215 0.744
-5.370 0.638 11.000 -2.314 -11.000 -4.694 8.126 1.182
-3.651 -4.884 -11.000 0.927 -1.067 2.011 1.321
PAPA 1121 PT1 2045077 1469179 0.782 -0.640 1.488 0.937
-1.690 -0.263 0.001 -0.717 0.053 11.000 0.625 2.572
1.181 4.746 2.167 0.266 -2.414 3.715 3.123
PAPA 1122 PT1 2122093 1525647 0.853 0.183 0.779 2.288
-1.673 -0.215 0.398 0.036 -1.091 0.524 2.416 2.652
1.014 11.000 11.000 0.444 -2.323 4.682 5.201
PAPA 1123 PT1 1823491 1300403 0.471 0.703 1.498 1.131
-1.565 -0.733 1.255 -0.018 -1.141 0.822 3.224 3.980
2.697 4.348 2.470 1.311 -3.824 5.645 6.184
PAPA 1126 PT1 2481014 1646229 -2.334 -1.304 5.707 11.000
-0.271 0.104 -0.311 -1.238 -1.066 -0.415 -1.539 -3.390
-2.809 -2.589 -2.861 -0.304 -2.114 -1.298 -2.310
PAPA 1128 PT1 2517754 1725457 0.820 1.491 -0.801 -0.181
-1.160 1.359 2.679 1.623 -0.561 1.140 0.297 -3.437
-3.125 -2.018 -1.637 0.559 -2.527 -1.168 -0.984

Table35.txt

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PAPA 1129 PT1  2861552       1938257      1.709     -0.267    -0.596    0.122
-0.446    0.909     1.158     -0.857    -0.072    0.081     -1.714    -3.890
-2.490    -2.871    -2.448    2.192     -1.305    -1.313    -2.068
PAPA 1130 PT1  2578566       1809637      0.788     2.044     -1.341    -0.250
-1.375    -0.294    2.400     -0.004    1.356     -0.010    1.165     -3.421
-3.254    -0.285    -2.368    0.446     -1.445    -0.411    -1.128
PAPA 1131 PT1  2689488       1917437      -2.390    -2.422    -3.556    -1.882
-1.421    -1.686    -0.017    -2.803    -1.663    -2.810    -3.236    -3.317
-3.293    -1.946    -3.111    -0.936    -3.381    -2.173    -3.482
PAPA 1132 PT1  2324546       1624624      0.947     2.070     -0.623    0.412
-0.363    0.533     0.987     0.284     -0.277    -0.104    0.841     -1.624
-2.231    -0.341    -1.531    1.202     -2.663    0.850     -0.087
PAPA 1133 PT1  2427399       1706783      0.253     -1.378    11.000    11.000
-0.907    0.269     0.137     -1.334    -0.273    -1.673    -2.017    -3.515
-2.278    -2.593    -2.892    0.871     -0.964    -1.397    -1.151
PAPA 1134 PT1  2948386       2057652      0.767     11.000    -2.073    -0.411
0.035     -0.513    1.183     -1.029    0.851     0.071     -2.061    -3.244
-0.196    -0.273    -1.130    0.072     0.321     0.152     -0.584
PAPA 1135 PT1  2915249       1959913      11.000    11.000    4.102     2.118
-0.971    0.466     4.945     5.231     -11.000   -5.205    -11.000   0.345
-3.125    -1.714    5.446     2.104     -11.000   1.389     11.000
PAPA 1136 PT1  2318145       1623377      3.727     2.434     3.851     3.905
0.041     11.000    11.000    -0.719    -11.000   6.563     -1.479    -0.299
-5.353    -4.964    -3.340    0.457     -2.783    -0.738    0.975
PAPA 1137 PT1  2041413       1430113      1.940     -0.796    -2.048    -0.027
-1.406    -0.601    3.128     0.325     1.947     1.892     -0.126    -3.836
-1.956    -0.175    -0.589    -0.592    -1.268    -0.764    -1.598
PAPA 1138 PT1  1824672       1301981      -2.348    -1.666    -6.399    -11.000
-2.369    -2.226    -0.315    -1.402    -3.659    -0.953    -1.911    -3.209
-4.070    6.069     11.000    -0.354    -4.046    -1.138    -2.658
PAPA 1139 PT1  1718637       1197099      0.080     11.000    7.180     -11.000
-11.000   -11.000   1.779     11.000    -11.000   11.000    0.576     -1.256
-0.541    -4.392    -0.170    11.000    -4.030    0.753     11.000
PAPA 1140 PT1  666116        476758       -0.072    1.230     0.020     1.935
-1.097    0.930     1.752     -0.081    1.167     0.622     -0.830    -4.322
-2.291    -1.188    -1.629    -1.888    -2.028    -0.975    -2.229
PAPA 1141 PT1  1636956       1138285      1.539     7.719     3.031     -11.000
-6.758    1.391     4.539     -0.838    3.814     5.317     -5.308    3.162
2.146     -4.120    5.579     -4.836    -3.799    -1.899    3.368
PAPA 1142 PT1  1400052       988790       -11.000   11.000    0.834     3.528
0.914     0.052     3.093     2.542     11.000    5.678     -0.865    -2.586
1.019     -2.761    4.119     -11.000   -11.000   -4.827    -1.978
PAPA 1143 PT1  1443909       1019093      -1.635    -0.859    11.000    11.000
-1.024    -2.095    0.403     -2.096    0.061     -1.348    -1.910    -3.323
-2.388    -0.242    -2.269    -2.698    -3.337    -1.669    -1.732
PAPA 1147 PT1  1037888       742981       0.709     0.378     0.743     1.897
-1.055    -0.305    2.077     -0.850    0.392     1.468     1.887     0.281
-0.867    2.972     0.681     -0.550    -2.403    0.910     2.483
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Table35.txt

PAPA 1148 PT1 1084548 708111 0.609 0.503 11.000 11.000
-1.379 -1.155 2.040 -0.077 2.504 0.865 -11.000 -5.804
-3.530 -2.320 -1.348 -0.223 -3.232 -3.203 -3.934
PAPA 1149 PT1 1512176 1046984 0.435 11.000 -2.468 -1.695
-1.510 -0.631 1.075 -0.880 -0.154 -1.100 -0.879 -4.256
-3.013 -3.625 -1.819 -0.772 -3.460 -2.692 -4.619
PAPA 1152 PT1 686941 486328 -0.097 -0.566 -2.740 -1.998
-0.568 -0.340 1.865 -0.638 1.457 2.383 -0.022 -4.314
-3.171 -2.838 -2.426 -0.914 -3.347 -3.137 -3.516
PAPA 1283 PT1 1047956 713526 -0.766 -1.523 -1.470 -0.892
-1.876 0.134 2.609 -0.630 1.150 1.076 0.632 -3.495
-4.022 -2.449 -2.519 0.632 -1.776 -2.082 -2.109
PAPA 1740 PT1 3135299 1223450 -6.473 11.000 11.000 -11.000
6.160 -11.000 -11.000 3.221 -0.687 -11.000 -11.000 2.371
-11.000 -4.137 3.126 3.900 -5.627 0.976 2.764
PAPA 1742 PT1 3337611 1485139 -0.349 0.009 0.040 2.015
-1.697 0.611 1.331 -0.668 -0.396 0.542 -0.369 1.559
-0.527 0.780 -0.554 -0.181 -0.326 0.330 0.836
PAPA 1743 PT1 4167149 1427505 3.180 11.000 3.628 5.167
2.782 3.797 -11.000 -11.000 -11.000 3.574 3.632 -0.888
-3.543 -5.604 -4.316 1.889 2.880 1.413 -2.359
PAPA 1747 PT1 4213185 1432954 -0.528 -0.274 -0.378 0.695
-1.706 -1.142 1.265 0.915 1.011 0.816 0.518 -2.469
-0.868 1.154 -0.641 -0.012 -0.820 0.118 -0.205
PAPA 1748 PT1 3153812 1236676 -1.221 11.000 -0.999 -1.295
-1.984 -0.681 0.228 -2.457 0.809 0.560 -1.629 -1.603
-1.432 -2.110 -2.471 0.688 -1.897 -1.918 -2.102
PAPA 1750 PT1 3976251 1262569 -0.007 -0.918 -2.332 0.011
-0.297 0.417 1.084 -0.026 1.992 -0.312 -0.869 -2.469
-2.198 -1.192 -2.470 0.330 -0.882 -1.273 -1.683
PAPA 1751 PT1 2849579 1133045 0.858 0.498 -1.379 -1.353
0.018 -0.292 0.644 -0.429 0.940 0.763 -0.666 -1.151
-2.184 -0.336 -2.053 -1.810 0.596 -2.074 -2.547
PAPA 1753 PT1 3917960 1481061 -0.327 11.000 -1.284 1.436
-0.025 -0.648 1.203 -1.693 -0.599 -0.006 -0.466 0.471
-1.152 0.497 -1.915 0.340 -0.381 1.179 -1.564
PAPA 1755 PT1 2380345 1029594 3.639 11.000 11.000 -11.000
-2.218 -11.000 -0.816 -11.000 3.056 6.197 -11.000 -2.752
-11.000 -0.042 -0.769 5.251 1.678 -2.781 11.000

PAPA 1756 PT1 3504144 1313187 4.847 6.914 -0.953 4.058
-11.000 4.473 3.163 4.299 -11.000 -0.180 1.426 1.220
-6.055 -4.351 -3.033 1.144 0.277 -0.444 3.012
PAPA 1761 PT1 3095945 1221982 0.627 -1.684 -1.116 0.817
-0.148 -0.236 0.946 -0.043 -1.385 0.637 0.329 -0.897
-0.115 1.179 1.187 0.162 -1.872 -0.328 -0.826
PAPA 1763 PT1 2792887 1187065 2.199 4.697 3.351 11.000
-11.000 11.000 3.190 -11.000 -1.433 -11.000 -3.432 0.430

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PAPA 1768 PT1  3789395       1554464      0.186     7.281     -2.330    -0.888
2.068     1.291     0.234     -1.593    4.439     0.090     -3.412    -2.977
-3.832    -1.643    3.355     -0.114    -1.317    0.436     5.914
PAPA 1773 PT1  4888867       1817621      -0.779    11.000    -0.726    0.163
-0.962    -1.237    -1.008    -2.122    -2.462    -1.827    -1.928    -0.717
-1.702    0.149     -0.735    -0.592    -3.841    -1.148    -0.081
PAPA 1775 PT1  3755399       1444463      -0.959    11.000    -1.133    0.154
-1.258    -0.820    -0.242    -1.398    -0.009    -1.584    -0.771    -1.449
-1.492    -0.499    1.098     7.607     -1.517    -0.524    -0.778
PAPA 1816 PT1  2426116       966724       -1.152    0.235     -1.525    -0.790
-0.991    0.442     1.011     -1.057    2.909     -0.650    -2.065    -3.042
-2.719    -2.669    -1.549    1.614     0.374     -2.133    -1.492
PAPA 1817 PT1  2597324       1065060      -2.020    4.603     3.121     -1.918
3.043     0.022     6.910     -11.000   -11.000   -2.979    11.000    7.578
2.077     -4.449    -7.034    2.757     3.773     0.103     -2.189
PAPA 1818 PT1  3062043       1194768      -0.854    -0.187    0.042     -0.818
-1.297    -0.114    1.551     -0.486    0.918     0.490     -1.220    -2.331
-2.295    -0.388    -2.761    1.483     0.571     -2.497    -3.017
PAPA 1819 PT1  4312947       1570494      -11.000   -11.000   11.000    5.598
-0.149    7.143     11.000    5.245     -5.707    1.548     -5.168    1.015
-5.026    -2.418    -1.660    -2.702    1.024     -0.174    -1.150
PAPA 1820 PT1  1041508       368045       -0.489    11.000    4.195     3.065
-3.478    -3.420    0.177     -3.229    -3.227    -3.427    -11.000   5.008
-3.831    -11.000   2.919     1.445     4.869     -1.837    4.980
PAPA 1821 PT1  3244432       1225904      4.297     5.370     0.811     -2.573
-0.389    1.524     0.575     -2.340    -11.000   -11.000   -2.607    -2.473
-11.000   -11.000   -11.000   0.325     0.584     -0.976    -2.453
PAPA 1823 PT1  2224738       743569       -11.000   11.000    7.049     8.014
-2.872    -1.551    7.617     11.000    -4.741    -6.937    -11.000   3.520
-11.000   -4.232    -5.607    -4.790    -11.000   -0.667    3.538
PAPA 1824 PT1  2592140       986919       -0.617    -2.308    -1.479    1.387
-1.078    -0.315    2.204     1.524     2.423     -3.937    -0.933    -3.319
-2.725    -2.319    -0.695    0.324     0.297     -3.482    -3.746
PAPA 1825 PT1  2612410       977897       -11.000   11.000    -2.152    -4.309
-11.000   -5.192    7.848     11.000    -1.430    0.572     5.513     0.819
2.229     -2.723    -2.592    -5.853    -11.000   2.527     4.485
PAPA 1826 PT1  2667674       1002811      1.232     1.535     -0.713    0.245
1.327     0.285     1.132     -0.262    0.167     0.509     -0.833    -3.397
-2.220    -0.966    0.240     0.076     -2.051    -2.311    -2.769
PAPA 1828 PT1  1540582       567838       2.187     5.857     -3.595    -0.194
-3.049    11.000    3.014     -11.000   -0.839    4.738     -11.000   -5.678
-7.034    -5.522    -0.367    -0.376    -2.823    -0.166    -1.403
PAPA 1829 PT1  3822385       1227467      -0.366    11.000    6.423     -0.825
-11.000   0.403     11.000    -0.305    -11.000   8.126     -5.996    -1.605
-2.814    -0.579    -5.305    -2.450    -5.702    0.971     1.954
PAPA 1831 PT1  2929157       1165645      0.347     0.479     -1.444    0.764
-0.528    -0.153    11.000    11.000    -0.576    1.238     -0.050    -2.095
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Table35.txt

-1.248 -0.311 -1.064 0.586 -0.864 -1.678 -2.399
PAPA 1832 PT1 2377039 892337 11.000 11.000 0.068 -11.000
-5.987 -7.034 11.000 11.000 -11.000 7.992 -6.024 -1.258
-11.000 2.201 0.752 1.793 0.244 -3.176 11.000
PAPA 1833 PT1 1208352 479702 8.077 11.000 -1.875 -1.853
-2.617 -1.735 1.169 -1.024 -1.896 3.679 -0.318 -3.007
-3.074 -4.733 11.000 0.661 -0.488 -0.740 4.005
PAPA 1834 PT1 2070779 817558 -0.362 0.864 -2.182 1.325
-1.901 -0.966 1.535 -0.338 1.440 0.533 1.795 1.048
-2.033 -1.157 -0.434 -0.595 -1.843 -2.543 -2.901
PAPA 1836 PT1 1648431 718151 0.942 1.181 -1.303 -0.389
-0.361 0.453 0.552 -0.917 2.081 1.079 -1.066 -2.794
-1.883 -2.050 -0.749 0.768 -0.290 -2.566 -3.346
PAPA 1837 PT1 2922537 1091596 -0.469 -0.266 -0.253 -0.115
-1.315 -0.638 0.980 -1.288 -0.974 -1.964 0.034 -3.168
-1.836 -0.932 -1.560 -0.133 -3.068 -1.751 -1.621
PAPA 1838 PT1 331653 119391 -2.983 -1.396 -0.100 0.181
-1.462 -2.929 4.330 2.832 -1.557 -2.384 -3.505 -3.241
-4.706 -3.255 -3.557 -3.235 -6.308 -2.603 -4.786
PAPA 1839 PT1 1723176 669732 0.216 0.908 -1.488 -0.507
0.267 -1.373 2.950 0.249 1.118 1.223 0.343 -1.746
-2.648 -1.504 -1.245 -0.864 -1.484 -2.540 -3.538
PAPA 1840 PT1 3572324 1283227 0.386 11.000 -0.781 0.963
-1.612 0.007 1.444 -1.593 1.241 1.001 0.019 -1.421
-0.323 0.027 -1.488 0.530 -2.523 -0.071 -0.678
PAPA 1841 PT1 3512971 1304223 -0.035 -0.283 -1.516 -0.956
-1.736 -0.558 2.050 0.030 2.207 1.004 -0.007 -4.284
-2.562 -1.479 -0.318 -1.009 -0.370 -4.143 -4.919
PAPA 1842 PT1 3078864 1047895 0.257 0.472 -0.532 0.430
-0.696 -0.650 0.859 -0.752 2.346 0.419 -0.535 -1.913
-2.115 -1.175 -1.350 0.924 -0.528 -2.117 -2.988
PAPA 1844 PT1 2249508 886795 -3.075 3.192 2.575 -2.739
0.625 0.276 1.572 -3.648 -11.000 -0.704 2.662 -5.932
-4.666 -11.000 -5.878 2.678 5.059 -1.019 1.636
PAPA 1845 PT1 1787850 633704 -11.000 11.000 7.729 6.093
1.606 1.903 11.000 -0.211 -0.663 -4.001 -3.312 -5.257
-11.000 -1.662 -1.058 -0.502 -11.000 -1.882 -2.658
PAPA 1846 PT1 1381772 520294 2.031 -0.016 0.406 -0.054
-0.203 -0.043 2.338 -1.793 0.143 0.298 0.706 -3.898
-3.318 -2.966 -0.280 -0.353 -1.333 -2.524 -2.147
PAPA 1847 PT1 2269646 914879 -0.760 11.000 -1.465 -1.203
-1.610 -2.247 11.000 11.000 -0.612 -2.150 -0.715 -1.536
-1.692 -1.825 7.758 0.064 -4.018 0.016 -2.324
PAPA 1848 PT1 228504 137963 0.237 11.000 -1.648 -1.112
-1.035 0.040 1.830 -0.014 0.873 -0.519 -2.391 -3.919
-2.795 -2.103 0.509 -1.436 0.682 -0.994 -2.269
PAPA 1849 PT1 3525796 1251306 3.305 11.000 11.000 11.000
1.653 1.780 2.077 2.694 -11.000 -11.000 2.847 1.160

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PAPA 1850 PT1  2235099       783392       4.890     11.000    0.745     -2.524
2.403     1.717     4.225     2.638     2.606     -11.000   2.333     -11.000
-4.126    -11.000   5.679     1.295     -11.000   11.000    4.019
PAPA 1852 PT1  2016960       784594       -0.016    0.453     11.000    11.000
-2.245    -0.979    0.795     -1.491    -0.039    -2.273    0.772     -3.185
-2.651    -3.156    -0.937    -1.725    -2.826    -4.330    -5.775
PAPA 1853 PT1  2523335       1068072      -11.000   11.000    -6.366    0.621
1.106     -3.730    0.682     -1.671    11.000    -6.937    2.137     0.016
1.215     5.603     3.078     -1.243    -2.155    -0.639    -1.047

PAPA 1855 PT1  2268620       822346       0.310     11.000    -1.298    -0.487
-1.081    -0.733    1.343     -0.031    0.599     0.826     -1.293    -2.573
-1.600    -0.803    -1.209    -0.841    -1.496    -2.105    -0.956
PAPA 1856 PT1  2220227       956230       5.474     11.000    -2.586    -2.533
-11.000   11.000    7.751     -11.000   0.596     -11.000   -4.757    -0.007
-3.188    -4.341    -3.698    -4.894    -11.000   0.068     -2.194
PAPA 1857 PT1  2747963       1185111      -0.194    0.476     -11.000   -4.597
11.000    11.000    -1.003    -3.371    -3.084    -1.913    -2.116    -1.066
-5.384    0.977     -5.894    -1.114    -2.935    -1.045    4.661
PAPA 1858 PT1  1747130       694150       0.293     1.198     -0.728    -0.140
1.207     -1.702    2.819     -0.059    -11.000   0.559     -0.029    -3.026
-2.009    -1.341    -1.913    1.061     -2.064    -1.713    -1.526
PAPA 1859 PT1  1423051       460381       -0.565    1.217     11.000    11.000
-0.874    -0.699    1.175     -0.722    -0.167    0.165     -0.559    0.523
-0.727    -1.070    0.286     -2.390    -1.645    -1.736    -1.608
PAPA 1860 PT1  3396582       1234140      0.054     0.162     -1.258    -0.396
-0.035    -1.141    0.684     -0.611    1.773     0.239     -1.219    -3.212
-1.858    -1.887    -3.368    2.036     0.999     -2.906    -3.354
PAPA 1861 PT1  2233471       677158       0.778     11.000    -0.818    0.726
-2.192    -0.934    1.472     -1.806    0.870     0.465     -0.929    -2.493
-2.868    -0.144    0.316     0.446     -1.116    -1.085    -3.125
PAPA 1862 PT1  1318847       457009       1.147     0.179     0.774     0.388
0.514     -0.011    1.355     -0.082    -0.592    0.505     -0.845    -2.749
-2.856    -1.767    -0.683    1.446     -0.142    -1.875    -1.671
PAPA 1863 PT1  3691409       1411911      3.628     11.000    0.699     3.172
-6.739    6.047     -6.430    -1.023    -11.000   -3.214    -5.732    1.034
-0.112    4.325     -0.062    7.162     -1.873    0.344     -0.308
PAPA 1864 PT1  2693623       1094546      4.249     4.696     3.252     -3.988
0.491     1.522     11.000    -6.080    -11.000   -4.535    -0.181    -2.313
-2.996    -1.810    -11.000   -1.706    -2.154    0.818     0.577
PAPA 1865 PT1  2314125       900578       6.015     3.098     -0.452    -11.000
-11.000   -0.385    7.200     11.000    -11.000   11.000    -11.000   -2.179
-6.464    -0.352    -0.783    0.860     -0.414    0.747     0.520
PAPA 1866 PT1  3309267       1229895      0.602     -0.299    -1.135    0.199
0.279     -0.848    2.199     -0.470    2.433     1.953     -0.829    -1.210
-1.770    -1.572    -0.965    1.797     -0.415    -1.129    -2.192
PAPA 1867 PT1  3043723       1137673      -11.000   -11.000   2.709     5.468
```

Table35.txt

-6.447	-6.480	7.420	11.000	8.014	-3.996	-7.034	-5.714
-6.096	-4.841	-5.091	-1.792	-4.792	-3.876	-6.539	
S100	2285289	1045123	-2.145	0.919	0.199	0.253	
0.184	0.004	-0.172	-2.039	0.132	-1.773	1.531	-1.832
-0.002	0.246	-0.035	-0.667	-1.059	2.054	-0.094	
S105	2095231	952972	11.000	11.000	1.282	0.788	
0.753	0.531	0.898	-1.149	0.028	0.911	2.458	0.244
0.883	0.722	-1.454	-0.098	-0.313	1.544	2.014	
S109	1686634	828108	-5.815	-5.092	11.000	11.000	
11.000	11.000	-4.984	11.000	-5.172	11.000	7.576	11.000
-3.212	-5.869	5.967	11.000	5.287	7.992	-4.341	
S109	2340188	1259849	-6.329	-6.937	-7.034	11.000	
7.540	7.594	-3.964	11.000	-4.897	-7.034	5.808	11.000
-4.801	-6.287	5.545	11.000	6.675	6.113	-4.343	
S110	1618305	876598	0.605	0.631	-0.663	0.231	
1.944	1.491	0.745	0.955	-0.275	2.009	0.198	-1.675
-0.304	-1.311	-1.488	0.962	0.917	0.462	0.051	
S119	2023106	1096432	0.503	-1.115	-2.213	-0.904	
0.295	0.417	0.211	0.246	-0.876	0.345	-0.024	-2.536
11.000	11.000	-1.588	0.755	-0.166	-0.066	-1.385	
S122	1621439	892805	-3.817	-4.046	-4.405	-5.508	
-2.925	-4.347	-2.413	-5.366	-4.153	-4.484	-3.439	-6.260
11.000	11.000	11.000	11.000	11.000	11.000	-3.939	
S127	1917135	1045092	0.021	11.000	-0.947	-0.349	
0.952	-0.132	0.656	0.093	0.331	-4.197	-0.159	-0.993
0.398	-0.217	-1.732	7.326	0.845	-0.083	-0.579	
S134	1809148	982232	-6.604	-6.647	6.165	11.000	
8.210	11.000	-4.271	11.000	-5.892	11.000	5.850	7.122
5.296	-5.896	3.797	7.906	-4.165	-5.586	-5.320	
S135	2047263	1184449	1.354	1.989	-0.858	-0.713	
-0.252	0.295	0.024	-0.691	-0.571	0.058	-0.260	-1.247
-0.028	0.199	-0.785	0.504	0.420	-0.835	-0.957	
S135	1957653	1042578	-2.931	-3.552	-3.301	-3.449	
-2.121	-2.583	-2.374	-3.370	-3.110	-2.621	-2.414	-4.594
8.210	11.000	6.097	11.000	-2.036	-2.546	-2.491	
S135	1749948	976767	3.372	2.023	-0.184	2.546	
2.331	3.275	0.205	1.383	0.265	1.737	-1.738	-1.276
-0.150	0.828	-1.541	2.742	1.435	-0.396	-0.468	
S136	2148240	1250988	-0.126	0.119	0.457	0.658	
0.783	1.790	0.611	0.334	0.228	1.279	-0.383	-0.010
-0.736	1.374	-2.163	1.366	0.819	1.191	-1.940	
S136	2217198	1418681	-0.385	-0.841	-0.247	1.061	
1.495	0.523	0.350	1.285	-0.338	1.475	0.440	-0.356
-1.020	0.934	-1.812	1.933	0.987	1.650	-1.303	
S136	1789315	1079965	0.665	-0.166	-1.180	0.517	
-0.151	-0.958	-0.251	-0.047	-0.383	1.311	0.068	-0.963
11.000	11.000	-1.648	-0.328	-0.794	0.459	-2.325	
S137	2044974	1021357	11.000	11.000	1.369	3.026	

Table35.txt

2.665	2.795	-5.418	-6.120	0.748	11.000	1.979	2.146
1.922	1.991	0.464	2.501	1.694	1.020	0.839	
S139	2093461	1027505	4.591	7.023	-1.851	-3.221	
5.377	5.264	-1.582	-4.652	1.903	6.706	-4.362	-7.034
11.000	11.000	-3.676	-4.774	1.608	2.361	-1.723	
S142	1884670	933444	-0.196	-0.054	-1.921	-0.732	
-0.460	-0.358	4.611	6.871	-1.508	-0.250	-1.899	-2.757
1.603	4.030	-1.441	0.192	-0.042	1.214	-2.965	
S143	2080754	1045090	1.766	0.924	0.343	-0.174	
0.888	0.111	1.570	0.641	-0.013	2.322	0.418	-0.976
-0.573	0.054	-1.845	0.930	0.098	0.711	-1.413	
S143	1925256	978889	1.220	0.215	-0.464	-0.573	
-0.430	-0.125	0.708	-0.179	-0.339	0.154	0.446	-1.712
0.262	-0.471	0.810	2.675	0.612	0.180	-0.646	
S157	2241734	1132216	1.899	1.763	-0.572	0.507	
2.375	0.638	1.575	0.671	-0.420	0.905	-0.544	-0.778
-0.228	0.878	-2.110	1.694	-0.603	-0.686	-1.061	
S168	4691615	2298576	0.105	-3.250	3.483	4.452	
-1.195	-0.270	11.000	11.000	1.204	1.416	3.036	2.840
1.632	3.458	1.471	11.000	2.134	1.376	1.938	
S172	2228743	1146077	0.236	-1.180	-0.641	-0.469	
1.335	0.429	0.553	1.245	-0.142	-0.159	-0.219	-3.042
11.000	11.000	-1.271	-0.725	0.357	-1.915	-2.363	
S178	2059262	1086269	0.918	0.815	-0.823	-0.510	
1.218	0.267	1.665	0.775	-1.182	0.965	-0.059	0.102
0.107	1.340	-0.038	1.419	0.250	0.904	-0.130	
S184	2459720	1228591	-1.495	-1.665	-1.740	-2.154	
0.162	0.383	11.000	11.000	0.376	-0.648	-1.325	-3.064
-1.770	-1.794	-2.336	-1.697	-0.655	-1.219	-2.108	
S22	4489593	1979066	-2.108	5.820	-1.180	0.045	
1.948	0.725	0.850	0.331	-0.417	1.817	-0.248	-2.937
-1.784	-0.320	-4.415	3.412	0.828	0.984	-1.057	
S48	3149092	1394968	1.819	1.000	0.654	-0.192	
0.850	0.700	1.047	-1.066	-1.938	-0.257	0.920	-0.796
0.074	-0.260	-0.444	0.054	-1.083	0.904	-0.310	
S60	717117	298379	1.805	2.249	0.023	-1.020	
-2.503	2.109	-4.282	11.000	-0.370	0.941	3.180	-0.885
11.000	11.000	11.000	0.773	0.367	0.230	1.103	
S69	2900693	1248849	1.185	0.324	-1.111	1.712	
-0.053	0.860	0.838	-0.676	-0.688	0.332	0.457	-1.380
0.200	-0.022	-1.031	-0.126	-0.167	0.178	-0.376	
S69	2652953	1140067	0.244	-1.359	-1.127	0.472	
-1.309	-0.045	-1.169	-2.933	-2.766	-1.217	0.780	-1.731
-1.684	-2.037	11.000	11.000	-1.958	-0.496	-0.152	
S69	3389303	1486208	1.790	-0.172	0.299	2.575	
0.339	1.047	0.522	-2.340	-0.892	11.000	1.694	-0.883
0.533	1.266	-0.233	0.234	-0.104	1.392	0.881	
S7	3082659	1456198	-2.068	0.251	0.119	0.752	

Table35.txt

2.230	-0.031	0.488	1.966	-0.258	2.248	0.492	-0.127
-0.252	1.465	0.188	1.348	1.399	0.343	-0.310	

chr10q	chr11p	chr11q	chr12p	chr12q	chr13q	chr14q	chr15q
chr16p	chr16q	chr17p	chr17q	chr18p	chr18q	chr19p	chr19q
chr20p	chr20q	chr21q	chr22q	chr1p_AI	chr1q_AI	chr2p_AI	chr2q_AI
-11.000	11.000	11.000	0.763	1.417	11.000	-11.000	-6.937
5.849	4.946	-3.012	-0.504	-2.656	-11.000	-0.767	-1.690
11.000	11.000	-5.168	-2.658	1.717	4.876	17.767	23.305
-0.318	-0.043	1.277	-0.301	-0.061	-1.056	-0.121	1.448
1.185	-0.128	-3.717	-1.946	0.783	-1.334	3.009	1.676
-2.120	-0.489	1.273	-0.470	-0.776	9.306	1.681	-0.232
-1.644	-0.890	-1.657	-1.596	-1.839	11.000	-2.603	-5.641
0.949	-11.000	0.372	-1.226	-0.787	-3.744	2.210	1.245
11.000	11.000	-0.612	-0.708	-1.719	-1.503	-1.467	-1.858
0.762	2.227	-11.000	11.000	4.498	11.000	3.404	-11.000
2.951	-4.983	-2.928	2.239	6.674	-11.000	2.955	5.642
-4.325	2.200	-4.080	-4.008	18.893	16.668	-0.903	20.757
-5.302	-4.887	-5.724	3.636	-3.707	0.403	5.482	-5.292
-1.802	-3.157	3.331	-3.904	7.287	-11.000	4.897	2.286
5.775	7.385	-6.493	-3.193	-0.535	13.807	1.316	19.755
-1.111	-1.079	-0.447	1.111	3.143	-1.072	-0.797	0.174
0.778	-0.697	-0.550	-2.635	-0.141	-6.012	2.787	1.036
-2.320	-0.471	-0.090	-2.194	-1.010	-0.248	0.139	-1.806
-11.000	-0.611	-11.000	11.000	5.374	11.000	-11.000	0.079
0.575	-6.407	0.411	-0.391	0.065	-11.000	1.249	1.684
4.170	11.000	0.203	-2.072	-0.446	15.239	-1.839	-1.163
4.262	2.641	3.570	3.768	4.264	4.027	3.353	-1.876
-2.059	3.498	3.441	3.572	-5.798	-11.000	2.015	3.354
11.000	11.000	1.455	2.204	15.783	3.051	-1.677	-2.055
-11.000	-1.121	-1.501	-3.561	-1.664	11.000	-11.000	-11.000
4.367	4.100	-6.692	-1.328	-4.060	-11.000	0.568	-0.017
-11.000	11.000	-1.160	-1.604	10.333	16.670	17.598	22.656
-1.502	0.622	-0.100	0.303	0.175	1.801	-0.200	-2.198
-1.516	-0.923	-1.698	-2.729	-1.766	0.416	-0.141	-0.990
-3.786	-2.254	0.254	-4.454	-1.282	-0.624	-1.337	-0.019
0.174	0.355	0.102	-0.334	0.085	-0.996	-0.649	-0.613
1.725	0.700	0.422	-1.361	0.275	-1.889	1.856	1.821
-0.580	0.650	-0.138	-1.561	-1.261	-1.747	-0.970	-3.349
2.932	2.620	2.946	2.227	3.509	11.000	-11.000	-5.540
2.118	2.293	-5.651	-11.000	-11.000	-11.000	2.215	2.514
1.342	1.864	-6.188	-11.000	-0.811	-1.358	-1.677	-2.176
-0.632	-3.188	-3.547	0.330	-0.021	11.000	-3.411	1.458
1.152	1.776	-4.294	-3.651	-11.000	-11.000	0.683	1.302
11.000	11.000	0.014	-5.062	0.069	-0.196	-1.136	10.099

Table35.txt

1.225	0.287	-0.167	1.096	-0.516	0.740	0.373	-11.000
-1.558	-0.760	-6.197	0.211	-3.090	-11.000	0.343	-0.279
7.274	4.209	0.030	0.344	-2.270	-1.062	-1.587	0.129
-3.049	0.253	-0.262	2.231	5.064	11.000	0.419	-11.000
3.014	3.322	0.060	-1.304	-11.000	-11.000	0.156	0.887
-0.797	11.000	0.438	-0.430	-1.293	0.430	0.346	-0.776
-5.304	11.000	-3.917	11.000	-4.882	11.000	-4.469	-4.000
-2.104	-2.831	-1.304	-0.707	-2.330	-11.000	-1.483	5.656
3.099	11.000	-3.062	-1.925	0.695	16.777	0.396	0.283
-1.427	1.352	11.000	0.642	-0.358	11.000	-11.000	1.058
0.268	0.848	0.792	0.378	-6.486	-11.000	0.444	1.581
-1.758	11.000	-0.715	-2.312	0.712	-1.454	-0.141	3.327
1.125	-6.657	-11.000	2.971	2.946	11.000	-6.504	-5.796
1.445	1.476	-4.013	-4.451	-11.000	-11.000	1.120	1.690
6.640	11.000	-2.210	1.068	7.507	8.734	8.798	11.114
-11.000	0.085	5.868	0.069	0.411	11.000	-11.000	-11.000
5.214	7.106	-3.614	0.108	-11.000	-11.000	0.302	0.145
6.821	11.000	-0.733	-0.928	1.504	-0.127	9.177	19.079
0.444	0.341	0.560	-6.839	-11.000	11.000	-11.000	-2.675
0.855	0.226	-4.076	0.487	-4.765	-11.000	0.355	0.602
11.000	11.000	-6.577	-4.533	9.190	16.619	-0.431	0.686
-0.084	-0.885	-1.220	-3.089	-2.949	11.000	-1.959	-2.002
-0.757	0.178	-2.226	0.246	-1.330	-6.025	0.019	-0.590
2.177	7.168	-1.647	-2.677	2.128	-3.179	-0.094	1.690
-6.355	4.909	-1.252	-0.858	-1.263	11.000	-11.000	-11.000
6.562	6.183	-4.975	2.273	-5.106	-11.000	-0.441	0.300
11.000	11.000	-5.354	-0.249	10.480	11.290	10.054	21.394
0.992	0.524	0.071	0.561	0.698	5.738	-11.000	1.186
2.037	0.539	-3.568	1.121	-2.606	-11.000	0.312	0.564
0.679	3.154	-0.391	-0.474	-0.527	-1.775	-1.712	-0.815
-2.989	3.756	3.491	8.041	-11.000	11.000	-1.902	-11.000
5.081	6.872	-6.062	-1.687	-6.260	-11.000	1.283	1.236
11.000	11.000	-1.407	-1.067	16.179	8.000	11.420	16.767
1.352	1.278	2.291	0.788	2.481	1.554	1.786	1.058
-0.017	1.258	-6.668	5.270	0.657	0.822	0.655	0.844
-6.590	0.952	0.522	1.032	3.654	12.451	-1.615	2.716
4.150	-2.516	-3.447	2.753	-11.000	11.000	-4.101	-11.000
-2.078	-3.428	-5.360	-11.000	-6.590	-11.000	-1.103	-1.035
3.079	2.783	2.796	3.013	5.924	8.295	-1.403	-0.276
-11.000	2.244	2.825	1.647	2.860	11.000	-11.000	-2.320
-0.630	-0.865	-5.084	-3.478	-4.489	-11.000	1.155	1.427
0.868	11.000	-6.807	-3.096	-2.049	-2.122	12.682	18.978
1.438	-11.000	-11.000	7.870	11.000	11.000	0.527	-11.000
11.000	-11.000	1.289	-4.296	-5.788	-11.000	0.585	11.000
11.000	11.000	0.887	-4.942	10.102	13.237	11.878	15.976
-3.050	-1.378	-2.142	-2.322	-3.030	11.000	-3.127	-2.294
-1.811	-1.914	-0.841	-0.813	-1.475	-3.137	-0.699	-1.232
4.451	11.000	-11.000	-1.432	16.943	18.665	12.605	-0.918

Table35.txt

-0.941	0.199	0.649	3.257	0.126	0.422	0.220	0.433
0.662	0.585	-6.464	0.967	-5.624	-11.000	-0.071	1.764
-3.318	11.000	0.255	5.691	-0.179	0.074	-2.188	0.184
-11.000	3.832	-1.232	-0.226	-5.439	11.000	-11.000	-11.000
1.834	-6.119	-4.255	-5.222	-11.000	-11.000	1.264	0.454
11.000	11.000	2.999	-3.862	18.305	15.774	12.632	16.664
-1.596	-1.109	-0.325	11.000	11.000	11.000	-2.009	-0.200
-0.480	-0.458	0.812	0.041	0.317	-1.487	-0.433	0.953
11.000	11.000	-0.195	0.141	-1.509	0.027	-1.219	-1.230
-0.669	0.810	0.444	-2.109	-0.227	-2.341	-0.180	-0.691
-1.031	-0.850	-11.000	2.697	-0.014	0.130	-0.131	0.491
11.000	11.000	-1.510	0.332	-0.708	0.572	-1.544	-0.474
3.696	4.128	-11.000	3.007	4.780	11.000	1.321	4.256
1.647	2.897	-5.831	-11.000	-5.719	-11.000	0.045	2.148
3.019	2.613	2.431	2.033	18.104	20.142	1.217	24.325
-0.116	0.170	0.393	0.097	0.294	11.000	-11.000	-11.000
-1.434	0.323	-5.607	0.750	-0.667	-11.000	0.269	1.046
0.614	7.830	1.372	0.392	-1.399	-0.959	-2.636	1.205
-1.888	-0.585	-0.884	-1.604	-0.310	11.000	1.558	2.200
-0.550	-0.346	-5.704	-0.306	-5.902	-11.000	0.617	-0.859
6.931	11.000	-0.849	4.019	-1.376	0.071	-1.497	-2.479
-3.051	1.323	0.299	-2.242	-3.480	11.000	-3.637	-11.000
5.006	3.541	-5.393	2.900	-5.895	-11.000	-0.841	-1.178
-0.861	11.000	-0.205	0.313	2.936	6.409	6.931	4.341
-3.811	1.204	0.583	4.363	-3.111	11.000	4.390	-6.739
0.485	1.695	-3.995	-5.964	-4.776	-11.000	2.546	2.097
-0.414	1.618	1.806	-2.917	3.013	2.616	3.698	0.335
-11.000	-0.838	0.792	1.355	-0.521	11.000	-11.000	11.000
2.538	-1.100	-11.000	0.512	-3.940	-11.000	0.903	1.268
5.237	11.000	-4.746	0.347	12.384	1.120	9.642	15.372
-2.497	-2.776	-2.638	-0.998	-3.231	-3.922	11.000	-11.000
4.817	6.242	-6.104	-11.000	-6.637	-11.000	4.387	7.469
4.072	4.780	-1.188	-1.135	11.445	12.520	12.525	15.199
-6.464	0.131	1.259	1.758	0.177	11.000	-6.158	-11.000
1.755	0.384	-3.670	-4.886	-7.034	-11.000	1.655	3.469
11.000	11.000	2.198	-3.139	-1.273	13.521	7.577	7.314
0.030	1.012	-0.465	1.519	-0.419	2.437	0.133	-0.785
-1.966	-0.704	-0.557	-0.426	-1.118	-4.629	1.616	-0.532
-1.389	2.831	-0.305	-2.584	-1.147	-2.660	-0.029	0.582
-0.127	-3.247	-2.810	5.682	4.884	6.496	-1.109	-2.141
-1.282	-1.820	-0.007	-0.880	-0.235	-5.003	-0.091	1.445
-0.575	0.223	-0.345	-0.520	-1.026	-0.386	-0.163	1.827
2.152	11.000	-11.000	11.000	2.334	11.000	1.545	2.232
0.580	0.021	0.975	0.371	-4.260	-11.000	0.428	1.411
11.000	4.479	1.319	-0.219	7.216	-1.284	-2.236	-1.836
2.148	1.713	1.884	1.915	0.189	11.000	-11.000	-11.000
2.977	1.046	-1.061	-1.990	-5.343	-11.000	1.790	1.772
1.648	11.000	1.059	-1.681	5.933	4.294	6.542	4.000

Table35.txt

3.450	-3.234	-3.709	0.099	-1.293	11.000	-0.682	-1.039
1.523	0.034	1.242	1.569	-0.162	-5.231	7.652	11.000
1.239	2.773	0.053	-0.317	-1.447	1.078	-0.107	1.303
1.793	0.209	-0.310	-0.667	-0.906	7.029	-5.669	5.939
-0.239	-1.033	-2.150	4.004	-0.912	-2.055	0.998	0.685
11.000	11.000	-3.591	-1.020	-2.217	-0.735	1.051	-0.278
-11.000	0.497	11.000	6.997	11.000	0.954	11.000	-11.000
7.621	7.077	-2.357	5.540	-4.683	-11.000	0.597	1.371
-1.972	11.000	-5.681	-4.943	7.674	6.923	8.278	12.087
-11.000	-0.651	-0.783	2.172	-0.079	0.691	0.897	1.486
1.017	-0.778	1.897	1.903	-11.000	-11.000	0.640	1.601
-11.000	11.000	-11.000	-0.482	-1.653	-0.201	-0.607	-0.600
-5.696	1.359	1.846	4.271	1.847	11.000	-5.861	-11.000
1.907	0.434	-1.126	-3.506	-6.432	-11.000	2.203	2.786
-11.000	11.000	-3.441	-1.349	2.223	4.544	-1.552	-1.095
0.925	-1.607	-1.205	1.622	-0.970	11.000	-11.000	-0.050
0.350	-1.140	-4.982	0.395	-1.309	-11.000	0.611	1.290
6.612	6.476	1.246	0.174	-0.452	-0.132	-0.953	0.382
0.424	-2.407	-11.000	7.928	11.000	-1.397	-0.683	0.173
1.033	-3.283	1.267	0.984	-1.051	-4.597	1.725	2.372
-11.000	11.000	-1.013	1.354	-0.356	-0.185	-0.953	0.185
-4.047	-2.245	-2.830	1.815	-1.460	11.000	-3.041	-11.000
2.277	2.802	-2.843	0.577	-4.375	-11.000	1.222	1.234
-1.298	2.563	-0.583	-4.826	-0.654	-0.451	2.111	0.915
0.010	-0.786	-0.591	5.391	6.622	11.000	-5.493	0.042
4.964	-0.376	5.094	3.572	-1.398	-11.000	0.900	6.695
11.000	11.000	4.642	0.828	15.396	18.583	13.823	21.120
1.754	-0.328	0.051	2.878	1.316	-0.751	-0.742	2.277
1.732	1.147	2.297	1.639	-0.201	-2.435	2.031	4.860
-0.236	1.949	0.648	1.673	-1.288	-1.724	-0.650	-0.480
0.547	0.788	-1.790	2.537	-0.569	0.848	-1.930	1.083
-0.492	-1.400	1.462	0.981	0.916	-3.386	1.935	0.897
-1.586	-0.243	0.417	-0.749	-1.883	-1.662	-0.610	-2.295
3.184	-1.020	-1.276	2.821	0.493	-1.685	1.565	4.204
4.663	2.243	6.588	4.365	0.442	-2.468	4.054	7.138
0.942	1.531	2.052	3.504	-2.734	0.817	0.867	-0.904
0.171	-0.701	-1.182	2.427	-1.475	-0.749	0.088	0.951
-0.367	-0.960	0.875	0.968	0.559	-3.951	0.002	-0.635
-1.387	0.276	-1.400	-0.773	-0.420	-2.915	-0.337	-2.643
-11.000	4.806	5.748	4.522	5.132	5.999	-11.000	-11.000
1.805	3.313	-4.977	-11.000	-5.563	-11.000	-3.138	0.764
3.401	11.000	-3.496	-5.147	-1.425	-1.280	0.190	-2.836
0.957	-0.852	-0.221	3.820	-0.031	11.000	-5.236	0.697
-3.062	-2.002	-0.504	2.152	-0.068	-3.126	-0.001	-0.692
-1.252	-1.845	-1.301	-2.413	-0.957	0.216	-0.628	-1.110
-1.120	-2.645	-3.194	1.393	-0.645	11.000	-2.383	-0.958
4.705	2.211	-2.222	0.217	-4.067	-11.000	0.973	1.938
7.896	11.000	-1.115	-1.303	-2.117	-2.126	0.490	1.405

Table35.txt

1.529	1.181	0.906	1.952	0.940	11.000	-11.000	-4.054
2.767	1.162	-3.332	2.163	-5.214	-11.000	3.345	2.863
6.088	11.000	-2.086	0.435	0.190	-0.443	-0.628	-1.635
3.610	0.034	0.992	2.239	0.600	-4.627	11.000	-11.000
6.386	6.724	-2.719	1.557	-5.736	-11.000	1.295	2.417
11.000	11.000	-4.976	1.212	13.585	13.966	7.083	8.390
1.256	-0.933	0.028	2.285	1.141	-1.629	-0.459	2.149
1.599	0.076	1.604	2.480	0.600	-3.686	2.925	3.851
-0.806	0.797	0.875	0.680	-0.447	-0.481	0.367	-3.076
-6.937	-6.432	-11.000	6.023	6.158	11.000	11.000	-6.470
3.700	3.615	-1.610	-4.071	-2.389	-11.000	4.496	5.375
11.000	11.000	-4.778	-2.919	0.018	-2.009	9.148	24.875
-1.714	-0.541	0.245	0.700	-0.337	0.733	0.289	1.081
-0.746	-2.191	1.040	-0.486	-0.318	-3.761	-0.216	0.038
-2.064	-1.117	0.832	-0.169	-1.181	-1.542	-2.279	-2.339
0.887	-1.314	-0.344	1.643	-0.626	11.000	-3.977	0.062
1.222	-0.149	-4.866	0.215	-5.514	-11.000	2.694	2.852
-4.690	11.000	0.117	0.774	-0.365	-0.942	-0.766	-0.530
-4.285	0.350	-5.212	2.892	-7.034	11.000	-4.703	-11.000
2.565	1.935	-3.623	2.600	-5.618	-11.000	2.347	3.239
-4.370	11.000	-2.264	1.404	16.263	15.184	15.786	21.308
-2.463	-2.630	-3.414	11.000	11.000	-2.549	-2.636	-2.548
-0.783	-2.334	-1.068	-1.487	-11.000	-11.000	0.590	-0.148
4.175	4.026	-1.635	-1.650	4.068	6.057	-1.918	-0.531
1.374	-2.221	-0.961	3.580	11.000	-2.414	0.355	1.024
0.964	-2.880	2.050	0.704	-0.341	-2.946	1.601	2.308
-0.843	0.526	0.478	0.563	-0.296	-0.359	-2.531	-2.159
1.938	-1.754	-0.744	1.641	-0.601	-1.409	-0.019	0.110
-0.064	-1.041	0.862	0.451	0.109	-2.732	0.227	0.814
-1.017	-0.144	-0.054	-0.462	-4.155	-1.653	-2.226	-0.735
0.132	-1.246	-1.049	0.376	-1.739	-0.623	-1.838	-1.238
-0.992	-1.319	-0.342	-0.414	-0.228	-3.721	0.371	0.022
-2.074	-2.075	-0.500	-1.152	-0.402	5.025	-0.989	-0.916
-2.009	-2.367	-0.699	7.536	2.832	11.000	5.058	1.670
-2.916	-1.660	0.355	-3.775	-4.585	-11.000	2.291	0.304
-0.786	1.853	0.231	-3.253	0.890	6.141	-1.039	7.576
-3.241	-4.130	-5.122	-1.991	-5.318	11.000	-4.625	-3.545
6.301	-5.843	-0.608	3.209	-2.486	-11.000	-1.251	-1.708
1.718	6.165	2.895	1.448	2.938	12.297	0.952	13.564
1.347	-0.466	-0.282	1.318	11.000	-0.727	0.627	1.783
-0.221	-1.003	1.030	1.097	-7.034	-6.383	-0.034	0.491
0.112	-0.536	0.000	-0.636	-0.471	-0.756	-0.027	-0.158
-0.158	0.924	-2.358	2.516	-0.585	11.000	-0.619	-2.233
0.349	-0.505	-2.179	-2.139	-1.209	-11.000	1.339	0.485
11.000	5.287	-2.935	-3.035	1.681	2.578	0.026	1.422
0.716	-0.217	-2.532	2.606	-0.696	11.000	-1.010	-0.533
2.047	1.030	-1.391	-0.603	-0.768	-11.000	1.415	1.655
11.000	7.209	-3.454	-1.586	3.269	1.230	-1.250	1.764

Table35.txt

1.130	-0.438	0.399	1.937	0.471	-1.911	-0.013	0.970
3.265	0.507	4.713	1.349	1.981	-3.283	6.925	5.633
-0.679	1.296	-0.472	1.365	-0.663	-0.672	0.065	-1.525
1.021	-1.420	-1.131	0.970	-0.759	11.000	-11.000	-11.000
1.843	0.132	-3.957	2.086	-5.441	-11.000	3.482	4.567
7.824	11.000	0.566	0.690	-1.174	-1.080	-0.519	-2.152
-0.818	-2.611	-2.328	0.771	-1.487	11.000	-3.016	-0.111
-0.912	-1.478	0.668	0.843	-0.708	-5.409	1.334	1.183
-1.906	0.210	-0.700	-1.556	-0.169	-1.049	-0.858	-0.667
-5.337	2.574	2.869	-0.170	-3.600	6.758	-1.845	0.802
2.144	1.390	-3.291	-1.562	-4.239	-11.000	-0.495	-1.315
2.818	11.000	-0.377	-1.086	4.558	6.424	3.722	5.104
-2.526	1.360	1.185	3.606	3.371	2.774	-3.072	-5.446
6.562	11.000	-4.760	7.487	-6.490	-11.000	6.304	5.131
-5.226	11.000	3.328	0.667	4.361	1.723	-0.090	2.590
-4.991	0.658	1.913	-1.994	-3.729	11.000	-4.868	-4.728
2.475	2.244	-5.795	-2.112	-4.330	-11.000	-1.146	-2.402
11.000	11.000	-5.096	-5.534	6.132	0.019	8.814	13.801
-1.452	0.396	0.660	0.255	-0.483	5.593	-3.860	-3.234
-2.184	-1.483	-3.548	-2.267	-1.068	-4.335	-1.000	-2.656
4.525	2.652	-0.468	-3.838	-2.569	-3.556	0.743	1.137
-0.410	-0.770	-0.461	0.908	-1.116	11.000	-0.815	0.935
-0.760	-0.907	-6.205	-0.512	-1.932	-11.000	0.376	-2.683
-11.000	11.000	0.368	-1.650	16.496	2.297	-1.645	-0.583
-0.447	-1.243	-2.035	0.662	-1.491	11.000	-0.900	-0.718
-1.009	-2.748	-4.065	-1.798	-1.469	-11.000	-0.663	-1.243
-11.000	11.000	-6.620	-1.708	15.577	3.060	1.122	2.033
1.144	0.237	-0.139	1.104	-0.299	2.199	11.000	0.227
7.346	-0.416	-4.443	-0.118	-4.344	-11.000	0.680	-0.286
-6.447	11.000	1.893	-0.345	-0.196	0.480	-2.769	-2.344
1.210	-0.329	-0.597	1.476	-0.082	11.000	0.307	0.099
8.126	-1.292	-5.682	0.471	-6.143	-11.000	0.610	-1.394
-11.000	11.000	5.889	-1.461	0.944	2.820	3.769	4.030
2.550	-0.570	-0.364	3.243	-0.176	1.933	0.808	1.411
-2.387	-2.514	0.528	-0.094	-0.245	-2.924	-1.661	-1.427
-0.322	-1.424	0.742	-1.730	-3.068	-0.435	-1.347	-1.138
-0.889	5.631	6.827	-0.213	-2.020	11.000	0.106	-11.000
3.761	2.943	-3.040	0.009	-4.335	-11.000	-0.052	0.408
11.000	11.000	0.161	-1.633	13.441	8.812	13.279	17.272
-3.447	1.439	1.591	-3.005	-11.000	11.000	-11.000	-11.000
-0.453	-0.446	-4.655	1.814	-6.253	-11.000	0.076	0.190
11.000	11.000	-0.835	-2.203	1.773	1.966	1.109	0.212
2.181	-1.267	-1.570	3.057	0.078	0.651	1.539	1.236
-0.752	-1.663	2.282	0.848	-0.529	-2.378	-0.031	-0.798
-0.671	-0.691	0.895	-0.780	-2.273	0.110	-3.747	0.129
-0.159	-0.109	-0.697	2.120	0.056	0.989	-0.668	0.301
-1.234	-2.436	-0.226	-0.962	-0.751	-3.218	-0.932	-2.293
-1.072	-1.677	-0.084	-2.209	1.132	-1.463	0.584	1.400

Table35.txt

0.218	0.112	-0.535	4.458	4.496	1.032	-1.519	0.011
-0.794	-2.049	0.361	-0.360	-0.782	-4.028	-0.559	-0.778
-1.004	-0.944	0.064	-1.697	-0.985	1.703	-0.436	2.342
-1.938	0.701	-0.788	0.224	-0.558	4.174	-1.064	-2.649
-4.788	-3.453	-3.691	-4.756	-0.792	-2.969	-2.179	-5.022
-2.542	-2.801	0.061	-5.957	1.165	2.153	2.874	2.072
0.050	-0.690	-1.118	2.122	-0.298	3.000	-1.041	-0.786
-2.770	-2.957	-1.416	-1.732	-0.966	-3.869	-0.295	-1.811
-1.682	-1.183	-0.159	-3.578	2.279	2.781	2.485	3.830
1.358	-1.442	-1.301	1.489	-0.566	11.000	-1.101	0.997
0.599	-1.802	2.184	0.174	0.441	-3.359	-0.298	0.544
-0.226	-0.887	0.726	-1.066	-0.702	-0.097	0.567	0.563
0.941	-1.449	-2.089	0.947	-1.784	0.455	-0.157	-0.566
3.787	-2.881	-0.595	-0.359	-0.766	-4.422	-0.724	-2.380
-1.466	-1.186	-0.716	-1.901	-0.551	2.753	-1.598	-0.759
-0.356	-0.215	-1.807	1.412	-0.337	-0.663	-0.854	-1.595
-4.243	-3.746	-1.787	-2.162	-0.462	-4.206	-1.940	-3.557
-2.353	-3.796	-2.169	-4.277	-2.753	-0.968	-0.465	-3.444
-2.098	-1.987	-2.781	3.081	4.173	11.000	-0.987	-2.829
-4.094	-4.402	-5.662	0.709	-4.355	-11.000	0.517	-0.563
0.461	-1.260	-1.775	-3.970	2.645	3.510	1.041	1.511
1.820	-1.363	-0.874	1.747	-0.594	1.021	0.105	0.572
-1.501	-2.602	0.269	-0.184	-0.298	-3.096	-0.105	-0.977
-0.606	-1.685	0.471	-2.067	-1.666	-0.787	-1.095	-0.895
-2.151	-1.396	-2.461	1.037	-0.606	11.000	-1.874	-1.067
-0.969	-2.465	-6.480	3.612	-6.263	-11.000	2.859	4.093
-1.348	11.000	-2.066	-2.348	2.499	7.498	12.750	18.130
-3.856	-0.509	-5.485	11.000	3.070	1.611	-1.683	-0.135
-3.068	-6.937	0.247	1.059	0.692	-11.000	0.932	0.103
-4.127	2.809	0.186	-5.185	-0.855	7.348	1.854	15.725
2.125	-0.040	-0.393	1.277	0.392	4.862	-11.000	-11.000
0.776	-0.239	-5.377	0.526	-6.937	-11.000	1.354	0.919
-11.000	11.000	0.179	-0.716	0.807	1.958	1.468	3.703
4.587	1.918	2.529	1.401	1.030	1.032	-11.000	-11.000
3.621	2.353	-5.342	2.305	-11.000	-11.000	2.512	2.799
-11.000	11.000	0.201	-0.911	6.908	6.181	3.647	6.103
2.121	0.309	0.143	3.738	-0.268	1.705	-0.263	0.168
0.815	0.623	-0.607	-1.206	0.108	-4.737	1.168	0.138
-0.051	-0.454	-1.240	-2.164	-2.413	-2.130	-3.173	-1.510
1.493	0.081	0.175	4.180	0.131	1.198	0.713	1.956
4.774	4.041	-1.769	0.437	-0.520	-6.668	1.420	2.249
0.074	0.516	0.924	-0.948	9.954	9.750	3.805	2.261
1.006	-0.079	0.018	1.861	-0.652	11.000	-6.048	-6.692
-0.096	-0.801	-5.242	11.000	-6.880	-11.000	3.601	5.954
-0.567	11.000	0.698	-0.106	2.880	1.474	2.648	1.067
1.225	-0.530	-0.228	2.635	11.000	11.000	0.210	-11.000
0.260	0.044	-3.741	11.000	-5.952	-11.000	1.772	1.600
-11.000	6.791	-11.000	1.276	-0.826	0.272	0.032	0.242

Table35.txt

3.309	1.199	0.965	2.640	2.606	11.000	3.245	-11.000
2.961	2.539	4.172	3.585	-6.880	-11.000	1.791	7.941
2.584	2.744	1.206	-1.962	-1.463	0.538	-1.438	-0.893
5.382	-4.791	-5.133	3.833	2.822	2.841	3.624	4.611
0.542	-0.125	-0.812	-2.802	-2.488	-11.000	1.553	1.987
2.363	1.047	2.421	-0.218	2.692	1.638	-0.994	0.813
-2.088	-1.209	-2.127	11.000	11.000	11.000	-2.442	-3.023
-2.323	-2.076	-1.174	-1.861	-0.809	-4.459	-0.887	-0.420
7.535	6.409	-0.352	-2.675	8.769	-1.233	-0.421	-2.426
-4.990	-3.499	-4.848	11.000	11.000	1.815	-5.417	-11.000
1.299	1.349	-3.805	0.263	-5.620	-11.000	-0.091	1.776
11.000	11.000	-1.854	-3.146	5.677	8.670	-1.053	-0.799
-11.000	-2.290	-2.727	-1.976	-3.368	11.000	-3.152	-2.382
-1.023	2.817	-4.571	7.371	-5.336	-11.000	1.950	3.465
11.000	11.000	-11.000	6.659	1.160	18.412	-1.644	-0.138
-5.818	2.938	2.843	-4.095	-6.070	11.000	-4.823	-5.527
2.458	-2.936	-1.606	5.202	-3.212	-11.000	11.000	5.269
11.000	11.000	3.396	-3.537	-0.915	10.114	11.118	15.797
2.912	0.020	1.006	11.000	11.000	11.000	-11.000	-11.000
-6.189	-11.000	-4.279	-11.000	-5.214	-11.000	0.705	1.210
11.000	6.022	0.908	-5.202	4.519	15.566	14.475	19.377
-2.295	-1.101	-1.570	11.000	11.000	11.000	-2.285	-1.989
-0.935	-0.945	-0.724	-1.630	-1.191	-4.788	0.512	0.107
-1.440	-1.727	-0.277	-1.883	-1.095	0.562	0.686	1.378
-0.112	-2.201	-0.660	0.077	-0.927	11.000	0.088	-4.615
-0.692	-1.802	-6.721	-0.300	0.993	-11.000	-0.058	-0.411
11.000	7.281	0.609	-1.141	2.957	2.002	3.264	3.328
-1.413	4.999	-1.416	-0.189	-1.900	11.000	-1.392	-0.378
-0.700	-1.633	-4.560	6.979	-6.188	-11.000	3.566	5.555
-11.000	11.000	-0.912	-1.549	-0.656	-1.195	-1.272	-1.110
-11.000	11.000	11.000	0.723	-0.226	-6.158	-11.000	0.037
6.372	11.000	-5.007	7.240	-4.521	-11.000	3.687	6.018
11.000	11.000	-6.104	-0.371	5.599	9.933	6.722	10.218
2.596	-11.000	-11.000	1.476	-0.324	11.000	-11.000	1.955
0.387	-0.204	-6.022	-1.976	-6.051	-11.000	0.991	1.098
4.391	11.000	-11.000	-4.537	2.517	-1.184	-1.509	-0.113
-1.984	-1.403	-0.804	8.210	11.000	0.058	-1.699	-1.608
-3.609	-3.001	-2.190	-2.074	0.098	-4.182	-0.351	-2.319
-2.676	-2.282	-1.440	-3.152	15.470	18.797	-0.963	-1.385
3.997	-1.516	-0.027	2.884	0.400	-0.077	1.372	1.564
-0.378	-0.965	2.023	1.340	0.521	-2.939	0.663	-0.054
0.336	-0.145	0.506	-0.256	-1.690	-2.044	-0.257	-2.473
-0.293	11.000	11.000	2.093	3.798	11.000	-11.000	-3.050
4.462	4.855	-5.179	-2.497	-6.657	-11.000	0.880	1.655
4.677	11.000	-2.996	-2.770	14.585	11.662	9.170	14.461
1.128	-0.521	-0.646	1.100	0.498	-1.482	-0.210	0.699
3.329	0.584	2.689	1.632	0.859	-3.673	3.478	4.027
-0.011	0.786	0.014	0.857	-1.403	1.365	0.557	-1.293

Table35.txt

0.184	-0.125	-0.885	0.958	-0.281	1.014	0.614	-1.815
3.757	4.291	-3.205	-1.694	-5.073	-11.000	2.043	2.324
-0.718	11.000	1.239	0.247	-3.417	-1.817	1.003	3.937
-3.373	-0.585	-0.925	-0.846	-1.757	11.000	-1.965	-11.000
-0.834	-0.481	-0.364	11.000	-11.000	-11.000	-0.588	-1.261
-11.000	11.000	-5.883	-1.750	0.035	-0.091	-0.977	0.752
1.778	-2.355	-1.889	-11.000	-0.454	3.439	-11.000	0.612
-0.941	-1.008	-5.516	-11.000	-5.515	-11.000	-2.103	0.147
6.974	4.214	-0.065	-6.181	0.850	13.368	3.406	3.376
-2.850	5.152	5.732	4.064	7.142	6.295	-5.411	-11.000
3.042	-11.000	-4.632	6.860	-5.936	-11.000	1.308	2.806
11.000	11.000	-2.436	-1.231	11.919	12.724	11.006	14.892
-11.000	1.058	-11.000	-3.318	11.000	-11.000	1.717	-11.000
1.660	1.193	-3.480	5.822	5.208	-11.000	0.896	1.730
3.242	5.756	5.996	-3.894	12.331	14.859	13.519	16.329
2.895	-1.783	-1.981	1.676	-0.537	0.205	0.469	2.134
1.046	-1.441	-0.568	0.038	0.061	-2.979	0.648	1.907
0.339	1.088	0.957	0.443	-2.211	0.418	-0.779	-1.761
-6.839	5.820	-6.758	3.855	-2.649	11.000	-2.677	-5.390
0.685	0.099	-1.651	-4.370	-11.000	-11.000	0.527	0.793
5.529	5.354	-1.325	-3.875	1.565	0.697	10.715	20.681
0.780	0.219	-0.197	1.599	0.007	11.000	-11.000	1.115
0.379	0.018	-5.567	0.675	-1.992	-11.000	0.755	2.673
-0.289	11.000	1.077	-0.723	0.734	0.965	0.770	-0.012
1.790	-1.028	-1.103	2.459	0.087	2.258	0.849	0.646
-0.744	-0.842	0.773	1.210	-1.903	-4.479	0.544	0.695
-0.597	-0.456	-11.000	-0.577	2.209	2.614	1.060	11.277
2.418	-0.944	-0.964	0.629	-1.789	11.000	-0.120	-1.533
-1.670	-2.470	-2.903	-4.021	1.576	-5.321	-0.878	0.015
-4.729	4.184	-5.951	-4.755	2.301	2.318	1.327	0.807
2.105	1.741	1.025	-0.351	1.829	11.000	2.636	1.662
0.699	-1.146	1.565	1.602	11.000	-11.000	0.275	0.933
0.951	11.000	-11.000	-6.383	10.823	2.364	4.044	1.124
0.792	-1.593	-0.812	11.000	11.000	-0.822	0.786	-0.337
-2.506	-2.505	0.083	-0.513	-0.663	-4.571	-0.340	-0.130
-0.657	-1.325	0.623	-1.278	-1.649	-0.030	-2.019	-1.729
-11.000	2.017	2.619	-5.980	-11.000	11.000	-11.000	-6.807
3.724	-4.871	-11.000	2.904	-3.161	-11.000	-0.433	-1.764
11.000	8.077	2.349	1.534	14.998	11.849	14.607	16.953
-3.507	-3.295	-4.210	-1.783	-3.982	11.000	-4.112	-3.857
-2.917	-3.532	-11.000	-3.193	-11.000	-11.000	2.347	3.744
-1.512	11.000	-2.526	-3.065	5.022	15.567	3.732	14.696
-0.012	-0.108	-1.680	0.554	-0.083	0.822	-0.677	0.009
0.299	-0.895	-0.251	-0.375	0.221	-3.489	-0.190	-0.161
-1.267	-2.314	0.747	-1.863	1.705	1.338	-0.568	0.723
0.972	0.350	-0.247	0.502	-0.179	-0.046	-0.452	-1.455
-1.957	-2.401	-0.018	-1.927	-0.562	-4.346	-0.495	-1.688
-1.960	-1.726	-0.964	-2.299	0.753	-1.930	-1.135	-2.796

Table35.txt

-0.707	-1.442	0.060	5.423	6.968	11.000	-0.251	-2.537
-5.587	-5.827	-0.297	-1.118	7.198	-11.000	-0.283	-0.386
4.314	2.550	-1.511	-4.762	6.172	0.216	6.266	4.983
-0.606	-1.669	-0.337	-0.399	-2.802	11.000	-1.440	-11.000
0.702	-0.845	1.208	0.382	-11.000	-11.000	2.058	2.139
7.703	11.000	-0.632	-1.439	0.507	2.695	-0.579	-0.602
-4.561	2.781	-3.876	0.381	-2.097	11.000	-5.944	-4.159
1.175	0.571	-2.020	-3.242	-2.499	-11.000	-1.296	-2.452
-3.078	5.236	-0.595	-3.251	4.224	6.638	1.226	5.889
-3.688	1.534	-3.256	0.634	-0.313	5.539	0.225	-2.857
-2.233	-2.336	-4.445	-4.618	-2.097	-3.872	-1.759	-3.807
-2.935	-2.568	-1.630	-11.000	-2.734	-0.267	1.757	-1.684
-5.930	-2.329	-5.813	-4.413	-11.000	11.000	-11.000	-11.000
-1.144	3.600	-2.179	-3.383	-5.168	-11.000	2.113	2.370
-4.901	11.000	-1.068	-2.472	12.236	13.673	12.386	22.379
0.059	-0.920	-0.490	-0.951	0.782	-1.505	0.291	1.179
-0.332	0.434	-0.814	1.689	4.029	0.476	1.208	-0.892
-0.299	-0.425	-0.445	0.766	0.000	-0.736	0.000	0.000
0.845	2.765	0.335	-1.033	-0.253	-2.498	0.456	0.401
-0.025	-1.094	-1.051	-1.413	0.697	2.470	0.951	0.241
-0.790	0.321	0.367	0.218	0.000	-1.009	-0.933	-1.517
1.179	0.786	2.510	11.000	-4.259	-3.674	-0.261	0.829
-11.000	3.315	3.229	-0.859	-2.133	-4.524	11.000	11.000
-11.000	11.000	-1.263	-2.557	-0.916	-1.036	-1.854	-3.529
11.000	11.000	11.000	11.000	-2.553	-1.335	-3.482	-3.047
-3.041	-5.185	-3.569	-3.261	-0.681	-1.784	11.000	11.000
-0.958	-0.993	6.828	-1.973	-0.535	-2.113	0.295	-1.593
6.180	11.000	11.000	11.000	-11.000	-0.494	-0.720	-0.819
-3.873	-11.000	-3.414	-3.893	1.270	2.928	4.916	6.223
-1.263	-1.587	-0.692	-1.185	-2.426	-1.815	-2.218	-1.613
-1.224	-2.555	11.000	6.329	0.109	-2.703	-1.864	-1.164
-1.398	-4.439	-1.611	-1.541	-0.754	-2.530	6.696	11.000
-11.000	11.000	-1.645	-1.421	0.000	-1.193	-0.877	-1.329
-0.763	0.582	-0.457	-0.878	1.182	-1.243	-0.318	0.789
-1.457	-0.492	-1.428	1.134	1.543	0.886	0.358	0.785
-0.932	0.280	1.115	2.176	-1.386	-0.256	-1.982	-2.678
-1.999	-2.937	-11.000	11.000	-6.379	-0.364	-1.465	-1.805
11.000	11.000	-2.559	-1.804	0.014	-1.540	11.000	11.000
-11.000	11.000	-0.337	-0.347	-1.242	-0.626	-0.299	-2.698
-1.557	-0.395	11.000	7.928	-5.372	-1.823	2.937	11.000
-2.758	-11.000	-6.240	-11.000	4.371	4.339	11.000	5.448
-11.000	1.984	7.602	4.356	1.146	0.646	3.168	4.702
1.974	4.735	11.000	11.000	-4.314	-4.024	-4.268	-4.175
-6.565	-11.000	-6.692	-11.000	0.101	-4.441	11.000	11.000
-11.000	11.000	0.570	-0.129	1.766	1.597	0.147	0.551
1.991	4.853	1.454	1.347	2.235	-1.005	-0.498	0.338
-4.663	-5.984	-4.470	-6.597	3.066	6.183	3.592	3.587
-11.000	11.000	0.755	1.094	0.000	0.309	-0.938	0.783

Table35.txt

-1.352	-1.933	11.000	11.000	2.762	-1.300	-0.946	-0.968
1.632	2.285	11.000	-11.000	1.176	1.769	1.683	2.341
-2.861	11.000	-1.107	-1.639	-1.510	-1.960	0.349	1.969
4.913	7.652	-2.162	3.999	-4.459	-5.711	-1.473	-0.655
-11.000	-11.000	11.000	-5.420	4.868	6.352	4.096	5.754
-5.203	11.000	-0.045	-3.410	-1.532	-0.736	0.000	2.986
1.866	0.469	1.560	1.970	1.643	-5.120	0.742	1.385
-0.043	-3.058	-0.953	1.796	2.792	0.463	1.942	1.741
-11.000	11.000	0.712	2.863	-0.768	-1.220	0.139	-1.861
-4.857	-3.321	5.553	7.092	-3.659	-2.464	-3.511	-11.000
-5.522	-11.000	11.000	-11.000	8.210	-11.000	11.000	11.000
-11.000	4.739	11.000	1.624	0.000	3.348	0.254	-0.873
-0.231	-4.022	11.000	11.000	0.767	-3.167	-3.111	-3.281
-11.000	-11.000	-2.886	-11.000	5.283	4.980	5.376	4.584
-11.000	11.000	-2.927	1.719	0.851	-0.074	-2.862	-3.018
-1.309	-0.080	1.803	-0.744	2.666	-4.093	-1.222	0.469
-1.485	-1.268	0.040	0.039	3.393	7.830	4.469	6.550
-5.264	4.717	-0.380	-2.455	0.553	-1.105	-0.537	-1.085
2.377	1.455	5.212	11.000	-1.899	-3.827	0.343	1.810
-11.000	-11.000	2.421	-0.746	1.787	0.385	2.766	3.371
-5.360	1.196	3.332	3.310	1.192	0.879	5.366	7.087
5.635	6.138	1.432	11.000	2.437	-0.865	-5.622	0.823
-5.856	-11.000	2.327	1.656	1.274	1.859	4.037	5.473
2.605	5.095	2.634	2.724	-0.491	1.676	-1.191	-1.367
0.094	0.869	0.244	-1.981	1.061	-2.095	0.053	0.216
-1.671	-0.398	-1.550	1.143	1.967	2.499	0.931	0.365
-1.817	0.109	1.144	1.599	-1.286	-1.044	-1.771	-2.804
-0.109	-4.228	-4.439	5.550	-6.430	-0.101	-2.249	-2.408
-2.172	-4.352	11.000	1.284	-0.589	-1.293	7.326	11.000
-5.022	11.000	-1.988	-1.279	0.000	0.000	0.000	0.000
2.075	1.992	6.197	11.000	1.175	-1.236	-1.506	-0.608
-1.620	-5.309	-1.865	-4.030	2.111	2.377	8.126	6.627
-2.515	-2.973	1.936	-2.166	0.218	0.203	-1.648	-1.116
-1.105	-2.800	11.000	11.000	0.634	-4.885	11.000	7.799
-2.355	-11.000	4.003	-4.099	5.208	1.435	5.428	2.740
-11.000	5.231	-1.340	-1.158	1.142	1.579	0.436	2.678
0.938	1.497	3.172	11.000	1.819	-3.757	0.273	0.828
-1.001	-3.117	-0.675	1.625	2.486	-6.201	1.429	1.132
-7.034	11.000	1.435	3.992	7.427	0.365	-0.842	4.401
-1.069	-2.704	0.157	0.954	0.426	1.432	-2.912	-2.778
-3.333	-7.034	-2.021	-1.733	0.180	-4.492	-0.786	-2.224
-1.038	-2.766	8.041	11.000	-2.596	-0.096	1.182	-1.898
0.451	0.372	-1.399	-0.217	-1.577	-2.011	-3.261	-2.891
-3.956	-6.583	0.916	1.481	-11.000	6.442	-3.339	-6.166
-2.849	1.226	8.210	11.000	-0.536	-1.225	0.034	-1.039
3.785	6.072	-3.565	11.000	-3.271	-2.371	-4.459	2.033
-4.828	-11.000	0.833	2.388	-2.180	-4.298	11.000	11.000
3.081	11.000	-0.987	0.248	1.526	1.006	-0.697	3.075

Table35.txt

0.062	0.269	-0.183	-1.691	-1.211	-1.637	-0.139	1.217
0.476	1.026	-0.974	1.390	1.791	0.540	0.130	0.759
-1.739	0.823	0.405	-0.279	0.027	0.492	-2.124	0.355
6.156	7.365	6.829	5.114	2.568	-3.220	-4.909	-6.029
-4.230	-6.706	-4.345	-5.639	4.819	6.516	5.030	6.835
0.466	6.232	-2.923	-4.524	1.433	5.128	-1.053	-1.500
11.000	11.000	3.451	11.000	-11.000	-7.034	-0.461	-0.588
-1.791	-2.850	-1.230	-1.508	0.623	0.146	0.954	-1.311
-2.012	11.000	-0.658	-0.067	-0.029	-2.748	0.016	-0.056
-1.684	-4.009	-2.679	-2.438	-1.733	-2.626	-3.014	-1.694
-3.557	-3.371	-2.540	-1.555	-0.841	-2.115	11.000	11.000
-3.075	-3.270	11.000	8.077	-0.769	-0.782	-1.601	-3.069
0.821	-0.624	-1.080	-1.272	-0.261	-3.228	-0.752	0.362
-1.264	-0.985	-1.798	-3.061	5.104	11.000	-1.365	-2.151
-2.165	-1.003	1.287	-0.756	-1.412	0.000	-1.093	-2.658
1.404	2.028	11.000	11.000	-1.463	-2.817	0.819	1.508
-11.000	-11.000	-1.866	-1.970	1.343	5.310	11.000	11.000
-11.000	5.756	3.423	2.760	2.441	0.607	-1.317	2.745
2.970	4.200	1.832	11.000	-5.355	-1.708	-11.000	-4.745
-0.531	-5.630	-0.264	-11.000	2.631	1.697	4.405	5.806
-4.943	11.000	-1.984	-2.641	-0.833	-0.313	-0.776	0.986
-0.824	-1.333	11.000	11.000	-1.263	0.145	-1.317	-0.667
-1.619	-1.917	3.496	7.047	0.793	0.197	6.950	11.000
-11.000	11.000	7.956	11.000	1.224	-2.214	-0.957	-0.020
0.365	0.291	-1.802	-0.876	0.453	-1.127	-1.423	0.188
-0.777	-2.737	-1.893	1.111	1.630	0.271	11.000	11.000
-1.795	-0.380	-0.041	0.120	-1.275	-0.678	-1.222	-0.709
11.000	11.000	-6.721	11.000	-2.506	-1.565	-5.981	-5.409
-4.118	-11.000	-4.910	-7.034	11.000	11.000	11.000	4.361
-11.000	11.000	-1.434	-1.840	-0.047	0.588	-1.661	-1.177
0.191	-1.997	2.016	11.000	-11.000	2.819	-0.522	-0.918
-1.858	-3.813	-2.095	0.041	2.504	-1.200	11.000	11.000
-3.026	7.691	0.712	2.685	0.022	-0.066	0.207	7.426
-0.050	-1.307	1.566	0.753	0.923	0.041	-0.289	-0.048
-1.165	-3.086	-3.311	-0.177	1.176	-1.663	3.955	6.170
-2.410	-0.687	0.820	1.628	-2.299	-1.381	-0.130	-3.372
0.480	-1.364	7.572	11.000	0.285	2.049	-1.000	-1.689
0.594	-1.128	-5.326	-0.773	2.079	-4.204	0.332	0.392
-3.466	-0.098	-0.768	-0.230	-1.604	-1.356	-1.099	0.002
0.716	0.443	-1.082	-0.403	0.141	-2.668	-4.920	-0.891
-3.346	-3.088	-0.897	2.683	1.677	2.625	0.627	0.733
-4.221	3.631	0.659	1.870	-2.989	-1.842	-1.790	-1.642
2.920	2.504	6.304	4.416	1.801	-3.126	3.064	3.431
-5.394	-11.000	1.654	4.250	0.917	3.674	2.608	2.536
-11.000	6.016	-2.414	-3.130	-1.663	-0.886	-1.990	0.426
0.729	1.334	11.000	11.000	-11.000	-0.978	0.319	-3.976
-0.487	-0.857	-1.666	-6.332	-1.639	-5.367	11.000	11.000
-1.229	1.306	1.028	1.684	0.379	-1.210	-1.516	-2.669

Table35.txt

-2.962	11.000	-3.855	11.000	-5.860	-1.616	-1.959	11.000
-4.791	-11.000	4.626	-11.000	1.316	-11.000	11.000	11.000
5.589	11.000	-2.355	-2.324	6.301	2.195	-0.223	-0.288
5.102	4.625	2.718	1.645	-0.256	-4.781	3.484	5.155
1.509	-11.000	-2.673	-11.000	3.834	5.989	11.000	-6.302
-11.000	3.615	-4.988	-0.304	0.481	3.650	-1.327	-0.289
-0.475	-1.522	11.000	11.000	4.533	2.138	1.584	3.154
-5.134	-6.516	-0.005	-0.491	3.479	4.042	11.000	11.000
-11.000	11.000	-6.076	-5.543	0.672	1.127	3.441	5.375
1.254	1.530	0.585	0.318	-1.581	-1.129	-0.526	0.893
-1.173	-0.131	-2.076	1.734	1.563	0.890	-0.078	-0.415
-0.543	1.254	0.135	-0.149	-1.703	0.175	-0.068	-0.819
0.710	-0.160	0.115	-0.920	1.129	1.069	0.085	1.183
-0.593	-1.638	-1.661	0.978	1.143	-0.111	1.843	0.695
-0.760	-1.220	-0.330	0.196	0.409	-0.877	-1.376	-1.266
6.383	8.126	2.749	2.488	-2.415	-2.187	-4.453	11.000
-4.346	-11.000	-4.821	-6.439	4.485	7.731	-3.130	-5.541
3.744	8.126	-3.846	-3.901	-0.954	-1.500	-1.567	-1.359
1.542	1.558	11.000	11.000	2.480	-1.901	-0.406	3.168
-4.422	-11.000	-0.272	1.021	3.605	3.492	11.000	11.000
-4.703	-3.056	11.000	11.000	9.729	10.299	9.083	14.399
-1.426	2.284	11.000	11.000	-3.726	0.152	3.672	-1.076
1.748	-11.000	-0.065	-11.000	2.156	-2.348	5.541	7.130
-11.000	11.000	4.812	11.000	1.481	1.507	0.521	-0.120
-0.144	0.113	0.682	-0.358	0.411	0.388	-1.054	1.031
-1.697	-1.491	-2.613	1.269	0.942	0.315	0.424	-0.196
-1.282	-0.025	0.579	2.664	-0.244	-1.431	-2.878	-0.597
2.176	-4.392	11.000	11.000	-0.894	-1.422	-2.614	-1.569
-5.922	-11.000	3.890	-11.000	2.378	3.795	11.000	11.000
-11.000	7.941	11.000	6.500	2.000	4.995	8.199	10.122
4.817	4.240	7.855	11.000	-4.151	1.456	0.083	0.850
-6.807	-11.000	-6.189	-11.000	1.521	0.482	11.000	11.000
0.836	3.888	6.965	7.597	-0.621	0.969	-0.707	-1.351
-0.182	-1.599	7.669	11.000	-2.769	2.006	0.787	-0.294
-5.086	-11.000	-3.785	-5.468	6.894	-11.000	11.000	11.000
-6.937	11.000	-2.485	-4.888	-0.053	1.752	-0.911	2.562
1.309	1.471	11.000	11.000	-5.303	-3.354	-0.727	0.254
-4.058	-11.000	4.665	11.000	-6.265	-11.000	11.000	11.000
-0.806	1.425	-6.508	-7.034	-1.515	-1.594	1.451	1.426
5.530	5.407	1.810	0.860	0.319	-1.321	-1.218	-0.409
-2.244	-2.586	-2.443	-1.505	-0.703	-1.579	11.000	11.000
-2.772	-0.525	-0.433	0.549	-1.681	-0.649	-2.666	-1.240
4.172	2.551	1.036	0.744	-0.970	-0.866	-0.201	-0.865
-2.229	-3.974	-1.711	-0.953	-1.950	-5.300	1.803	5.201
-1.470	5.208	0.051	0.859	-3.814	-1.765	-0.101	-2.088
-3.044	-5.129	4.212	8.126	-1.262	-2.286	3.154	4.955
-4.533	-11.000	1.153	3.720	4.038	4.886	11.000	11.000
-11.000	8.014	3.216	4.078	0.032	0.225	-1.609	-2.799

Table35.txt

0.792	2.122	-0.653	-0.486	-11.000	-0.614	0.194	0.359
0.023	-0.024	-1.172	1.572	1.831	2.119	-5.800	-0.861
-1.969	0.175	-11.000	-2.226	-1.471	0.579	-0.625	-1.637
6.613	7.917	1.461	1.244	-3.054	-0.890	-2.740	6.653
-11.000	-11.000	11.000	-11.000	4.189	-0.533	6.263	6.362
2.140	5.210	4.490	4.718	-1.256	0.456	0.000	0.000
6.013	6.525	-0.895	-0.935	-0.779	-0.497	-1.827	-1.656
-5.314	-4.315	5.347	7.301	-0.470	-2.953	11.000	11.000
-11.000	5.269	-0.281	-0.707	-0.694	-1.270	-1.241	-2.598
0.703	0.131	0.694	0.561	0.341	2.013	-1.882	-2.713
-3.180	-11.000	-3.484	3.424	0.756	-3.204	11.000	11.000
-11.000	-2.137	-0.388	1.586	-1.201	3.438	-2.553	-2.016
1.073	0.426	0.614	0.665	-11.000	0.641	-0.597	-0.199
-1.795	-2.516	-2.652	0.468	2.663	0.277	0.619	1.571
-1.833	0.801	0.058	1.956	-3.019	-1.188	-0.150	-2.243
1.952	11.000	11.000	11.000	-4.409	-2.705	-11.000	-1.379
-1.383	-4.234	4.305	-6.083	-0.921	-1.973	4.210	11.000
-1.141	4.620	5.637	2.679	1.591	-0.018	0.571	-2.844
-4.828	-11.000	11.000	11.000	-2.980	-1.151	11.000	11.000
-5.417	-11.000	-5.193	-6.464	7.941	5.678	6.560	11.000
-11.000	-3.878	2.383	3.259	-0.255	-1.945	0.000	0.000
-2.078	-1.593	1.660	0.447	-4.862	2.056	5.434	-4.349
-11.000	-11.000	7.567	-11.000	-3.340	-11.000	6.436	11.000
-1.244	11.000	11.000	-6.397	2.311	2.209	3.495	5.827
5.597	-1.139	0.072	-4.877	-1.805	11.000	-11.000	5.900
-1.028	-6.388	0.950	-1.414	-4.351	-11.000	1.803	1.209
8.210	11.000	-6.088	-3.102	11.443	11.364	-1.541	0.577
4.929	-1.687	-1.393	-1.952	-1.886	11.000	-11.000	4.169
-1.037	-5.694	1.557	0.099	-3.505	-11.000	0.149	-0.081
6.283	4.485	-5.717	-1.411	9.061	11.328	-0.802	-0.597
-2.668	-3.472	-3.517	5.431	7.669	-11.000	-3.484	-2.147
-7.034	-11.000	-4.644	6.435	0.098	-11.000	-0.949	-0.629
6.081	5.189	-11.000	-5.947	18.131	14.821	14.719	19.097
3.381	1.830	11.000	-1.058	3.168	-0.599	-2.498	-1.765
-0.536	0.144	1.810	2.586	1.337	-2.285	-1.108	-0.735
0.615	1.504	-1.264	0.931	-1.826	1.816	3.368	15.820
2.204	-1.876	-1.772	0.358	0.572	-2.192	1.503	6.741
-0.589	-2.075	1.990	2.261	-0.405	-1.875	-0.512	3.604
0.586	-0.899	-2.381	0.410	-2.075	9.511	0.415	0.717
1.046	-0.984	-2.009	0.416	1.780	3.838	0.964	2.808
2.243	0.164	-0.039	11.000	-1.684	-11.000	-0.429	0.645
1.448	0.136	1.407	2.974	10.722	7.536	0.013	3.437
2.537	-1.304	-0.468	1.976	1.904	-2.051	0.623	-1.670
1.532	0.173	0.363	5.159	-2.576	-5.809	-0.189	1.238
0.500	0.267	0.723	1.407	0.281	-0.896	1.098	0.689
3.247	-1.531	-1.148	0.940	1.498	-1.776	0.361	-1.541
2.645	-0.656	0.823	4.556	-2.095	-6.080	0.181	0.882
1.046	0.018	1.255	2.180	0.431	0.300	0.838	-1.441

Table35.txt

0.161	-1.563	-1.462	-0.773	3.844	-0.245	-2.595	-0.583
4.713	-2.467	-4.545	-0.052	11.000	-3.939	-0.745	-0.918
4.994	2.097	-3.055	3.294	15.492	14.493	9.733	1.688
1.956	-2.693	-4.338	0.061	1.788	1.807	-0.154	2.143
4.944	-0.406	0.568	2.456	1.493	-4.387	0.076	-1.360
1.985	0.005	0.115	3.923	11.672	9.526	8.405	2.992
2.360	0.542	-6.322	6.060	3.363	11.000	-1.795	-1.978
5.598	-2.418	0.514	-0.224	-0.121	-2.655	0.911	2.747
8.014	4.865	-3.171	-1.040	7.310	8.369	12.682	15.599
0.940	2.227	-0.550	11.000	11.000	11.000	7.079	0.660
-4.113	-6.434	-2.429	1.674	-4.332	-11.000	0.032	11.000
11.000	11.000	-5.225	-3.177	17.307	15.137	10.787	15.377
1.796	0.394	-2.793	11.000	11.000	11.000	5.487	1.787
-1.836	-4.925	-0.053	3.032	-2.337	-6.839	0.008	2.155
3.999	2.120	-2.583	-0.727	14.189	12.865	10.745	13.853
1.683	-4.618	-0.907	-5.389	-11.000	11.000	-11.000	-1.278
-4.378	-1.143	-3.076	1.823	2.740	6.254	-0.505	0.970
4.036	11.000	11.000	1.743	6.434	7.854	13.956	21.060
-11.000	4.686	4.423	-3.066	-5.374	11.000	-5.423	-5.474
-3.094	-2.912	-6.483	2.657	-5.877	-11.000	-2.149	-3.396
3.550	11.000	-2.490	-1.562	7.533	-1.484	-1.169	-1.988
5.341	-5.479	-1.912	-1.858	2.931	8.126	-3.464	-1.257
4.916	-3.695	1.060	4.409	1.058	-2.606	-0.491	-3.337
3.156	2.743	-0.492	1.350	9.913	5.428	8.151	5.552
-11.000	0.904	2.510	3.880	0.908	0.793	1.538	3.723
1.849	-11.000	-5.979	1.147	8.210	5.443	-1.860	11.000
0.699	2.129	1.229	-0.234	-1.007	-1.344	10.220	-1.356
1.177	-1.682	-3.436	6.896	1.809	-0.342	1.906	-6.706
0.212	-2.238	-0.529	3.571	2.271	-4.013	0.195	1.860
2.747	1.225	-4.667	1.348	7.192	2.299	5.467	9.866
1.648	-0.884	-1.591	3.198	3.354	1.287	-0.245	1.459
1.561	-3.837	0.722	1.768	-0.809	-4.098	0.385	0.519
0.584	-1.579	-1.178	-0.654	1.161	0.731	-3.074	-1.414
-0.762	-0.495	-0.594	0.965	-1.619	11.000	-2.615	-0.544
-0.260	-0.974	-4.386	-5.997	-0.752	-1.322	0.837	0.097
0.200	-1.482	-2.345	1.279	-1.878	-1.295	-1.424	8.388
1.383	-1.627	0.125	-0.339	-0.159	11.000	-1.385	0.447
4.623	2.897	-1.075	11.000	-0.137	-11.000	2.247	4.344
-0.362	0.980	-0.443	4.950	-1.214	-2.162	16.428	20.916
2.483	5.338	6.858	0.924	0.161	1.750	2.290	-11.000
-5.231	-7.034	-4.587	-1.577	0.440	-11.000	-2.532	11.000
5.643	5.020	-5.237	-5.107	16.844	10.880	6.576	15.834
2.040	-1.171	-0.974	0.973	0.611	0.893	0.359	11.000
1.554	-0.470	2.969	2.315	-4.634	-1.795	-0.103	0.442
0.736	-0.449	0.628	1.897	-2.056	17.341	-0.307	-1.143
0.859	-2.670	-2.839	0.053	0.068	0.758	-0.993	0.585
1.860	-0.980	-3.797	11.000	-1.202	-2.578	-0.343	-0.312
0.151	-0.996	0.148	1.296	-1.237	14.398	-0.111	0.847

Table35.txt

3.262	-1.171	-2.516	1.303	0.863	4.153	1.398	2.639
2.865	0.328	3.530	3.055	1.101	-0.632	-1.425	-3.339
0.729	-0.578	2.522	2.454	-2.521	10.062	0.416	-0.161
-5.287	-1.540	-3.355	0.920	-0.508	2.066	0.691	2.583
0.812	0.003	-1.052	5.096	0.860	-1.744	-0.605	-1.614
0.981	-0.408	0.448	2.302	-1.651	11.859	1.197	1.139
5.230	1.016	-11.000	2.353	3.993	-11.000	3.195	-11.000
3.063	0.381	-0.456	3.800	1.598	1.085	1.482	1.895
2.560	1.111	-5.694	2.751	-0.384	14.963	0.605	-2.986
3.086	-1.284	-1.666	0.225	-1.263	-6.758	0.362	-1.431
2.226	0.225	3.362	2.737	-1.938	-4.209	-0.317	0.797
5.255	3.118	-1.398	1.597	2.776	-0.761	1.999	0.654
0.490	-3.364	-3.669	3.240	2.554	-7.034	-2.105	2.231
1.723	-2.751	-1.254	-2.386	1.900	-0.397	3.095	4.100
11.000	-2.995	0.094	1.478	3.936	5.658	-1.054	-2.164
-11.000	-11.000	11.000	4.575	-1.811	-11.000	7.956	-1.033
0.303	-0.552	0.113	2.272	2.629	-11.000	1.346	-2.199
-3.825	5.141	-6.549	1.659	2.425	4.635	16.845	14.062
-0.288	3.467	4.082	-0.472	-1.800	-11.000	5.730	1.196
1.352	0.238	1.200	-0.236	-1.029	-2.524	-1.743	-0.966
11.000	11.000	2.722	-0.898	1.870	6.718	5.826	0.171
-11.000	0.122	-11.000	1.039	0.419	0.068	-11.000	2.515
0.327	-11.000	-11.000	-1.491	0.495	0.142	2.527	11.000
0.149	1.616	1.181	11.000	-0.214	-0.703	-1.465	-3.059
2.913	7.768	-0.528	-2.809	11.000	-11.000	6.001	0.495
-2.125	0.954	0.668	-0.652	4.226	-11.000	-1.218	0.779
11.000	11.000	-4.053	-0.056	18.443	15.752	11.439	21.766
4.204	3.677	-2.691	-2.428	7.992	-11.000	3.675	1.953
-0.745	-0.035	3.001	1.569	3.383	-6.486	-1.113	-0.595
6.256	4.377	-1.987	0.601	13.145	12.778	6.861	15.290
-1.417	-0.205	0.911	0.362	-1.091	-0.697	0.479	0.092
1.782	0.683	0.681	-2.062	-0.117	-1.305	1.213	1.126
-0.356	0.399	-0.036	0.524	-1.366	-1.092	-0.506	-1.633
1.378	-0.474	-0.590	6.763	-4.327	-0.065	11.000	-5.797
-3.313	-4.458	1.900	2.398	0.986	-11.000	-0.505	1.221
5.749	5.429	-6.839	-2.873	6.913	-0.171	9.396	8.799
-1.911	-0.534	0.084	-1.147	0.556	-4.025	-2.157	-1.051
2.785	2.210	-3.768	-2.765	0.659	-6.313	0.605	-1.422
3.377	2.913	-2.160	-2.183	-0.671	-1.020	-0.014	-0.675
-6.182	-5.191	-11.000	5.734	-5.054	-11.000	-11.000	8.210
-2.439	-4.550	-2.515	-4.714	3.026	6.534	2.774	5.573
3.520	3.921	5.232	-2.814	13.178	15.012	-0.865	-0.280
-0.360	-11.000	-11.000	0.444	1.408	-11.000	1.901	1.462
2.565	-0.092	0.876	1.054	0.414	11.000	1.314	-3.114
0.438	-0.315	1.037	0.294	2.111	17.807	-2.216	0.932
-1.246	1.205	0.309	1.364	0.730	-0.877	0.324	2.018
1.238	-0.265	1.073	0.104	0.050	-11.000	1.985	1.628
1.080	0.832	1.531	0.226	-0.989	-3.899	-1.384	-2.664

Table35.txt

0.627	-4.208	-3.910	-2.463	-6.191	-11.000	1.896	2.306
4.209	7.764	-0.212	-3.765	0.180	0.357	1.158	6.792
0.836	1.978	2.019	-2.066	13.177	3.639	0.304	-0.786
-0.652	-3.249	-3.890	0.637	-0.603	-3.614	3.763	-3.430
-1.280	-3.054	0.730	1.440	-1.170	-1.432	2.032	2.600
-1.875	-2.001	0.283	-0.941	-1.125	2.687	1.118	3.142
-11.000	-0.397	0.219	2.169	-0.565	-2.993	-1.055	-2.536
-11.000	-11.000	0.963	0.579	8.126	11.000	1.787	2.097
11.000	8.210	1.309	0.310	-0.610	-0.590	0.786	0.320
3.274	-2.335	-1.924	1.856	-1.111	5.426	2.336	4.771
2.204	-0.309	3.574	1.268	1.664	-0.825	0.736	1.874
3.582	1.174	1.908	2.199	0.300	-0.542	-0.163	-0.170
-4.086	6.585	7.159	11.000	-2.646	-11.000	7.153	-11.000
-0.064	-1.260	0.739	-1.804	-2.896	-2.759	1.056	0.475
3.462	2.390	-5.800	-0.560	6.203	5.521	7.074	4.203
0.247	-1.275	-2.300	5.136	-0.930	-1.659	11.000	3.442
0.577	-1.451	-0.157	-1.714	-0.468	-6.284	-0.164	0.308
-1.088	-1.987	-0.892	-2.116	-0.461	-0.791	-0.425	11.285
-3.985	6.124	11.000	-1.271	-0.757	-6.807	2.528	2.114
-0.588	0.045	0.518	4.239	1.676	-4.231	6.453	11.000
5.982	5.084	-0.700	1.616	14.587	14.967	1.560	13.785
0.908	-0.687	-11.000	0.913	-0.692	-11.000	-5.538	5.820
2.104	1.089	0.323	-0.853	0.827	-2.754	1.592	1.465
-0.484	-0.530	0.735	-0.386	-0.647	9.542	-1.554	-2.590
2.849	0.907	-11.000	2.835	0.996	0.810	-4.160	-1.021
11.000	1.079	2.814	-1.275	0.789	-0.095	3.641	2.879
1.443	11.000	1.437	-5.115	0.218	0.374	-0.930	21.745
2.845	0.351	-5.676	3.833	3.295	1.077	-3.796	2.604
1.604	1.032	1.865	2.230	-0.228	-5.160	-0.257	0.392
2.168	1.162	-1.151	4.539	0.934	10.648	2.214	13.233
3.285	-0.684	-11.000	2.580	0.260	-11.000	3.634	-1.026
1.509	0.819	3.096	1.109	0.593	-1.939	-0.345	3.436
7.495	4.829	0.954	0.440	1.045	0.872	-1.208	-1.903
-11.000	-1.824	0.007	4.011	-1.136	-11.000	4.201	3.959
-0.263	-3.534	2.360	2.554	1.526	1.361	0.422	11.000
-1.820	2.898	-4.837	1.350	10.722	6.816	0.575	1.910
-0.852	1.640	3.197	11.000	11.000	7.886	0.355	-1.983
-1.217	-2.005	0.082	6.806	1.892	-11.000	-0.419	-0.465
-1.148	-0.726	-2.944	-0.548	0.610	-0.167	-0.828	-0.408
1.338	3.806	4.103	4.549	-2.085	1.519	-3.081	3.676
-1.878	0.212	1.399	2.477	-6.692	-11.000	2.356	2.794
1.308	-1.979	-11.000	1.777	15.343	-0.458	13.504	14.127
-3.356	-0.457	-1.305	3.436	3.177	-2.909	2.381	-4.433
1.672	0.824	1.950	2.536	4.455	-1.043	1.820	2.187
3.222	3.077	3.330	-1.360	1.870	-0.825	0.007	2.104
-11.000	-11.000	-1.404	4.968	6.790	-11.000	5.849	11.000
4.947	6.129	0.455	1.925	-0.429	-11.000	-0.093	0.063
-4.117	-0.667	-1.375	-0.865	16.008	-0.211	13.765	21.773

Table35.txt

-1.379	-1.439	2.625	-1.176	-1.952	11.000	-1.697	-1.187
-0.578	-0.922	-0.342	-1.094	-0.543	-3.320	0.251	-0.308
-1.243	0.217	-0.884	-0.889	-0.162	-0.091	14.738	20.378
-1.975	-1.094	-0.042	11.000	11.000	-3.287	-11.000	-0.256
-0.433	-4.896	-0.136	-1.461	0.556	-1.290	1.230	-0.352
11.000	-3.843	-0.338	-0.028	-1.149	-1.638	0.059	-1.096
0.480	-0.578	0.401	0.433	-1.510	-1.886	0.975	0.272
0.125	-0.655	-0.004	-1.257	0.417	-1.125	1.869	2.517
-0.997	0.814	1.300	2.151	-1.704	-0.316	-1.408	0.152
-0.244	11.000	11.000	0.067	0.604	11.000	0.817	0.919
0.689	0.466	0.124	-1.269	-0.219	-11.000	0.396	0.365
0.574	1.820	-0.073	-0.512	-0.714	-3.041	-0.528	-0.460
-0.122	-2.711	-11.000	-0.765	-0.737	4.733	11.000	-1.312
-5.069	2.029	5.337	-1.213	2.781	0.908	-0.200	-4.923
-3.913	-0.150	-6.277	-1.512	6.529	10.581	10.287	4.941
-0.089	0.282	-0.290	0.533	0.960	-0.454	-0.158	1.240
-0.415	0.227	-1.897	-0.400	1.335	-6.085	-3.661	0.218
-0.324	1.180	0.037	2.160	-1.511	-1.144	-0.814	-2.846
-5.426	-11.000	5.372	3.864	-3.473	-3.635	-6.051	-5.846
-5.754	-11.000	-4.893	-6.937	-3.591	-7.034	4.163	5.533
5.170	11.000	-3.053	-4.519	3.404	5.605	5.552	5.547
6.842	11.000	2.668	2.811	0.643	-4.260	-2.191	11.000
-3.096	-5.898	11.000	-11.000	7.830	-3.434	-1.685	6.064
-11.000	4.367	-1.833	4.385	-0.647	1.153	-1.805	-2.035
-0.729	-0.856	-0.061	0.035	1.335	0.425	0.420	1.207
-1.143	-2.426	-1.327	-0.168	1.403	-0.515	0.609	0.437
-1.557	-0.217	0.780	1.234	-0.627	0.479	-3.089	0.662
-1.175	-1.836	11.000	11.000	-1.737	11.000	-2.291	-2.633
-1.371	-3.034	-1.735	-1.779	-0.167	-2.512	-0.162	0.072
-0.139	0.694	1.126	1.136	-0.372	-3.038	-2.330	-2.214
-3.829	-4.239	2.112	2.004	-1.609	-0.075	-2.479	-2.876
-2.290	-4.827	-3.558	-11.000	-0.377	-11.000	-2.695	-3.065
11.000	11.000	11.000	11.000	7.822	7.862	-1.481	0.978
-11.000	-0.884	-1.092	-0.072	-0.772	-1.974	-1.223	-0.009
-2.572	-3.315	11.000	0.102	1.555	0.598	-1.604	11.000
-1.299	0.336	0.327	1.318	-0.189	0.153	3.154	-2.756
-1.421	0.893	-1.167	0.037	0.728	-1.814	-0.432	0.823
-0.418	-1.801	0.625	0.910	-0.028	1.065	0.699	1.179
-1.473	-0.014	-1.977	1.438	-0.800	-1.033	-1.318	-0.858
-1.141	0.149	-1.215	-1.156	-0.259	-1.176	-0.966	0.418
-0.305	0.439	-0.315	-0.462	-0.903	-11.000	-0.665	1.139
-1.027	11.000	0.042	0.723	-0.750	-0.842	-2.518	-0.855
0.544	-0.145	0.748	0.458	0.810	-5.245	0.805	-1.481
-0.554	-3.488	-0.964	-0.501	2.434	0.010	-0.224	-0.034
0.053	0.502	-0.901	2.243	-1.527	-1.884	-1.542	-1.154
1.353	0.911	-1.755	-0.174	-0.319	-0.787	0.235	0.402
-2.525	-1.966	-0.724	0.077	1.748	0.515	0.002	0.465
-1.675	-0.852	0.165	1.106	-2.800	-1.493	0.814	-1.540

Table35.txt

-1.581	0.644	-1.742	0.343	-0.633	3.466	-0.559	0.982
-1.093	1.375	-1.322	0.013	0.197	-11.000	-2.693	1.634
-1.266	-0.350	11.000	0.820	-0.291	-2.113	-1.113	0.693
0.011	-0.003	-1.517	-0.945	1.539	-0.461	1.814	0.817
-1.966	-1.218	0.009	-1.251	0.890	-11.000	-1.070	0.194
-0.348	-1.075	11.000	0.621	-0.389	-0.875	-1.184	-0.884
0.373	0.209	-0.017	-1.322	0.460	-1.163	0.476	1.392
-2.522	-1.070	-0.355	-0.126	1.091	-4.200	-1.007	0.301
-1.705	-0.131	-0.365	0.781	-2.206	-0.616	-1.908	-1.342
-0.164	-0.838	0.200	1.782	0.430	-0.277	0.916	-1.419
-0.525	11.000	-1.506	0.209	2.132	-0.462	0.085	0.658
0.283	0.622	-0.293	1.141	1.334	2.922	0.124	-1.464
-1.404	-0.718	-1.906	-0.296	-0.179	-0.380	-0.879	1.194
-1.427	-2.584	-0.978	-0.444	1.026	0.293	11.000	11.000
-0.268	-0.308	-0.297	1.607	0.832	-1.162	-0.527	-1.608
-0.192	1.774	-1.544	-0.579	0.105	-1.151	-0.876	1.257
-0.699	-0.278	-0.038	-1.254	1.412	0.493	0.335	0.682
-1.164	-0.032	1.183	0.944	-0.720	-0.974	0.245	-2.423
-0.123	0.582	-0.901	-1.300	-0.426	11.000	0.316	1.302
-0.706	-0.175	-0.248	0.162	1.263	-11.000	0.563	-0.230
-0.762	-0.035	-0.067	-11.000	-3.345	-1.822	-0.825	-1.404
-0.037	-0.049	0.374	1.439	0.397	1.071	0.931	0.704
-1.407	-1.469	-1.613	-0.695	-0.097	-11.000	0.202	-0.328
0.733	-0.521	11.000	1.074	0.886	0.895	-0.513	-1.816
0.364	1.966	-1.113	-0.252	-0.576	-2.088	0.745	-0.105
-2.594	0.779	0.049	0.454	0.235	0.974	-2.074	-0.450
-0.655	-0.099	-0.248	1.066	-1.047	-1.350	-1.294	-0.222
0.566	0.031	-0.949	-0.418	-0.084	-1.981	0.016	0.570
-1.872	1.298	-0.409	0.029	1.881	1.130	-0.037	0.570
-1.631	0.411	-0.624	-0.351	-0.363	-1.420	0.254	-1.097
-2.317	-0.462	-0.699	0.215	-0.370	0.427	-1.281	0.277
0.072	2.806	-0.932	-0.707	-1.034	-0.216	-2.759	-0.847
-1.113	0.258	3.624	3.639	0.655	-2.091	1.135	-0.670
0.904	-1.207	-0.612	-0.516	0.102	-1.212	-0.112	0.538
-2.184	-1.045	-1.112	0.593	1.237	1.372	-0.560	0.206
-1.228	0.365	0.255	1.088	-0.263	-0.785	-2.911	0.236
-1.288	-1.921	3.782	3.238	-5.583	-4.384	-11.000	11.000
-11.000	-11.000	2.798	-3.448	6.204	11.000	11.000	11.000
-6.880	11.000	4.911	-0.143	0.586	3.502	6.373	7.834
-0.323	2.760	11.000	4.830	-1.463	3.234	-2.635	-0.839
0.105	-2.369	1.902	2.829	2.036	-4.020	-1.076	-2.631
4.000	2.372	-6.145	2.013	10.231	9.684	7.605	14.256
-0.764	-3.304	3.454	2.349	-11.000	0.555	-6.056	11.000
2.341	-11.000	3.256	6.183	3.602	-0.491	11.000	-2.257
-11.000	11.000	2.042	1.619	0.335	0.448	0.017	12.689
0.243	-11.000	-2.823	3.382	2.515	-0.084	2.233	2.733
-0.753	-0.725	-0.961	0.282	-3.568	-11.000	-0.054	1.262
11.000	11.000	3.092	1.630	-0.479	-1.039	-0.718	-2.055

Table35.txt

-1.781	-2.876	7.386	3.500	-6.278	1.969	-11.000	11.000
-4.845	-3.395	-2.497	-11.000	-0.287	-2.411	0.283	11.000
-7.034	8.014	11.000	-3.451	5.098	1.169	0.975	-0.401
-0.240	-1.621	-0.394	0.687	3.102	1.805	-5.021	-1.600
-0.384	-3.575	0.999	-2.439	-0.432	-1.929	0.363	0.054
-3.137	2.236	-1.340	3.501	-1.369	0.424	-1.138	-0.882
-5.966	-11.000	11.000	11.000	-2.597	-2.606	-5.467	11.000
-4.378	-7.034	11.000	-4.265	-3.606	-5.313	-4.675	7.228
11.000	11.000	-3.733	11.000	-0.066	0.183	10.516	-0.114
-0.558	-11.000	7.352	1.540	-0.421	0.397	-4.010	5.796
0.711	-1.692	4.731	-11.000	11.000	-4.041	1.886	-5.272
-11.000	11.000	2.122	-4.421	8.348	2.734	4.622	2.083
0.618	0.606	11.000	-0.167	0.371	-1.957	-11.000	0.439
-2.032	-2.048	-1.940	-1.239	11.000	0.901	0.434	-0.182
-0.268	0.310	0.305	1.959	-1.761	0.543	0.039	-1.703
-0.333	1.379	5.344	2.789	-0.104	0.068	-11.000	7.274
-4.803	-11.000	11.000	-11.000	6.185	-0.446	4.785	11.000
-11.000	11.000	-0.363	7.193	-0.412	-0.156	4.265	5.336
1.150	-11.000	11.000	3.549	-1.644	-0.160	-11.000	7.390
-0.149	-11.000	11.000	-11.000	0.792	3.727	11.000	1.746
-11.000	11.000	0.196	1.798	11.086	10.265	0.035	13.945
2.126	-11.000	0.577	1.178	-5.824	-3.210	-11.000	11.000
-2.055	1.016	4.412	11.000	2.536	-1.465	11.000	2.807
-2.409	7.261	-11.000	-6.357	1.972	12.224	4.197	10.514
3.772	2.941	0.091	1.863	1.876	0.007	-11.000	4.556
1.486	4.036	0.482	-4.927	2.578	-4.543	2.004	3.150
-11.000	11.000	-11.000	2.578	2.140	1.787	0.091	8.719
3.620	-4.453	-3.807	2.735	-1.505	-3.613	-11.000	-4.107
2.525	3.135	6.808	-11.000	3.485	5.918	2.477	4.908
-5.963	11.000	-11.000	-11.000	0.821	1.285	-1.354	5.007
2.066	-2.462	-11.000	0.458	-0.322	0.654	11.000	1.188
0.952	-0.053	4.337	2.066	0.595	-2.639	-0.431	1.755
0.370	-0.580	-1.374	5.707	-1.475	-1.378	0.421	-1.407
0.463	1.561	-0.359	0.719	-2.843	5.598	-11.000	11.000
-1.017	0.715	-1.396	0.792	1.153	1.979	-0.016	0.341
-11.000	11.000	0.872	11.000	-1.245	-2.657	-1.275	9.419
0.051	-0.533	-0.300	0.189	0.649	-0.091	-1.755	0.431
-1.344	-1.653	-0.878	0.381	1.524	0.536	1.518	-0.593
-2.061	2.984	-1.643	1.994	-1.621	1.790	-1.353	-0.047
1.855	-2.158	-0.185	0.124	0.406	0.387	4.744	1.010
1.157	-0.716	2.611	2.199	1.943	-4.761	3.405	0.122
-2.980	-0.539	0.454	2.526	-0.712	-2.142	2.164	1.782
-0.359	0.621	-4.632	0.231	0.076	0.965	-11.000	11.000
-1.985	-4.523	-3.092	-0.728	1.339	11.000	4.124	-0.608
-11.000	11.000	0.795	0.024	-0.606	-0.410	-0.995	5.608
3.548	7.460	-1.397	11.000	2.191	3.669	-11.000	0.668
5.897	7.709	11.000	-11.000	2.425	1.761	5.627	11.000
-6.780	6.422	-3.333	-1.176	11.188	16.644	3.367	13.775

Table35.txt

-0.133	-0.695	-0.436	0.940	1.116	-1.191	-11.000	11.000
-2.485	-4.248	-1.901	-2.300	5.952	3.232	-0.380	-0.272
-11.000	11.000	-4.804	1.564	-0.347	-1.254	-1.664	-1.089
0.707	1.492	0.623	0.099	-6.780	0.763	-11.000	11.000
-0.950	-11.000	0.286	2.810	1.690	2.182	0.327	0.785
-11.000	11.000	1.781	11.000	8.122	-0.777	-0.456	14.489
1.251	2.916	11.000	11.000	-11.000	-0.290	-11.000	11.000
-11.000	-0.133	-1.658	-11.000	-2.017	2.089	0.705	1.313
6.078	11.000	1.236	11.000	12.001	16.179	5.909	15.891
1.598	3.221	2.077	4.518	-11.000	-1.514	-11.000	11.000
-11.000	-11.000	0.603	3.009	-1.666	-5.454	0.275	-0.152
11.000	11.000	11.000	11.000	8.977	11.737	1.827	3.482
4.789	-11.000	11.000	11.000	-1.221	-3.950	-11.000	2.153
-11.000	-11.000	4.836	-11.000	-0.079	-3.998	5.654	11.000
3.529	7.830	0.654	4.633	11.382	15.902	4.704	11.755
0.640	-0.035	-0.858	-0.615	0.055	-0.941	1.247	0.813
0.536	-1.944	0.142	1.030	0.773	0.827	1.106	-1.290
-0.477	-0.067	1.438	-0.524	0.457	0.089	-1.190	-1.161
0.310	-1.422	0.065	2.307	2.385	-0.228	0.342	1.877
0.833	-1.045	0.302	0.712	0.939	-0.908	0.852	0.339
0.776	0.323	-0.245	-0.059	0.000	0.000	0.000	0.000
-0.814	-1.647	0.600	0.507	-1.682	-0.706	-3.215	11.000
-0.988	-6.525	-1.203	-0.035	2.040	4.145	2.027	-3.244
-4.096	11.000	-1.814	3.006	2.735	0.012	-0.853	0.408
-0.676	0.339	2.019	-0.302	-0.194	-1.291	-3.567	5.684
0.620	-0.596	-0.801	-5.939	3.398	1.783	0.407	1.840
-4.764	5.644	-2.218	2.498	-1.697	-0.941	-1.665	-1.523
5.655	7.896	-0.124	-1.372	-3.964	-0.778	-11.000	11.000
-11.000	-4.455	-2.553	-11.000	-1.197	2.378	7.658	7.761
4.022	5.663	-11.000	5.154	0.000	0.000	0.000	0.000
-0.877	-2.344	-2.467	-1.119	-0.427	1.368	-1.904	-0.042
-1.101	-2.823	3.891	-1.566	1.088	0.713	-0.426	0.903
-1.112	7.136	-0.842	0.465	-0.445	-0.867	-0.734	0.309
-2.873	-3.098	-1.033	11.000	-0.892	-0.140	-3.365	11.000
-3.803	-5.358	-3.842	-3.002	-11.000	-2.704	-2.672	-2.504
11.000	11.000	-2.301	-0.656	-0.415	-2.423	0.124	-0.864
-2.820	-3.648	0.273	1.131	-3.751	-1.068	-11.000	3.960
6.240	-3.545	0.867	-3.178	3.335	4.522	-0.500	-0.284
-6.311	11.000	11.000	3.401	-0.132	0.442	-0.836	-0.771
0.931	0.848	0.515	0.566	0.321	0.296	-11.000	11.000
0.090	1.305	1.107	-5.593	1.305	1.478	0.100	1.563
-0.001	2.418	-11.000	1.982	-0.980	0.355	-0.136	0.018
0.071	-11.000	4.302	3.001	-3.539	1.025	-11.000	11.000
-5.935	-11.000	11.000	11.000	-3.895	-11.000	-4.974	-5.967
5.923	11.000	11.000	11.000	2.431	2.673	1.510	2.398
-3.356	-4.255	1.435	0.491	2.277	-0.232	-11.000	1.105
-5.677	1.332	0.871	2.353	2.026	-11.000	0.604	2.086
11.000	11.000	1.408	0.222	-0.518	-0.861	-1.342	1.236

Table35.txt

0.019	0.322	11.000	3.031	1.206	1.374	0.410	1.071
-2.026	-1.089	-1.903	0.735	-11.000	1.324	-11.000	0.642
11.000	11.000	0.718	1.433	-1.454	0.477	-1.322	4.570
-1.926	-1.175	11.000	7.345	-2.548	-1.032	-11.000	11.000
-0.783	11.000	-1.277	-1.852	-1.203	-1.851	-2.160	-0.747
-11.000	11.000	-6.458	-1.047	-0.178	-1.221	-1.351	-1.771
0.528	0.425	-0.517	-1.714	1.709	-1.036	-2.638	6.410
-1.402	-2.714	-0.502	-0.258	-0.142	0.985	-0.278	-0.361
-0.134	6.361	0.209	1.194	-0.543	-1.129	0.661	1.427
-11.000	-11.000	-11.000	2.678	11.000	-2.341	-11.000	0.570
3.657	4.766	-11.000	0.432	-5.433	-11.000	-4.192	3.147
11.000	11.000	-1.507	-6.647	4.525	7.429	-1.061	-3.640
-1.541	-0.127	0.013	1.086	-0.626	11.000	-0.699	-11.000
-1.830	-0.931	-0.895	0.178	-5.177	-11.000	3.177	4.180
11.000	11.000	-11.000	-6.780	-1.269	12.748	3.769	8.551
-0.942	-0.946	-1.241	2.710	-0.812	11.000	-2.195	0.104
-2.898	-2.661	-5.399	11.000	-3.490	-11.000	-0.998	-2.301
-1.239	6.141	-1.349	-2.974	-0.810	-1.274	-0.452	-2.531
-7.034	1.747	2.110	-4.274	-11.000	11.000	-11.000	-5.623
0.145	0.852	-3.306	8.041	-3.372	-11.000	-2.399	-4.251
-4.490	11.000	-3.429	-4.091	-0.786	15.101	13.052	17.528
-1.050	-0.792	-1.283	11.000	6.645	11.000	-1.254	-0.678
5.259	-0.838	-3.717	6.228	-4.608	-11.000	1.155	1.552
-0.915	11.000	5.098	-1.939	3.579	2.955	1.918	3.591
-0.831	0.650	0.734	1.459	-0.248	11.000	-11.000	0.481
-0.064	-4.131	-6.308	0.478	-5.268	-11.000	-1.953	-3.306
11.000	11.000	-0.913	-3.060	-1.302	-2.178	-1.417	-2.646
-11.000	-2.777	-3.583	4.599	5.490	6.479	-11.000	-4.021
0.850	0.873	-6.577	2.724	-2.970	-11.000	0.111	-0.377
2.698	11.000	-11.000	-3.255	2.946	5.260	7.086	15.174
3.964	-1.816	-2.258	-0.099	-2.170	11.000	-11.000	-11.000
1.972	2.097	-1.313	-0.709	-6.721	-11.000	0.675	0.363
7.150	11.000	1.621	-1.046	1.639	4.954	7.649	15.814
-11.000	0.716	0.714	0.237	-2.341	11.000	-0.378	-0.358
-3.861	-2.092	-6.937	1.567	-5.002	-11.000	-1.458	-3.009
-3.434	11.000	-11.000	-5.830	-2.759	-3.659	2.776	-0.082
-0.849	0.149	-2.289	7.992	11.000	-0.352	0.326	0.341
-4.237	-3.718	-2.186	-1.309	-1.229	-3.517	0.629	4.240
-1.857	-2.560	-2.214	-4.442	0.559	-2.371	-1.521	-3.706
1.752	-0.492	0.353	2.511	-0.221	0.429	1.039	-11.000
-4.284	-1.716	-0.105	0.164	0.241	-2.473	-0.075	-0.668
-2.494	-1.623	-1.031	-11.000	-2.333	-0.048	-1.975	-2.311
-0.008	-0.362	1.263	3.477	0.776	-0.595	-0.435	0.874
-5.550	-3.067	-1.568	2.372	-1.780	-2.427	-1.169	-2.887
-0.118	-1.808	-0.408	-2.646	-1.666	-1.019	0.095	-4.040
-0.739	11.000	-6.490	0.206	0.766	0.158	-0.757	2.411
-11.000	-11.000	2.785	7.870	-0.639	-1.396	-1.492	-3.509
5.165	4.295	-1.365	-3.885	0.558	0.734	-0.339	-1.574

Table35.txt

0.172	2.050	0.164	2.773	1.126	0.778	-11.000	0.780
-2.753	-2.296	-0.957	-2.713	0.182	-1.209	-1.334	-1.756
1.458	11.000	-0.077	-4.608	0.000	-1.042	-0.654	0.537
-1.667	-0.923	11.000	-0.061	3.074	-0.503	-2.192	-11.000
-3.067	-5.695	-5.236	8.126	-1.889	-11.000	-1.626	-2.731
11.000	7.906	-1.649	-2.070	-1.613	-2.449	-1.270	1.454
-1.488	-11.000	-1.661	1.939	0.180	11.000	-11.000	-1.344
0.269	2.772	-5.125	-1.045	-5.683	-11.000	-2.753	-3.584
11.000	6.085	-1.086	-2.898	-2.671	-0.950	-2.960	-3.034
-5.715	-0.140	-0.841	3.574	-5.041	11.000	-11.000	-11.000
-2.450	-1.222	-6.565	6.769	-5.921	-11.000	-1.052	-1.895
3.074	11.000	-0.118	-1.957	-0.913	0.259	-2.079	-1.400
0.827	0.293	1.375	0.573	-0.943	1.903	2.230	-0.112
-1.719	-2.183	0.142	-0.518	-0.201	-1.998	0.586	-1.832
-1.290	-1.223	1.989	-2.053	-0.108	-0.908	-1.061	-2.008
1.442	0.367	-0.305	0.418	0.483	0.229	6.090	0.668
-0.708	-3.480	0.739	0.350	-0.776	-2.032	1.074	-0.745
-0.835	-0.381	0.284	-0.632	-0.896	-0.368	-0.507	-0.388
-11.000	-6.259	-11.000	11.000	8.077	-0.285	5.318	-0.572
-3.247	-2.005	-0.075	0.156	1.931	-11.000	-0.272	-0.210
5.301	6.420	-5.604	-5.941	0.176	-3.624	3.953	3.064
4.142	1.033	3.250	-1.104	11.000	-2.802	3.037	-0.254
-0.559	-7.034	-4.707	-3.789	-4.069	-11.000	0.431	-0.094
-2.769	5.393	0.407	-5.990	0.727	-0.949	0.678	-2.002
6.833	-0.397	-2.167	11.000	3.419	-5.298	5.000	0.164
-0.500	-1.041	1.132	0.152	-4.633	-1.599	0.276	1.294
2.879	3.042	-1.511	-0.300	0.078	-0.789	0.058	-0.134
-1.278	0.126	0.096	0.347	-0.025	0.003	0.950	0.880
0.629	-0.309	0.253	-0.176	0.595	1.008	0.309	-0.590
-0.595	1.363	1.688	-2.266	0.000	0.000	0.000	0.000
-11.000	-7.034	2.579	-6.544	6.394	1.124	6.054	-3.830
-0.705	-0.959	-4.979	2.217	3.453	11.000	-1.319	-2.476
4.483	3.478	4.212	2.819	2.779	4.208	-0.921	-0.023
-4.378	-4.543	-4.619	-2.604	-5.130	-5.717	-5.316	-11.000
3.990	3.981	-1.754	-3.380	-2.108	-5.758	2.145	3.747
3.863	2.856	5.973	-3.537	6.538	7.275	0.341	-1.711
-2.969	0.341	0.555	1.749	1.524	-11.000	0.134	0.305
-3.044	-11.000	-4.607	-0.699	0.594	-2.640	-1.281	4.793
5.547	3.913	-0.899	-1.876	-0.364	0.529	-0.014	-0.193
-3.460	1.671	2.953	-0.447	-3.571	11.000	-3.085	-3.687
-4.413	-1.054	-2.886	-1.684	-4.825	-11.000	-0.979	-2.649
-3.673	6.983	-4.355	-4.295	-2.881	-2.146	-1.212	0.457
-11.000	3.772	3.069	3.564	3.033	8.041	-11.000	-11.000
0.126	-0.297	-11.000	-5.805	-4.073	-11.000	-0.419	-1.439
1.995	4.103	-5.744	-2.856	2.513	2.875	3.572	5.144
1.846	-3.601	-0.524	-2.921	-5.689	6.894	-11.000	-11.000
-1.220	0.752	-5.689	-2.773	-3.770	-11.000	-1.682	-3.281
-0.779	3.263	-3.462	-4.473	0.569	-1.933	-0.056	-0.517

Table35.txt

0.282	1.090	1.854	-2.455	-6.357	11.000	-11.000	-5.027
-2.922	3.603	-6.282	4.582	-5.634	-11.000	0.233	-1.224
11.000	11.000	-2.371	-4.412	2.119	5.598	3.230	5.359
-1.850	-2.355	-4.920	-1.130	-3.879	11.000	-2.233	-2.036
-3.099	-3.868	-4.477	3.873	-4.727	-11.000	-1.407	-2.321
-11.000	11.000	-1.478	-1.505	-0.371	-1.594	-0.770	-0.924
-1.806	-0.202	-0.567	1.686	-0.984	11.000	-11.000	-6.721
-2.916	-2.766	-6.399	0.118	-6.372	-11.000	-0.643	-2.178
11.000	11.000	1.324	-2.061	-0.510	-1.475	-0.072	2.448
-0.035	-1.304	-1.511	11.000	11.000	11.000	-1.904	-3.452
-4.121	-3.587	-2.335	-2.535	-1.114	-3.472	-1.208	-3.609
-11.000	-3.141	-1.816	-4.812	-1.794	0.604	-1.122	-2.625
0.785	-0.096	-0.501	4.354	5.899	1.460	0.031	0.831
-1.942	-2.342	-0.935	-1.825	-1.406	-2.082	-0.630	-0.627
-0.781	-2.331	-1.351	-1.506	-0.604	-3.254	-1.024	-1.515
-1.381	-1.142	-2.183	0.670	-0.213	11.000	-11.000	-1.182
2.221	1.087	0.495	1.778	-3.697	-11.000	2.355	-0.243
-1.445	11.000	-2.332	-3.046	0.000	0.050	0.633	0.000
-0.284	-0.678	-0.818	6.639	5.943	11.000	-2.326	-0.825
-2.523	-1.783	-6.039	-1.694	-0.941	-2.454	-0.567	-1.459
3.977	3.453	-0.319	-2.565	-2.182	0.902	-1.013	-2.512
-3.163	-1.200	-0.570	1.800	0.721	11.000	0.725	-4.442
-5.978	-2.371	-3.710	-3.618	-2.934	-11.000	-0.559	-3.090
3.555	2.270	-1.793	-5.878	-1.978	0.965	-0.947	-0.692
0.206	-1.985	-0.227	0.903	-1.321	11.000	-1.717	-4.813
5.672	-11.000	-5.937	0.780	-5.209	-11.000	0.232	-0.950
7.062	4.558	-1.077	-0.899	-0.298	-1.607	-0.755	-1.957
0.346	-3.209	1.176	0.943	-0.806	11.000	-1.741	-1.115
-0.702	-1.164	-0.558	-1.702	-0.416	-3.758	0.496	0.611
1.619	1.735	1.031	-1.791	0.000	0.000	-1.120	0.591
-0.360	-1.245	-1.448	1.061	0.823	11.000	0.778	-1.254
-2.997	-2.452	-4.283	-1.180	-2.904	-6.571	-0.338	-3.121
2.140	1.264	0.844	-1.758	-1.926	-4.121	-0.736	-1.615
1.234	0.590	-0.326	1.720	0.339	1.424	0.103	0.085
4.467	4.502	-0.649	-0.751	-0.282	-2.257	-1.236	-0.562
-1.895	-2.265	-0.272	-5.308	-1.351	-0.459	-2.118	-1.410
2.320	0.924	0.586	2.235	0.359	11.000	-2.455	0.942
-0.428	0.590	-4.662	0.442	-5.553	-11.000	0.362	0.219
1.878	11.000	1.501	-6.549	-1.055	-2.952	-1.344	-1.829
-0.630	1.024	0.857	1.729	1.303	0.163	2.853	0.826
1.355	0.312	-0.677	-0.380	-1.585	1.274	1.764	1.371
-0.629	0.027	-0.118	-2.603	0.000	0.000	0.000	1.236
-1.774	-2.157	-0.685	5.232	4.157	-5.647	0.723	-2.302
3.741	0.492	-3.266	3.425	-3.567	-11.000	0.680	0.927
0.846	0.554	-0.678	-5.679	-0.123	0.465	0.975	-3.735
7.290	-2.841	-2.428	5.181	7.145	-3.467	-11.000	-11.000
3.321	7.442	3.074	2.922	-5.681	-11.000	-1.644	-1.962
2.087	2.251	4.580	-6.097	0.000	4.051	5.594	6.552

Table35.txt

0.033	-1.302	0.622	0.570	2.407	-1.946	0.507	2.119
-0.623	0.796	-2.670	3.862	-1.566	-3.454	-0.206	-2.704
-0.039	5.838	-0.600	-1.178	2.718	1.504	-1.145	-0.321
2.058	-0.027	0.093	0.474	-0.072	3.002	-1.032	1.314
-0.447	-1.034	-1.438	0.067	-1.184	-3.641	2.189	2.991
-0.163	-0.093	-0.085	0.516	1.149	-2.039	0.000	-2.118
0.713	-1.159	-0.982	-0.090	-0.560	11.000	-11.000	-2.969
-1.040	-2.441	-4.570	-5.688	-5.912	-11.000	-0.631	0.072
-0.756	0.816	0.661	-1.889	-1.837	4.629	-2.770	-1.172
0.326	-0.178	0.111	1.187	0.088	2.388	0.793	0.324
-1.908	-1.400	0.126	-1.139	-0.248	-1.900	-1.451	-1.437
-1.818	-1.236	-0.132	-2.184	-1.140	-0.707	-1.288	-1.248
-3.428	-4.153	-4.486	2.177	0.217	-11.000	1.715	3.912
-1.186	-3.779	-2.304	-1.775	-2.214	-4.127	-0.340	-0.559
-2.856	1.569	-2.076	0.443	-0.499	-0.512	-0.151	1.535
0.805	1.153	-0.120	1.594	1.078	0.569	-1.709	0.706
-2.831	-1.157	0.337	-0.196	-0.762	-3.012	-1.278	-1.604
-1.358	-2.001	0.059	-2.783	1.572	1.988	-1.039	-3.588
2.233	-0.471	-1.635	0.549	0.904	0.111	-0.841	0.720
-3.366	-2.123	-0.911	-0.172	-0.391	-2.308	-0.400	-1.011
1.016	-2.133	-0.777	-3.429	-4.313	0.852	-0.422	-0.105
11.000	-2.207	-1.772	-1.049	-2.899	-11.000	2.312	-0.888
-5.179	-6.420	-3.055	-1.079	-0.373	-0.231	0.312	0.866
2.275	2.655	4.948	1.246	-0.610	6.762	2.068	1.384
-1.295	-6.188	5.118	4.691	-0.861	-7.034	11.000	-1.534
1.298	1.167	1.425	1.062	6.031	-4.860	2.682	-1.506
0.728	1.386	-3.794	3.866	0.458	0.122	0.018	2.008
-0.051	0.441	0.543	1.117	0.200	1.725	-0.539	-0.874
-2.857	-1.478	-0.754	-0.931	-1.303	-2.200	-1.323	-1.919
-2.814	-2.465	1.233	-3.534	-0.914	-2.508	-0.354	-1.796
-2.618	-2.760	-3.266	2.817	3.522	7.689	4.270	-11.000
-11.000	-11.000	4.769	6.854	-0.067	-2.593	1.009	2.021
3.415	3.028	6.106	-1.049	3.090	3.090	0.000	3.090
-2.672	-2.584	-2.903	-0.777	-2.589	-1.870	-2.625	-2.894
-2.650	-3.473	-0.513	-2.409	-1.962	-5.529	-1.045	-1.937
-2.360	-3.018	-1.619	-3.740	-1.164	-0.417	0.072	-0.580
-2.311	-5.318	-1.599	3.417	3.005	11.000	7.570	-1.880
2.191	2.807	-3.723	-6.072	-4.062	-11.000	-0.302	-2.219
-4.262	-1.000	7.764	-5.824	1.506	-0.074	-1.464	-1.461
-2.806	-1.708	-2.486	-0.561	-2.274	11.000	-2.318	-2.571
-3.267	-2.713	-7.034	11.000	-11.000	-11.000	-1.339	-1.939
-6.668	11.000	-1.259	-2.700	1.310	-1.452	-1.694	-0.357
-0.564	-0.640	-1.822	2.748	-0.018	-1.163	0.421	0.428
-11.000	11.000	0.514	-11.000	0.295	-0.262	-0.417	-0.457
-2.755	11.000	-0.215	-0.976	-0.631	0.509	0.009	13.826
1.319	0.827	-1.052	11.000	0.687	-1.618	-0.763	-0.315
-6.739	-11.000	0.889	0.936	1.611	1.270	11.000	11.000
7.216	11.000	-5.485	-6.880	-0.170	5.010	1.073	2.235

Table35.txt

-11.000	-0.242	-0.399	-6.311	0.099	4.492	-11.000	1.126
-0.583	-0.958	-4.474	0.440	-4.316	-11.000	0.421	-0.083
3.091	4.060	0.926	-1.007	-0.121	-0.001	-1.367	-1.671
-2.521	3.855	4.245	7.709	11.000	11.000	0.792	2.394
0.353	0.606	-4.495	7.011	-5.031	-11.000	1.029	0.464
-11.000	6.569	-3.608	-1.408	5.156	-2.529	-2.225	-2.772
0.992	-0.179	-0.264	0.410	-0.410	1.975	1.141	0.921
-1.910	-1.666	0.594	-1.038	-1.118	-4.007	-0.250	-0.850
-1.966	-0.345	-0.069	-1.697	-1.675	-0.555	-0.671	-1.996
-3.248	-1.160	-1.802	2.989	4.916	11.000	-4.112	-7.034
-2.492	-2.487	-4.899	-2.024	-0.368	-11.000	2.217	-1.560
3.017	2.756	-0.214	-2.563	-0.830	0.079	-0.552	-0.734
-3.282	-5.158	-5.212	-0.062	-3.074	11.000	-2.174	-11.000
-2.093	-2.572	-1.185	-0.733	-2.381	-11.000	-0.228	-1.616
1.105	11.000	-2.443	-1.324	0.000	-1.820	-1.956	-1.463
-5.409	-6.394	11.000	7.836	-7.034	-3.215	-4.937	3.430
-5.104	-11.000	11.000	-5.939	3.828	7.134	11.000	-4.402
-4.105	11.000	-3.357	-6.246	-2.236	-1.071	-0.193	1.213
-0.404	-0.542	-0.225	-0.182	-0.345	-1.732	-0.091	0.688
-0.101	0.307	-0.542	0.372	1.651	1.326	-0.512	0.061
-2.502	-0.511	0.280	-0.836	0.000	-0.909	-1.069	0.000
1.785	1.920	11.000	11.000	-0.425	-2.312	0.095	2.269
0.434	1.452	1.087	1.927	1.025	1.098	0.852	0.657
-1.846	0.785	1.050	-0.611	-0.844	-1.706	-0.731	-0.630
-1.395	-0.549	-3.338	-2.350	-1.711	-3.612	-0.738	0.281
-2.795	-1.269	-2.848	0.224	1.137	0.781	11.000	11.000
6.228	11.000	-2.269	0.132	-0.447	-1.636	-2.214	-1.371
-1.159	2.438	0.107	11.000	-2.171	-2.713	-2.291	-0.190
-1.292	-11.000	6.347	-11.000	5.056	5.668	7.719	11.000
-6.780	11.000	-1.077	-6.256	-0.757	-1.487	-0.727	-0.965
-2.994	-2.855	11.000	11.000	-0.284	-4.178	-3.323	-2.007
-3.389	-3.175	-3.551	-3.580	11.000	11.000	4.847	11.000
-11.000	11.000	5.668	4.829	-0.970	2.825	1.312	1.159
4.287	3.808	11.000	11.000	-2.993	-5.176	-1.371	-0.710
-3.649	-11.000	0.119	-4.511	4.827	6.505	11.000	11.000
-11.000	11.000	-2.000	-2.827	0.489	5.313	3.932	4.254
0.332	-0.462	-2.737	-1.727	2.725	-1.935	-1.066	0.117
-0.673	-0.003	0.610	0.588	0.428	1.559	8.077	11.000
-2.291	0.133	0.126	-0.808	0.003	-1.416	-0.239	-1.462
-0.529	0.747	-0.216	-0.321	-1.586	-1.746	-2.185	-4.293
2.141	-0.489	3.530	1.534	-2.220	-2.119	-0.653	1.105
3.771	7.630	5.916	3.939	-1.317	-1.398	-2.776	-3.777
-0.404	3.242	11.000	11.000	-0.865	-0.800	-0.933	4.625
-5.335	-5.960	0.433	-5.861	0.625	1.313	11.000	4.540
-4.286	11.000	11.000	3.100	5.581	5.436	4.319	4.805
0.645	-3.147	-2.986	-1.444	-0.364	-1.659	3.483	11.000
-3.351	-5.250	-2.215	-2.145	-1.257	-3.345	4.055	5.424
-1.571	7.077	2.273	2.339	-1.285	1.880	3.973	3.975

Table35.txt

4.292	-1.866	-0.776	-1.170	0.581	-1.584	-0.073	6.954
-2.525	-2.673	0.436	-1.026	-1.176	-0.351	4.707	0.830
-1.001	0.756	1.086	-0.026	-0.726	-0.924	-1.831	-0.871
11.000	11.000	1.216	1.106	3.751	0.472	-5.979	0.062
-2.707	-11.000	-4.212	-6.372	11.000	11.000	2.478	5.118
-5.435	2.108	-2.449	-2.078	-3.635	-2.180	9.512	12.505
-1.570	0.434	-1.500	-1.014	1.564	-1.536	0.363	1.658
0.978	1.106	0.860	-2.898	1.153	1.829	0.653	1.087
-1.539	-0.394	0.435	0.019	0.017	0.470	-2.501	-0.618
0.120	-0.291	0.435	2.973	-5.378	-2.161	-1.116	11.000
-6.554	-5.118	0.093	-1.184	2.265	-5.832	1.419	2.254
5.424	11.000	-3.514	-2.590	-0.547	-0.569	-0.412	0.859
0.938	1.120	-1.302	0.166	0.341	-1.274	-1.050	1.033
-0.590	0.815	-1.894	1.473	2.607	1.759	1.220	0.965
-1.721	0.559	0.278	0.283	0.185	-0.906	-1.829	-0.510
5.104	7.448	-1.154	-0.997	3.315	0.430	-11.000	11.000
-11.000	-11.000	-1.060	-11.000	-0.959	-3.098	11.000	6.110
1.223	11.000	4.100	3.419	9.043	10.499	-1.808	11.119
-0.137	-0.758	0.682	0.580	-0.292	-5.502	0.834	1.396
-11.000	-11.000	11.000	11.000	1.394	2.513	1.352	1.734
-11.000	11.000	-3.572	1.134	0.583	-0.969	-3.590	-2.296
6.423	-11.000	1.356	-0.136	11.000	-1.087	-11.000	11.000
-0.870	0.406	11.000	-11.000	0.901	0.417	-11.000	11.000
-4.478	4.375	-11.000	-0.471	1.462	-1.950	-1.581	-0.769
4.038	-1.853	-4.721	-0.946	2.934	-0.888	-11.000	5.778
-1.171	-1.526	2.751	-5.209	3.140	-0.430	11.000	-0.017
-0.986	11.000	-5.858	-0.732	0.838	1.796	-2.096	1.014
2.798	-4.939	5.146	3.580	-3.904	1.756	-11.000	11.000
3.761	-5.198	11.000	-11.000	0.906	1.338	11.000	11.000
-0.503	11.000	2.179	-6.937	-1.185	2.151	-1.264	2.496
2.614	2.679	11.000	11.000	1.980	-0.591	1.094	3.326
-11.000	-11.000	5.658	-1.685	2.921	2.389	0.510	1.841
-0.741	2.440	0.782	0.709	-2.102	6.709	-1.445	1.098
7.764	11.000	11.000	11.000	-11.000	-2.280	-4.507	-3.871
-3.135	-5.076	-1.033	-0.355	-2.397	-4.231	6.978	11.000
2.111	5.494	2.048	2.871	1.918	3.542	5.395	7.038
6.226	6.553	7.534	6.431	3.071	-5.004	-11.000	-11.000
-5.989	-11.000	4.167	7.496	4.769	8.210	3.775	-2.416
1.196	4.980	-6.219	-11.000	0.370	-2.781	-1.055	-2.315
-0.778	-0.007	-0.707	-1.647	2.014	-1.183	-1.685	-0.327
-0.814	-1.625	-2.418	-0.659	1.713	0.842	-0.402	-0.376
-2.209	0.228	0.119	0.354	0.518	0.353	-3.336	-0.408
-0.736	2.590	-3.226	0.274	1.851	-2.652	-0.766	2.734
0.479	-4.900	0.222	4.102	4.017	-1.866	2.170	3.025
-5.587	5.376	0.207	-0.737	-0.080	-0.578	-0.911	-0.536
0.678	0.562	-0.460	0.100	2.334	-1.781	-1.177	2.253
-0.469	0.542	-0.485	1.801	1.236	2.715	-0.300	-3.088
-1.049	11.000	1.229	0.473	-0.419	-0.411	-1.399	0.710

Table35.txt

-6.604	4.532	11.000	11.000	-2.610	1.173	2.062	4.681
-4.916	-11.000	-6.232	-11.000	7.129	11.000	11.000	11.000
-4.077	4.529	-4.813	-4.937	-1.089	-0.607	2.159	5.028
2.716	0.753	-1.686	-0.681	1.236	-0.999	-0.570	1.139
0.827	0.725	0.172	-0.097	0.386	1.339	-0.437	1.781
-1.413	-0.520	-0.514	-0.625	-0.069	0.458	-2.088	-1.035
-0.115	0.276	-2.537	-1.684	0.484	-1.746	0.165	0.700
-0.203	0.896	-0.253	0.312	0.891	1.890	-0.458	0.387
-2.267	0.576	1.133	0.825	2.969	-1.150	-1.918	-2.896
-0.788	0.620	-1.513	-1.536	0.491	-0.950	-1.157	1.003
-2.210	0.601	-3.497	1.857	2.059	0.108	-1.350	0.430
-1.775	-0.582	0.422	1.186	-1.308	-0.797	-2.592	-0.332
0.988	0.136	1.502	0.823	2.991	-0.805	2.174	3.332
0.058	-3.324	11.000	11.000	3.687	5.023	0.280	1.143
-11.000	11.000	-2.386	-2.993	-1.869	-1.498	-2.267	0.733
0.173	0.055	-5.300	11.000	1.304	-1.885	0.027	0.478
-1.364	-1.551	-11.000	11.000	0.233	0.305	-0.852	0.136
-11.000	11.000	0.775	1.453	-0.393	-1.690	-2.325	-0.162
-0.559	0.065	11.000	11.000	-5.022	-3.972	1.258	11.000
-6.880	-11.000	3.254	-3.874	1.472	-1.733	11.000	11.000
-11.000	11.000	6.563	7.045	2.752	2.859	6.408	-0.688
2.769	-0.028	5.778	7.311	-3.835	-0.795	-4.344	5.055
-11.000	-11.000	11.000	1.406	-0.029	4.758	6.120	2.199
-5.688	11.000	-11.000	-11.000	-1.428	-1.635	-1.648	-0.746
1.430	-0.637	-0.669	11.000	1.159	-4.984	-0.199	1.376
-11.000	-11.000	11.000	-11.000	0.849	1.679	11.000	1.912
-11.000	11.000	1.073	1.123	4.001	5.138	4.629	2.834
-11.000	-11.000	0.990	0.530	3.339	-0.785	-2.410	7.562
-3.394	-6.807	-1.397	-0.954	11.000	11.000	-0.614	-0.808
-11.000	11.000	-5.727	-4.652	-0.949	6.590	-1.751	-0.998
-1.199	-3.083	2.259	-1.621	1.259	-2.342	-2.316	-2.357
-2.461	-2.270	7.016	-1.292	3.668	11.000	0.772	1.964
-4.822	11.000	-0.967	-2.916	0.000	-0.790	-2.315	-0.433
0.979	-1.773	6.905	11.000	-0.069	-2.777	8.210	4.941
-4.769	-11.000	-0.049	-11.000	2.099	-5.615	11.000	11.000
-11.000	2.185	3.758	2.717	0.000	0.000	0.000	0.000
4.330	4.907	0.680	-0.877	-5.577	-4.595	-2.267	5.050
11.000	-11.000	3.398	5.906	2.914	-11.000	2.616	3.617
1.059	4.104	1.681	2.329	0.089	-1.449	0.043	0.118
-3.940	-3.634	-4.193	11.000	11.000	11.000	-4.987	-2.548
-5.736	-4.923	-3.189	-2.054	-3.542	-5.392	-0.063	0.332
3.591	2.830	-3.975	-4.512	-0.469	4.290	5.881	7.013
-2.130	4.041	-1.850	4.035	0.098	0.600	1.824	-2.408
-5.947	-2.296	-1.445	-1.897	-1.608	-6.307	0.115	-1.967
-2.995	1.566	-1.205	-3.929	0.092	-0.432	0.353	-0.465
-1.650	-0.929	-0.665	0.837	-1.234	11.000	-2.562	-4.634
-3.186	-2.249	-2.563	-1.212	-3.373	-11.000	-2.512	-3.910
5.157	2.885	-4.228	-5.562	-2.071	2.063	-0.559	-0.312

Table35.txt

-0.455	-0.546	0.620	3.172	0.445	-0.951	-1.250	1.252
-2.114	-2.114	-0.155	1.070	-0.231	-2.539	2.901	2.806
-1.123	0.460	-2.672	-2.511	0.810	-2.512	-0.302	-2.832
2.342	-5.026	-6.758	0.243	-2.322	11.000	-11.000	-5.148
-0.883	0.041	-5.900	3.019	-6.290	-11.000	-2.125	-3.802
11.000	11.000	-11.000	-4.401	-0.484	7.677	1.817	-2.172
-2.011	-1.283	-0.463	4.038	2.406	-0.923	-0.534	-0.699
-1.940	-1.397	-0.347	0.641	-1.225	-2.960	-1.519	-1.415
0.019	0.112	-1.150	-2.248	-1.120	0.727	-1.683	-2.023
-0.428	2.891	-4.213	3.511	4.377	11.000	-5.737	0.522
-4.130	-6.081	-0.662	-1.748	-0.100	-3.474	0.314	-1.508
0.932	2.470	-1.040	-2.613	-1.544	-2.053	-1.401	-2.417
-6.247	3.082	2.460	-1.025	-1.028	0.623	5.415	-4.904
0.129	-0.084	-2.290	-3.953	-3.644	-11.000	1.185	0.260
5.951	11.000	-4.418	-4.455	9.919	3.588	3.375	2.557
-11.000	2.035	2.843	2.978	3.691	11.000	-11.000	-5.929
1.053	3.388	-2.948	2.992	-3.706	-11.000	-0.216	2.432
6.074	11.000	-5.369	-4.383	4.032	5.344	3.716	5.424
0.193	-6.247	-11.000	0.778	-0.072	11.000	-11.000	5.063
-2.705	-1.494	-3.558	-5.236	-6.009	-11.000	-0.959	-1.794
11.000	11.000	-0.295	-5.485	2.418	2.273	0.474	0.671
-3.383	-2.295	11.000	0.433	-2.167	5.825	-2.873	-11.000
-4.142	-1.773	-5.332	3.652	-1.618	-4.877	-1.365	-3.047
0.014	5.458	-5.425	-3.168	2.481	2.267	2.309	-0.263
1.995	-0.293	-2.998	7.544	11.000	-0.545	-4.163	5.227
-1.138	-0.592	-4.249	-0.924	-2.017	-11.000	-1.370	-1.246
6.554	3.596	-2.992	-2.287	-0.844	-0.941	-2.032	-1.804
-1.827	-2.168	-0.560	11.000	11.000	-0.270	-4.984	-1.031
-4.165	-3.161	0.004	-0.714	-1.181	-3.236	-1.356	2.570
-2.751	5.127	-1.927	-2.901	-1.311	-0.749	-0.613	-1.638
-0.850	1.442	-0.445	1.360	-0.394	11.000	-2.099	-1.186
-3.570	-2.302	-1.950	-0.029	-7.034	-11.000	-2.363	-3.665
4.983	3.964	-11.000	-3.518	-2.379	-1.451	-1.983	-1.641
0.166	-0.236	-1.138	1.183	-0.052	-1.215	-2.151	0.368
-3.699	-1.023	-1.119	0.401	-0.267	-1.644	-2.079	-2.782
-1.782	-1.403	-1.835	-1.697	-1.469	11.000	-2.287	-1.173
-1.461	-0.505	11.000	0.241	11.000	-1.674	-11.000	-0.761
-4.906	-3.592	-11.000	-0.979	-1.661	-11.000	-1.236	-3.288
6.480	3.507	-2.240	-3.204	-2.480	1.369	-2.565	3.542
-2.380	-3.681	-3.459	2.107	0.878	7.504	0.382	-3.073
-3.986	-3.000	-5.962	-0.952	-3.577	-11.000	0.413	-2.624
-3.393	2.652	1.139	-3.017	-4.109	-1.180	-2.051	-0.969
-0.532	-0.750	-0.671	2.156	0.111	-1.533	-1.986	-0.163
-3.735	-2.803	-1.262	0.625	-0.806	-3.331	-1.422	-2.797
-1.544	-1.624	-1.562	-3.180	-1.234	-0.394	-1.297	-1.560
-7.034	3.168	-11.000	3.927	-0.698	6.793	-6.305	-6.255
-4.481	-0.431	-4.400	-0.757	-3.593	-11.000	2.516	2.092
-2.425	7.878	-4.096	-5.527	6.345	-1.658	0.484	-0.185

Table35.txt

5.090	0.851	0.504	-1.995	-4.481	11.000	-11.000	-3.616
-0.374	1.681	-0.701	-2.931	-2.382	-4.152	-1.461	-2.241
11.000	6.206	-11.000	-3.624	1.191	0.960	2.477	5.796
-11.000	-0.497	0.389	3.464	0.355	11.000	-11.000	-0.550
-0.937	-0.961	-4.000	-11.000	-6.706	-11.000	0.421	-5.357
-11.000	6.703	-0.422	-5.395	-2.139	0.782	-0.689	-0.051
-0.175	-0.765	0.370	1.612	-0.335	1.362	-0.480	-1.700
-3.358	-2.512	-1.078	-0.666	0.024	-2.043	-2.017	-1.761
-1.260	-0.987	-0.160	-2.048	-0.884	-0.536	-0.109	-2.266
-1.224	-1.044	0.145	2.670	1.033	0.580	-0.105	0.312
-3.023	-1.323	-1.020	-0.103	-1.511	-2.347	-0.956	-3.388
-0.809	-0.990	-1.547	-3.748	-2.036	-1.411	1.147	-2.562
-1.448	-0.544	-1.829	0.683	-1.478	1.324	-0.773	-2.346
-3.417	-2.903	-0.130	1.030	-0.192	-2.763	-0.600	-2.437
0.338	0.844	-0.004	-3.464	0.058	0.368	-0.517	-1.488
-2.317	4.169	-7.034	5.856	11.000	6.081	1.626	-1.633
1.361	-6.480	-3.005	-4.407	6.575	-11.000	0.455	-1.204
-0.384	2.417	-5.604	-5.833	-0.125	-2.909	1.007	-2.207
-2.922	-2.345	-2.500	0.429	-2.306	11.000	-6.100	-11.000
-4.868	-3.191	-5.557	11.000	-4.193	-11.000	-1.954	-2.996
1.822	3.766	-0.608	-2.703	3.200	2.175	-1.139	-0.155
-11.000	-0.568	0.479	1.093	-0.639	11.000	-11.000	-11.000
-1.129	-2.898	-3.688	4.933	0.534	-11.000	0.179	-0.527
11.000	11.000	-1.356	-4.889	-1.046	6.485	5.007	11.163
-5.463	3.188	4.020	-2.621	-5.698	11.000	-4.848	-4.724
-1.727	-4.865	-11.000	1.340	-5.906	-11.000	-1.317	-2.772
11.000	11.000	-1.229	-4.621	3.248	-0.957	-0.789	-1.393
-0.759	-0.292	-1.971	4.415	0.091	-2.206	1.854	11.000
-2.506	11.000	-2.201	-1.892	11.000	3.951	-0.794	11.000
-11.000	11.000	-0.848	-1.695	2.166	2.001	3.217	4.301
-5.744	-5.106	11.000	11.000	1.407	-1.802	-0.166	7.014
-2.678	-11.000	-2.225	3.753	4.517	4.324	3.067	-2.130
-11.000	5.397	-1.419	0.352	-1.085	-1.840	-1.796	1.880
5.774	-1.546	8.210	11.000	-6.612	-0.337	-2.925	-1.907
-1.608	-3.155	3.448	-11.000	11.000	11.000	7.028	-2.238
3.983	11.000	-1.891	-2.092	-1.644	-2.642	4.903	6.893
11.000	11.000	11.000	11.000	-1.215	-6.091	-1.834	-0.391
-11.000	-2.346	-2.493	-0.716	1.033	-0.654	11.000	11.000
-11.000	11.000	-1.597	-0.645	3.090	4.771	-1.167	-0.662
3.949	4.822	-11.000	11.000	-11.000	-2.530	-0.629	6.104
2.505	5.990	0.392	0.997	-0.914	-4.663	6.909	11.000
-4.196	-1.092	-2.837	-3.740	1.541	1.747	1.310	1.999
-0.862	0.874	-1.902	-1.965	0.238	-2.961	-0.537	1.853
-1.508	1.501	-1.675	1.562	2.096	3.153	-0.189	1.632
-2.576	2.157	0.459	-0.407	-2.359	-0.313	-0.770	-2.414
2.889	4.494	6.939	6.462	-4.705	-1.604	1.183	-1.905
-11.000	-11.000	-11.000	-11.000	-5.667	-11.000	11.000	11.000
0.490	2.548	1.094	1.911	3.760	6.930	-0.272	-2.382

Table35.txt

1.900	3.903	-0.476	11.000	-1.313	-3.845	-0.959	-0.373
-3.846	-2.779	-2.035	-2.091	5.138	6.606	11.000	11.000
1.148	3.866	1.123	1.137	4.957	-2.104	0.970	0.365
2.982	5.609	3.844	11.000	-3.990	-0.856	-4.604	11.000
4.264	-6.679	-1.199	-11.000	2.229	1.670	11.000	11.000
-11.000	11.000	-2.045	-2.151	0.075	4.301	-1.164	1.565
-2.413	-2.419	-2.188	7.308	-2.985	-2.270	-5.452	-1.184
-1.954	-11.000	8.126	-3.339	7.199	7.043	5.278	6.351
-11.000	11.000	-0.872	-1.898	0.000	0.575	0.000	0.000
1.882	2.769	0.542	-0.188	2.274	-0.196	2.879	3.324
0.446	-11.000	1.124	3.498	11.000	-11.000	1.386	2.589
-11.000	11.000	1.720	1.993	-1.374	-2.504	-0.028	-2.086
-5.856	-3.903	3.920	5.221	-4.661	-1.554	-1.793	6.243
2.020	2.314	2.888	-11.000	8.210	-5.175	1.406	11.000
-2.088	4.350	2.794	2.834	2.909	0.388	-0.183	7.168
-0.314	-0.229	-0.377	-0.822	0.208	-1.487	1.397	1.585
-0.254	1.907	1.248	1.008	0.916	1.664	0.110	0.956
-2.180	-0.366	0.861	0.646	-0.643	-0.678	-2.342	-0.685
4.100	5.866	11.000	11.000	0.480	-5.754	2.561	3.764
-11.000	-11.000	-1.159	-5.318	3.633	-3.726	2.731	4.774
-6.219	11.000	3.194	4.132	1.336	4.191	-1.386	-0.616
4.370	4.188	6.470	11.000	-6.612	-0.312	-11.000	11.000
-3.894	-11.000	0.830	-2.425	7.351	4.538	11.000	3.760
-3.052	11.000	1.207	-2.772	3.718	-1.175	0.291	11.301
-0.201	2.004	-0.289	-0.597	-0.898	-1.241	-0.988	1.148
-1.027	1.417	-3.779	2.028	3.032	0.913	0.108	0.484
-1.780	-0.322	-0.811	1.680	-1.543	-2.427	-0.806	-2.508
0.623	0.612	-3.248	-0.660	0.181	-2.917	-1.899	0.816
-1.012	-0.580	-0.616	-0.173	3.368	1.691	2.431	3.422
-4.364	1.291	3.780	3.419	-2.112	-1.538	0.085	-1.862
1.428	2.899	0.150	-0.426	-0.915	-1.178	-1.686	2.833
-11.000	-11.000	-2.531	-1.617	-11.000	-11.000	11.000	11.000
-11.000	11.000	-0.016	-0.713	0.631	-4.148	0.221	-3.409
-0.961	0.230	2.178	11.000	0.728	-1.608	-0.211	0.070
-2.061	-1.623	-2.249	-0.797	2.820	1.847	11.000	11.000
-11.000	11.000	-2.237	-0.661	-0.369	1.293	-2.271	-1.598
0.880	1.593	2.669	11.000	-0.482	-6.807	0.924	11.000
-1.706	-1.377	-1.638	-11.000	2.363	1.418	11.000	8.077
-2.221	-0.824	0.063	0.874	4.866	0.603	-1.175	-2.960
-1.186	8.126	11.000	11.000	3.209	-5.321	5.280	8.077
-6.739	-11.000	-2.410	-2.417	3.145	-1.306	5.718	4.023
-11.000	11.000	3.892	4.495	0.885	0.146	1.027	-0.725
1.538	-0.310	-1.520	-0.585	0.754	-1.354	-1.396	-0.553
-0.616	-0.574	-0.523	-0.386	1.245	-0.902	0.343	11.000
-2.868	1.741	0.000	0.893	-0.887	-1.068	-1.445	-1.862
-3.899	-0.728	4.709	11.000	-5.887	-3.332	-5.188	-0.623
-5.903	-7.034	-0.096	7.495	7.443	5.234	11.000	11.000
-4.590	11.000	-11.000	11.000	1.575	-0.777	2.233	2.797

Table35.txt

-0.634	1.494	-1.954	-2.508	-1.077	-4.252	-0.286	2.081
0.454	2.817	-1.488	1.126	1.110	2.020	0.574	0.284
-3.067	0.602	0.112	-0.248	0.659	-0.286	-1.596	-2.689
2.121	2.116	7.529	11.000	-11.000	-0.002	-2.851	0.457
-11.000	-11.000	-0.448	-1.561	-0.847	11.000	11.000	11.000
-2.732	-0.289	-2.039	-1.605	0.256	5.093	2.842	4.880
1.851	2.470	-2.860	-1.640	1.727	-2.020	0.377	4.071
-1.830	-1.644	-1.260	1.332	4.133	1.103	3.192	1.176
-4.631	7.824	-3.478	-1.811	-1.125	-0.643	0.280	-2.265
1.040	0.981	-6.444	4.857	1.447	-0.589	1.427	3.609
-2.850	-2.007	6.212	-11.000	3.994	4.626	0.095	1.600
-6.439	11.000	-0.382	1.933	-1.556	-2.582	-3.203	4.781
-1.576	-0.757	-7.034	11.000	0.589	-1.376	-2.556	0.200
-2.024	-2.010	-2.241	1.449	1.620	-0.330	-1.243	-1.673
11.000	11.000	-2.088	1.468	-0.976	-1.421	-1.589	1.205
3.226	5.727	-2.242	11.000	-2.142	-4.662	-2.025	-4.342
1.957	-11.000	0.178	-3.045	1.730	2.459	6.585	3.532
-11.000	5.271	-6.739	0.377	4.275	2.756	-0.590	-2.571
3.639	3.024	-0.470	1.153	1.175	-2.703	-6.180	11.000
-5.269	-1.137	2.060	-4.858	5.301	4.118	1.238	-2.545
-4.340	-3.001	-4.362	-6.227	-0.688	0.532	0.690	1.370
1.493	7.241	-2.744	1.215	-0.376	-4.544	-4.720	-0.181
-3.518	-1.398	5.377	-2.159	6.483	-0.105	0.133	6.289
-5.523	2.459	5.084	3.473	-0.326	1.322	-1.059	0.541
-0.721	0.818	2.237	1.263	-4.649	-1.744	7.992	11.000
-11.000	-11.000	3.977	11.000	2.184	-4.854	0.597	0.982
-2.456	-0.059	5.341	6.547	-1.945	-0.958	2.094	1.265
-2.588	0.504	6.612	7.021	-1.937	-2.594	-2.582	0.485
-1.275	0.283	11.000	0.194	2.230	0.236	11.000	11.000
-3.555	-0.816	-11.000	-0.502	-0.449	-0.048	-1.438	-3.226
11.000	3.495	7.660	11.000	-0.820	-2.948	-0.168	1.514
-6.339	-11.000	-2.183	-0.377	6.980	-6.512	11.000	-0.818
-5.718	-1.823	5.567	-1.994	-0.917	0.061	-2.335	0.566
-0.957	-1.838	-2.201	-1.674	0.850	-2.320	-0.764	0.038
-1.800	-1.540	-1.989	-1.222	0.801	0.709	-0.133	0.890
-2.131	11.000	-0.739	0.360	-1.092	-2.068	-2.398	-1.337
1.008	4.171	1.687	2.869	-0.761	-4.288	1.462	2.427
-3.259	-3.955	-0.091	1.522	2.078	5.886	-1.133	-1.254
-11.000	2.228	0.793	1.703	-1.084	-1.238	-1.695	-0.294
-2.053	-2.206	11.000	11.000	-1.357	-5.362	-2.975	11.000
-11.000	-11.000	11.000	-1.804	6.972	11.000	11.000	5.006
-5.277	-1.451	8.126	0.315	8.444	9.066	0.192	-1.877
0.542	0.789	-1.117	-1.336	-0.700	-2.280	-1.264	0.360
-1.416	-0.422	-2.204	1.830	0.738	1.832	-0.622	-1.203
-11.000	11.000	-1.192	-1.285	-0.440	-0.354	-0.399	-0.376
11.000	11.000	0.882	11.000	-0.465	1.919	-0.713	0.309
-0.431	0.654	-2.677	-11.000	2.976	-0.460	1.312	3.200
-11.000	11.000	-0.045	1.321	0.175	-0.778	-2.121	0.417

Table35.txt

3.018	5.096	11.000	11.000	0.893	-5.480	-11.000	11.000
-11.000	-11.000	-0.382	5.469	4.856	3.684	7.928	-1.686
-11.000	-1.248	0.625	1.729	6.136	4.220	-2.373	-1.372
2.029	-4.352	11.000	8.210	-11.000	-0.515	2.220	3.819
1.443	0.569	-0.096	-3.715	2.547	-0.834	1.011	-3.179
-4.023	2.198	11.000	-11.000	-1.325	-0.709	-0.510	-2.326
-2.888	-1.255	5.446	5.517	-2.082	-2.780	-4.144	-4.118
-3.773	-5.783	-3.722	-4.114	8.041	6.732	11.000	11.000
6.694	11.000	11.000	11.000	-1.831	-0.999	-1.611	-2.442
11.000	11.000	3.525	11.000	-11.000	-1.638	-0.918	-0.443
-1.899	-1.958	0.296	-2.151	0.335	-1.074	6.066	7.226
11.000	11.000	-1.382	-0.446	-1.273	0.160	-1.301	-0.649
-1.506	5.564	-2.225	11.000	-0.427	-1.373	-2.397	-1.327
-2.856	-4.112	-2.452	-1.719	0.627	-2.683	11.000	11.000
-11.000	11.000	5.090	4.063	-0.307	-1.575	-1.081	-2.021
-1.331	-0.609	-2.340	-1.931	-1.564	-2.510	-2.215	0.559
-2.714	-1.855	-3.420	-1.244	1.164	-0.875	8.041	11.000
11.000	11.000	-1.213	-0.543	-0.398	-0.601	-1.843	-0.956
5.068	8.077	-2.689	-1.953	2.083	0.303	5.498	7.530
-11.000	-11.000	3.514	6.542	5.574	8.077	4.545	5.209
-11.000	-2.190	-11.000	-11.000	3.000	10.370	3.696	2.004
1.984	2.274	-0.657	-0.666	5.074	-2.425	-2.994	11.000
2.342	-11.000	-2.713	-3.190	11.000	-11.000	11.000	11.000
-1.478	-0.015	-2.175	-2.120	1.132	4.900	4.487	3.125
-2.442	-0.573	1.580	-0.023	-3.947	-0.184	5.150	7.569
7.270	-1.530	-2.548	-11.000	7.142	6.392	-2.465	-1.613
-7.034	11.000	-11.000	-0.900	0.514	-0.110	-0.187	3.623
-11.000	4.427	1.845	3.420	1.868	-5.347	3.339	5.711
-11.000	-11.000	11.000	-11.000	3.468	-11.000	3.189	4.395
-6.357	11.000	2.294	3.668	-0.254	1.631	-2.350	-1.358
-0.166	0.944	-1.174	0.417	-0.374	-2.228	-0.863	1.029
-1.996	0.959	-3.229	1.053	3.716	1.825	-1.073	0.416
-2.638	0.387	0.539	1.381	-0.157	-2.259	-2.422	-2.190
-0.580	1.851	0.225	2.701	3.328	-1.933	0.614	3.992
-11.000	-11.000	5.017	-5.433	11.000	3.138	7.131	11.000
-11.000	2.249	6.821	1.322	0.002	0.537	0.230	4.260
-1.410	-1.377	11.000	11.000	-0.261	-2.326	-1.657	0.161
-0.492	-1.510	-2.059	-4.593	0.038	0.098	6.866	11.000
-11.000	11.000	-0.464	-1.698	2.197	1.001	-3.023	0.376
1.120	2.051	11.000	11.000	-5.496	-5.336	0.500	1.336
-0.625	1.379	6.588	-3.267	1.926	1.888	1.110	1.122
-2.080	8.210	0.203	1.700	-0.817	-3.184	0.000	3.090
0.924	3.124	2.154	11.000	-11.000	-0.595	1.737	3.774
-11.000	-11.000	0.814	3.552	3.335	3.344	1.413	1.840
5.036	11.000	1.296	3.428	-0.089	-1.171	-1.371	-0.930
1.946	1.088	8.210	11.000	-4.260	-2.274	-2.908	1.047
-11.000	-11.000	0.058	-11.000	3.405	7.824	11.000	11.000
-11.000	11.000	-0.012	-6.230	0.984	4.289	-1.571	-0.812

Table35.txt

-5.585	-3.179	-2.779	2.435	2.789	-5.358	-11.000	7.174
-11.000	-2.461	2.797	-1.638	6.111	5.638	6.193	7.330
-11.000	7.004	3.353	0.998	0.517	3.611	-1.760	9.942
5.369	7.488	-3.625	2.302	-2.378	-5.767	-3.711	-2.523
-11.000	-11.000	-11.000	-11.000	11.000	11.000	4.112	6.378
-11.000	11.000	-2.311	11.000	0.294	-0.933	2.296	5.338
-4.104	6.776	-3.993	11.000	-3.275	-3.001	5.110	11.000
-5.344	-11.000	1.965	-5.561	6.128	6.292	11.000	4.724
1.600	11.000	-2.995	-5.026	3.988	-1.959	-2.132	-2.323
1.910	4.044	11.000	11.000	-5.439	-5.422	5.880	7.428
-11.000	-11.000	0.748	4.107	3.611	4.414	11.000	3.000
11.000	11.000	1.782	2.495	3.080	6.563	3.919	5.183
5.649	6.863	0.619	1.427	-2.395	-3.091	-3.241	11.000
-4.552	-6.430	-4.716	-5.580	4.594	5.403	-4.553	-3.953
-11.000	11.000	3.533	5.230	3.215	7.065	1.536	0.470
7.584	11.000	11.000	2.518	-6.937	-3.956	-7.034	-6.706
-4.486	-11.000	6.020	11.000	4.814	11.000	-4.516	-6.059
-5.605	-11.000	5.878	7.591	1.694	-0.785	7.973	7.772
0.491	0.869	-0.775	8.077	-0.129	-0.989	-0.441	1.062
-4.639	-6.679	-0.958	1.292	4.494	3.880	11.000	2.372
-5.822	2.976	0.835	4.025	-1.467	-0.775	-1.943	-2.536
4.778	11.000	4.591	11.000	1.131	-6.378	3.676	3.079
-3.762	-6.103	1.834	-4.454	3.643	-2.076	11.000	11.000
-11.000	3.697	4.285	5.857	-2.398	3.864	3.980	2.654
0.030	1.138	-11.000	11.000	0.779	-1.662	1.205	1.633
-0.049	1.859	0.302	1.963	1.885	2.436	11.000	11.000
-11.000	11.000	1.452	1.322	-2.385	-0.081	4.249	0.255
3.058	5.612	1.499	11.000	-1.150	-5.916	3.420	4.633
-11.000	-5.822	-11.000	-11.000	4.245	-3.105	11.000	11.000
-11.000	11.000	3.045	1.764	-0.780	3.090	3.683	-2.114
4.433	5.892	2.624	2.499	-0.766	-3.643	-11.000	11.000
-11.000	-11.000	3.652	7.545	4.763	5.966	11.000	11.000
-6.620	5.894	-5.946	-5.777	-0.007	1.486	2.226	3.467
-1.502	-0.670	-2.110	-2.089	-0.430	-2.861	-1.295	0.432
-2.943	-1.166	-3.453	-4.027	-1.291	-6.058	3.441	11.000
-11.000	11.000	-1.119	0.026	-1.252	-0.357	-2.460	-1.291
-3.043	-1.280	-3.634	11.000	-3.191	-3.318	-1.388	-0.101
-0.568	0.302	-2.514	0.223	-0.199	-0.761	11.000	11.000
-11.000	11.000	8.210	11.000	1.946	4.008	3.102	4.760
3.396	6.070	11.000	11.000	-4.186	-5.269	-4.098	6.246
-3.046	0.738	3.706	-11.000	5.722	7.495	11.000	7.015
-6.679	2.438	-5.143	-5.213	0.404	0.225	6.404	7.030
0.826	1.776	-0.071	5.805	0.607	-5.334	0.253	1.969
11.000	-11.000	-1.271	2.459	-2.822	-1.954	-0.573	1.648
-11.000	11.000	-11.000	1.064	-0.624	-3.218	-1.071	-0.838
1.564	1.682	-0.136	-0.018	-4.288	6.942	-11.000	11.000
-11.000	11.000	0.253	-4.925	0.093	-11.000	11.000	-4.307
-11.000	11.000	1.177	11.000	-1.219	-2.266	-0.385	3.542

Table35.txt

5.962	11.000	-5.684	11.000	-2.439	-3.309	-5.812	4.101
1.913	-0.581	11.000	-11.000	-2.156	-0.726	11.000	8.077
-5.782	11.000	-5.500	-2.607	1.769	1.876	7.553	4.574
-0.077	0.767	7.587	11.000	-3.675	-4.405	-11.000	2.331
-11.000	-11.000	2.395	2.965	0.881	2.488	11.000	11.000
0.673	2.820	11.000	0.370	1.149	2.901	5.409	9.810
-0.110	0.249	-0.409	-0.791	1.527	-1.428	-0.893	0.423
-1.424	-0.457	11.000	11.000	1.825	0.822	-0.912	0.178
-3.025	-0.440	-0.032	1.586	0.385	-2.505	-1.804	-1.480
1.227	2.843	-1.204	7.917	2.732	-2.455	1.952	2.734
-2.703	-5.577	-2.586	-5.064	-1.288	-2.751	7.420	11.000
-11.000	11.000	-1.249	-0.833	-0.109	-0.139	0.159	-1.093
0.353	3.900	-0.445	11.000	-4.140	-3.464	-2.320	1.415
-4.492	-11.000	5.554	-11.000	2.739	3.207	3.312	11.000
-11.000	7.175	-0.691	0.329	2.699	1.542	2.604	3.726
-0.762	8.210	-6.839	2.286	7.956	0.590	-11.000	2.706
-2.480	-6.237	11.000	7.814	0.901	1.891	11.000	-11.000
-11.000	11.000	-3.605	-2.304	-0.771	4.231	3.747	3.155
-1.447	6.856	2.430	-1.129	4.806	0.649	-11.000	11.000
-11.000	-3.001	2.677	-4.845	-3.149	-5.200	1.483	4.640
-4.856	11.000	4.663	7.048	-1.474	-0.363	-0.969	6.607
4.434	6.105	1.166	0.934	0.261	-0.194	2.971	4.360
-11.000	-11.000	1.943	5.940	4.490	3.830	2.633	2.116
-0.759	11.000	2.244	4.585	2.208	3.141	-1.895	-0.572
3.246	5.557	4.546	4.124	2.740	-6.470	4.680	5.224
-3.364	-11.000	1.666	-11.000	2.524	3.595	2.732	5.835
-4.230	11.000	2.954	4.792	3.750	3.341	-0.741	10.523
1.153	0.273	-4.994	5.773	-1.249	-0.879	-1.423	3.696
-5.144	-11.000	0.208	-1.179	0.942	-1.111	11.000	-0.421
-11.000	11.000	5.769	3.302	0.560	1.787	1.351	0.850
1.188	2.296	2.035	11.000	1.863	0.142	1.384	2.583
-4.417	0.996	-1.715	-11.000	2.396	1.424	4.937	8.126
-6.354	11.000	-5.573	-5.146	-0.486	1.137	-2.532	0.537
2.648	3.930	0.576	0.530	2.140	-11.000	-2.968	2.249
1.133	-0.143	0.127	2.653	3.184	3.330	1.793	3.242
-11.000	6.105	2.094	3.753	-1.174	9.059	-1.451	-1.313
1.495	-11.000	0.351	0.488	3.036	-11.000	2.988	4.285
2.113	4.396	2.851	4.506	2.593	4.954	2.785	3.587
-5.337	11.000	1.972	3.186	-0.665	-1.188	0.008	-1.177
1.683	1.669	2.100	1.124	0.834	0.086	-11.000	11.000
-2.679	-11.000	5.355	2.735	1.908	1.909	5.858	-2.070
-5.740	11.000	-11.000	-6.035	0.746	1.972	10.706	-1.370
0.972	0.232	0.683	0.036	0.221	-2.830	-1.009	0.382
-5.627	-11.000	1.866	3.091	0.305	2.225	3.333	4.921
-6.937	2.554	-3.161	4.104	2.821	3.698	-0.420	-0.315
-0.799	11.000	11.000	5.448	-0.134	-0.538	-11.000	5.443
-1.331	-1.765	-2.387	3.121	5.928	-11.000	5.062	11.000
1.368	-3.560	-11.000	-11.000	3.305	1.891	5.642	7.576

Table35.txt

11.000	11.000	-0.072	-0.069	1.286	0.132	1.506	1.181
-1.192	-5.315	0.586	2.167	2.822	2.083	-0.133	-4.940
-11.000	-11.000	-2.414	1.251	-0.498	-0.303	-1.471	-1.991
11.000	11.000	-3.626	11.000	-6.458	-1.195	-11.000	0.192
-11.000	-11.000	-3.829	-11.000	7.671	11.000	6.793	11.000
4.056	11.000	-1.370	0.423	3.377	3.810	4.599	5.650
2.258	4.475	-5.435	11.000	1.588	-4.577	-0.448	2.955
-11.000	-11.000	-1.297	-11.000	11.000	5.407	11.000	11.000
-11.000	11.000	2.478	3.251	1.929	10.585	-2.318	11.005
1.274	1.826	-6.148	0.066	1.103	3.861	-11.000	11.000
-0.721	3.142	-0.359	-0.998	1.214	0.575	1.227	0.608
-11.000	2.996	-11.000	0.857	-1.762	-2.643	-1.270	6.833
3.781	2.566	11.000	11.000	-3.806	-0.248	-0.398	1.301
-11.000	-11.000	-0.574	1.746	0.947	1.971	2.683	11.000
-1.094	0.455	-0.678	0.530	-0.984	-2.696	5.805	5.956
-3.742	-3.411	-3.434	-2.119	-3.136	-1.825	-3.723	-2.361
-2.947	-3.916	-2.775	-3.155	8.126	11.000	5.639	11.000
3.379	11.000	-0.483	-1.574	-2.712	-2.179	0.655	-1.687
3.594	11.000	8.077	11.000	3.215	-3.861	-11.000	-11.000
-6.175	-11.000	1.659	-3.251	4.962	5.528	2.971	3.803
7.509	11.000	-4.713	-4.790	-2.038	-1.163	2.610	4.071
-1.460	-0.877	6.362	11.000	-0.873	-0.828	-1.667	-0.714
-11.000	-5.336	-2.538	-1.780	1.966	-1.058	11.000	11.000
-4.427	11.000	-0.292	0.724	1.043	0.050	-2.826	-3.398
-0.683	-2.688	-0.751	-1.247	-1.334	-1.801	-1.763	-0.324
-2.222	-2.556	-2.692	-0.270	1.458	0.199	-0.622	-1.420
11.000	11.000	11.000	11.000	-2.226	-2.077	-2.677	-0.984
-1.241	-0.846	2.404	7.502	-0.591	-4.880	-11.000	11.000
-11.000	-11.000	-1.683	6.223	8.210	11.000	-0.229	-1.222
-11.000	-1.586	6.437	0.038	6.486	5.805	-1.805	6.375
1.356	3.002	2.785	11.000	-1.903	-3.374	3.630	6.674
-3.563	-4.540	1.321	-3.848	4.933	6.109	4.974	7.555
-11.000	11.000	-2.562	-1.790	3.684	3.784	-0.590	0.494
1.397	2.460	11.000	11.000	1.232	-4.537	4.785	6.036
-11.000	-11.000	-6.350	-11.000	11.000	2.701	11.000	11.000
-11.000	11.000	-5.525	-2.871	9.642	3.175	-1.576	-1.019
-3.882	-4.403	-0.629	11.000	-4.240	-3.502	-4.277	-3.241
-2.177	11.000	11.000	4.896	-3.123	-2.676	11.000	11.000
-11.000	11.000	-4.617	-2.958	-1.136	-2.779	-2.378	-2.857
0.993	2.055	-5.668	11.000	-2.755	-2.433	0.947	3.600
-5.107	-11.000	1.909	2.686	0.946	-0.378	11.000	3.526
-11.000	11.000	0.041	-0.385	-2.019	-2.087	-1.219	-2.186
-2.585	-3.834	-6.692	11.000	-1.629	-1.028	-2.484	-1.889
-3.963	-4.666	-0.396	-11.000	6.382	11.000	11.000	-0.654
-11.000	11.000	-1.837	0.349	1.052	0.941	-0.043	-0.403
11.000	11.000	4.177	3.282	0.661	-0.508	-11.000	-11.000
-1.300	-0.549	-1.553	0.639	-6.571	-11.000	11.000	11.000
-2.727	-1.601	-0.714	1.046	2.346	4.267	2.638	3.721

Table35.txt

-0.127	-0.583	-0.858	-0.497	-0.310	-0.836	-0.885	1.495
-3.058	-1.108	-3.111	1.431	2.024	1.064	0.011	-0.811
-1.917	0.233	-0.647	1.887	-0.383	-2.349	-1.316	-0.340
3.707	3.963	1.368	0.807	0.870	11.000	-5.589	1.564
-3.623	-5.619	-2.129	-1.211	1.922	-0.364	-2.226	-3.592
11.000	11.000	3.498	-3.572	-1.429	-1.706	4.589	15.614
-1.001	0.961	-11.000	11.000	0.093	0.203	0.334	1.038
-0.675	-0.420	-1.331	-11.000	11.000	1.032	11.000	11.000
-2.189	5.071	1.027	2.000	0.109	-0.399	-1.417	0.341
-2.049	-0.485	-5.820	11.000	-6.165	-4.529	-6.739	1.947
-11.000	6.938	5.609	0.469	0.417	-11.000	11.000	11.000
-6.322	8.210	-1.635	-2.711	9.934	6.209	10.635	10.370
0.301	-0.770	-0.731	2.203	0.026	-0.870	-1.722	-0.268
-2.394	-11.000	-0.529	3.342	-1.220	-2.380	-0.254	-1.511
-0.206	-0.580	-2.329	-1.726	-2.192	-1.885	-3.257	-1.690
3.623	-6.937	0.286	11.000	-4.212	-3.630	3.858	11.000
-6.369	-11.000	2.201	6.207	4.456	-11.000	11.000	11.000
-11.000	4.364	1.502	-5.306	9.935	8.890	13.236	14.758
6.306	11.000	-11.000	11.000	-2.417	-2.226	-4.634	-3.902
-4.007	-11.000	-4.224	-4.881	7.197	11.000	11.000	11.000
2.911	11.000	-3.027	-2.117	6.421	5.788	4.550	6.442
-3.076	-2.023	-1.899	-1.992	-1.382	-1.602	-1.764	-0.996
-2.642	-3.591	-3.493	0.002	0.243	-0.806	11.000	11.000
-3.163	-1.382	1.153	2.748	-0.481	-1.356	-1.309	-0.013
-2.674	-2.224	-6.409	11.000	-5.678	-4.898	-5.649	11.000
-11.000	-3.941	6.361	-2.462	11.000	-11.000	7.973	11.000
3.064	11.000	-1.688	-1.135	3.825	4.467	2.779	1.234
0.822	-2.232	2.548	2.721	0.811	-2.077	-1.804	-2.100
-2.122	-4.060	1.883	4.205	4.504	4.097	1.612	3.426
-3.199	3.685	1.786	3.567	-1.469	-1.522	-1.206	0.996
4.778	7.525	-0.417	11.000	-4.616	0.671	-11.000	11.000
-5.174	-11.000	-4.766	-4.489	0.877	-11.000	11.000	11.000
0.639	11.000	4.546	5.513	6.434	7.644	-1.631	0.530
-0.799	-0.197	-11.000	11.000	-1.227	1.365	3.330	4.324
-1.937	-11.000	-4.162	-5.094	5.065	6.356	5.220	6.909
-11.000	11.000	-0.630	0.187	6.327	9.603	2.382	1.925
-3.120	-3.853	-4.571	11.000	-1.843	-0.574	-3.033	-3.746
3.097	6.562	2.413	6.962	-0.815	-4.652	11.000	11.000
-11.000	11.000	-1.890	-1.454	-1.740	-1.328	4.830	4.101
3.567	3.226	5.553	11.000	-4.413	-2.662	-11.000	0.774
-5.354	-11.000	11.000	-11.000	11.000	-2.492	11.000	11.000
0.053	3.351	-0.279	1.200	0.334	0.005	4.604	9.092
4.412	6.584	11.000	11.000	-1.872	-1.314	-11.000	-11.000
-11.000	-11.000	-0.853	-2.775	3.522	6.688	2.934	5.123
1.627	7.526	-4.797	-6.432	-0.055	0.043	3.141	3.083
0.398	2.314	-1.648	-1.382	0.986	-2.431	0.658	0.305
-1.155	0.046	-0.728	4.047	-0.237	1.527	-0.252	-0.813
4.279	3.296	0.122	1.416	-0.091	-1.460	-2.169	3.760

Table35.txt

-0.879	1.081	0.017	-0.791	0.845	-0.976	-0.340	1.765
-2.202	0.077	-0.654	1.230	2.024	2.097	-1.523	2.171
-2.990	0.669	-0.176	1.525	-0.824	-0.225	-0.698	-0.464
3.417	6.616	0.753	1.081	3.397	-5.865	-2.733	-2.385
-2.949	-3.738	5.667	11.000	-0.666	-0.400	2.945	5.225
-3.489	11.000	-1.692	-1.588	-0.750	-1.112	0.616	1.463
-0.791	0.414	-1.185	-1.437	0.198	-1.554	-1.426	0.947
-0.505	0.638	-1.949	2.282	1.701	1.797	-0.021	0.341
-1.882	-1.658	0.231	1.528	-1.822	-2.859	0.930	-1.854
0.569	-0.636	1.768	4.957	0.279	-3.294	-2.092	11.000
-2.351	-11.000	11.000	0.169	-3.231	-1.238	0.333	1.237
-11.000	2.602	1.072	0.198	-2.013	-0.474	2.449	9.422
11.000	11.000	-3.356	-2.669	-0.827	-4.004	11.000	11.000
-3.590	-4.593	-3.155	-3.227	0.248	-2.071	5.769	11.000
-3.916	-2.215	-4.337	-2.149	0.706	6.656	-1.263	-1.405
-3.222	-2.307	-3.846	-0.266	0.949	-2.752	-2.454	1.075
-3.804	-2.681	-3.388	-11.000	11.000	11.000	-3.824	-0.216
-0.639	11.000	5.327	5.468	-1.641	-1.993	-2.046	1.082
-2.028	-1.689	0.700	6.338	4.113	-4.237	-4.500	3.126
-11.000	1.718	11.000	-11.000	11.000	11.000	-3.836	0.873
-11.000	11.000	3.664	-6.409	-1.776	-0.911	2.079	3.925
-0.260	-11.000	5.463	11.000	-1.044	-2.167	-11.000	1.651
1.115	3.767	11.000	2.575	0.882	11.000	6.637	11.000
0.831	11.000	-11.000	-1.664	0.002	-0.481	-0.590	-1.979
0.921	2.066	-0.689	1.487	1.954	-6.323	2.168	2.560
1.287	3.994	1.040	2.792	-3.440	-5.017	-3.239	2.126
-11.000	11.000	-11.000	0.640	-2.226	-0.499	-0.336	1.754
-2.923	-3.140	-11.000	11.000	0.573	-2.862	-2.466	-1.876
-2.827	-2.727	-1.907	-1.551	-1.133	-1.318	7.703	11.000
4.250	11.000	-1.248	-0.156	-0.746	-1.588	-1.071	-0.813
2.346	4.176	-0.831	0.612	2.615	-0.448	2.377	4.059
2.455	4.590	2.089	3.170	-11.000	-11.000	2.736	6.118
-3.626	-3.402	3.244	3.388	0.167	1.635	-1.918	-0.092
11.000	11.000	-2.036	-1.408	-0.010	-1.558	-2.114	-1.359
-3.006	-4.304	-2.989	-1.905	-1.629	-1.732	11.000	11.000
-4.825	-3.395	11.000	11.000	-0.057	-0.446	0.048	-0.838
4.873	5.863	0.187	0.784	-0.052	-0.182	-5.637	11.000
-4.956	-5.446	3.442	0.294	3.327	-1.813	11.000	-0.008
-4.493	11.000	-5.255	-0.569	0.000	0.827	0.637	-0.170
1.267	1.303	0.930	1.305	-0.315	-11.000	2.889	-11.000
-11.000	-11.000	-2.017	-0.253	0.113	-1.812	-0.281	-0.505
0.138	-0.329	1.320	-11.000	0.187	8.446	-0.091	-1.890
-3.731	0.054	0.231	0.329	-0.173	11.000	-11.000	-4.542
-0.222	-3.129	0.066	-0.449	-4.406	-6.807	0.851	-2.215
11.000	7.246	5.582	-2.503	-1.736	-1.245	-0.458	-0.603
3.500	0.276	-3.015	3.594	0.532	5.357	4.607	-6.065
1.631	-11.000	-4.836	1.273	-5.340	-3.273	-0.926	-2.501
6.404	5.169	2.055	-5.132	1.981	1.653	-1.077	1.884

Table35.txt

2.990	-4.246	-4.544	-2.457	-5.064	2.534	-3.624	-2.627
4.029	-11.000	-5.592	0.763	-6.383	-5.935	-0.727	-0.270
-4.463	3.396	-3.465	11.000	-0.436	-2.075	0.970	0.067
1.503	1.372	1.159	1.966	1.176	11.000	1.044	1.763
-0.016	-1.098	-5.392	-11.000	-4.923	-11.000	1.025	0.620
7.164	5.594	-0.034	-7.034	-1.453	-2.128	0.093	-1.139
2.184	-2.177	0.374	2.847	1.653	1.247	-1.284	0.393
-0.081	-0.094	0.508	0.678	1.139	-1.430	1.120	2.191
1.272	1.953	1.258	-0.229	-3.090	0.000	0.226	0.137
0.085	-0.432	0.167	2.555	1.187	2.182	-2.428	-0.406
0.921	-1.514	0.137	0.611	0.570	0.743	1.561	1.565
-0.527	2.050	0.797	-0.368	0.000	-1.256	0.000	0.000
0.482	-0.353	-3.909	0.166	-0.911	-0.108	0.099	0.749
-0.286	-0.951	-0.683	0.347	0.162	-0.702	-0.990	0.168
0.007	-1.185	0.778	-2.289	0.403	-0.279	-0.563	-2.323
1.069	-0.460	1.100	2.260	1.185	-0.088	1.717	-0.703
0.628	1.150	-1.229	0.578	-0.247	0.610	0.122	-0.665
1.013	3.952	-1.521	-1.047	0.000	0.000	0.000	0.000
-2.518	0.785	0.671	2.824	0.655	-2.026	5.994	4.423
-0.959	-0.789	0.542	-0.855	-1.790	-4.360	1.436	-2.781
0.168	0.387	-0.158	-1.923	-0.505	0.490	-2.887	0.237
0.493	-4.563	-4.965	2.180	1.902	0.089	-0.614	-1.637
3.034	-1.291	-1.115	0.106	0.089	-2.162	-0.041	1.189
3.478	2.898	1.036	1.356	-2.832	-1.774	-0.420	0.253
2.272	-3.721	-1.798	5.133	4.632	-6.647	-4.269	-4.859
3.979	-6.067	-0.288	-0.256	-1.678	-4.426	-0.277	-2.319
5.140	3.928	-0.541	0.699	1.717	0.819	-1.860	2.015
-4.216	-0.532	-0.098	1.576	0.702	-0.451	0.262	1.601
-2.307	-2.361	-0.041	0.627	-1.180	-3.113	-0.609	-0.470
6.569	4.244	-0.306	-2.420	-1.255	-0.823	-1.881	-1.482
-4.524	-1.627	0.199	1.875	1.283	1.347	1.988	6.900
-0.226	-2.301	-2.591	7.234	-1.944	-3.873	1.062	2.766
-3.556	1.364	2.771	-0.817	0.000	0.389	-0.592	0.146
-2.031	-2.948	-2.821	2.408	4.176	11.000	-11.000	-1.676
1.815	2.431	-2.999	2.636	-4.124	-11.000	-0.107	4.419
-2.828	11.000	-2.114	-2.729	-2.842	-0.258	-0.451	-0.964
-1.487	-1.376	-2.001	-0.664	-2.717	-2.483	-2.303	11.000
1.812	2.900	-0.447	-2.231	-1.790	-4.410	-0.277	-2.017
6.403	4.810	0.281	-1.805	4.531	7.423	6.745	9.470
-0.046	1.124	1.357	-0.975	-0.223	3.693	-0.605	-0.416
0.714	0.698	-1.875	1.696	-0.814	-0.505	0.874	-0.270
0.842	0.889	0.463	-0.975	0.000	0.000	0.000	-3.090
-1.213	0.569	-0.125	-0.440	-1.147	0.315	-0.932	2.315
1.824	-1.426	-1.206	0.920	-0.769	-0.881	-0.369	0.464
4.100	3.025	-0.156	-1.805	0.000	0.000	0.000	0.000
0.046	0.221	-1.672	2.103	2.613	-1.539	0.857	-1.350
0.543	-0.376	-0.018	3.874	-0.551	1.700	-0.467	1.028
1.088	-0.614	0.303	0.014	0.000	0.000	0.000	0.000

Table35.txt

2.322	-3.992	11.000	0.959	1.280	11.000	1.195	-6.516
0.542	-1.592	-2.997	-3.708	-1.362	-5.212	-0.462	-0.548
-3.417	5.334	0.775	-0.099	-0.637	-0.747	-1.171	-1.105
-2.377	-3.652	-4.109	1.102	-3.527	-11.000	-11.000	-6.739
0.535	-11.000	-0.573	2.055	2.105	6.363	0.081	-1.496
0.919	7.287	11.000	-1.041	2.518	11.176	2.796	8.301
2.702	0.874	-2.102	-1.177	1.698	0.213	0.055	0.360
-2.944	-2.004	-3.135	-2.541	6.603	11.000	-1.195	-0.232
-4.466	7.217	11.000	0.764	-0.474	-0.960	0.353	0.154
3.203	2.936	-0.432	11.000	-3.234	-0.063	4.449	5.156
-11.000	-0.023	-0.531	-11.000	2.569	3.318	5.967	3.442
-3.433	2.261	4.738	2.297	-1.089	0.459	-2.828	-1.802
-3.565	5.186	7.290	3.139	-1.037	-1.462	-5.137	-3.961
-4.728	-11.000	0.671	5.269	4.903	5.172	11.000	4.820
-11.000	11.000	7.642	-1.495	2.413	3.349	-0.296	0.180
-0.919	-1.820	-2.533	11.000	0.099	-1.367	-1.433	-2.051
-2.326	-2.180	-2.163	-11.000	-0.517	-0.567	5.739	11.000
-6.807	11.000	5.849	2.533	-0.683	-1.318	0.891	0.783
-0.287	-1.964	1.829	7.878	11.000	11.000	-0.634	-1.177
-3.139	-1.388	-0.884	-0.887	-0.323	-3.165	0.268	0.044
-1.980	-0.493	-1.358	-2.844	-1.241	-1.104	-2.032	-1.407
-3.585	-0.871	-1.174	0.246	-0.216	11.000	-11.000	-5.763
-0.990	-1.773	-3.962	4.221	-5.046	-6.692	0.231	1.945
2.761	6.877	-3.949	-3.543	0.647	-2.318	-0.129	-0.829
3.617	0.562	-11.000	2.064	5.713	-11.000	2.679	11.000
3.027	-7.034	-5.065	0.040	1.797	6.179	5.318	4.501
1.703	8.077	2.556	-6.199	-1.784	-1.387	-1.974	-1.093
-2.707	1.794	1.087	2.323	-0.740	3.896	-2.516	-2.280
2.705	4.048	-2.128	-3.142	-3.924	-11.000	-0.150	-2.656
-4.581	7.123	-3.429	-1.393	-0.170	-0.757	-0.974	-0.914
-3.991	1.585	-11.000	2.888	-3.517	11.000	-11.000	2.001
3.711	3.735	-3.643	-2.676	-5.273	-11.000	-1.102	1.637
6.028	7.094	-3.561	-5.395	-2.646	-0.743	-1.700	-1.222
-0.438	-1.946	-11.000	-4.498	11.000	-1.203	-0.249	-0.957
-1.535	-1.512	0.688	-2.248	0.183	-2.778	-0.143	-0.611
6.878	5.293	1.077	-1.690	-0.923	-0.893	-1.336	-1.652
-6.414	-3.877	-5.893	2.385	5.944	0.814	-0.564	-0.658
-6.512	-6.937	-0.715	-1.032	-4.253	-11.000	-1.034	-1.252
1.308	0.524	1.663	-4.444	-0.719	0.672	1.123	0.873
-0.350	-1.789	-2.167	4.203	5.500	-0.223	-3.792	-1.292
-2.194	-3.487	-0.259	0.228	-0.604	-1.975	-0.435	0.189
-2.200	-1.529	0.286	-2.909	-0.951	-0.266	0.155	-1.977
3.611	-0.873	-0.808	2.667	2.413	-0.319	-3.351	3.244
-1.300	-1.773	1.143	-0.684	-0.245	-3.423	-0.248	-0.183
-3.119	-0.888	1.894	0.168	-0.836	-1.003	-2.722	-1.276
-6.312	1.854	3.676	1.030	1.101	11.000	-11.000	-1.814
6.756	5.841	-2.149	0.244	-3.591	-5.823	1.714	0.019
-4.450	11.000	-2.141	-4.345	0.000	-3.090	-1.712	1.153

Table35.txt

-1.035	0.246	0.266	-5.853	2.576	-11.000	0.044	1.158
-0.533	-3.294	-4.420	0.013	-1.181	-11.000	0.172	-0.101
11.000	4.387	0.684	-0.403	-1.284	4.874	3.090	-0.033
-5.525	-0.230	0.774	11.000	-2.953	-4.386	-5.807	-3.078
-1.021	1.389	-2.155	6.524	0.712	-2.264	0.721	1.969
1.737	3.306	-1.334	1.269	2.815	-0.603	2.594	1.804
-2.465	3.002	3.029	-1.279	-2.487	11.000	-3.666	-1.406
1.165	0.508	-2.147	2.018	-2.862	-11.000	-0.919	-0.706
1.343	11.000	-1.640	-0.651	0.000	0.137	-2.284	-1.357
0.107	-0.718	0.774	1.074	0.059	11.000	-11.000	-6.001
-3.005	-2.281	-3.596	-1.471	-3.738	-7.034	2.164	0.616
11.000	8.210	-1.703	-2.842	-0.966	-1.545	0.000	2.380
-0.546	-1.677	-1.160	4.822	5.878	11.000	-11.000	5.729
-2.198	-11.000	-1.410	-1.707	-3.673	-11.000	1.606	-1.950
5.579	4.004	-1.739	-3.529	0.247	-0.205	-0.683	1.432
-3.013	-1.808	-2.371	-1.716	-4.521	6.714	-1.145	-1.024
6.205	-5.731	-3.705	3.567	-1.390	-4.666	3.078	2.302
2.379	3.639	-1.411	-2.606	-0.030	4.575	0.000	0.000
1.239	-0.318	-0.598	0.795	0.365	0.717	-0.594	-0.764
-2.993	-1.286	0.230	-0.870	-1.944	-2.743	-1.608	-2.320
-0.780	-1.460	-1.170	-1.797	-2.021	-0.903	-1.656	-2.239
-0.468	11.000	-11.000	0.755	0.963	-11.000	-1.328	-5.380
3.307	-5.131	-2.307	0.524	-0.708	-2.073	1.584	-1.342
-0.620	7.595	1.739	3.149	-0.892	-0.802	-0.610	-0.728
0.173	-0.877	-0.443	0.703	-2.332	-6.095	4.005	2.865
0.542	-4.450	-1.106	-2.372	-1.296	-2.421	1.374	-1.052
0.218	-1.015	-1.045	-2.705	0.366	1.461	0.000	-0.571
-0.285	-0.216	-0.119	0.474	-0.410	0.628	-11.000	-11.000
-0.760	-0.917	-5.686	-0.055	-6.637	-11.000	3.779	1.086
-5.733	11.000	0.531	-0.959	-1.635	-3.580	-2.355	-3.012
1.310	1.360	3.220	3.388	-2.626	-3.163	-2.813	2.691
-0.060	-0.017	-0.244	-0.727	-1.042	-1.109	0.655	0.937
-1.835	-1.618	-2.028	-1.626	0.000	0.000	0.139	-1.814
2.702	1.482	2.398	0.149	0.363	0.460	-0.501	0.612
0.199	-1.101	0.943	-0.547	-0.557	1.218	-0.038	1.098
-1.446	-0.621	0.989	1.039	0.000	0.000	0.000	0.529
-11.000	-1.176	-1.613	4.378	5.813	-1.950	-11.000	-11.000
1.503	0.690	-3.645	-1.751	-5.895	-11.000	-2.502	-1.806
1.223	3.912	-3.676	-4.963	1.653	0.000	-0.399	1.173
0.746	3.617	3.345	3.792	0.321	1.201	1.117	4.327
0.989	0.838	-0.111	1.353	0.292	3.609	1.320	0.121
-0.199	-1.698	0.240	0.932	0.000	0.000	0.000	0.000
-2.234	-0.979	-0.807	3.556	3.925	-11.000	-2.158	-5.383
-1.518	-6.339	-3.979	-1.787	-0.606	-3.457	-2.107	-1.746
-0.503	-1.546	-2.523	-1.169	-1.084	4.118	-0.834	-1.043
1.145	2.869	0.834	0.373	1.395	-3.050	1.461	0.374
3.308	-1.825	-0.950	-1.584	-1.274	1.277	1.089	0.964
0.627	-1.472	-1.980	-0.284	0.000	0.137	0.000	0.000

Table35.txt

-11.000	0.129	-0.505	-2.682	-6.341	11.000	-1.130	-11.000
-0.269	-0.773	-3.664	-3.626	-4.188	-11.000	0.117	-0.756
-5.674	11.000	0.361	-0.636	-0.605	0.000	-0.170	-4.528
1.174	0.140	-0.302	0.259	-0.697	-1.145	-1.615	0.632
-2.895	0.526	1.097	-0.502	-0.339	-2.773	0.546	-0.557
11.000	11.000	0.682	-0.727	-0.730	13.858	-2.795	-1.820
3.472	-11.000	3.365	-4.874	-11.000	1.123	-11.000	-6.628
1.253	-6.668	-2.580	0.220	0.797	-11.000	1.575	1.634
0.542	5.967	2.051	0.532	-1.365	-0.517	-1.734	-0.580
1.169	-1.737	-2.411	1.134	-2.526	8.126	-4.661	2.439
-2.763	-3.487	-1.058	0.936	-2.238	-5.252	-0.454	-1.915
0.112	-0.176	-1.875	-2.901	0.000	0.000	-0.790	1.873
1.994	1.523	-0.790	0.283	-0.207	4.643	-0.751	0.830
0.378	1.074	0.207	-0.302	0.648	-0.437	-0.166	0.210
-0.858	1.968	0.280	0.401	0.000	0.000	0.000	1.011
1.779	-0.813	-0.057	0.453	-0.650	1.167	0.161	0.287
-1.342	-0.697	0.530	-0.537	-1.396	-2.202	1.523	1.105
-0.964	-1.284	-0.290	-2.060	-1.169	-0.786	-1.287	-0.702
0.206	-1.866	-0.741	0.676	0.445	0.579	-0.948	0.901
-0.338	-0.654	0.432	0.395	-0.184	-2.719	-0.688	-0.391
-0.788	-1.125	0.400	-2.304	-0.686	-0.156	-1.535	1.593
1.437	0.403	0.456	1.018	-0.069	0.493	0.683	1.536
-0.781	-2.478	1.043	0.253	-0.627	-3.327	-0.918	-0.578
-0.440	-1.788	-0.132	-2.191	-1.115	-1.688	-1.110	-0.951
-0.473	-0.063	-1.998	1.036	-0.878	0.081	-0.083	-0.051
5.178	-11.000	-1.131	-0.645	-0.989	-1.812	-0.208	-0.969
-0.926	-1.906	0.689	-2.589	-1.387	6.461	-1.102	-3.447
-2.710	-2.890	-2.480	-1.613	-3.441	11.000	-3.509	-2.087
1.353	-0.688	-1.798	0.133	-2.020	-4.326	-0.435	-0.721
3.034	6.675	2.586	-2.578	0.000	0.000	0.865	0.347
-2.937	-0.617	-0.472	-0.261	-3.210	11.000	-11.000	-5.602
-2.700	-1.498	-3.312	-0.033	4.638	-11.000	-1.510	-2.025
-3.473	2.729	1.127	-1.490	-2.868	2.316	-2.726	-1.204
-0.939	-3.180	-1.096	-0.286	-11.000	7.257	3.288	1.096
-1.020	-0.609	-3.817	-4.335	-0.109	-3.247	-0.669	0.488
0.617	-1.998	-2.596	-1.191	-2.709	1.486	0.194	0.287
-0.770	8.077	-4.915	3.802	3.560	-11.000	3.822	4.076
1.003	-11.000	-4.756	2.276	-5.332	-11.000	-3.245	5.144
0.594	0.656	1.688	-6.565	-0.172	-1.264	-0.569	-2.148
1.749	0.795	2.683	2.577	2.039	2.851	2.403	0.951
-1.130	-1.127	1.172	-0.508	1.064	-2.340	-0.091	-0.839
-1.383	-0.837	0.727	-2.403	-2.674	-1.795	-0.240	-3.950
0.529	-4.278	-0.007	-3.936	-0.601	1.621	-1.954	-0.400
-2.182	-2.119	-3.394	-0.283	-3.532	-6.034	-0.403	-1.907
-4.845	5.738	-1.274	-4.709	-0.969	-3.433	-1.701	-0.505
0.958	-0.666	-3.740	-0.019	6.330	-11.000	-2.413	1.343
-1.565	-5.951	-2.424	-2.730	-1.097	-6.937	0.005	-0.681
-0.363	-0.722	-0.313	-2.336	0.725	-3.822	0.034	-1.369

Table35.txt

6.573	-11.000	-11.000	-3.742	3.875	-0.077	-6.937	6.939
0.564	-0.751	-0.913	-5.199	0.126	3.542	1.631	0.114
3.954	3.004	-4.272	-0.868	3.227	-2.188	-0.764	-2.878
-11.000	2.134	-2.747	-0.028	-1.410	-4.304	11.000	-4.819
0.853	1.881	-3.537	5.993	-2.076	-11.000	2.628	1.719
-5.497	2.832	-2.712	-2.768	2.455	5.082	-2.098	1.072
-3.067	-4.092	-3.542	0.710	0.787	4.048	-3.141	-3.381
2.082	0.103	-4.443	6.520	-3.821	-11.000	-3.664	-3.264
-1.155	0.498	2.656	-5.695	-1.065	2.655	0.121	-2.267
-2.877	2.398	-11.000	-11.000	-5.324	-11.000	-4.959	-2.208
5.698	-1.258	-4.861	6.861	-4.718	-4.619	1.102	2.105
1.611	1.006	2.652	-3.598	-0.117	11.367	-0.863	3.259
-11.000	1.012	1.622	-2.892	0.463	-0.099	-5.833	2.397
-0.858	-6.668	-3.699	3.996	-1.121	-3.305	-0.174	0.399
-0.382	-0.377	-2.677	-6.197	0.717	-1.619	-0.747	-0.975
0.010	-1.991	-2.174	-0.517	-4.643	11.000	-11.000	-2.257
-0.705	-1.312	-5.000	-0.124	-5.082	-11.000	0.848	0.939
-5.519	11.000	-1.484	-5.817	1.428	0.533	-1.390	-1.561
-0.231	0.151	0.440	0.977	1.557	0.727	0.200	-0.549
1.609	-1.264	0.233	-0.604	1.274	0.205	1.574	-0.300
-2.427	0.695	-0.969	0.473	0.000	0.000	0.000	0.000
-2.088	-1.424	-1.934	0.063	-11.000	0.824	-1.413	-1.423
4.855	-11.000	-6.937	-0.370	-6.023	-11.000	-1.093	-0.600
-1.802	-0.923	0.028	-11.000	-2.748	8.170	-2.916	-2.303
-2.377	5.831	7.992	0.078	-0.906	11.000	-11.000	-11.000
-1.963	-2.341	-1.131	-0.880	-3.830	-11.000	-1.348	-2.074
11.000	11.000	-6.364	-5.783	1.020	1.546	-2.093	-1.783
-3.187	-2.885	-3.614	11.000	6.036	11.000	-3.617	-0.161
-3.437	2.089	-2.821	2.112	-3.474	-4.508	-2.134	-2.753
-1.650	7.520	-2.069	-2.952	-1.851	2.847	5.073	7.070
3.879	3.340	-0.900	3.802	-3.948	11.000	-11.000	-11.000
3.565	-5.207	-5.094	11.000	-5.861	-11.000	2.100	2.207
6.641	11.000	-4.466	-6.461	-1.398	-0.958	-0.417	0.523
-1.807	-1.575	-0.682	1.247	11.000	11.000	-1.103	-4.479
-1.373	-2.006	-1.377	-0.665	-0.941	-3.011	-2.025	-1.456
-1.485	-1.689	-0.956	-2.947	-0.939	-2.067	3.130	-2.167
-4.431	2.777	4.311	-0.406	-2.815	11.000	-11.000	-1.892
4.715	1.980	-5.334	3.600	-5.864	-11.000	1.594	1.328
-2.678	11.000	-1.233	-2.896	2.360	2.157	1.097	-3.160
2.975	-7.034	-11.000	3.883	2.718	11.000	4.330	-11.000
0.371	1.002	-1.353	7.267	-3.881	-11.000	-1.063	1.339
5.706	4.903	-1.070	-4.789	-0.800	-1.603	1.693	2.226
-1.393	-1.487	-1.736	0.969	-1.423	11.000	-1.490	-11.000
-2.486	-3.501	-6.692	7.621	-5.693	-11.000	-0.547	-3.258
-1.859	11.000	5.644	-3.485	-0.288	1.159	-2.155	-0.164
-1.349	-2.370	-2.740	11.000	-1.506	11.000	-3.245	-2.230
6.384	11.000	-0.673	-0.623	-11.000	-11.000	-1.724	-0.561
11.000	11.000	-1.240	-1.762	-2.047	-1.144	-0.978	0.156

Table35.txt

2.043	0.950	-11.000	1.835	11.000	11.000	1.064	-4.586
7.164	-0.672	-0.940	4.685	-5.903	-11.000	-0.043	4.442
-0.588	6.522	0.894	-11.000	-1.920	-1.117	-0.594	-3.243
-0.744	-1.459	1.127	2.283	-0.067	0.631	-0.725	2.144
-3.026	-2.625	-1.434	0.945	-1.077	-2.732	-2.938	-3.174
-0.182	-0.652	-2.904	-2.404	-2.185	-3.139	-0.560	2.406
-6.739	-5.786	-6.880	2.996	2.791	2.870	7.535	-11.000
11.000	-11.000	-1.339	0.745	-0.189	-3.377	-0.663	-2.144
1.357	2.026	1.947	-11.000	4.123	12.495	-0.127	-3.704
-1.991	-1.338	-0.624	11.000	11.000	0.621	-0.084	-0.735
-2.398	-2.548	-1.546	-2.020	-0.503	-2.202	-0.540	-2.653
-2.071	-0.778	-1.407	-2.814	-2.865	-1.540	-1.598	-1.756
-4.068	0.463	-2.193	3.426	3.019	-11.000	-2.294	2.802
-2.783	-1.469	-5.076	0.322	-0.773	-1.911	-1.256	-2.971
1.490	2.367	-3.292	-5.400	-2.430	0.224	-2.578	-2.128
-1.725	-1.314	-1.232	3.435	2.642	1.898	0.407	-11.000
0.040	-0.886	-11.000	-6.409	-6.077	-11.000	0.420	-2.004
-1.318	4.972	-0.415	-11.000	0.449	-1.217	-1.811	-0.898
0.232	-0.433	0.723	1.437	0.510	0.705	-1.533	1.062
-3.703	-2.812	-2.526	2.190	0.131	-4.063	-1.398	-2.773
-1.981	-2.009	-1.546	-4.016	-1.559	-1.319	-1.753	-2.482
-3.648	-2.059	-3.118	-0.698	-2.887	11.000	-2.834	-2.582
7.234	11.000	-11.000	-2.196	-11.000	-11.000	-1.381	-2.598
-1.216	6.880	-2.458	-2.961	-0.274	-1.544	5.807	5.756
-6.347	-6.379	-4.212	4.520	5.837	-6.157	2.091	3.840
-3.211	1.778	-4.598	-3.413	-1.118	-4.216	-1.442	-3.421
-1.240	1.587	1.817	-0.645	0.983	4.211	-3.933	-0.870
-2.371	-0.232	-0.428	11.000	-3.799	5.810	-2.768	-3.735
-1.097	-2.427	-2.742	-1.579	1.059	-5.042	-1.022	-2.578
-0.688	1.432	4.093	-2.276	-1.534	-1.474	-1.937	-1.555
4.847	-5.919	-0.840	1.924	0.258	0.673	-6.291	6.678
-2.655	-1.008	-4.040	0.018	-2.477	-11.000	-2.647	-2.631
-3.736	0.109	4.737	-5.357	-2.157	2.847	-0.940	-2.119
-11.000	0.909	5.959	5.248	-11.000	-11.000	-1.988	-11.000
-5.218	-11.000	-4.465	-5.481	0.478	2.672	0.426	-1.366
-0.439	0.632	1.393	-4.953	3.723	-2.179	6.873	0.875
-11.000	2.283	-11.000	2.820	2.432	4.670	0.759	-3.032
-1.639	-1.835	-4.773	11.000	-0.080	-3.124	-1.648	-1.970
11.000	11.000	-0.344	-2.320	-1.103	1.612	-1.842	-1.515
-0.155	-1.072	-1.179	1.511	-0.826	0.732	0.046	1.365
-3.279	-1.952	-1.461	0.469	-0.168	-2.861	-0.365	-2.809
-2.099	-1.627	0.947	-4.108	-0.995	-1.988	-1.804	-1.485
2.295	-0.750	-0.035	1.612	11.000	-11.000	0.222	-0.439
-2.469	-1.931	0.196	0.718	-3.606	-6.758	-0.411	2.298
-1.283	6.907	-0.234	-2.293	-2.525	-1.743	-0.637	-1.880
-0.487	-5.327	-5.527	2.792	1.283	-4.331	4.461	3.330
-1.068	-11.000	-0.887	-1.017	1.379	-11.000	1.185	-1.029
-6.231	-1.792	2.291	-1.212	-0.027	3.270	0.132	-1.203

Table35.txt

-0.230	-1.847	0.469	2.618	1.202	-1.055	-0.236	0.874
-4.822	-2.648	-0.684	1.094	-0.986	-2.049	-1.288	-1.851
-2.075	-0.900	-1.529	-3.702	-2.866	-3.600	-0.963	-2.364
0.695	2.546	-11.000	3.449	4.285	-11.000	-6.739	-5.591
11.000	-5.320	-6.583	2.623	2.012	2.671	3.303	1.168
0.906	1.162	-4.654	-11.000	-1.873	-2.428	1.126	3.184
-11.000	-2.107	-11.000	5.671	8.014	-11.000	0.761	-2.709
7.389	-11.000	0.649	11.000	2.333	4.248	-1.182	-3.271
1.596	2.592	-11.000	-2.102	-0.277	2.279	2.703	4.873
-0.950	7.366	7.809	2.816	-0.869	1.762	11.000	-4.601
-1.847	-2.267	-5.057	2.809	-3.441	-11.000	-1.148	-1.954
-6.020	7.941	-6.376	-2.235	1.656	0.610	0.402	1.700
-3.404	0.450	-11.000	-1.107	-3.024	11.000	-11.000	-1.219
-3.107	-2.911	-4.658	-1.234	-4.988	-11.000	2.217	1.376
11.000	11.000	3.725	-2.654	0.000	0.000	4.854	7.034
-0.242	-0.300	-0.308	1.520	0.810	11.000	-11.000	-11.000
4.734	6.805	-4.743	-6.880	-5.237	-11.000	-1.029	-0.156
1.455	11.000	-11.000	-5.914	3.812	3.455	1.160	5.632
0.376	-0.188	-2.077	3.049	1.268	0.438	-2.109	0.132
-3.879	-2.778	-2.357	0.010	0.174	-2.705	-1.726	-3.186
-3.308	-2.041	-0.025	-3.174	-0.513	9.833	-0.753	-0.189
0.355	-0.055	-1.033	2.718	-0.064	-0.829	-0.566	0.426
-4.104	-3.588	-0.399	-0.877	-1.260	-3.146	-2.173	-1.917
-2.229	-2.206	-4.939	-2.582	-0.498	-1.979	-0.233	-2.155
1.098	-0.711	-0.239	1.377	-0.765	-0.331	0.648	-0.185
-0.743	-2.882	-0.892	-0.714	0.796	-1.343	1.132	-1.008
-1.281	-0.467	0.777	-0.833	-1.433	-1.742	-2.942	-1.316
-2.276	-0.370	0.583	0.624	-0.051	7.158	0.287	-0.213
0.093	-1.425	-1.117	0.559	-1.458	-2.187	1.483	0.037
-0.859	1.986	-0.169	-0.517	0.000	-0.736	0.000	0.000
-0.440	2.221	3.039	0.093	-2.101	11.000	-6.590	-1.937
1.039	1.124	-2.387	-1.382	-3.714	-11.000	-0.505	1.452
11.000	8.210	-0.899	-4.578	1.052	-0.046	-0.036	1.430
-5.331	-0.757	-2.257	0.404	-2.510	11.000	-1.022	0.594
-1.827	-2.011	-2.157	4.092	-3.544	-6.679	2.329	1.611
3.637	11.000	-5.063	-1.615	0.529	-0.506	1.903	0.584
2.407	0.921	-0.010	-0.781	0.465	1.135	-1.234	2.370
-0.886	-1.785	0.920	-0.646	0.146	-1.264	0.270	0.226
-0.382	-1.457	-0.125	-1.590	-0.027	0.000	-0.144	0.204
1.041	0.499	0.452	1.660	1.172	11.000	0.619	-11.000
-0.082	-0.527	-5.315	1.094	-6.493	-11.000	0.019	6.982
11.000	11.000	1.110	-0.489	-2.053	-2.331	-1.337	-0.508
-2.130	-0.838	0.207	1.035	-3.567	-0.061	0.260	-0.229
0.025	0.572	-0.643	-0.057	1.334	-1.750	0.969	-0.506
-0.830	2.118	-0.025	-1.829	0.000	0.000	-3.090	0.104
4.154	-0.837	-2.189	3.327	5.022	-11.000	3.465	-0.391
0.031	-2.321	-2.640	-0.147	-2.970	-11.000	-2.149	-2.391
0.427	2.843	1.990	-1.366	2.394	5.199	-0.405	4.955

Table35.txt

4.626	-3.628	1.922	3.339	2.495	-3.812	2.650	1.264
0.754	4.472	0.995	-0.420	3.909	-11.000	-0.581	-1.898
4.103	-0.733	-1.344	-0.527	0.880	-1.279	0.178	0.367
-0.390	-1.320	-11.000	0.000	-5.989	-11.000	11.000	-1.809
11.000	-11.000	-4.616	11.000	-5.149	-11.000	-0.771	2.348
2.664	1.799	-5.240	-2.008	2.174	0.640	3.258	3.623
2.338	-3.069	-0.936	2.965	2.348	3.906	-4.125	-1.032
-2.085	-2.735	-1.549	-1.831	-2.385	-6.218	-1.326	-2.542
0.947	-1.948	-1.084	-3.543	0.406	-1.292	-0.460	4.135
0.545	0.986	0.464	1.956	0.459	11.000	-0.592	-0.443
-1.062	-1.847	-2.385	-0.889	-0.132	-11.000	-0.579	-0.530
-1.557	0.107	-0.644	-1.703	-3.052	-4.083	-0.316	-2.784
-11.000	2.980	-4.910	4.112	4.423	-11.000	-11.000	4.979
4.633	-5.846	-3.405	6.196	2.078	1.139	-0.174	1.064
1.781	3.296	-2.481	-3.112	0.836	-1.141	1.765	-1.402
2.811	-1.700	-11.000	-6.549	11.000	-11.000	-6.628	-0.961
-2.131	-2.084	-0.453	6.006	-4.731	-2.603	0.504	1.010
-2.060	-1.831	-11.000	-3.256	-1.139	3.950	-1.434	-0.080
0.509	0.288	0.726	-0.199	-0.201	2.815	0.181	-2.048
-2.395	-1.078	-11.000	-11.000	-11.000	-11.000	-0.375	-2.103
11.000	11.000	-11.000	-2.993	-1.857	-1.586	0.000	4.367
3.879	1.785	-4.716	11.000	2.886	-11.000	11.000	3.793
-1.747	-0.849	1.426	1.969	6.676	-11.000	-3.775	1.241
11.000	11.000	-6.612	0.233	-0.602	1.732	13.643	18.418
-5.779	-1.529	-2.676	-0.995	-4.099	11.000	-0.751	-11.000
3.412	4.594	-5.040	-0.081	-2.857	-11.000	0.341	-2.958
6.183	5.544	-3.543	-2.154	11.372	11.199	-0.355	4.789
-2.823	1.155	11.000	-4.974	-4.890	11.000	-11.000	-0.335
-0.938	-1.588	-2.068	-5.798	-4.627	-11.000	-3.100	-0.665
11.000	11.000	-5.152	-6.590	0.189	2.685	4.591	4.298
-5.398	-11.000	11.000	7.754	11.000	-3.939	5.371	7.228
-5.380	-11.000	11.000	-5.696	11.000	-5.308	4.208	7.303
11.000	11.000	3.445	3.405	0.366	-1.214	0.000	-2.348
3.161	-6.807	1.471	1.573	0.825	-11.000	1.514	2.414
2.079	-11.000	2.408	11.000	1.463	-0.148	0.179	0.423
-4.512	8.077	-5.133	-11.000	2.011	12.079	-1.391	1.444
-5.125	-4.928	-5.486	1.937	1.047	11.000	6.433	-5.600
2.874	-0.360	-3.430	-3.723	-4.622	-11.000	-2.611	-2.576
3.767	4.047	-3.704	-4.139	0.000	1.054	0.000	2.469
0.200	0.579	0.524	0.538	0.104	0.302	1.880	1.232
-2.401	-1.015	0.071	1.221	-4.014	-11.000	0.214	-1.455
-5.560	2.138	-0.042	-4.010	-3.090	0.050	0.000	-1.074
-4.241	-3.477	-2.948	3.367	-3.535	11.000	-3.650	3.517
0.707	2.583	-3.039	-2.961	-2.172	-6.199	-1.447	-1.533
1.262	0.314	-2.111	-2.808	0.000	-0.256	1.396	0.974
-0.360	4.440	4.596	0.123	-0.460	6.112	-2.055	-4.720
-1.736	-1.972	-3.194	-4.884	-3.925	-11.000	-1.403	-2.923
3.424	1.984	-5.374	-1.461	-1.169	-0.194	0.561	0.406

Table35.txt

0.253	-0.181	-1.235	-3.096	-0.611	2.797	-1.716	1.401
-0.503	-3.394	-1.670	0.118	0.824	-1.099	0.452	0.045
0.785	-1.450	-3.895	0.210	0.000	-0.242	0.000	-1.687
-1.675	-1.710	1.767	0.502	1.586	5.268	-1.407	-1.057
-0.621	-0.773	0.083	0.105	-0.319	-0.571	-0.597	-0.440
-0.461	5.339	0.783	0.048	0.000	0.000	0.000	-0.445
0.610	-0.985	-1.008	1.325	-3.289	11.000	0.982	-4.034
-0.936	-3.693	-4.479	-0.988	0.718	-11.000	-0.187	5.991
3.508	4.140	-0.632	-3.602	-0.146	-1.012	-2.237	-0.837
-4.531	-4.872	2.737	1.033	-1.492	-4.869	7.917	11.000
-3.277	-5.130	6.895	11.000	-3.082	-4.389	5.374	7.525
3.926	11.000	5.819	5.145	-0.808	-0.505	-0.269	-2.296
1.075	-0.243	2.986	2.498	1.687	0.195	1.410	11.000
-3.774	-11.000	4.712	-2.057	4.855	8.210	-1.574	-0.431
-11.000	11.000	5.856	-4.550	1.528	0.762	0.000	2.013
2.267	6.422	2.562	-2.929	-6.880	1.896	-11.000	11.000
-11.000	-3.560	5.882	-11.000	4.610	0.397	4.972	4.679
1.451	11.000	-0.586	-1.548	1.595	2.072	-2.790	3.426
-3.701	0.896	11.000	11.000	-1.560	-3.121	4.295	5.780
-11.000	-11.000	11.000	-11.000	2.111	5.512	2.507	5.561
1.990	11.000	-2.500	-2.754	-0.145	0.003	-1.066	-0.273
-1.387	-1.377	4.225	3.019	-2.379	-3.081	-2.304	-2.328
-3.224	-4.211	11.000	11.000	-0.151	-2.266	11.000	11.000
-11.000	11.000	-1.607	-2.687	-1.335	-0.439	-1.451	-2.178
3.730	2.896	-6.136	11.000	0.078	-4.595	-0.513	11.000
-4.725	-5.233	0.598	1.050	11.000	-3.370	6.820	11.000
-11.000	11.000	3.324	-11.000	-0.702	0.309	0.563	-0.345
5.354	3.027	0.178	3.287	-11.000	-4.055	-1.928	1.406
-11.000	-11.000	0.078	3.283	3.513	5.157	2.455	5.915
-1.784	11.000	0.900	1.978	-0.934	-2.898	0.928	0.750
-3.298	-1.112	-1.800	-1.224	1.457	-1.245	-1.085	-0.339
-0.454	-1.869	-1.711	0.415	0.668	0.561	-0.697	0.524
11.000	11.000	-0.681	-0.414	-2.623	0.427	-2.606	-1.564
-1.022	-0.725	0.217	11.000	0.694	-1.812	-2.003	1.329
-2.604	-1.964	-0.846	-0.417	0.201	-2.567	0.308	-0.792
-1.208	-0.609	-11.000	-2.217	-1.575	-0.137	2.991	-4.024
-5.953	0.076	-0.279	2.368	0.990	11.000	1.647	-11.000
-1.221	-1.032	-3.429	-4.123	-4.635	-11.000	-0.204	-1.788
1.989	11.000	-5.801	-4.661	-0.715	-0.142	-2.241	-1.791
-3.977	0.545	1.799	1.884	0.162	0.397	0.535	-0.684
-2.707	-1.933	-0.992	-1.076	-1.188	-0.773	-0.973	-3.154
-1.550	-0.287	-0.567	-4.372	-3.443	-3.175	-1.675	-3.288
-4.953	0.195	1.996	1.705	-0.396	2.791	-3.208	-0.065
-2.333	-3.626	-3.738	-2.206	-1.198	-5.774	-1.019	-4.869
-3.236	-3.495	-1.516	-3.032	-0.893	-0.174	-2.026	-3.403
4.450	-11.000	-11.000	3.541	3.730	5.115	-11.000	-4.361
4.182	-4.077	-2.687	5.481	-5.400	2.869	0.572	-0.578
-3.906	-3.675	-6.085	-6.577	-2.970	5.452	0.096	2.355

Table35.txt

-2.110	-2.052	-6.880	0.962	1.051	3.776	-2.136	-3.022
-3.730	-2.948	-1.800	-2.154	-1.438	-3.333	-0.354	-2.510
-2.185	-2.477	-2.832	-3.577	-2.792	8.793	-1.719	-3.302
-11.000	-2.844	-3.569	1.523	7.265	-11.000	-1.335	-2.402
4.165	-5.275	-2.561	6.528	0.451	4.903	-1.116	-0.879
2.539	3.048	11.000	-5.833	-2.106	0.000	-0.976	-2.064
-6.512	-0.838	-0.227	-0.088	-3.132	-11.000	-6.937	-1.638
0.063	-11.000	-3.707	-0.703	-1.164	-1.997	1.742	0.988
0.735	3.105	4.281	1.408	-2.809	0.101	-0.529	-1.561
-2.725	-3.081	-3.139	-11.000	11.000	-1.832	-2.693	11.000
5.245	-11.000	-1.463	-2.774	-1.067	-2.777	-0.362	-3.031
-2.890	-1.688	-2.389	-2.573	-2.229	12.045	-2.746	-1.795
-4.813	-4.206	-4.455	-1.278	-4.125	-4.266	-3.405	-3.400
-4.073	-3.542	-2.152	-3.373	-2.006	-5.268	-0.377	8.041
5.114	3.353	-1.891	-3.513	0.628	11.538	-4.249	-0.993
2.891	1.512	1.693	2.939	2.453	-11.000	0.917	-11.000
0.797	0.954	1.482	-0.256	7.154	-4.388	-2.838	3.801
1.032	11.000	0.101	-11.000	-0.255	8.434	-0.902	-4.440
-5.511	0.450	1.272	1.102	0.462	6.299	-0.166	-11.000
-2.132	-2.612	0.306	11.000	-2.747	1.902	1.775	1.228
11.000	6.312	-1.525	-3.067	-3.298	-1.601	-2.021	-3.264
-1.777	-2.907	-2.320	4.508	5.414	11.000	4.820	-1.303
-3.924	-5.300	-5.917	4.915	-4.511	-11.000	-1.447	-2.941
-11.000	6.157	-6.807	0.097	0.705	0.075	3.238	5.517
-11.000	-6.647	-4.697	-0.859	-5.471	6.435	4.098	3.871
-1.550	-1.245	-4.178	-1.622	-0.111	0.208	-0.242	-1.818
-1.391	5.275	-3.204	-2.868	-1.292	0.358	1.523	2.399
4.043	-0.917	-1.099	11.000	4.689	-0.439	-1.050	-0.091
-6.350	-11.000	-3.429	2.645	-3.757	-11.000	-2.064	0.721
1.892	1.235	-4.430	-5.588	-0.591	0.611	-1.821	2.142
0.741	-0.002	1.329	1.961	0.279	11.000	-11.000	-11.000
-0.937	-0.743	-7.034	-0.306	-11.000	-11.000	-1.111	-1.456
-3.505	11.000	-11.000	-1.868	2.663	-0.564	-1.794	-0.577
-0.472	-0.326	-0.150	1.182	-0.856	11.000	-11.000	-4.159
-1.732	-1.666	-11.000	0.834	-11.000	-11.000	-0.952	-1.715
-0.206	11.000	0.229	-2.295	-0.221	-0.687	-1.391	2.844
0.108	-1.543	0.545	2.090	-0.349	-0.236	-0.935	-0.110
-3.891	-2.966	-0.833	-1.015	-1.156	-3.389	-0.546	-3.027
-1.968	-1.631	-1.387	-3.109	-2.978	-2.275	5.703	-2.979
-5.559	2.130	2.451	2.575	1.499	3.669	1.102	2.038
-0.412	-0.094	-2.384	-1.478	-2.541	-11.000	-0.370	-0.584
-0.533	0.387	-0.900	-1.009	0.000	0.000	0.460	-0.834
1.535	-3.043	-4.026	0.038	1.901	-11.000	-11.000	-11.000
-1.686	-0.739	-4.154	0.751	1.105	-0.828	-1.953	1.202
-1.378	-0.838	-11.000	-2.011	-2.862	4.084	-1.855	-0.651
0.306	-0.903	-0.224	1.343	0.190	-0.879	-0.328	1.651
-2.343	-1.945	-0.722	-0.815	-0.813	-2.893	-0.583	-1.503
-0.760	-0.682	-0.645	-2.893	-0.577	-1.489	-1.796	-3.818

Table35.txt

-3.086	-1.084	5.389	-0.492	-1.504	11.000	-2.500	-0.682
-3.355	-1.503	-3.712	7.508	-5.118	-11.000	-1.609	-3.072
-1.686	11.000	-11.000	-1.181	-1.725	0.137	0.284	-1.175
-1.055	-0.284	-0.591	-0.640	-2.978	0.739	0.403	-1.073
-0.097	-1.748	0.519	-1.522	0.646	-3.622	1.148	-0.996
-3.339	0.005	0.221	-2.438	-3.130	-0.656	-0.755	-2.928
-0.831	-1.437	0.164	1.230	-1.043	-2.535	7.386	-0.288
-3.252	-11.000	-3.488	-6.291	-4.055	-11.000	-0.045	-0.596
-3.297	0.760	-0.384	-1.370	-4.710	6.109	0.017	0.152
-0.278	0.911	1.460	2.484	3.204	11.000	-11.000	-3.337
-3.732	-5.239	-2.785	0.135	-4.822	-11.000	-1.235	4.365
5.174	4.939	-5.317	-3.949	0.346	-0.056	-1.531	0.269
0.894	-0.211	1.096	1.275	-5.372	11.000	-0.475	2.048
-0.914	-0.469	-6.439	-6.041	11.000	-1.519	0.527	-1.035
-0.555	0.207	-0.218	-6.937	-0.046	2.058	-0.962	-1.866
2.409	-6.130	0.276	2.379	2.614	0.349	1.061	2.888
-2.728	-6.937	-4.483	-0.655	-2.691	-11.000	-0.845	-2.129
-0.988	-1.535	11.000	-1.205	-2.419	-0.115	-0.831	-4.345
-1.757	-1.455	-1.550	0.422	-1.828	11.000	-2.222	-2.340
-2.703	-2.237	-1.322	-0.091	-7.034	-11.000	-1.396	-4.274
-4.991	11.000	-1.135	-11.000	-2.763	-3.252	-1.395	-1.258
0.219	0.510	3.678	0.397	-1.067	11.000	1.210	-11.000
-1.022	-0.042	-11.000	0.193	-7.034	-11.000	4.775	-6.176
-11.000	11.000	0.858	-1.877	1.526	-0.382	-0.914	11.515
-2.068	-0.454	0.451	7.413	0.256	11.000	-0.791	-0.443
-0.070	0.800	-6.217	11.000	-5.716	-11.000	-0.309	-1.244
-5.456	11.000	-1.060	-2.038	-1.211	-0.590	-1.077	-1.875
2.086	0.195	1.805	1.939	0.687	11.000	1.422	-11.000
-3.182	-3.392	-2.089	1.653	2.957	-11.000	0.212	-1.205
-1.092	0.365	0.869	-0.913	8.510	-2.241	-1.117	-0.929
-5.576	-5.693	-4.699	1.596	4.579	0.794	-5.759	-5.596
-1.406	2.141	-1.994	-2.379	-5.202	-7.034	-1.026	0.025
-2.876	1.271	-4.619	-5.427	-2.355	4.110	0.393	1.795
-3.781	-5.323	-0.130	-3.528	-5.710	-4.532	-0.438	-4.592
-2.178	-2.059	-1.014	-0.596	-0.203	-1.351	1.157	0.865
-3.847	-0.199	-4.088	0.139	0.435	7.847	-0.871	-2.103
1.774	0.072	0.173	1.894	1.101	-0.474	0.214	1.247
-2.366	-11.000	-7.034	-11.000	-11.000	-11.000	0.112	-1.603
-1.458	0.814	1.416	0.118	-3.381	3.170	-1.026	-3.674
-2.838	5.949	2.819	4.206	4.487	-3.409	3.808	-3.071
-2.981	-2.914	-5.706	-11.000	-5.604	-11.000	-0.655	-2.045
0.328	0.818	1.725	-1.160	-2.518	9.052	-2.224	0.072
-4.433	0.738	-0.026	1.397	-0.018	4.122	0.999	-3.346
-2.176	-0.346	0.020	-0.520	-1.338	-5.759	-1.705	-1.383
5.678	3.904	-3.662	-2.772	0.050	-0.169	-0.054	-0.919
0.369	0.111	0.052	2.517	1.093	-0.427	0.186	0.429
-3.758	-2.664	-0.719	0.829	-0.205	-2.023	-0.766	-1.882
-2.330	0.348	-0.929	-2.684	-2.361	-2.823	-1.816	-2.623

Table35.txt

-4.029	4.083	4.117	-2.309	-4.316	11.000	-11.000	-2.537
-0.126	-5.947	-5.526	0.402	-5.727	-11.000	-0.282	-0.297
0.054	11.000	-2.504	-2.695	3.271	-1.307	0.672	-0.730
-4.031	7.754	-4.571	0.903	-0.710	11.000	-6.807	-4.520
1.812	-0.278	-5.116	-1.444	-1.363	-11.000	-1.987	-3.396
-3.205	11.000	-1.051	-6.336	-0.276	1.989	-2.623	-1.454
-11.000	-3.862	-2.347	3.570	-4.830	-11.000	11.000	5.914
0.030	2.579	-2.620	0.798	1.000	2.421	-4.031	-0.306
6.294	6.164	-11.000	0.109	1.251	-1.919	-1.737	-2.793
11.000	-0.673	-1.554	-0.726	-4.518	11.000	-1.936	-11.000
1.846	3.744	0.023	0.676	-4.581	-11.000	-3.942	0.664
4.600	3.040	-5.334	-6.019	-1.276	-0.052	2.001	-0.008
-0.005	-11.000	-1.229	3.973	-0.814	-1.851	-2.552	3.874
0.792	-4.344	0.583	0.025	-2.133	-4.895	11.000	6.162
-1.242	11.000	6.716	-0.405	-1.084	-0.550	3.382	2.992
-11.000	6.515	4.994	2.963	3.850	-3.760	5.554	11.000
2.389	-11.000	11.000	-4.385	11.000	-4.026	3.644	4.997
-11.000	5.972	4.240	4.434	4.093	5.858	0.000	0.000
0.080	0.420	-2.028	-0.891	0.865	-2.451	-1.286	2.277
-0.746	0.804	-2.110	0.339	1.423	2.115	0.013	0.992
-1.940	0.941	1.127	1.434	-1.514	0.077	-1.953	0.855
11.000	11.000	7.314	5.219	-4.891	-4.454	-0.530	0.882
-11.000	-11.000	-5.842	-11.000	0.617	3.213	7.364	11.000
-11.000	11.000	0.006	0.011	-1.016	3.460	-1.534	3.467
-4.436	-11.000	-1.460	1.639	-1.060	-4.846	-11.000	11.000
1.363	-5.375	11.000	-11.000	11.000	7.154	4.009	11.000
-5.702	11.000	-6.211	-7.034	0.000	3.090	-1.905	-0.853
0.799	0.824	-1.656	-0.982	1.844	-0.523	-0.874	1.461
-0.950	-0.335	-1.447	2.564	2.570	1.484	-0.185	0.350
-1.611	-0.704	1.478	1.143	0.190	0.044	0.426	-0.357
11.000	3.919	11.000	3.039	-0.937	0.025	-6.880	11.000
-4.908	-11.000	11.000	-2.432	-2.042	-2.974	-1.792	-1.275
-5.885	2.522	1.618	7.716	-1.804	-3.610	10.694	13.850
2.333	2.531	-0.507	-0.951	2.064	-1.470	0.786	1.837
-0.149	-4.119	-0.577	2.344	2.009	2.827	-0.329	1.625
-2.371	0.429	0.925	1.375	0.018	-1.279	-0.658	-0.090
7.243	11.000	0.338	11.000	-11.000	-0.628	4.183	2.152
3.985	0.977	-11.000	-11.000	3.726	6.362	7.173	11.000
-11.000	11.000	-5.528	-5.028	1.410	1.942	11.153	1.078
1.888	3.355	-11.000	0.528	0.684	-6.420	1.998	2.763
1.631	0.309	11.000	1.076	3.371	11.000	11.000	11.000
11.000	11.000	-0.242	2.788	-2.797	0.609	1.431	1.168
0.718	-3.042	1.019	1.218	5.879	1.018	-6.937	2.031
2.928	-2.566	-4.118	-11.000	0.119	-1.628	11.000	3.476
-11.000	11.000	-6.062	-6.604	-1.619	5.655	8.676	8.501
-11.000	-11.000	1.544	2.568	-11.000	1.604	5.498	8.210
2.628	6.502	3.183	7.878	6.664	-11.000	3.230	6.851
-11.000	7.692	2.720	3.167	0.600	6.325	-1.011	-0.470

Table35.txt

6.661	11.000	-0.208	3.672	-0.110	-1.530	-11.000	7.824
-2.010	2.581	-2.477	-2.247	-0.030	-3.388	6.019	2.512
-3.111	11.000	-3.096	-6.211	-1.210	0.794	0.382	3.594
-1.204	1.063	5.751	4.977	7.180	-1.715	-7.034	-3.168
-1.660	-3.384	8.210	11.000	3.449	-1.108	5.624	4.544
-11.000	11.000	-4.256	-4.390	1.375	4.293	0.407	0.437
2.096	4.612	-0.109	-0.263	1.669	-1.744	1.879	7.063
0.386	-11.000	1.267	3.587	11.000	-11.000	11.000	11.000
-11.000	3.820	1.801	2.879	-0.421	3.090	-0.007	-0.094
1.842	-6.483	3.080	2.003	2.252	-2.955	-5.192	-3.857
0.440	-11.000	-1.032	11.000	7.848	6.029	4.217	6.785
-11.000	-4.207	-1.995	4.306	-3.707	1.960	-0.263	2.854
2.238	-4.366	0.195	11.000	-2.537	-4.612	4.355	5.867
-11.000	-11.000	6.593	11.000	3.009	-1.558	1.821	4.856
3.077	11.000	-1.782	-2.970	0.865	-0.184	-1.258	1.424
-0.639	-1.849	0.486	11.000	-4.887	-0.090	-0.189	3.344
3.295	11.000	2.468	2.690	-5.407	-11.000	0.353	-4.105
-11.000	11.000	-11.000	-1.932	-1.248	0.728	-0.852	4.674
1.079	11.000	-4.842	7.351	-3.056	-3.958	-3.571	11.000
-11.000	-11.000	1.482	-11.000	4.102	-6.079	11.000	6.575
-0.910	11.000	-4.622	-4.241	-1.517	-1.132	5.097	4.647
2.973	-6.340	7.758	-1.481	2.571	-0.551	0.399	5.016
-0.681	-3.341	2.149	-0.149	7.529	-3.629	-1.687	11.000
-11.000	11.000	-6.577	11.000	-0.617	0.171	0.481	6.317
1.417	1.777	3.920	4.082	2.041	-0.082	11.000	11.000
-6.439	-11.000	-0.141	-3.079	3.053	-11.000	11.000	11.000
-6.122	2.175	0.117	1.148	-1.843	2.112	2.096	7.612
1.376	-3.235	-4.650	2.994	0.449	-3.983	-2.960	-0.677
1.831	0.513	-0.979	5.825	1.788	0.319	4.478	-2.964
0.450	2.344	2.131	-1.906	-2.101	-0.330	-0.260	1.202
1.610	-1.636	0.204	1.492	0.851	-0.493	-0.855	2.486
-2.076	-4.510	-2.260	0.755	-1.171	-1.986	1.160	-0.020
-1.911	1.299	1.015	-1.366	0.000	1.118	0.000	0.969
-6.151	-2.317	-2.840	3.086	3.180	0.003	11.000	-11.000
-2.456	-4.135	1.150	11.000	-2.173	-5.273	2.236	6.303
11.000	3.903	11.000	-0.345	10.689	16.454	8.741	12.075
-0.611	-0.659	0.937	0.383	5.948	-5.014	6.580	11.000
-11.000	-11.000	0.585	4.303	11.000	-0.139	2.097	3.256
-0.691	1.727	1.195	3.051	-0.161	0.902	-1.376	-0.721
-11.000	-11.000	7.742	7.020	3.813	-4.085	-11.000	-11.000
3.863	7.973	3.177	4.230	-5.761	-11.000	3.809	2.876
5.160	11.000	-5.207	-6.407	3.202	7.605	5.321	8.262
2.290	4.937	11.000	11.000	4.561	1.044	6.665	11.000
5.289	11.000	2.706	7.124	-11.000	-11.000	5.136	-11.000
11.000	5.529	-11.000	-11.000	-2.596	7.508	5.741	0.972
11.000	11.000	6.997	5.744	0.410	-0.896	-3.707	-2.305
-1.556	-11.000	4.228	-11.000	11.000	3.057	4.802	1.097
-5.769	-11.000	2.048	-2.995	7.978	3.265	2.757	3.317

Table35.txt

4.803	-1.215	4.410	11.000	-4.556	3.703	0.611	0.366
-11.000	-11.000	11.000	-11.000	7.477	-4.231	7.327	11.000
-11.000	-0.131	-6.534	-1.141	-1.315	0.897	0.151	0.602
5.363	1.440	-0.110	1.404	1.359	0.409	-1.982	2.326
0.286	-4.953	1.999	-2.350	2.883	-4.946	11.000	7.040
-0.494	11.000	-11.000	-1.750	2.724	1.212	-2.011	3.742
-3.059	-2.623	4.582	0.554	1.829	-2.816	0.249	11.000
0.342	1.407	-0.786	5.728	2.704	1.993	0.104	0.993
-11.000	2.192	-11.000	0.384	1.424	-0.544	-0.791	-0.381
-3.903	-4.996	-4.068	-3.279	-1.836	-3.436	5.045	6.007
3.269	7.692	3.747	7.497	5.520	-11.000	-4.273	-5.614
1.517	5.807	-4.399	0.506	-0.506	1.363	1.373	1.499
0.272	-11.000	1.481	11.000	-11.000	-4.749	0.933	3.671
0.484	1.729	-4.435	3.643	2.728	-2.671	11.000	11.000
-4.676	11.000	-5.650	-3.170	-0.115	-0.879	11.040	11.361
0.016	6.494	1.462	1.996	-11.000	0.569	-4.374	-2.811
3.509	7.337	3.160	-1.968	6.186	8.077	3.316	5.012
1.718	6.785	2.727	4.179	-0.755	8.414	-0.870	-0.099
-0.467	5.058	-4.496	1.906	6.243	-0.628	1.974	11.000
-4.465	-2.930	-5.938	-11.000	4.608	2.379	0.126	11.000
5.438	11.000	-4.788	2.960	0.542	2.579	0.000	2.141
11.000	1.421	-5.854	2.993	5.892	-0.787	-11.000	1.183
-1.728	-0.115	-0.250	0.130	1.270	7.213	6.613	11.000
-11.000	3.718	-11.000	6.719	2.171	3.987	1.876	0.895
0.245	1.768	-4.719	11.000	-2.270	-4.988	11.000	11.000
-4.094	-11.000	0.572	-11.000	-0.840	-1.079	1.222	1.965
-5.124	2.131	7.130	4.553	-1.838	-0.009	-0.219	4.227
6.411	11.000	1.442	1.274	4.640	2.540	-11.000	-1.766
-6.937	-5.075	3.003	-11.000	3.179	1.163	4.076	2.544
-11.000	11.000	-1.193	-1.428	-0.782	-2.150	-0.857	2.152
2.117	2.662	0.739	0.843	3.416	-0.527	-6.880	2.230
-11.000	4.996	-3.470	-11.000	11.000	2.533	-5.113	11.000
-2.255	11.000	11.000	-3.256	-0.786	-0.479	-0.737	-1.881
3.641	1.743	1.748	6.475	-3.849	-4.823	-11.000	11.000
-11.000	-11.000	11.000	-11.000	-5.610	-11.000	7.283	5.164
2.901	11.000	-5.267	7.745	0.000	0.000	-1.981	3.942
-3.005	7.642	-3.066	-0.764	-0.840	-3.678	-11.000	11.000
-1.771	-5.893	5.322	1.234	2.223	1.906	2.854	11.000
-4.660	-0.811	-11.000	-3.170	0.545	2.754	-1.509	-0.309
0.113	0.788	-4.576	11.000	-4.113	0.999	-11.000	11.000
-5.950	-1.445	4.860	0.736	6.820	8.126	11.000	-11.000
-3.605	11.000	-11.000	-0.293	-1.278	8.176	0.028	2.495
3.033	-11.000	0.505	-0.263	-3.816	-2.306	-3.399	11.000
1.122	4.929	11.000	-11.000	-3.650	-4.565	11.000	11.000
0.794	5.671	11.000	-6.780	-0.128	4.312	0.912	3.829
4.517	-3.523	11.000	5.099	-11.000	0.041	-6.226	11.000
-5.343	-11.000	2.090	-1.808	-4.896	-11.000	11.000	11.000
-6.019	11.000	-5.202	-6.099	3.154	6.461	2.703	2.393

Table35.txt

3.114	-6.483	11.000	11.000	-3.919	0.807	-6.937	11.000
-0.908	-11.000	11.000	-11.000	5.966	-6.267	1.548	-1.842
-11.000	11.000	-5.712	-5.689	5.652	-1.692	0.556	6.052
-1.839	-2.625	-2.679	2.716	-0.426	-1.490	-11.000	11.000
-1.420	-3.857	11.000	-11.000	0.039	0.580	3.744	0.957
1.982	7.819	2.620	-1.115	-0.555	0.165	-0.125	-1.412
-1.813	11.000	11.000	4.880	-4.551	-0.628	-11.000	11.000
-2.802	-11.000	1.156	-11.000	-3.728	6.558	6.424	2.442
-0.777	11.000	2.129	-0.034	2.089	1.144	11.195	13.255
2.158	0.540	1.299	1.285	3.011	-1.280	-11.000	11.000
-11.000	-11.000	11.000	-11.000	6.030	11.000	2.404	3.237
2.656	11.000	-0.331	-1.386	-0.059	2.030	-0.714	-1.836
7.640	-2.213	11.000	0.448	2.453	-0.107	-11.000	11.000
-7.034	-11.000	6.448	-11.000	-0.628	1.431	11.000	-7.034
0.260	11.000	0.563	11.000	0.000	3.024	4.041	5.004
-0.240	1.159	-1.154	-0.440	1.512	-11.000	-0.987	1.362
-2.297	0.453	-0.412	-0.903	3.414	1.823	-0.573	-0.223
-3.494	11.000	-0.990	-4.984	-1.263	-1.451	9.863	5.790
8.126	11.000	-3.848	-0.526	1.565	-4.570	-2.495	11.000
-11.000	-11.000	-2.231	-3.217	2.496	-2.315	1.413	7.627
-11.000	11.000	6.386	-5.033	0.462	1.844	0.385	-1.729
-4.881	-4.431	-3.601	-3.369	11.000	-4.634	-2.867	-3.146
-3.348	-4.212	11.000	3.771	11.000	-0.466	11.000	11.000
-1.538	4.218	-2.039	-2.823	-0.596	-1.746	-1.558	-2.513
4.165	6.081	1.714	1.361	-0.893	3.416	-4.158	-0.649
-5.654	-11.000	-2.526	-11.000	4.716	3.387	11.000	11.000
-6.464	-3.178	-5.497	-6.257	0.756	-1.395	3.908	3.454
-0.029	-3.188	11.000	11.000	-1.506	-4.225	-2.968	1.440
-5.143	-11.000	-11.000	-11.000	11.000	-2.499	11.000	11.000
-11.000	11.000	-4.725	-5.364	5.298	2.415	5.050	7.262
-1.886	11.000	11.000	11.000	-1.361	-11.000	-3.196	-0.965
-11.000	-3.380	-1.605	-0.684	-5.450	-1.219	7.992	3.437
2.458	11.000	-11.000	-11.000	2.434	7.891	8.631	11.756
5.527	-11.000	4.578	5.437	3.613	-0.106	-4.093	2.266
-5.661	-11.000	1.049	4.356	-2.755	-11.000	5.600	7.037
1.087	8.210	-0.576	4.667	0.405	0.550	6.189	5.534
-1.337	5.418	1.316	6.478	-0.586	11.000	5.742	11.000
3.549	-2.486	3.252	-11.000	4.332	11.000	-4.533	-6.084
-11.000	11.000	-3.520	5.138	1.514	6.338	9.535	6.513
8.041	11.000	-4.671	-2.086	-6.612	-6.706	-0.209	1.216
-2.529	-4.087	1.263	-11.000	0.049	-1.585	4.369	-0.845
11.000	11.000	3.420	5.012	2.236	-0.653	-1.559	-0.964
-3.415	6.362	7.791	7.771	-1.467	-2.572	-1.729	11.000
-11.000	-11.000	0.949	3.588	7.344	6.061	11.000	11.000
-11.000	-3.101	-11.000	-11.000	8.723	10.074	10.574	13.786
-2.529	11.000	8.126	8.210	-1.464	-3.082	-4.342	11.000
-11.000	3.460	0.300	-11.000	11.000	11.000	-0.779	-4.477
-11.000	11.000	-2.991	-3.662	-2.464	0.214	3.208	2.717

Table35.txt

2.668	3.739	0.717	1.461	3.404	-2.577	-3.369	6.436
2.989	-11.000	-5.770	-11.000	-1.074	5.736	2.195	4.564
-3.965	11.000	-4.841	3.859	-1.446	-2.301	0.474	-1.117
1.318	3.607	-1.767	-0.057	-11.000	-0.603	2.509	4.068
1.906	5.716	1.049	4.751	-0.842	1.307	1.985	11.000
-11.000	11.000	-11.000	1.024	-0.384	-4.183	-0.931	-1.898
1.403	0.647	0.263	-2.229	1.076	-1.034	-0.023	2.097
-0.284	2.200	1.312	1.010	1.687	1.999	1.537	0.525
-2.005	-0.138	2.252	0.779	0.000	0.000	0.000	0.000
2.877	3.295	0.730	0.544	-3.271	-3.169	2.428	4.466
-1.977	-1.581	1.558	4.604	-1.610	-5.317	3.040	3.229
1.284	4.154	-1.829	1.712	0.000	-0.512	0.110	-1.232
2.813	0.227	1.114	2.004	1.115	-6.486	-11.000	1.545
2.418	-1.202	3.119	2.036	-0.223	-0.814	1.377	2.216
2.010	7.196	-11.000	1.532	-0.737	10.345	-0.663	-1.703
4.744	0.761	3.076	-0.092	-1.439	-6.242	11.000	3.565
-11.000	-11.000	6.203	6.389	2.176	0.995	1.945	5.279
5.882	5.718	0.015	2.185	18.041	17.591	4.945	8.124
6.125	1.628	2.838	0.702	3.478	2.366	-0.434	1.298
-11.000	-11.000	2.468	0.404	1.441	1.356	3.004	2.884
2.348	11.000	2.435	0.759	17.630	17.153	-0.166	-0.804
3.761	-3.484	-3.564	-5.219	-5.264	-11.000	-11.000	1.713
11.000	11.000	3.374	2.510	-7.034	-11.000	3.902	4.516
-5.216	-0.919	-5.105	-2.853	1.017	1.180	3.676	16.307
2.735	-0.238	1.499	1.240	0.948	-2.841	-0.026	1.758
-0.125	0.190	1.985	-0.308	0.741	-2.487	2.406	2.531
-0.292	-0.528	0.608	-0.112	-0.487	-4.119	-1.924	-1.687
0.116	1.031	1.948	1.322	2.678	-0.716	0.748	2.413
-0.417	1.930	-2.189	-4.807	0.559	-11.000	3.154	1.642
-0.689	0.288	1.049	-3.983	-3.082	-1.082	-0.418	-1.907
0.490	0.692	2.389	-4.539	0.474	1.814	2.646	1.109
-0.049	0.621	-2.759	4.892	0.022	-11.000	2.709	2.281
0.514	0.764	1.028	-1.393	-3.036	-1.632	-1.049	-3.185
-0.598	1.310	3.075	2.708	-1.324	-0.647	-0.220	-0.931
-0.077	-0.325	-3.087	-0.065	0.072	-11.000	1.642	-0.143
-1.129	-0.341	-1.895	-3.518	-1.987	-0.270	-1.420	-2.122
-3.212	-0.377	1.093	11.000	-0.355	-0.469	1.176	11.000
2.274	0.730	2.950	1.836	0.756	-11.000	2.606	2.650
0.021	1.753	0.840	1.690	-2.007	-2.767	-0.219	-2.924
-0.409	1.854	2.644	1.169	2.894	-2.767	2.588	5.138
5.370	6.915	-1.409	0.115	0.671	-2.504	-1.435	1.807
1.254	5.508	-2.014	-0.940	0.000	0.000	0.000	0.000
-0.177	0.273	0.515	1.567	0.494	-1.072	0.320	1.496
-1.110	-0.168	1.414	0.606	-0.599	-1.207	0.870	-0.811
-1.275	0.197	1.274	-0.942	0.000	0.000	0.000	-0.378
1.785	0.422	1.887	1.354	-2.824	0.636	-4.252	2.974
-0.995	-0.040	0.436	-0.465	2.692	-1.292	-0.197	2.056
0.303	0.725	0.568	-0.858	0.000	0.000	0.000	0.000

Table35.txt

3.217	2.973	3.892	-1.340	-2.803	11.000	-1.510	-11.000
2.859	2.740	0.529	2.887	2.360	-11.000	3.199	11.000
1.592	1.139	-11.000	8.077	-2.213	-1.018	-0.311	-1.932
1.590	0.566	0.975	0.896	-0.405	-0.199	-1.219	1.900
1.965	0.066	0.896	-1.845	1.614	-4.817	0.470	2.088
-0.653	0.474	-0.654	0.495	-1.329	0.000	0.000	0.000
1.141	0.503	-0.162	-0.714	-0.095	2.804	-0.935	-0.938
0.470	-0.049	2.228	0.916	0.076	-4.687	2.889	4.060
0.144	2.047	0.726	-2.397	-1.431	-1.925	-0.872	-1.447
0.311	1.416	0.590	7.037	1.658	0.217	-11.000	-2.314
-1.757	0.304	0.145	3.693	4.026	-11.000	0.726	1.323
-0.191	2.588	0.214	0.172	-1.087	-1.943	-0.546	-1.690
0.679	3.180	5.018	-4.208	5.198	-11.000	2.788	-0.966
-0.115	-0.067	-2.961	5.245	1.869	-11.000	1.854	5.607
0.985	2.711	-4.327	-0.859	-1.266	4.066	-1.686	-1.407
-6.265	-5.187	-5.536	0.445	-0.046	4.782	5.336	-4.984
0.753	0.414	-1.867	0.972	4.312	-11.000	0.847	1.183
0.474	5.186	0.373	0.413	-2.155	-2.571	-1.317	-0.340
-4.043	3.042	1.516	2.762	-4.804	-5.185	0.071	2.279
2.653	0.402	-0.530	-1.601	0.641	-4.487	0.212	5.236
0.335	-0.112	2.184	-0.344	-0.483	0.011	-1.515	-1.032
6.702	-0.269	-0.112	0.380	-1.355	5.010	-0.334	1.141
0.870	-1.867	-0.128	-2.117	-0.628	-5.856	0.121	0.255
-1.694	-0.913	3.029	-2.548	-0.571	-0.139	-1.489	-3.061
-0.416	-0.247	0.417	1.628	-2.355	7.181	-1.233	6.133
-1.360	-1.901	-2.131	0.319	0.775	-11.000	-0.905	4.272
0.083	-0.026	-4.074	1.509	1.300	-0.413	-1.661	-1.979
-0.928	2.680	4.844	-2.653	-6.022	-5.102	1.887	0.614
-0.210	-1.703	-0.012	4.183	-0.769	-3.205	1.755	0.994
-0.758	0.228	-0.144	-0.718	-1.838	-4.119	-3.111	-2.732
1.298	-0.935	-0.040	1.895	-0.324	-0.230	-0.974	-0.103
-0.865	-1.067	1.116	0.166	-1.050	-4.681	1.686	1.070
-1.280	-0.937	1.364	-0.418	-0.591	-0.469	-2.988	-3.431
-0.009	1.112	1.214	11.000	0.957	2.038	-0.559	1.572
2.335	2.324	-2.649	4.611	-0.850	-11.000	-1.265	6.196
-2.157	3.495	-1.035	-2.265	1.762	-0.482	0.215	-0.894
2.773	2.563	3.576	-1.972	-3.483	2.601	0.012	0.952
-0.632	1.183	0.400	-2.001	-1.378	-4.103	-0.956	4.856
1.400	0.995	-0.579	0.331	0.000	0.000	0.000	-1.214
0.309	2.694	1.993	-6.807	-3.563	11.000	2.132	-0.584
-0.440	0.629	-6.739	-6.937	0.117	-11.000	1.750	1.754
3.498	3.414	-4.339	-4.433	-0.668	-3.168	-1.524	-2.650
1.300	1.691	0.280	2.766	0.114	0.821	0.663	0.729
0.398	0.666	-1.958	-1.177	-0.876	-1.015	0.507	2.632
2.050	3.378	-1.192	-0.315	0.000	0.000	0.000	0.000
-0.101	-0.635	0.715	1.977	-1.809	1.296	1.178	1.059
-0.185	-1.388	-0.819	1.522	-1.209	-4.893	3.085	2.760
-1.125	-0.230	-0.028	-0.738	-1.739	-1.887	-2.218	-1.920

Table35.txt

1.926	1.726	4.360	-11.000	-0.806	2.458	-0.677	1.886
0.767	0.572	-4.113	-1.204	-4.215	-11.000	1.500	1.786
0.623	0.050	-6.455	-0.642	-0.856	-2.297	-3.282	-3.090
-6.807	-1.324	-1.319	0.122	-2.140	-2.082	-0.732	-6.091
-3.786	-5.075	0.828	0.284	2.174	-2.634	-0.082	6.639
11.000	11.000	7.906	-3.239	3.090	3.090	0.000	0.000
2.731	-3.126	3.874	11.000	-11.000	11.000	3.490	3.231
11.000	-11.000	-3.133	0.673	1.996	-11.000	-4.650	5.254
1.739	1.263	-0.457	-3.097	5.328	-1.727	0.668	-2.032
1.587	11.000	11.000	0.880	1.835	-0.479	-0.425	1.522
0.970	4.406	-1.973	0.221	-1.497	-11.000	-1.527	11.000
4.096	6.187	-4.020	-4.063	-1.604	2.734	0.111	-1.571
2.198	1.573	2.980	-11.000	1.319	0.999	-7.034	1.883
1.859	1.081	-4.305	0.271	0.696	-11.000	1.896	-0.708
0.158	0.994	1.179	-7.034	-1.483	-0.900	-2.419	-4.473
2.621	0.851	-11.000	11.000	-11.000	-11.000	1.859	-6.839
-4.774	-4.831	-0.942	2.916	2.371	-11.000	3.224	3.492
1.372	1.522	0.221	-3.808	-3.866	10.306	3.095	-2.377
-1.363	-0.839	3.472	-0.515	-1.845	2.213	0.086	-0.388
-0.948	-1.475	0.195	-1.162	-0.379	-3.430	1.647	3.826
-0.033	0.784	0.348	-2.892	0.158	-2.143	-0.826	-1.838
0.547	-2.472	-0.710	11.000	1.985	5.900	-0.032	0.674
4.002	2.091	-3.778	1.901	-1.370	-11.000	1.746	2.044
2.289	2.066	-0.878	-1.368	11.296	2.861	4.135	4.622
-11.000	2.490	3.000	-4.847	-11.000	3.524	3.430	-6.455
0.877	0.398	-2.381	2.492	1.891	-11.000	2.254	-2.237
6.940	4.761	-0.902	4.032	6.615	-2.490	1.810	3.513
2.954	-0.173	3.261	3.184	-11.000	4.256	-11.000	-11.000
1.535	1.428	-5.004	-4.555	1.342	-11.000	-1.315	2.385
1.127	0.956	0.161	-1.395	-2.009	0.211	0.600	-1.821
1.227	0.108	2.000	2.753	1.022	1.465	1.199	1.608
1.283	0.362	-0.976	-0.636	1.256	-11.000	3.378	2.965
0.124	0.183	1.027	-0.633	6.973	5.242	-0.277	-3.665
0.159	-11.000	-0.396	11.000	2.455	-3.005	0.000	1.938
-11.000	11.000	1.696	0.806	6.801	-11.000	1.170	1.351
0.454	0.062	0.031	-11.000	-1.382	-1.918	-1.533	-0.729
6.327	-0.476	-11.000	3.621	3.032	11.000	4.437	3.545
3.495	3.608	-3.653	0.764	-1.074	-11.000	-0.233	0.000
3.087	2.887	-0.785	1.034	6.580	11.866	-2.322	-1.345
0.386	0.507	-2.156	-1.882	0.178	7.519	0.499	-0.156
0.305	0.008	-5.384	-4.847	-0.343	-5.188	2.804	1.607
-0.431	4.690	-3.695	-6.486	6.120	1.142	-0.892	-1.644
-0.515	-2.177	-4.202	0.465	-0.660	5.110	5.043	-0.938
1.876	2.419	-2.010	-1.971	-1.517	-5.879	2.311	1.932
-1.581	0.318	1.201	-1.237	-1.289	-1.493	0.856	-1.154
-2.876	1.629	1.906	-1.292	-5.157	11.000	2.807	1.770
5.692	0.874	-4.578	-2.110	3.380	-11.000	0.579	-0.980
-3.105	3.475	-3.500	-1.921	-0.999	-0.110	1.103	-1.270

Table35.txt

-11.000	2.755	3.963	-1.828	-4.620	11.000	3.240	-2.625
4.887	-1.846	-4.666	-2.030	2.966	-11.000	-1.268	-1.300
-2.023	4.991	0.849	-3.865	-0.650	-2.145	0.204	2.686
0.305	3.165	4.384	0.699	-1.009	11.000	0.786	-11.000
-3.114	-2.896	3.487	2.235	6.099	-11.000	3.606	3.824
-0.738	-0.015	-2.969	-2.169	1.684	6.683	7.458	8.544
1.067	1.883	2.480	-2.785	-5.362	11.000	1.818	-11.000
-3.289	-3.897	4.854	4.450	7.768	-11.000	2.168	2.331
0.477	0.878	-3.752	-0.744	7.988	10.863	13.247	18.305
-2.032	-0.747	-2.443	2.622	-4.041	2.789	0.973	-3.361
-3.915	-2.451	-3.895	-2.280	-0.284	-3.409	-1.828	-0.494
-3.954	-3.242	-1.572	-4.970	-0.739	-1.316	-3.657	-1.199
2.466	2.043	1.123	-3.515	-1.685	3.327	1.161	0.733
1.142	-0.471	-2.566	-0.824	-0.974	-11.000	1.356	4.012
-0.521	0.361	-2.013	-0.696	-1.780	-1.851	-3.050	-2.190
0.763	-0.734	0.561	1.194	-1.179	3.231	0.988	0.620
-1.330	-0.030	-1.485	-1.363	0.737	-4.170	1.308	0.599
-0.900	0.565	-0.833	-1.805	0.000	0.000	-1.214	-1.622
1.591	-0.642	-1.186	1.613	0.318	11.000	-4.874	2.698
-1.498	-0.002	-3.698	2.760	0.027	-6.000	1.527	2.350
-0.235	-0.800	1.375	0.165	0.069	9.084	-0.100	-1.709
-0.110	1.721	0.415	1.392	5.336	1.954	5.477	0.441
-2.608	-2.299	-3.659	-0.539	5.222	-11.000	-0.218	0.734
-3.972	2.991	0.974	-3.603	-0.713	-1.385	-1.370	-3.288
0.806	0.118	0.009	2.795	-1.060	2.048	0.425	-1.674
-1.317	-0.944	-0.716	-1.049	-1.225	-2.537	-0.435	-1.568
-1.864	-1.809	0.756	-0.856	-0.426	0.000	-0.144	0.000
-1.794	-0.479	-1.212	5.302	-1.664	1.419	1.052	-0.756
1.375	1.816	-1.020	-0.258	1.423	-0.233	-0.583	2.415
1.087	1.569	-1.103	0.874	0.000	0.000	0.000	-0.472
1.358	-3.414	-0.626	1.402	-11.000	0.678	0.937	5.364
1.432	-0.122	-1.496	0.438	-3.479	-11.000	1.477	2.016
0.219	3.633	1.666	-3.057	-2.263	-2.102	-0.831	-1.932
1.256	0.876	0.882	0.534	0.413	7.583	0.383	-1.398
-1.316	-1.257	-1.728	0.262	4.339	-6.612	0.705	1.290
-0.660	-2.048	0.640	-1.216	-3.305	0.037	-1.951	-2.141
1.124	3.043	3.809	0.017	-0.688	2.207	2.794	-3.932
4.324	2.944	1.303	0.530	-1.334	-11.000	0.504	1.800
-3.042	3.427	-3.237	0.313	4.450	0.277	-1.032	-2.566
2.375	0.621	1.010	3.187	3.213	4.991	0.286	-2.296
3.474	3.064	1.380	-2.302	-0.468	-5.836	3.415	1.953
-2.241	-0.134	-2.512	-2.737	-0.664	-0.575	-0.150	-1.058
-0.306	1.916	0.410	1.931	0.438	1.831	0.660	0.548
-0.833	-2.348	-0.776	1.401	-0.503	-5.460	-0.066	3.775
-1.313	-2.621	0.454	-1.371	-0.642	-1.416	-0.687	-1.858
0.486	0.936	-0.375	5.442	-3.500	4.725	1.242	0.531
-0.929	-2.047	-0.834	1.812	-1.567	-4.361	1.100	3.738
-0.343	-0.595	1.569	-2.218	-1.838	-0.749	-1.025	-2.724

Table35.txt

2.109	-0.814	-0.257	0.460	-1.662	1.862	1.637	2.271
2.260	-0.158	0.560	0.884	0.760	-6.721	0.670	1.083
0.856	-0.283	1.539	-0.317	-1.227	-0.257	-0.055	0.446
0.961	-0.196	-0.605	0.320	-2.652	2.960	3.544	2.069
-0.773	0.391	0.459	-2.437	-2.087	-4.023	0.439	-0.416
1.338	0.749	-0.179	-2.006	-2.446	-0.856	-0.355	-0.794
0.494	0.559	0.366	2.199	-0.488	4.934	0.113	0.071
0.708	-0.654	-0.168	0.378	-1.200	-3.217	0.551	-0.370
-1.247	-0.361	0.865	-1.750	-2.445	-2.282	-1.902	-2.054
0.203	1.503	1.024	5.029	11.000	-6.222	-2.270	-4.620
-3.113	-3.458	-2.142	1.529	0.794	-6.145	-2.867	-4.836
-1.894	-3.409	-1.422	-3.672	4.664	3.131	-1.388	-0.511
1.950	1.867	1.054	3.001	-4.741	2.546	-2.129	0.893
2.956	1.969	-0.666	1.862	1.007	-5.239	1.736	3.610
1.286	0.212	1.146	1.098	-1.554	0.272	0.069	-3.599
0.799	2.534	2.808	-5.832	1.180	3.340	3.052	-3.392
1.003	1.076	-3.884	-6.288	1.516	-6.839	0.442	3.601
-4.149	4.331	-1.979	-4.367	-1.018	0.074	-1.009	-1.205
-1.063	-0.551	-3.098	2.127	1.676	3.438	3.916	-0.707
0.503	4.380	2.196	-0.790	-2.207	-6.780	0.484	4.988
4.685	0.217	-0.820	-0.738	-0.988	4.294	-0.883	-1.766
-1.179	1.792	1.385	1.607	1.299	0.251	1.785	0.729
-2.727	-2.867	-0.579	1.540	0.570	-5.076	-0.564	-0.915
-1.137	-1.981	-1.212	-3.138	-2.351	-1.815	-2.634	-1.954
1.237	-0.093	-0.449	-3.048	0.177	0.274	2.723	0.144
0.391	-0.425	0.829	-0.539	0.124	-11.000	0.159	0.353
-1.121	-0.569	0.963	-1.306	-1.493	1.125	-0.865	-2.040
1.515	3.231	4.353	0.220	-3.945	3.371	1.691	-1.912
-2.571	-1.772	-2.512	-2.906	-0.080	-0.785	-1.168	-2.574
-4.851	-2.614	0.574	-3.732	-2.475	-0.488	-1.983	0.046
3.631	3.268	0.865	3.811	3.614	1.505	2.966	-11.000
2.120	1.819	-3.001	2.110	0.353	-11.000	-2.530	-0.155
1.723	1.020	-6.253	-4.692	6.037	-1.123	-1.004	-1.089
2.697	-0.140	1.798	-0.714	-1.543	0.896	0.136	-1.566
-1.929	-1.362	-0.101	-1.373	-1.348	-6.706	1.687	-0.787
-0.153	-0.426	0.026	-1.217	-1.873	0.469	-0.542	-1.917
-4.009	-4.249	-5.564	-3.008	-5.367	-5.358	1.447	5.408
-1.857	-3.722	-1.498	-2.685	-0.409	-2.658	-0.861	-1.716
-3.072	-3.679	-5.441	-2.775	10.029	0.292	4.272	5.767
4.726	0.578	-0.677	0.780	-0.160	-2.898	0.462	1.153
1.291	-0.366	0.585	1.994	-0.424	-2.091	1.461	-0.265
0.224	-0.618	-0.891	0.122	-0.043	0.032	-2.145	2.879
-1.695	2.577	-0.579	1.396	-0.653	2.285	-1.290	3.352
0.863	0.866	-0.175	-0.391	-1.306	-5.255	-0.634	7.485
-1.978	2.501	-1.693	-2.241	-1.441	0.385	3.284	1.366
0.506	-4.191	-4.075	-0.113	-3.027	-2.932	0.040	6.801
1.461	-0.706	1.943	-0.531	0.039	-1.310	0.760	1.525
-0.518	-1.183	-11.000	-0.011	-1.284	3.528	2.410	0.654

Table35.txt

-0.204	1.065	0.501	1.579	-0.013	-0.092	0.992	1.197
0.140	-0.680	2.046	0.760	-0.530	-3.017	0.760	1.616
-0.670	-0.057	0.179	-1.412	-0.135	-2.783	-1.476	-0.533
5.383	3.456	-3.397	11.000	11.000	11.000	-1.467	-5.274
0.690	2.338	-1.356	-1.708	-3.334	-6.937	-2.294	3.479
1.851	0.088	-2.534	-3.307	3.246	2.288	0.999	-0.938
2.682	-0.868	0.615	2.435	-0.004	-0.899	-0.882	0.742
-0.716	-1.349	-0.225	0.347	-1.032	-0.562	-1.430	2.195
-0.090	0.737	-0.036	-0.472	0.000	0.000	0.000	-0.623
-6.033	-5.282	5.437	11.000	-11.000	4.015	-6.577	3.328
1.883	-1.636	-2.522	2.625	-3.267	-4.848	-2.351	-1.060
1.094	-0.119	-3.522	-1.435	-0.031	-1.775	0.215	-1.810
3.980	1.867	-2.615	0.267	-0.632	0.184	1.011	3.269
2.642	-0.508	1.726	1.726	1.334	-2.280	0.667	1.238
2.439	-0.693	2.099	2.784	-0.669	-0.027	0.206	0.738
0.802	-0.066	0.502	1.368	-0.028	1.597	-3.771	0.072
-0.369	-0.695	-0.687	1.630	1.442	-4.337	1.315	0.508
0.477	-0.118	0.459	0.120	-1.478	-0.929	-0.688	-1.401
3.859	-0.301	-1.307	0.877	-0.898	11.000	-1.296	2.101
0.132	-2.311	-0.612	-1.509	-1.041	-11.000	2.075	1.548
0.986	0.737	1.742	-3.097	-3.166	-1.357	-0.122	-0.071
-1.141	-3.173	-0.241	0.627	-4.179	1.617	3.409	1.186
1.015	-0.874	-0.944	-0.180	3.794	-4.810	0.532	0.861
-0.016	-0.888	0.458	-1.393	-0.913	-0.755	-1.976	-1.794
-1.413	-0.669	0.266	-0.260	-1.511	11.000	-1.311	-1.094
-0.747	-1.355	0.516	-1.667	-6.222	-11.000	1.310	1.049
-11.000	-1.409	-5.320	-11.000	6.335	10.062	-0.405	-0.122
-0.941	6.854	7.488	-0.142	-2.096	-3.907	-11.000	-0.318
2.444	1.195	-4.045	5.650	-2.303	0.127	0.378	11.000
4.344	5.203	-0.463	-2.269	3.109	-1.306	6.267	4.930
-6.807	0.054	0.870	1.726	-4.378	7.004	-11.000	-1.345
6.140	1.972	-3.427	-0.237	1.652	-11.000	1.956	0.396
0.652	3.392	-0.144	-1.005	1.144	2.958	-0.509	-1.242
0.976	2.350	3.094	3.978	-11.000	3.283	3.545	-2.159
2.057	1.140	-2.365	0.184	5.699	-11.000	4.213	4.058
-5.397	1.077	-6.005	-2.928	-2.282	1.026	-1.366	-1.000
4.258	-0.116	-0.999	-3.630	-1.166	7.742	-1.231	-0.316
4.461	-1.222	-1.142	0.907	1.416	4.183	3.719	4.821
-0.818	4.349	1.709	-1.522	-0.063	-1.756	-1.051	-1.261
-0.023	0.187	2.610	-0.083	0.164	1.196	0.715	-1.837
1.052	-0.360	-1.074	-2.382	0.334	-3.422	2.864	3.011
-3.500	-0.541	0.205	-2.790	-0.264	-1.646	-2.095	-3.744
1.851	1.803	3.340	0.988	-7.034	1.875	2.308	2.622
0.316	0.849	-3.816	-0.344	2.527	-11.000	-0.221	4.394
-5.338	-0.070	-1.937	-3.875	-1.629	-2.050	-1.893	-1.641
-1.277	0.882	1.941	1.339	-6.461	-0.316	-0.008	-0.660
2.193	0.112	-1.763	-0.873	1.213	-5.556	-0.180	0.740
-1.070	0.233	1.149	-0.128	-0.468	-1.275	-2.415	-1.665

Table35.txt

-6.839	2.131	4.001	5.685	-11.000	-11.000	3.954	2.197
2.444	1.143	-4.636	2.718	2.548	-11.000	-0.952	4.838
1.158	2.110	-5.715	1.826	-2.196	-2.107	-4.262	-3.476
-5.937	2.015	3.789	3.836	-11.000	-11.000	2.463	2.231
0.436	0.465	-2.983	0.488	1.156	-11.000	-1.500	1.086
0.491	1.187	-7.034	-0.471	-0.781	-0.480	-1.717	-4.084
-0.798	-1.301	0.173	11.000	-11.000	-3.106	3.329	2.899
3.747	3.150	-2.373	-4.704	-1.244	-11.000	0.412	11.000
-0.029	-0.799	-4.088	-1.464	1.581	-0.669	-1.377	0.884
1.802	0.492	1.934	-1.086	-0.244	-2.810	0.246	2.024
4.460	-1.179	-3.557	-2.480	-0.014	-2.263	2.823	3.632
-0.292	1.265	-0.961	-6.386	-1.818	0.306	-1.550	1.453
-0.214	8.210	11.000	0.910	-11.000	-11.000	-0.275	6.853
-0.417	-6.407	-4.025	0.220	1.515	-11.000	-3.056	3.161
-4.894	1.978	0.423	-4.887	-0.368	2.536	0.118	-2.560
0.579	0.354	0.638	0.644	0.035	0.003	-0.441	1.796
-2.608	-1.700	-1.312	-1.258	-0.236	-2.433	-0.299	-1.161
-2.325	-2.445	0.407	-1.762	-2.483	-1.300	-1.054	-1.811
0.309	-0.259	0.377	1.291	-0.095	-1.148	-0.506	-4.382
-1.048	-2.288	-5.809	-1.121	-0.233	-11.000	-1.523	0.967
-0.061	3.427	-1.952	-1.414	-1.591	-1.667	-0.301	-1.988
0.875	0.494	1.672	2.385	-1.340	1.412	0.192	0.611
-3.071	-2.841	-3.836	-2.709	-2.448	-2.950	-0.720	-3.413
-3.323	-2.210	-1.943	-4.265	0.198	-3.155	-0.868	-0.920
-0.564	0.896	-1.176	2.211	-0.104	1.058	0.791	-2.349
-4.592	-3.619	-2.687	-2.512	-0.845	-1.075	-0.876	-2.806
-2.757	-4.262	-1.683	-3.148	-0.988	-0.790	-1.424	-2.316
-0.659	-0.455	0.472	1.243	0.072	-0.371	-0.750	-1.872
-4.692	-1.656	-1.283	-1.598	-0.248	-0.311	-0.676	-1.009
-2.223	-1.118	-0.308	-2.549	-2.290	-2.083	-1.893	-4.065
2.141	1.063	2.532	2.092	1.041	0.209	0.302	2.804
-0.205	0.283	-0.443	1.460	2.164	0.642	-1.194	-0.815
-1.095	0.018	2.148	1.808	0.000	0.000	0.000	0.000
0.812	1.054	-0.956	1.353	-0.905	11.000	0.179	0.610
-1.757	-2.092	-0.333	-0.684	-0.714	-3.391	0.000	-0.133
-2.019	-1.784	-2.624	-1.551	-0.306	-0.446	-0.378	-2.757
1.998	2.386	0.059	2.283	1.135	0.043	0.221	-3.214
-1.393	0.594	-3.520	-3.178	-4.483	-4.434	-0.369	-0.148
-0.660	-0.566	-6.226	-5.280	-0.714	-0.882	-1.652	-1.475
-11.000	-1.725	-2.570	1.854	-11.000	-1.691	-2.107	-4.712
7.286	-2.678	-4.492	1.710	6.659	-11.000	1.914	11.000
-2.726	-0.423	-2.604	-2.673	-0.055	-0.616	-1.384	-2.618
1.179	-11.000	1.448	11.000	-0.555	0.551	0.326	3.179
-4.849	-5.104	-4.261	-1.718	0.014	-6.309	-0.468	-2.126
-2.434	-1.428	-2.532	-1.951	-1.938	-2.272	-0.562	-2.325
-1.350	-0.015	-0.032	2.761	1.271	0.807	-0.340	-2.615
-4.797	-3.277	-1.916	-1.384	-1.406	-3.033	-0.380	-2.992
-4.167	-3.386	0.031	-4.815	-2.964	-2.775	-1.230	-2.287

Table35.txt

0.565	1.494	0.076	1.299	-0.504	1.369	2.112	-1.248
-3.106	-2.604	-1.809	-2.705	-0.403	-6.483	-0.587	-2.736
-2.664	-1.433	-0.464	-5.309	-0.376	-2.187	-2.413	-0.244
0.013	1.651	1.335	0.431	0.779	0.881	-0.525	-0.164
-1.580	-1.313	-3.179	-1.872	2.818	-4.216	0.230	-1.304
-2.920	-2.334	1.213	-4.682	-2.751	-3.904	-0.417	-4.082
0.588	0.489	-1.995	0.783	-0.587	0.734	1.603	-0.052
-0.907	-1.743	-3.537	-1.295	-1.498	-11.000	0.303	-2.131
-2.352	-1.328	-2.042	-2.564	0.413	-1.707	-1.627	-2.589
2.249	0.621	0.907	0.757	-4.215	-5.175	3.138	2.369
-0.625	-0.792	-3.676	-2.856	1.456	-5.609	2.190	2.376
-0.980	-0.989	-3.747	-4.282	0.869	2.108	-2.397	-2.919
0.999	0.234	-3.611	0.263	-0.053	2.241	-4.090	-0.171
-1.466	-1.222	-4.196	-1.972	3.624	-7.034	-0.337	2.028
-2.963	-0.680	-3.236	-3.525	-2.356	-2.741	-0.246	-5.551
1.051	0.730	0.919	0.758	-1.222	2.601	-11.000	1.158
-0.739	-0.658	-0.195	-1.369	3.288	0.338	0.653	-0.204
-3.144	-1.060	1.077	-1.833	-2.947	-0.220	-0.517	-2.373
-6.442	0.510	1.215	5.088	3.234	6.196	-5.342	-3.735
-0.489	0.720	-3.686	-3.079	-4.454	-11.000	-1.329	-4.962
0.682	2.302	-4.366	-0.831	-1.400	-2.181	-1.431	-2.003
-0.748	0.150	0.696	-0.535	-0.113	1.734	-1.009	-3.989
-3.269	-2.099	-3.115	-3.054	0.418	-3.134	-1.403	-1.233
-4.119	-3.092	-0.380	-3.351	-1.664	-0.865	-0.320	-3.034
4.346	-2.391	0.130	-2.648	3.193	4.165	2.512	3.420
-0.663	1.368	-4.972	1.140	-3.991	-11.000	0.482	0.140
-6.604	4.769	-1.212	-5.717	-2.500	3.895	0.192	-2.278
0.477	0.055	0.474	2.256	-4.966	1.421	1.606	-0.013
-2.213	-1.019	-4.715	-3.539	0.004	-11.000	-1.053	-0.505
-3.609	-1.163	-1.299	-2.443	-2.151	-3.104	-1.489	-3.080
-0.116	3.356	2.161	1.977	-11.000	6.235	-2.066	1.856
-3.051	-5.011	-1.808	-1.006	5.220	-11.000	-0.271	1.029
-2.507	0.333	1.831	-1.480	-0.706	5.573	-1.284	-0.063
-0.390	1.368	2.338	-0.809	-3.950	4.028	0.861	-1.152
-2.976	-1.959	-3.706	-0.382	-0.070	-5.931	0.608	-1.262
-0.800	-0.217	-1.163	-3.359	-2.637	-1.636	-2.330	-3.207
-0.438	1.478	0.084	3.832	1.329	1.294	-0.327	-1.160
-2.522	-2.976	-5.413	-1.280	1.396	-1.092	-1.396	-2.191
-1.359	-0.941	-0.467	-2.339	-1.508	-2.208	-0.376	-3.294
1.391	1.376	1.062	0.687	0.965	2.325	0.624	1.713
-1.092	-0.270	-5.939	-1.368	1.290	-11.000	0.613	-2.189
-3.513	-1.877	-0.629	-2.402	-0.827	-1.842	-0.171	-0.871
0.589	-1.303	-0.885	11.000	-2.792	4.894	-3.141	-1.744
1.159	0.789	-1.376	-1.066	-2.909	-6.215	-1.121	1.520
-2.729	-0.435	-3.038	-0.776	-1.214	-1.912	-1.685	-1.120
0.558	0.096	1.353	-0.163	0.137	-0.211	0.814	1.270
-1.729	-1.762	-0.383	-1.404	0.023	-3.474	1.361	-1.006
-2.942	-0.732	-0.316	-1.238	-3.469	-2.975	-1.716	-3.236

Table35.txt

-3.751	2.555	3.555	4.845	4.089	3.404	-2.076	2.541
-0.107	-0.144	-3.369	1.152	2.113	-11.000	-1.868	0.068
4.161	0.562	-7.034	-2.169	0.736	1.539	-3.205	-3.231
-2.732	-0.716	-2.137	1.041	-1.946	-6.692	-1.579	-5.217
-6.739	-5.087	-3.900	-3.294	-1.579	-3.054	-3.566	-5.615
-5.320	-4.406	-1.575	-5.624	0.243	-0.155	1.229	-2.692
1.611	2.455	1.338	-1.018	1.552	-4.043	2.452	-5.061
-2.703	-3.424	-3.771	0.412	-0.404	-11.000	-1.666	0.231
-2.360	-1.485	-4.094	-3.226	-1.805	0.276	-2.158	-2.974
2.071	3.204	2.873	0.930	0.899	-2.675	1.995	1.153
0.858	1.507	-3.226	1.273	-1.329	-11.000	0.442	-0.371
-0.436	-0.089	1.756	-1.476	-0.961	-1.485	-1.217	-2.189
-1.299	-1.132	1.013	0.873	-2.373	-3.037	-1.228	-0.328
-4.899	-6.069	-1.564	0.078	1.350	-5.045	-2.017	-2.635
2.058	2.075	-1.891	-3.767	-3.562	-2.622	-1.789	-1.910
-0.670	-2.600	-3.483	-1.222	-2.828	11.000	2.935	0.115
-2.501	-1.804	-4.670	-1.972	3.804	-5.180	-1.079	2.642
-2.286	-0.813	-0.977	-2.245	-0.760	-0.284	-2.444	-2.225
-3.188	-1.861	-1.587	7.315	-4.061	6.512	5.364	3.430
-1.169	-0.966	-4.963	1.404	1.309	-11.000	-0.395	3.351
4.445	4.188	1.480	-2.613	-1.416	3.623	0.955	9.779
0.412	-3.599	4.280	-0.435	-11.000	6.721	4.129	0.671
-1.300	-0.819	-4.026	1.546	1.581	-2.987	0.254	-2.163
1.456	1.539	0.617	-3.414	-1.580	-0.524	-1.704	-1.515
-1.072	1.086	0.578	2.338	1.678	1.359	-0.277	-2.278
-2.249	-1.122	-1.320	-3.820	1.069	-2.821	-0.597	-3.458
-4.048	-2.105	-0.303	-4.088	-0.956	-2.730	-3.032	-1.864
1.212	0.741	7.870	1.261	0.555	11.000	0.524	-5.528
-0.959	-5.954	-4.142	-5.513	-1.159	-11.000	-0.349	0.218
4.806	4.536	-2.318	-5.235	-0.390	4.258	7.473	-1.766
1.004	-0.658	1.921	0.940	0.839	-2.446	0.161	-1.473
-2.282	-2.094	-2.209	-2.024	-2.565	-11.000	-0.422	-1.164
0.548	3.076	-0.458	-3.969	-0.488	-0.869	-2.119	-1.517
2.030	1.706	2.829	1.752	0.757	2.934	2.742	1.255
-2.582	-1.645	-3.980	-2.008	-1.810	-2.202	-0.944	-2.496
-5.478	-5.352	1.914	-3.357	-2.761	-1.362	-2.919	-1.239
0.016	0.083	2.037	0.082	2.044	1.540	-0.947	-0.656
2.325	0.524	0.324	2.400	1.796	2.087	0.512	0.497
1.047	-0.378	0.540	1.846	0.000	0.000	0.000	0.000
-1.523	0.389	0.785	-0.688	-1.458	-1.171	3.984	1.678
-0.408	1.560	-1.311	-1.293	0.259	0.524	-0.552	0.652
1.006	-0.138	-1.753	-1.518	0.000	0.000	-3.090	0.316
0.745	0.246	-0.534	0.817	0.568	-0.416	1.712	-0.530
0.569	-0.950	0.241	0.434	-0.287	-1.795	0.146	-0.831
0.095	0.395	-2.526	-1.222	0.000	0.000	0.000	-0.121
-2.897	-1.789	-0.604	3.853	-3.707	-0.643	0.049	-0.367
0.854	0.845	0.110	0.455	2.863	3.294	1.608	0.996
0.373	-0.410	1.226	-1.720	0.000	0.000	0.000	0.000

Table35.txt

0.732	-0.551	-0.661	1.238	-1.237	-1.672	-0.153	1.284
0.639	-1.507	-0.779	0.813	-1.528	-2.875	0.049	2.928
-1.954	0.408	1.261	0.507	0.000	0.000	-1.214	0.000
-0.747	2.196	2.373	-0.550	2.900	2.347	2.520	2.903
0.644	0.267	6.008	0.708	2.014	2.513	-0.638	-0.496
2.582	-0.598	3.351	2.527	0.000	0.000	0.000	0.000
3.244	0.400	1.289	1.528	1.885	0.161	1.443	1.018
-0.074	-0.554	-1.219	-0.756	-1.197	-3.859	0.834	0.160
-0.295	1.491	-1.590	-0.486	0.000	0.000	0.000	0.000
-6.628	1.455	3.859	-3.431	-11.000	2.839	3.827	-4.457
-3.385	-4.393	-1.641	6.441	0.990	0.253	1.130	1.316
4.628	3.922	-5.317	-1.773	0.000	-1.606	-0.147	-1.322
1.812	-4.152	1.574	0.914	0.455	1.668	2.307	-0.522
-3.537	-2.711	-4.814	-3.478	-2.199	-7.034	-1.126	-2.457
-1.276	-1.658	-0.591	-4.021	-0.932	-2.310	-1.549	-2.014
-0.275	0.784	-0.391	0.195	0.979	1.147	-0.152	-2.944
-4.063	-3.412	-2.141	-1.727	-0.895	-2.843	0.484	-2.217
-3.960	-4.124	-0.030	-4.094	-2.024	-2.956	-0.729	-3.457
2.880	3.648	4.090	3.490	5.560	4.458	-11.000	0.671
-3.679	-3.693	-6.037	2.525	1.990	-11.000	-1.215	1.130
0.610	1.007	-0.835	-0.694	-1.740	-0.663	-0.719	-0.881
3.346	2.586	2.918	3.670	-11.000	4.752	2.301	1.148
-3.822	-1.426	-5.375	-2.755	0.881	-2.425	-0.164	-1.234
-3.539	-0.041	-6.163	-3.037	-1.996	-0.336	-3.174	-2.836
-6.269	-1.200	0.658	1.454	0.781	2.251	0.668	-1.396
-3.248	-1.925	-3.507	-1.860	1.219	-3.794	-1.113	0.246
-2.764	-1.884	1.033	-3.704	-2.338	-1.797	-2.071	-1.984
-3.627	4.619	5.584	5.477	6.966	8.126	-3.130	-2.474
1.234	3.440	-3.192	1.539	-4.917	-11.000	-2.444	-1.994
11.000	11.000	-11.000	0.630	0.597	-1.425	-3.336	-4.646
-1.002	-0.132	1.006	3.352	-3.590	0.904	0.056	-0.224
-2.726	-1.591	-4.470	-0.476	1.319	-11.000	0.294	-1.031
-6.807	-2.358	0.595	-2.222	-2.376	1.422	-0.904	-1.976
-1.802	-0.324	0.773	-0.992	-0.366	0.894	0.366	-0.496
-1.633	-1.148	-1.547	-2.873	-0.666	-2.220	1.180	-1.050
-2.172	-0.605	0.543	-2.044	-0.267	-2.509	-0.335	-3.536
1.763	-1.115	0.688	0.421	-0.876	5.058	0.804	-1.024
-1.214	-0.939	-1.889	-2.511	-0.621	-3.229	-0.051	1.245
-1.529	-1.243	-1.622	-2.489	-4.137	-1.627	-2.169	-2.710
-11.000	-0.415	7.349	6.260	-11.000	5.619	11.000	0.192
3.616	4.705	-4.566	-1.269	7.761	-11.000	-0.287	-0.597
-1.131	4.371	-0.923	-1.557	0.613	2.117	-1.745	-0.939
-0.623	0.837	0.840	1.731	0.124	1.242	0.938	-11.000
-4.129	-3.464	-5.300	-2.221	0.372	-5.162	-1.785	-2.963
-3.210	-2.635	0.444	-4.118	-2.013	-2.386	-3.109	-0.770
2.107	2.818	2.012	2.251	2.961	11.000	-11.000	-11.000
-3.654	-3.244	-4.957	-4.751	2.827	-5.162	-1.295	-1.607
-4.971	1.921	-3.860	-5.529	-0.839	0.106	1.475	1.415

Table35.txt

0.473	1.000	1.673	3.258	-11.000	3.083	1.424	-1.277
-1.363	-1.420	-4.738	-4.077	-0.195	-6.880	-1.705	5.933
-1.433	-1.422	-0.659	-3.227	-0.507	-1.316	-1.559	-1.224
-6.231	1.952	0.947	0.034	-11.000	-11.000	-5.587	0.650
-1.094	-5.702	-1.647	-0.247	0.305	-1.493	-2.393	5.033
-4.547	-0.470	1.003	-1.734	-2.782	-3.267	-2.030	-2.731
2.033	3.404	-2.608	3.087	2.523	2.096	2.554	-4.774
0.092	-1.716	-3.175	-0.901	0.961	-6.668	1.906	1.154
0.651	1.188	0.422	-2.374	-0.396	-4.089	-0.127	-1.905
-1.702	4.536	6.095	-0.100	-3.995	6.970	-2.829	-2.075
-3.468	-3.758	-2.794	3.230	0.755	-11.000	-1.552	6.718
6.550	6.347	-1.713	-3.125	-1.214	-0.699	0.530	3.233
-6.758	0.247	1.359	0.181	-11.000	2.616	1.200	1.961
-0.700	0.321	-2.370	-0.892	2.133	-6.937	0.833	0.730
-5.381	-1.387	1.552	-1.739	-4.345	-1.324	-1.680	-3.427
2.733	2.272	2.119	-1.520	-0.759	5.513	0.714	1.889
-1.513	-2.399	0.299	0.497	0.437	-5.597	0.729	-1.633
-1.612	-1.353	0.162	-0.652	-0.798	-0.782	-1.795	-3.396
-6.112	6.671	11.000	5.940	11.000	4.249	-5.657	6.756
1.723	2.057	-1.478	-4.351	-1.460	-4.979	0.510	-1.772
4.860	5.020	-4.642	-2.801	0.168	2.070	-0.316	-1.074
-0.059	0.161	0.396	1.202	0.471	0.631	0.071	-1.869
-1.047	-0.581	-0.740	-1.906	0.951	-3.631	1.877	-0.228
-3.084	0.783	-1.394	-2.323	-3.634	-2.851	0.369	-3.156
-1.690	-1.576	-0.990	0.797	-0.773	-4.151	-4.838	-2.742
-1.137	-0.883	-2.192	-0.168	-0.034	-11.000	-0.790	-2.975
0.130	-0.012	-1.073	-2.320	-0.920	0.283	-3.501	-3.506
0.592	3.255	-4.521	-0.877	-0.236	-4.513	-2.650	4.830
0.346	0.502	2.037	1.810	0.095	-0.963	2.540	3.556
-4.219	11.000	0.467	-0.502	0.000	-0.736	-0.217	-0.823
1.277	0.581	-2.072	-0.297	0.553	1.844	0.878	1.527
0.626	1.073	-1.403	3.096	1.846	-5.073	-0.023	0.409
-3.849	0.856	-3.185	0.692	-0.558	0.166	-1.328	-0.948
-0.120	1.181	-0.331	-1.362	0.204	-2.154	-0.228	4.091
0.743	1.723	1.345	3.068	-2.593	-4.979	1.213	0.607
-2.499	4.230	-3.472	-3.699	-0.191	-0.045	-3.058	-1.240
6.547	11.000	1.491	7.270	3.550	-4.055	-1.685	-2.099
-1.867	-3.055	1.230	5.590	-3.057	-6.340	11.000	5.566
-1.943	-0.892	1.536	-3.784	0.000	-1.368	-0.445	-1.169
1.985	3.624	-1.945	-2.690	0.389	-4.018	-1.373	2.786
-1.838	0.610	-1.479	1.403	-0.381	4.985	2.364	2.651
0.160	2.880	1.477	-2.959	0.226	-0.440	-2.686	-1.874
1.270	11.000	-0.517	-0.421	1.700	-1.268	0.569	1.131
-0.346	-0.855	-0.787	0.641	1.152	-11.000	0.438	0.280
-11.000	0.530	-4.247	0.500	-0.933	-0.652	-2.960	-2.518
-4.406	4.553	2.955	1.840	-0.704	-2.562	-4.535	0.889
-3.288	-5.062	4.712	-1.652	4.309	3.133	3.052	2.781
-0.145	4.311	-6.061	-5.693	0.235	-0.522	-0.953	-2.253

Table35.txt

1.200	1.669	1.209	-0.844	-1.559	-1.357	2.059	2.971
0.978	1.687	0.732	3.900	-3.582	-4.822	1.576	0.387
-4.299	0.071	-2.304	-0.411	-0.378	-1.482	-1.395	-0.029
1.067	0.469	-0.522	-2.164	0.010	-3.225	0.066	0.422
-0.826	-0.203	-0.296	1.140	0.771	-1.602	4.983	0.053
-3.496	11.000	-0.392	0.331	-0.673	0.968	-1.385	0.812
-1.216	0.545	-0.097	-2.209	-0.021	-4.327	-0.973	1.228
-0.650	0.382	-0.224	1.278	0.000	-0.685	6.194	7.689
-5.911	3.501	-0.592	-0.711	-2.560	-3.334	-0.816	-1.915
0.616	1.200	0.257	0.073	1.723	-1.261	-4.783	11.000
-5.850	-11.000	-0.991	1.649	0.650	0.722	0.930	0.367
-1.013	2.460	-4.434	0.316	-0.889	-2.839	-0.498	-1.537
1.822	0.586	0.087	-0.413	0.397	-1.564	0.510	0.115
1.419	1.923	2.259	3.961	-1.170	-0.898	0.332	-1.289
-0.489	0.680	-2.322	-3.326	0.000	0.000	0.137	0.000
1.318	1.661	0.513	-1.975	0.680	-0.996	-3.696	1.186
-0.263	1.637	-0.347	1.621	1.231	1.656	0.803	-1.107
-2.550	6.699	-1.113	-0.358	-2.489	0.050	-0.957	-0.847
2.764	3.180	-1.435	-0.911	-0.370	-2.645	-2.588	3.097
0.529	2.171	6.078	0.323	-3.658	-0.447	2.046	1.801
-6.202	1.465	-3.629	-4.653	-0.868	-0.313	-0.791	-1.194
0.503	0.496	1.204	0.192	0.040	1.552	-4.385	11.000
-4.918	-6.082	-4.676	-6.054	8.014	-1.992	5.524	4.611
2.635	7.125	-3.914	-5.409	0.000	-0.342	-0.261	-1.214
-5.152	1.681	-5.317	-2.859	0.463	-2.158	0.939	4.587
2.579	5.112	1.138	3.981	-7.034	-11.000	2.975	3.126
-0.284	2.540	-4.747	0.269	0.000	-0.228	0.249	-3.352
-1.336	0.007	2.362	0.733	-3.403	-3.725	-7.034	-5.484
3.376	-2.976	4.307	7.176	1.950	-11.000	11.000	4.932
3.166	7.060	-6.554	-11.000	0.000	0.382	0.000	-1.663
2.604	3.280	-4.204	-0.235	1.820	-2.662	-6.126	4.982
1.028	1.493	2.315	6.034	2.314	-11.000	2.948	0.943
0.481	2.939	-4.060	-2.317	-1.218	-1.207	-1.222	-0.372
1.297	0.720	-1.522	-1.391	1.726	-0.768	-0.052	1.576
0.188	1.319	2.971	3.218	1.460	-1.090	2.065	-0.302
-3.582	3.108	-1.858	-2.974	0.218	-2.254	-0.541	-0.389
0.260	2.216	-0.156	-0.808	1.955	-0.826	-1.735	0.743
-2.914	-5.262	0.132	4.105	1.289	-1.396	1.416	-0.653
0.160	4.042	-0.620	0.176	0.000	0.000	-0.790	0.000
-0.353	0.567	-1.039	-2.110	-1.126	0.112	0.941	3.015
0.346	-1.524	6.037	1.850	-1.110	-3.499	-0.229	-0.024
-0.947	3.521	-0.708	0.686	0.516	5.302	0.312	-2.732
0.354	0.536	0.575	-0.952	1.526	-2.041	2.354	2.814
0.608	1.513	-0.783	1.723	-0.026	-3.752	1.280	0.915
0.171	6.717	0.138	-0.111	0.000	0.000	0.000	0.000
2.045	0.824	-2.034	11.000	5.813	-0.935	1.288	1.797
-4.861	-5.820	0.751	-5.029	1.428	2.721	1.106	5.619
0.831	11.000	0.436	2.468	0.000	0.000	-3.090	-0.224

Table35.txt

2.403	3.452	1.688	-0.886	-1.056	0.277	-11.000	6.804
-5.990	-11.000	7.599	-6.420	4.289	5.148	3.399	5.342
-5.669	11.000	0.287	-0.487	0.000	-0.445	-0.105	-2.282
0.583	1.396	0.307	-1.472	1.312	-1.325	0.008	-0.999
-1.214	0.144	0.016	2.009	1.310	-1.606	0.609	1.211
1.767	4.792	-1.853	-1.240	0.000	0.000	0.000	0.000
0.349	0.480	-0.254	-0.805	-0.595	-1.138	-5.949	8.210
0.876	1.043	0.263	3.132	-0.604	-1.081	5.833	0.602
-5.332	7.079	-4.716	-0.660	0.000	0.000	0.000	0.000
2.353	0.849	-0.585	-1.960	1.207	-1.712	1.069	11.000
-1.490	-1.563	1.489	1.810	1.235	-1.607	0.137	1.618
0.509	2.125	-3.309	-2.609	0.000	0.000	0.000	0.000
0.886	1.143	-3.414	-1.385	-0.525	-2.129	-0.089	-2.908
1.174	1.268	-0.411	2.545	1.992	2.366	1.027	1.526
-1.260	6.227	-1.863	-3.231	-0.432	-2.771	-0.787	-0.886
0.585	2.269	-3.050	-0.196	1.588	-5.118	-1.006	1.574
-0.225	1.452	0.436	2.186	-4.917	-11.000	11.000	11.000
-5.436	0.469	1.640	0.980	0.000	-0.631	-0.736	0.000
2.443	3.989	1.710	-0.071	2.084	-4.883	1.621	7.928
0.398	2.113	0.249	-0.449	2.817	-0.718	3.015	3.236
-0.448	2.263	-11.000	-11.000	-1.226	-0.009	5.331	12.648
1.579	3.125	0.697	-1.424	-1.917	-0.313	1.799	3.429
-0.087	3.158	0.502	3.640	1.095	-5.392	1.196	2.098
-0.808	2.330	1.417	1.992	-2.616	-0.400	-1.274	-4.025
2.294	3.555	-1.296	-2.209	1.305	-2.425	1.500	2.506
0.985	4.008	0.507	4.330	0.400	-11.000	1.300	1.203
0.095	2.828	1.418	0.238	-1.195	-0.027	-2.833	-2.016
-0.804	5.955	0.637	-1.234	-0.865	-1.997	-3.284	1.731
3.451	6.896	6.716	-0.344	-3.577	-5.131	4.485	3.148
-2.353	11.000	-4.059	-2.846	-0.736	-0.200	-1.338	0.529
1.335	0.755	-3.568	0.928	1.926	1.676	0.439	0.089
-0.456	-1.077	-0.943	1.926	-11.000	-11.000	2.405	0.020
7.619	11.000	0.953	-11.000	-2.167	-0.524	-1.722	-0.220
0.123	4.821	-1.160	-1.905	6.365	-3.780	-2.827	0.813
-0.476	0.615	3.340	-0.774	-1.075	0.649	8.126	6.651
-4.766	-0.397	0.176	-2.428	-0.910	-0.846	-1.128	-1.200
1.418	2.290	-0.700	-1.907	-2.740	-1.619	2.456	2.231
0.855	1.601	0.584	2.633	-2.243	-3.015	1.235	1.613
-2.636	5.690	-3.236	-0.441	0.000	-0.874	-1.150	-2.375
0.643	1.133	-2.573	-2.747	0.408	-2.979	1.793	2.941
0.841	1.844	0.622	2.719	0.651	-2.808	1.978	1.308
-0.735	1.036	0.669	-0.684	-0.868	-0.541	-3.050	0.055
-2.361	11.000	2.930	2.524	-1.507	-5.498	-2.908	6.866
-3.411	-5.911	-3.393	11.000	-2.029	-11.000	5.804	11.000
-11.000	-1.816	-6.937	1.833	2.307	6.612	0.206	-2.857
-0.078	-0.886	-0.200	0.503	0.988	-0.038	-0.083	-0.382
-1.410	-2.618	-0.087	0.733	0.418	-0.071	0.757	-0.299
3.550	7.568	-6.571	-2.461	-1.169	-0.337	-1.746	-0.702

Table35.txt

-0.357	1.775	-1.471	-2.676	1.129	-2.528	1.734	2.315
0.309	3.867	2.315	3.772	0.148	-1.229	0.437	0.764
-2.654	5.094	-1.952	-3.407	-0.897	-1.925	-0.241	-0.260
1.161	0.835	0.145	-0.752	-1.691	-2.389	2.406	5.754
0.505	1.119	5.807	3.398	-2.296	3.032	1.036	1.212
-0.705	2.788	1.319	1.667	2.595	4.337	-2.036	-1.784
2.976	4.154	-0.856	-0.806	0.958	-4.268	3.169	5.171
-6.807	-11.000	3.459	-11.000	1.714	-11.000	5.838	2.868
-6.434	4.210	-5.085	0.007	-0.094	2.229	-2.295	0.357
3.946	4.178	0.990	-0.822	1.316	-0.613	1.450	7.166
-1.764	-11.000	-6.508	-3.783	-1.632	-1.824	2.236	2.603
-2.192	4.686	-5.247	-5.087	-0.347	-0.176	0.161	1.719
1.587	1.001	0.213	0.782	1.048	0.210	-0.577	-0.775
-1.841	-3.838	0.129	1.747	-0.844	-11.000	0.633	-1.073
-1.014	1.284	-4.041	-1.251	-1.306	-1.101	0.484	-2.195
-5.892	-2.063	-0.123	0.303	-2.004	-2.079	-0.909	4.619
-0.375	1.305	-1.316	-2.003	3.746	2.496	-0.077	-0.556
-6.049	11.000	-3.239	-0.721	-1.540	-1.988	-0.508	-1.382
1.827	3.492	1.748	1.635	1.288	-1.602	-6.455	4.329
1.580	-11.000	-2.632	0.021	-2.342	-5.610	3.369	1.605
-4.612	11.000	-4.549	1.920	-0.658	-0.433	-1.153	-1.090
-0.091	0.450	2.418	1.486	1.666	1.720	-0.962	1.334
-1.140	-1.022	-1.634	-1.117	1.953	0.412	1.405	0.711
0.032	1.992	-2.059	-2.567	0.888	-1.499	-2.026	-1.427
2.453	2.235	0.314	-1.070	-3.960	-0.692	-11.000	11.000
0.665	2.038	1.933	3.963	1.376	3.498	2.214	2.384
-11.000	6.659	-5.674	0.431	0.475	0.749	-2.010	-1.086
0.443	1.956	0.675	0.000	-1.139	0.220	-4.624	3.600
1.708	2.349	1.326	3.225	0.293	-1.007	0.602	0.857
0.843	2.682	-2.360	1.245	0.000	0.000	0.000	0.000
-0.405	0.202	-2.327	-1.019	0.062	-1.125	-4.485	3.612
1.579	0.623	0.846	4.428	1.550	-4.284	1.161	1.097
-2.406	6.985	-1.377	-0.918	0.000	0.000	0.000	0.260
0.544	1.374	-1.768	-0.813	0.612	-1.077	1.692	1.615
0.445	1.046	0.405	1.614	2.112	-2.265	0.110	0.476
-0.483	-0.499	1.073	0.231	0.000	0.606	-1.316	-0.668
2.025	2.859	-2.957	-0.165	2.490	-0.713	-11.000	6.430
1.780	4.006	1.378	3.121	-0.175	-11.000	1.539	3.307
-6.692	3.963	-5.669	1.263	-2.832	-1.277	-1.981	-0.470
0.239	1.451	-2.888	-2.186	0.835	-2.670	0.718	1.902
1.544	-4.250	0.922	2.028	-0.867	2.555	0.923	0.614
-3.207	3.786	0.437	-0.619	-1.129	-1.281	-0.828	-0.667
-2.052	1.628	0.567	1.573	-2.490	0.488	-2.052	-0.253
-0.500	0.180	-2.255	-2.312	1.401	-3.360	0.840	-1.425
-2.207	-1.035	-2.157	-2.927	-0.217	-1.096	-0.968	-2.338
0.543	0.527	2.160	7.073	-4.543	-6.335	4.628	-6.183
-0.384	0.800	-2.278	-0.483	0.754	-11.000	0.865	2.089
1.228	3.256	-3.586	-4.110	2.802	5.098	-0.129	-1.375

Table35.txt

-1.470	1.412	1.157	-0.225	-0.204	0.059	2.546	0.947
-1.477	-0.643	-0.744	-1.036	2.857	-11.000	1.643	3.670
-1.687	-0.609	0.635	-2.670	-1.937	-2.187	-1.769	-1.914
0.675	1.174	0.780	6.967	0.373	-4.564	2.193	0.484
-2.994	-1.788	-11.000	-6.780	5.211	-11.000	-1.178	-4.717
-11.000	1.677	-0.414	-7.034	-2.218	-1.456	-0.741	-1.015
2.641	2.411	2.177	-6.046	1.725	11.000	-1.447	0.427
-0.778	0.274	-5.760	-3.545	0.727	-11.000	-0.906	4.814
-6.271	-0.199	1.433	-6.721	-3.013	-0.043	-1.318	-2.231
1.922	5.283	0.661	-1.914	-11.000	-1.267	4.419	-2.428
0.360	-1.895	-3.114	-4.815	-3.543	-11.000	1.676	2.382
-3.561	2.533	-0.042	-3.433	-0.785	2.314	-1.332	-1.728
-5.427	0.115	2.056	5.886	-1.031	1.500	1.911	-2.827
-1.754	-1.685	-4.665	-1.744	6.883	-4.693	-0.535	-1.651
-2.853	1.003	-0.528	-2.917	-2.392	-3.349	-2.540	-4.220
3.872	4.612	4.644	-0.988	-2.487	5.272	-1.721	-2.695
3.502	-2.013	-4.251	2.514	1.725	-11.000	-3.773	3.900
-2.829	0.059	-5.959	-0.047	0.204	6.803	-0.886	-1.896
-5.872	1.556	1.507	4.617	-1.923	4.153	-0.889	1.317
-1.915	-2.648	-2.417	-0.911	0.109	-0.173	-0.794	-1.506
1.337	1.198	-3.395	-3.076	-2.091	-0.948	-0.243	1.113
-11.000	3.051	3.077	-5.785	-0.284	-11.000	2.377	0.573
0.538	0.581	-3.142	-0.496	1.043	-11.000	2.455	-0.365
-0.537	5.625	-6.054	-2.540	-2.793	-0.749	-1.622	-1.767
-2.119	-0.778	-1.451	0.393	-0.814	11.000	-4.648	-0.310
-1.615	-1.497	-3.163	-1.358	0.265	-2.416	0.476	-2.330
-0.203	-1.404	1.176	-2.502	-3.681	-0.977	-0.744	-1.191
2.296	2.036	1.295	-2.650	1.583	-11.000	11.000	4.273
0.402	-0.350	-3.259	6.561	-3.324	-11.000	0.618	0.566
-0.238	-0.823	-4.248	-4.849	-0.736	-0.050	-0.056	-2.227
-2.390	0.823	0.514	2.268	1.550	-0.255	0.993	1.020
-1.806	-0.712	-11.000	-1.699	-4.651	-11.000	0.794	-2.172
-0.826	-0.202	0.237	-3.144	-2.709	-3.842	-1.442	-0.900
-0.606	-0.567	-2.176	2.398	-6.053	2.513	-1.651	3.082
-1.095	-1.385	-2.463	-1.429	-2.359	-11.000	-0.571	2.499
-0.901	-0.233	0.235	-4.294	-2.701	-2.678	-0.178	-2.308
-0.365	-0.544	-1.670	-2.903	-2.450	6.566	-1.037	5.719
-1.653	2.889	-0.941	2.251	-0.050	-2.763	0.038	2.029
0.742	2.070	-2.141	-1.568	-2.553	-1.895	-2.013	-3.851
-3.070	-3.032	-2.380	-5.679	5.369	11.000	-1.847	-2.375
-0.137	0.902	-2.649	2.664	3.214	-1.009	2.291	1.251
-5.789	4.428	-5.203	-5.112	0.361	-1.773	0.370	-2.034
5.009	3.827	4.497	11.000	6.182	-3.993	-6.008	11.000
3.158	2.148	-6.201	-2.101	-5.057	-11.000	-0.940	0.134
0.528	2.050	-4.526	-3.241	1.811	3.633	-0.102	-2.760
1.208	1.318	1.210	3.003	-1.492	2.715	0.755	1.957
0.162	0.125	-4.182	-0.605	0.287	-11.000	-0.859	4.597

Table35.txt

-0.401	5.658	0.497	-1.500	-0.995	-2.242	-2.601	-2.960
2.065	-0.398	2.187	3.074	-1.574	-3.535	0.538	-1.525
-2.362	0.893	-3.802	-2.408	1.973	-11.000	-1.639	0.197
-1.388	-1.933	1.157	-4.537	-0.917	-2.384	-1.691	-2.842
-3.601	1.558	-4.379	1.598	0.085	1.521	2.296	-2.575
-2.322	-1.234	-3.822	-1.040	0.388	-3.263	-0.539	-2.401
-1.166	-1.182	-2.032	-4.570	-2.461	-0.990	-0.809	-2.340
1.593	0.225	0.685	1.268	1.112	2.286	1.132	-1.920
-1.255	-0.894	-1.193	-1.298	1.455	-5.174	1.472	-0.105
-1.873	-1.417	1.411	-0.681	-3.620	-5.299	-1.590	-2.297
0.146	0.893	0.510	2.440	-0.947	2.537	-0.025	0.557
-3.040	-0.858	-1.746	-1.539	-1.927	-5.704	-0.300	-1.596
-2.176	-0.916	0.159	-3.472	-3.098	-1.554	-1.482	-0.906
0.339	0.972	1.315	-5.616	-0.051	1.335	-0.516	-6.317
-6.037	-5.004	-1.705	2.672	-0.490	-7.034	-0.981	4.282
-1.296	-0.643	-1.855	-5.162	-0.395	-1.234	-3.199	-2.344
-1.491	-1.374	0.104	-4.058	-0.590	0.718	-0.389	0.076
-1.947	-0.468	0.163	-2.208	4.206	-11.000	0.159	-0.284
-1.701	-1.459	-1.541	-1.039	-0.760	-2.717	-0.627	-0.623
-0.805	1.528	-11.000	1.504	-2.187	11.000	5.079	-11.000
-4.146	-4.786	-4.828	-2.962	2.579	-11.000	-2.116	6.477
2.399	2.343	-1.250	0.207	-0.419	-1.448	-1.938	1.231
0.918	-0.188	1.758	2.318	6.705	2.139	0.399	-0.705
-1.732	-1.399	-5.657	-0.330	-0.509	-4.874	0.941	-1.729
-1.920	-0.537	0.337	-1.883	-1.090	-3.059	-4.186	-2.034
-5.605	1.363	2.183	1.853	-3.483	1.540	-0.691	-0.821
-0.941	-0.247	-3.220	0.140	0.304	-11.000	-1.840	6.478
-1.502	0.212	-1.973	-1.457	-1.773	-1.949	-1.454	-2.378
0.875	-1.767	-1.223	11.000	-1.742	-0.246	-2.127	0.489
-2.730	-0.774	-1.530	0.765	-2.245	-11.000	-0.640	-1.041
-1.186	-0.226	-5.378	-2.616	-1.093	-2.460	-0.536	-1.020
5.940	3.547	5.168	11.000	-1.187	4.422	-4.184	-6.430
1.613	1.608	-4.016	-4.192	-4.291	-11.000	0.897	2.220
2.109	11.000	-4.907	-5.574	5.904	-4.459	1.124	-1.151
-0.196	-1.053	1.522	1.673	4.676	1.149	-6.137	2.074
-1.545	-1.544	-4.414	-2.189	-2.253	-2.765	-0.755	-2.421
-5.989	-2.241	-4.455	-5.167	-1.376	0.211	-1.840	-1.649
0.153	0.825	1.145	0.977	-0.401	0.629	1.051	0.172
-0.100	-1.196	-3.881	-1.032	1.916	-11.000	-0.508	-1.227
-0.740	-1.610	0.542	-1.610	-0.007	2.507	-3.337	-4.395
1.182	-0.852	1.275	-0.886	-3.963	2.337	1.285	0.671
-1.027	-0.764	1.274	1.165	0.014	-5.290	0.916	-0.703
-0.021	0.008	1.210	-1.515	-1.587	4.887	-1.650	-1.653
-1.441	-2.760	-0.414	3.539	-4.069	-0.039	-4.263	2.069
-0.269	1.311	-5.872	1.399	5.892	-11.000	1.167	0.070
-6.243	6.153	-11.000	-0.133	-1.039	2.336	5.329	5.707
1.543	-1.349	-0.267	-1.095	1.504	1.363	0.293	-0.042
-2.633	-0.889	0.160	-0.732	0.522	-1.970	-0.096	-0.794

Table35.txt

-1.176	-0.263	-0.929	-1.526	-2.847	-0.599	-1.107	-3.398
0.633	0.849	0.956	1.878	0.154	-0.270	1.362	0.478
-1.747	-1.549	-1.064	-2.031	0.046	-2.313	0.204	-1.796
-2.358	-0.100	-1.073	-0.455	-1.056	-0.223	0.335	-1.710
1.810	1.157	4.605	1.283	-3.217	-6.015	0.008	1.025
-0.607	5.133	-2.079	0.973	0.513	-6.692	0.405	-2.891
1.006	5.139	1.750	-1.334	-0.308	-0.911	-1.137	-2.556
4.042	2.094	2.823	2.273	-11.000	2.081	2.801	2.129
2.760	-6.364	1.132	0.749	0.781	-11.000	2.506	2.465
-4.931	2.523	0.726	-0.931	1.245	0.512	-0.195	-1.753
-4.880	2.962	3.697	11.000	-2.848	-3.679	2.800	1.141
-2.676	-0.558	-4.817	-1.394	0.693	0.802	-1.620	1.927
-1.530	-1.766	-11.000	-1.566	-0.605	-2.279	-1.006	1.766
3.481	3.340	4.071	11.000	-4.450	4.122	5.425	-1.876
1.378	1.637	-4.981	4.964	-4.863	-11.000	-0.236	-0.076
4.045	3.290	-1.027	1.338	0.781	-0.550	1.478	-1.420
-1.863	1.398	1.171	-2.723	-3.031	-5.560	2.484	0.827
-0.650	0.636	-3.150	-0.075	1.037	-3.567	-0.642	3.739
0.537	1.111	-0.396	-2.339	-0.899	-2.377	-0.929	-0.718
2.001	1.475	2.912	-11.000	-11.000	2.071	2.916	2.008
0.201	-0.215	-5.459	-4.880	2.369	-4.602	1.933	0.577
-0.264	1.157	1.581	-0.654	-1.171	1.083	-2.321	-3.200
5.149	2.941	5.190	4.663	-0.751	-5.481	-11.000	8.210
2.180	3.781	-1.766	-3.661	-2.661	-11.000	-2.796	7.158
6.769	5.864	-2.357	-3.077	-0.062	-1.980	0.200	0.293
-4.782	0.264	-1.973	1.504	-0.788	-2.470	0.062	-3.169
-2.635	-1.534	0.528	-1.985	-0.267	-6.937	-0.120	0.979
-1.389	0.109	-2.903	-2.591	-1.730	-2.556	-0.892	-0.700
-0.134	0.222	0.398	5.128	3.281	1.338	1.572	-4.357
-0.693	-0.445	-4.243	0.192	7.468	-11.000	0.543	0.944
-0.574	-0.377	-3.086	-1.585	-0.755	-0.499	-1.651	6.545
-1.495	-1.216	-0.140	0.338	-0.623	0.769	-1.616	0.245
-4.505	-2.286	0.641	-0.482	-1.234	-2.801	-1.708	-1.323
0.455	1.481	3.466	-2.944	-0.899	-2.760	-1.870	-1.358
0.704	0.637	0.890	0.029	-0.099	-0.559	0.697	0.729
0.982	0.369	0.182	-2.400	-0.297	-3.033	1.997	1.040
-0.233	0.410	-0.477	-1.164	-1.912	-2.906	-1.025	-2.546
1.174	0.628	1.763	0.864	3.078	11.000	1.506	2.307
-1.792	-0.726	-4.674	0.651	0.910	-11.000	-1.241	-0.652
-0.612	0.296	0.239	-6.430	1.334	2.596	-2.640	-1.330
0.682	1.253	1.142	4.113	-2.092	11.000	0.916	0.108
-1.371	-0.388	-2.690	1.736	1.299	-11.000	-0.899	-0.380
-0.253	0.054	0.623	-5.521	2.031	1.667	-1.713	-2.370
-1.522	1.142	0.544	2.321	-0.621	0.708	-1.008	0.905
-0.991	-2.641	1.132	-1.668	0.700	-2.413	1.385	-1.256
-0.598	1.607	0.771	-0.257	-0.736	0.000	0.000	-1.169
-4.683	-0.034	-0.353	1.507	3.143	-1.431	0.214	0.916
-0.055	-0.997	-1.213	0.292	0.228	-11.000	0.662	0.886

Table35.txt

-1.614	3.015	-0.788	-1.055	-0.013	1.944	-1.713	-2.963
-11.000	1.159	1.843	2.793	-11.000	-11.000	1.756	-7.034
1.072	0.247	-3.086	-4.086	0.920	-11.000	0.980	1.049
-4.822	0.974	0.029	-0.137	-0.723	-1.669	-1.632	-1.978
-11.000	3.331	3.706	3.514	-11.000	5.204	4.674	3.552
1.770	1.857	-3.605	1.852	-1.393	-11.000	1.542	2.260
0.891	1.680	-5.921	-5.029	0.346	-1.866	-1.907	0.671
-2.273	5.809	6.984	-1.866	-2.682	5.528	-4.115	1.638
-1.264	3.293	1.020	4.512	-5.040	-11.000	-1.006	-1.504
-2.514	-2.042	-2.924	-2.447	-2.119	-1.888	0.930	1.403
6.150	4.780	6.452	-0.419	-3.882	5.189	-11.000	-2.891
2.692	3.214	0.016	-1.196	-5.365	-11.000	-0.383	-0.595
11.000	7.286	-2.240	-2.315	2.768	-0.954	1.220	3.506
0.611	0.567	-1.478	2.062	1.485	11.000	0.621	-0.492
-2.131	-1.166	-1.331	-0.502	-0.089	-6.529	-0.357	-1.432
-2.278	-1.322	0.162	-3.262	1.173	-0.444	-0.918	-4.205
-1.181	-1.160	-0.892	0.487	-0.910	1.909	-2.005	0.418
-2.422	-3.525	-0.661	-0.514	-0.421	-3.775	-0.778	-2.073
-2.236	-2.322	-1.701	-4.795	4.980	8.219	7.726	11.064
-2.140	-2.775	-2.542	2.566	-0.014	-6.880	11.000	-4.272
1.965	2.026	-4.146	0.420	-0.500	-11.000	2.173	2.529
1.233	1.740	-6.212	0.149	0.544	-2.984	7.848	0.400
0.960	0.730	-0.788	1.233	0.579	1.263	-6.493	0.113
-2.276	-1.467	0.592	-1.111	-0.195	-1.760	-0.302	-0.954
7.469	5.930	-0.542	-3.153	-0.169	-1.073	-1.685	-3.068
0.391	-0.987	0.725	1.180	0.900	6.561	-0.749	-6.483
-1.199	-0.383	-2.124	2.976	-2.806	-5.426	1.596	1.050
-0.347	0.423	0.516	-1.015	-0.895	0.788	-2.443	-2.035
-5.016	0.405	-2.228	1.292	2.320	1.921	-0.128	-2.921
-2.041	-0.917	0.016	-1.764	-0.021	-5.076	-0.521	-0.365
-0.491	-1.523	0.169	-3.215	-1.317	-0.397	-2.682	-0.693
-11.000	0.360	-0.199	11.000	5.374	3.967	11.000	-0.494
-0.199	1.965	-3.654	-2.140	-3.027	-11.000	0.567	1.217
0.351	0.355	-1.371	-4.282	-0.533	-0.053	-0.046	-1.967
0.322	1.376	2.636	2.256	0.634	1.623	-4.205	0.936
0.730	-0.376	-2.931	-0.431	0.159	-2.722	0.114	-0.799
-1.091	-0.149	1.359	-2.573	0.000	-1.622	0.024	-1.931
1.058	2.940	1.741	1.351	-7.034	1.558	1.624	0.761
-1.083	-0.742	-3.134	0.619	-0.721	-4.610	-0.760	-0.172
-3.189	3.040	-4.571	-1.364	-0.023	0.132	-0.426	-2.280
2.031	-1.538	0.628	1.938	-0.840	3.056	-3.820	-2.014
-1.074	0.886	-2.039	-3.328	-2.457	-5.380	-1.702	0.457
-1.077	0.813	-0.766	-4.427	0.000	-0.334	-0.675	-0.304
-11.000	5.640	7.297	0.877	-0.624	6.872	7.768	-1.078
-1.350	-1.398	-2.894	2.711	2.127	-11.000	0.146	1.458
5.462	4.459	-4.489	-1.725	-0.013	-0.330	5.242	-0.664
-0.369	0.275	1.012	1.553	-0.113	1.601	0.679	-0.487
-2.231	-1.626	-0.262	-0.384	-0.217	-1.480	1.014	-0.424

Table35.txt

-1.226	-2.103	1.189	-4.113	-1.187	-3.388	-2.417	-3.961
0.769	-1.155	2.770	5.346	-1.525	0.022	3.416	5.916
-0.284	-0.019	-3.513	-2.249	-1.669	-11.000	-1.307	1.720
-0.442	0.781	2.119	-1.742	-1.926	-0.497	-1.228	-1.838
-0.203	1.286	1.102	1.728	-2.428	1.697	0.642	1.176
0.275	-0.670	0.442	-0.213	-0.484	-0.203	1.858	1.171
-0.506	-2.121	0.167	-0.466	-1.333	-0.007	-3.758	-1.036
-0.195	0.183	-0.346	0.867	0.893	0.776	1.075	0.250
0.148	1.044	-1.905	-0.356	1.330	-0.879	1.463	-0.533
0.839	-1.164	-0.442	-1.242	0.000	0.000	0.000	-3.090
-0.474	-0.349	-0.034	1.107	-0.731	0.123	0.006	-0.999
-2.171	-3.840	0.234	-2.579	-1.165	-2.407	1.179	-0.625
-0.748	-1.116	1.123	-2.973	-1.876	0.251	-0.196	-3.493
-0.543	7.135	0.291	-0.765	-1.430	-0.206	-2.050	-1.043
-1.474	-1.753	-4.300	-0.983	4.456	-11.000	1.143	-2.977
-1.963	-0.677	-2.262	-2.969	-1.488	-1.887	-1.677	-1.503
-0.049	-0.144	-1.394	2.593	2.699	-3.247	2.153	-3.051
1.443	0.085	-0.831	1.905	-0.096	-4.384	-1.204	1.473
0.580	-0.041	0.826	-2.401	-0.977	-3.017	-1.064	1.192
6.027	1.411	0.895	1.096	-2.742	1.797	-1.118	3.013
1.291	-0.730	-1.969	0.487	-2.442	-6.628	0.850	0.791
-0.631	-2.651	0.877	-1.724	3.995	-0.903	-3.201	-0.282
-0.490	-0.496	0.222	1.319	-0.534	4.524	-1.136	0.677
-1.809	1.195	-1.907	-3.079	-0.269	-3.193	-0.008	-0.434
-1.623	-2.245	-0.547	-2.382	-1.645	-3.105	-0.656	-1.092
1.825	1.100	-0.314	0.890	0.270	1.294	0.343	1.193
-0.660	-0.940	1.921	-1.246	0.533	-2.195	0.118	0.644
-0.137	-0.473	0.111	-0.654	-1.532	12.183	-1.178	-2.841
1.609	1.019	1.646	2.373	0.289	2.261	1.072	-1.609
-0.561	-0.193	-0.506	-0.748	-0.190	-1.997	1.301	1.467
-2.612	-3.046	-1.553	-2.061	0.199	-2.681	-1.238	-1.378
1.886	1.111	-1.183	0.164	0.321	0.231	-0.181	-3.648
4.199	3.316	1.878	-1.527	-0.549	-11.000	0.864	2.022
-2.411	0.062	-0.655	-2.549	-2.499	-1.418	-0.779	-2.287
0.919	1.439	1.613	0.606	1.075	1.822	1.402	0.800
1.591	1.241	-0.458	0.159	-1.484	1.081	-0.038	2.068
-1.035	-0.002	-0.563	0.696	0.000	0.000	0.000	0.000
0.589	-2.529	-2.202	3.136	-0.840	11.000	-0.355	-0.056
-2.199	-1.273	-4.966	-2.664	2.310	-11.000	-1.669	-2.321
-6.363	-3.149	-1.334	-6.668	0.323	-2.599	1.727	-1.873
0.362	1.714	0.049	2.057	-2.350	3.400	1.818	2.765
4.392	3.501	-3.991	-2.701	-0.003	-11.000	-1.039	-0.742
-2.272	-2.871	-1.235	-2.672	-0.896	0.452	-2.644	-2.245
2.096	2.161	2.473	1.215	-11.000	-0.723	-1.125	-1.490
1.019	-0.448	-3.869	0.713	3.136	-11.000	-0.465	0.540
-4.165	-0.424	-1.922	-3.792	-0.693	-0.729	-2.225	-3.071
-1.171	-0.776	-1.682	1.991	1.094	1.885	3.205	-1.071
0.793	0.125	-0.793	-1.712	0.218	-2.121	0.515	0.519

Table35.txt

2.480	4.885	-1.413	-0.200	0.000	0.000	0.000	0.000
2.415	-0.106	-1.866	1.416	-2.592	0.783	-0.238	-2.260
-0.608	-1.661	0.024	0.597	-0.640	-1.092	-0.630	0.433
-1.646	1.276	-0.687	-0.766	0.000	0.000	0.000	0.137
-0.443	1.361	1.344	0.334	-0.169	0.183	-0.587	0.782
0.036	0.231	-0.221	0.075	-0.382	2.024	-1.289	0.750
-0.596	-0.761	0.633	-0.826	0.000	0.000	0.000	0.000
2.515	2.162	2.708	2.329	0.591	0.104	1.716	0.382
-0.443	5.048	-1.889	0.143	1.768	-11.000	1.227	-0.104
-0.212	0.393	-6.378	-0.428	0.311	-2.048	-1.393	-2.628
-1.956	0.042	-1.094	2.226	3.343	-5.973	-6.111	1.948
2.004	-2.277	-2.488	0.315	-0.810	-6.937	-0.939	3.509
0.596	-1.349	-1.439	-3.989	-0.199	0.791	-1.180	-2.366
-2.038	0.735	3.046	1.742	-1.785	-0.949	2.135	-0.095
0.137	0.956	2.336	1.641	0.182	0.420	-0.980	-0.726
0.197	2.551	-0.153	-0.587	0.000	0.000	0.000	0.000
-3.468	1.215	-1.332	3.354	-5.798	5.059	-1.407	-2.800
-4.817	-1.142	-5.768	-5.148	-3.786	-5.159	-0.980	-2.474
-2.085	-2.693	-2.805	-7.034	4.325	-1.296	-1.926	-2.719
2.404	1.538	0.835	3.879	0.661	0.853	1.131	0.684
2.049	0.349	-3.234	0.955	2.599	-11.000	-1.515	3.099
-11.000	-2.561	-6.196	-5.295	-2.078	-0.664	1.222	12.179
1.276	1.172	1.411	11.000	11.000	-11.000	2.297	1.231
4.501	-0.633	-4.708	2.203	-0.913	-6.668	-0.983	2.827
-6.880	-0.150	-2.229	-0.688	-1.213	-1.392	-2.648	-2.076
0.626	-0.185	-0.450	1.255	-1.099	0.341	1.055	-0.484
0.072	-1.258	0.104	-1.410	-0.334	-5.354	-0.117	0.794
-1.189	-2.096	-0.616	-1.823	-1.511	-0.484	-1.115	-2.370
-11.000	2.202	3.282	7.547	-11.000	1.263	3.083	2.832
-0.366	-0.139	-3.794	0.077	2.270	-11.000	2.673	1.282
-0.639	0.130	1.423	-0.338	-0.075	-0.553	-2.677	-2.813
-2.022	0.693	2.178	0.411	-0.036	1.823	-0.158	-0.287
-0.532	0.064	2.257	0.491	-0.322	-3.707	0.974	0.275
-2.249	-0.793	-0.724	-1.567	-0.560	0.595	-3.090	-1.883
1.743	0.552	-0.156	0.767	1.976	11.000	-0.125	-1.047
-0.763	0.427	-2.163	3.227	-0.856	-11.000	-0.490	6.224
-0.815	4.279	-0.015	-3.451	2.557	0.219	-0.280	0.795
0.194	1.559	1.511	-2.997	1.121	1.694	1.716	-3.016
-0.614	-1.152	-1.208	-1.278	-3.766	-3.864	-0.597	-1.027
-1.073	-1.509	0.911	-6.140	-0.680	0.293	-0.634	-2.581
3.595	1.072	0.476	0.495	-0.056	0.324	-0.148	1.061
1.126	-0.513	1.424	1.919	1.468	1.244	0.338	-0.279
-1.299	-0.258	0.515	-0.028	0.000	0.000	0.000	0.000
0.607	1.696	2.256	0.534	-4.605	0.023	-4.023	1.023
0.649	-0.182	1.601	0.065	0.311	-4.474	0.694	1.623
-2.996	-0.353	1.991	-3.170	-0.926	-1.311	-0.451	-2.833
0.636	0.640	1.105	2.270	0.164	0.572	0.577	-3.913
-0.858	-0.866	-2.419	-0.502	-3.140	-11.000	0.534	0.824

Table35.txt

-1.600	-2.662	1.042	-1.972	-1.642	-1.800	-0.876	-1.420
-0.236	0.981	2.083	1.149	2.464	-3.473	-3.416	1.060
1.220	0.586	-1.568	0.792	1.014	-11.000	2.683	3.999
1.599	1.235	-2.526	-0.414	-0.802	-0.505	-0.688	-0.270
-0.643	3.530	1.423	0.417	1.807	-1.487	2.860	2.345
-0.631	1.180	-1.351	1.527	0.306	-0.155	1.671	-1.162
-4.861	-2.153	-0.571	0.528	0.000	0.000	0.000	0.000
0.409	1.812	-0.420	-0.535	0.072	-0.711	0.023	1.428
1.265	3.203	-11.000	2.933	-1.307	-11.000	1.489	2.470
-0.199	3.122	-6.013	3.184	3.655	-1.624	-1.812	-1.471
4.821	2.985	-0.071	-0.075	-3.612	-1.076	-3.282	11.000
-0.045	-3.564	-0.084	11.000	2.531	-5.064	0.385	-1.668
-6.521	-0.100	-6.113	-2.825	-2.169	-1.051	-0.579	-0.437
0.885	1.100	-0.754	-1.939	1.308	-1.746	0.614	1.008
-0.491	4.837	1.592	-0.074	-0.349	1.831	0.752	0.875
0.223	2.050	0.637	-1.364	-0.378	-0.602	0.008	-2.250
2.113	2.904	1.578	0.902	0.746	-3.750	2.461	2.314
0.886	-0.425	0.077	4.776	1.207	-4.996	2.257	3.553
0.411	1.684	-11.000	1.018	-0.736	-0.052	-0.258	-0.105
1.894	11.000	-0.557	-0.877	-2.724	-0.276	-5.788	5.963
-0.094	1.535	-0.321	0.601	-4.529	-11.000	1.048	0.139
-5.157	7.346	0.460	0.349	0.000	0.000	0.000	0.000
3.082	4.015	-2.979	2.215	2.866	0.569	-1.151	0.092
-4.372	-7.034	-0.383	3.181	3.415	2.796	1.094	-2.206
-3.686	-0.869	-3.913	-3.876	-1.671	-0.904	-0.380	0.297
0.302	-0.975	0.843	-0.655	-1.673	-3.093	-1.290	-0.553
-0.967	-0.798	2.811	4.975	-0.039	-3.670	3.430	4.197
0.417	2.941	-4.339	-2.369	0.000	0.050	0.000	0.000
1.712	0.709	0.682	0.342	-0.177	-2.041	0.901	1.391
0.937	1.034	-0.083	3.572	-4.290	-4.703	0.680	0.681
-4.398	1.656	-4.026	2.349	0.000	0.000	0.000	0.000
-0.744	-1.610	2.373	1.047	1.622	-2.682	0.039	1.905
1.390	1.010	2.209	3.683	2.317	-6.403	3.493	2.936
-2.611	-2.096	4.595	4.265	0.000	0.000	0.000	-0.335
2.258	2.351	-0.271	0.111	1.596	1.655	0.992	2.202
-2.541	-3.838	-5.055	-5.496	1.175	-1.704	1.399	1.611
3.486	11.000	0.996	1.837	-0.115	-0.104	-0.122	0.977
0.277	1.172	1.161	5.013	-2.181	1.504	-11.000	-11.000
-1.163	1.837	11.000	11.000	-5.620	-11.000	11.000	5.175
-11.000	11.000	-3.130	-0.822	0.775	-0.683	0.433	0.765
0.979	1.029	0.657	-0.587	0.258	-2.242	-0.426	5.750
0.193	-3.167	-1.188	2.124	2.032	1.121	1.584	1.075
-3.606	5.052	0.622	-2.571	0.000	0.000	0.000	0.000
4.719	6.557	2.077	1.327	-2.665	2.990	-4.975	-6.076
0.424	0.200	11.000	-4.849	1.046	-5.612	4.038	4.442
-3.855	6.205	-1.855	1.631	-0.593	2.382	-0.279	-0.416
0.827	1.320	2.219	-0.602	-3.551	-1.058	0.244	6.903
-4.663	-11.000	1.079	2.168	0.269	-1.554	11.000	2.739

Table35.txt

-2.418	0.288	-5.429	-7.034	-1.241	-0.566	-0.897	1.397
1.470	1.310	0.524	0.677	-3.087	-1.981	-4.271	11.000
-0.802	-0.014	0.259	7.623	1.205	-11.000	1.859	1.470
-5.641	1.975	-4.709	1.377	-1.010	-0.752	-0.604	-1.530
1.300	2.062	1.891	2.525	-0.378	-1.486	1.833	3.256
1.027	1.325	0.258	2.075	-1.974	-11.000	1.806	0.741
-0.093	0.958	0.684	0.920	-0.767	0.144	-1.246	-1.108
1.746	1.205	0.561	0.013	-6.047	1.468	-0.122	2.295
-11.000	-11.000	0.225	3.323	2.616	2.276	2.692	2.006
11.000	11.000	1.238	2.318	1.000	-1.975	-2.683	-1.091
0.610	0.059	1.308	1.321	1.253	0.604	0.231	0.645
-1.967	-2.640	-3.153	0.524	-0.631	-5.051	0.378	1.009
-3.415	0.212	-1.131	1.240	-0.284	-0.395	-1.784	-2.139
-0.677	-1.729	-0.611	0.114	1.015	0.712	0.763	-0.524
-1.279	-1.789	-1.187	0.854	2.058	-2.564	-0.698	0.594
-3.315	-0.769	0.340	1.764	-0.197	-1.122	0.074	-2.317
1.546	1.814	-1.479	-1.000	2.249	-1.682	-6.937	2.544
1.398	1.509	-0.254	2.486	2.459	-11.000	5.463	6.250
-2.949	2.393	-4.605	3.046	-1.352	-0.861	-0.477	-2.111
-0.841	-1.367	1.291	1.812	-0.978	-1.079	1.903	2.848
-3.835	-6.706	2.771	-2.628	1.831	-2.296	2.858	4.197
-1.561	0.500	-2.458	5.880	-1.472	-1.473	-0.346	3.141
2.528	1.468	0.040	-0.947	-1.721	-2.718	2.703	1.908
-0.628	1.769	0.730	2.049	-0.785	-5.375	5.203	-1.626
-2.015	1.897	-3.501	0.511	0.000	0.000	0.000	0.000
0.341	1.084	-1.539	-1.563	1.550	-1.397	0.569	0.409
-0.906	-0.551	0.085	1.042	1.205	1.923	1.654	0.966
-0.674	1.756	1.461	0.591	-0.538	-1.410	-1.936	0.100
2.138	2.526	-1.883	0.114	1.080	0.918	-4.870	2.615
0.296	1.646	-0.068	4.492	-1.201	2.980	2.762	1.982
-5.329	11.000	-0.050	-2.022	-1.143	0.369	-1.206	2.451
2.909	3.498	1.488	0.775	-0.088	0.608	2.944	1.367
1.408	1.690	0.803	3.060	3.044	-4.826	2.274	2.174
-3.485	1.910	-2.367	-3.983	0.000	0.000	0.000	0.000
-1.097	2.532	0.009	-1.321	-2.672	0.514	1.384	1.996
-0.025	1.880	-0.029	4.403	-3.097	-11.000	1.794	11.000
-5.667	11.000	-4.582	2.120	-0.923	-1.164	-1.392	-3.322
11.000	-1.788	0.537	0.232	0.171	-1.121	-1.748	0.299
0.676	0.148	-0.075	-0.848	-2.012	-2.634	-0.173	0.771
-0.772	-0.475	-1.073	-0.807	-1.923	-1.215	-0.803	0.116
0.144	-1.534	0.490	1.249	0.635	0.328	0.315	-0.749
-0.953	0.035	0.200	0.724	-0.882	-0.250	0.133	-0.639
-1.188	-0.393	0.958	-0.511	-1.107	-1.857	-1.475	-0.098
-0.564	-1.621	4.558	3.796	-0.990	0.119	0.151	-1.581
-0.784	-2.497	-0.020	-1.873	0.240	-0.873	1.579	0.570
-1.006	-1.438	0.639	-1.130	1.103	3.171	-1.723	-0.269
0.535	-0.040	-0.260	0.407	0.706	-0.620	0.728	1.263
-0.417	-1.506	-0.672	-0.477	-1.269	0.162	0.162	0.789

Table35.txt

-0.360	-0.002	-0.210	0.920	-0.369	8.976	-3.772	14.772
-0.201	0.846	-0.051	-0.721	-1.759	-0.754	-0.247	-1.406
-0.516	-1.958	-0.480	-2.562	-1.319	-0.593	-2.245	-0.011
-0.637	-0.283	0.409	0.368	2.034	3.265	-2.971	0.547
-1.837	-0.443	-0.366	0.025	0.023	-1.570	0.346	1.942
-0.759	0.019	-0.410	-0.101	-0.126	0.240	-1.021	-0.967
-0.292	0.610	1.024	0.891	-2.268	-0.430	-0.995	-2.199
-0.667	-1.563	-0.746	-0.544	-1.447	-0.289	-0.800	-0.555
-0.127	0.656	1.185	-0.395	-0.851	-0.959	-0.775	1.374
-0.605	-0.941	-0.559	0.659	5.227	7.464	-2.128	-1.099
11.000	-3.479	-0.172	-0.409	-1.948	-2.145	-3.057	-4.012
-1.980	-4.201	-2.131	-3.998	11.000	-4.265	11.000	11.000
-2.038	-3.436	-2.121	-1.176	4.222	4.872	-0.992	-1.037
0.226	0.999	0.537	1.057	0.669	-1.344	-1.299	-0.710
0.554	-1.874	-1.496	-0.351	-0.064	-1.242	-1.573	-0.107
-0.426	-0.173	0.712	0.070	-3.101	-1.555	-3.308	0.072
0.875	1.714	0.140	-0.182	-0.140	0.719	-0.311	-0.015
-0.602	-1.723	-0.435	-0.246	-0.510	0.042	1.097	-1.203
-1.332	0.645	0.465	0.304	-0.397	4.809	-0.162	-0.705
-1.123	0.221	-0.387	-0.344	0.940	-0.812	-0.792	-0.272
1.958	0.246	0.478	-0.814	0.308	0.146	0.682	-1.680
0.066	2.854	0.032	1.175	-1.146	1.858	-1.722	-1.851
1.298	-0.242	-0.476	0.920	-0.193	-0.887	0.634	0.168
-0.031	-2.302	-0.983	-0.834	2.156	1.738	-0.676	-0.433
-0.306	-0.830	-0.283	2.049	-0.582	-0.843	-1.163	-1.636
-1.665	0.901	-0.189	0.911	-1.366	0.447	-0.307	0.007
-0.109	0.994	-1.497	-1.449	0.986	0.690	0.183	0.708
-0.428	-0.392	-1.406	1.624	-2.203	-0.780	-1.702	-1.113
1.771	-0.559	0.640	-0.083	1.265	-1.627	-0.549	0.213
-1.117	-1.210	-0.622	-0.438	0.896	-0.666	-0.201	-0.853
-0.698	-0.654	0.391	1.202	-1.704	-3.903	0.403	-0.756
3.030	3.993	1.992	-6.372	-4.868	-0.055	3.185	11.000
0.758	3.327	1.022	-11.000	11.000	-11.000	-3.807	11.000
6.905	11.000	2.318	2.548	1.291	1.588	-0.243	5.375
-0.608	0.316	-11.000	-0.023	-1.900	-1.270	1.435	0.433
0.615	2.046	-1.739	-0.635	-0.022	1.517	0.230	1.677
-0.856	11.000	0.833	0.757	-0.655	-1.507	-2.283	-3.214
3.632	4.396	-0.799	6.246	11.000	-2.369	-2.655	-3.197
-3.705	-5.790	-3.981	-5.089	-2.059	-3.643	11.000	11.000
11.000	11.000	-2.097	-2.309	1.431	2.421	6.154	9.672
5.506	1.805	3.041	1.304	-11.000	-5.358	-11.000	11.000
11.000	-11.000	3.604	2.071	5.333	-11.000	-11.000	1.130
-11.000	11.000	-5.470	7.791	-0.613	-1.501	-2.192	2.826
0.791	-3.934	6.710	5.305	0.524	-0.203	-6.176	1.366
-2.153	-0.924	-0.517	-0.212	1.301	0.554	-0.249	0.234
11.000	11.000	0.963	2.377	-1.751	-1.345	-1.076	-1.904
1.066	-0.967	-1.167	-0.392	0.071	-1.975	-0.343	0.150
-3.495	-2.043	-1.476	-0.029	1.120	-1.144	-2.297	0.010

Table35.txt

11.000	11.000	0.074	0.918	-3.362	5.418	-0.017	-1.778
-0.179	1.177	1.142	-0.387	-0.620	-0.285	-1.338	-0.498
-0.847	0.741	-1.517	0.684	-0.687	-0.786	-0.467	0.916
-1.129	0.773	0.352	-0.509	-2.704	-1.808	-2.736	-1.111
1.274	-0.865	0.195	0.414	0.806	0.066	0.229	0.902
-2.039	-2.663	-1.642	-0.343	1.545	0.021	-0.436	0.246
-1.321	0.029	-0.005	0.895	-2.058	-0.066	4.404	1.244
0.402	-2.061	0.475	-1.188	0.296	-0.602	-1.336	-0.372
-1.414	-1.695	-0.980	-0.661	1.985	-1.510	11.000	11.000
-1.635	-1.478	-1.089	-0.077	-3.626	-1.883	1.980	-2.221
-2.166	0.239	-1.442	-0.212	1.151	-2.461	-0.853	0.491
-1.369	-0.398	-1.441	0.057	-0.407	0.243	1.405	5.746
-1.949	0.168	0.609	0.457	-0.693	-0.002	-2.839	-1.315
11.000	11.000	1.704	11.000	-1.222	-2.264	-1.966	11.000
-11.000	-11.000	2.376	-11.000	2.853	-6.668	-4.746	-2.846
2.657	11.000	-6.539	-3.379	4.238	5.792	6.564	10.254
0.557	-0.102	0.118	0.266	-0.194	-0.359	0.032	1.217
-3.476	-1.014	-0.797	-0.586	2.087	0.704	-0.660	-0.348
-1.577	1.249	-1.056	-0.471	-2.038	-1.059	-0.003	-2.285
5.610	7.383	3.429	4.448	3.828	-1.388	-11.000	11.000
-3.618	-11.000	-2.617	-3.176	7.739	11.000	11.000	1.945
-3.006	2.507	-11.000	-1.780	-0.884	1.073	8.431	9.259
2.177	-0.485	3.599	2.449	1.674	-3.190	3.439	4.439
-0.062	7.322	0.564	-6.320	2.592	7.517	1.800	3.130
-11.000	11.000	1.021	-2.871	-0.123	-0.355	-1.894	-0.508
-2.393	-6.065	0.342	4.187	2.915	-4.621	5.398	11.000
2.156	-11.000	11.000	-11.000	0.750	-11.000	-3.369	5.457
-6.008	11.000	1.015	5.944	-1.084	2.958	10.438	10.035
11.000	11.000	-2.788	-2.244	-1.561	-2.763	-4.702	-3.874
-2.828	-2.785	-3.583	-4.528	-1.805	-4.368	7.492	11.000
-3.408	-3.006	-2.407	-2.725	0.000	-2.821	0.000	0.217
-0.969	-0.323	5.007	3.831	5.269	-2.346	0.282	11.000
8.077	-11.000	11.000	-11.000	2.595	-5.966	0.180	1.873
-4.785	11.000	-4.196	-11.000	4.734	0.364	7.354	4.222
6.362	4.192	2.666	3.168	2.004	0.561	1.974	11.000
-11.000	-11.000	11.000	-11.000	11.000	-1.817	1.456	2.882
2.078	2.808	11.000	3.236	6.610	6.544	0.087	1.669
1.250	0.855	1.946	0.048	-0.454	-11.000	1.511	2.665
-0.450	-0.812	-0.528	2.241	1.926	0.927	1.280	-11.000
1.143	11.000	-1.166	-0.441	-1.301	-3.559	-0.406	-2.644
11.000	-1.729	-0.692	11.000	11.000	0.304	1.359	0.884
-2.752	-3.899	-11.000	-11.000	-0.763	-11.000	6.427	-6.539
7.973	11.000	-1.980	-1.362	7.944	5.217	2.387	3.059
2.840	3.632	1.050	0.463	1.926	-11.000	3.930	4.194
1.291	2.775	1.201	-11.000	-2.563	-11.000	1.628	3.491
0.917	3.520	-11.000	-11.000	-1.203	-0.959	-1.416	-1.574
11.000	2.266	-0.127	0.740	-2.883	0.213	-4.328	11.000
4.358	11.000	11.000	-11.000	-5.249	-11.000	0.415	11.000

Table35.txt

-7.034	11.000	-6.210	0.873	2.356	-1.368	0.807	-0.582
0.294	6.906	-6.739	2.031	2.257	-5.772	2.301	11.000
2.796	-11.000	11.000	3.838	-2.190	-11.000	-3.658	11.000
-3.836	11.000	-6.937	2.999	-2.900	0.039	-0.479	0.077
0.225	-3.340	0.529	7.482	-1.361	-1.859	2.437	7.145
-11.000	-11.000	0.273	2.589	5.810	-0.906	1.546	11.000
-5.145	11.000	7.228	2.566	1.273	4.270	-2.969	-0.888
-4.719	1.047	1.469	2.624	-1.676	-0.033	11.000	11.000
6.100	-6.255	2.662	-11.000	4.087	-11.000	0.140	-1.173
-3.984	11.000	-11.000	-3.140	2.261	9.428	2.545	10.828
11.000	6.798	11.000	6.118	1.766	-2.251	0.090	11.000
2.151	-11.000	1.370	-11.000	1.354	-0.959	2.504	3.129
-4.769	-2.525	-11.000	-1.610	1.556	4.989	3.265	3.570
3.623	4.044	1.652	-1.461	0.551	-1.567	2.003	11.000
-11.000	-11.000	4.306	-0.480	3.347	-2.333	-0.225	7.520
-11.000	11.000	-2.913	-11.000	2.311	0.252	5.717	4.170
-3.144	4.113	0.341	1.374	1.249	-7.034	1.075	7.685
0.265	0.096	11.000	-11.000	0.411	0.236	-2.369	11.000
2.299	11.000	-11.000	1.159	-1.579	-0.968	-1.189	3.464
-0.339	-0.304	-0.017	0.213	0.944	-1.116	0.150	-1.025
-1.661	-0.832	-1.168	0.270	1.164	-0.375	-0.639	0.654
-0.725	0.185	0.751	1.881	-1.805	-0.166	-3.105	0.311
0.247	1.897	-0.697	-1.064	-0.380	-1.592	-1.528	-1.726
-1.288	-2.849	-1.753	-1.989	-2.026	-1.610	-3.564	-1.625
11.000	11.000	-1.720	-1.541	6.814	8.386	-1.740	-2.629
-0.823	0.619	-0.281	0.543	-0.493	-1.138	0.638	-0.186
-1.354	-1.034	-1.857	0.608	-0.547	0.743	0.226	0.789
11.000	11.000	-0.544	2.073	0.282	-0.463	-0.060	-1.211
-2.957	-2.709	-2.174	-1.628	-0.117	-1.856	-1.097	-1.375
-2.269	-2.843	-1.698	-1.023	-1.823	-1.685	-2.193	-0.620
11.000	11.000	-0.417	-0.752	9.384	10.246	-0.815	-0.810
-0.371	0.583	-0.887	-0.560	-1.387	-0.298	11.000	11.000
-3.938	-6.620	-1.720	-0.873	-0.503	-0.066	-1.771	-0.697
1.827	2.709	-1.010	0.581	-0.899	1.148	-0.728	-1.385
-0.122	-0.935	0.931	0.591	1.227	-0.361	-0.215	-0.501
-1.763	-0.391	-1.616	0.771	1.256	0.209	-0.601	-0.055
-2.195	0.114	0.901	2.025	-0.291	-3.311	-0.699	-0.705
-1.931	-1.190	11.000	11.000	0.500	-0.889	-0.986	-1.563
-2.424	-3.052	-2.168	-1.351	-0.093	1.111	-1.045	-1.166
11.000	11.000	0.116	0.551	-0.761	7.055	-1.591	-1.183
-1.517	-1.634	-1.836	-0.423	0.121	-1.899	-1.816	-2.464
-2.210	-1.770	-2.049	-2.546	-2.197	-0.892	-1.275	-0.847
11.000	11.000	0.022	-0.571	7.263	6.162	0.259	-2.141
-0.230	-0.411	-0.053	0.784	0.198	-0.462	0.513	0.560
1.456	2.601	0.385	-0.843	-0.944	-1.115	-0.468	0.261
1.116	1.479	1.454	0.363	-1.749	-2.581	-0.295	-1.181
-0.773	-0.278	-0.969	-1.090	-0.838	-1.105	-1.480	0.709
-1.954	-1.991	-1.717	-1.145	-0.297	-1.079	-1.625	-1.344

Table35.txt

11.000	11.000	-0.903	-0.987	6.707	7.733	-0.987	-1.245
-1.208	-0.897	0.807	1.818	0.223	0.465	0.779	-0.591
1.406	0.736	0.799	0.453	-0.413	-0.565	-0.256	-0.502
0.669	1.289	-0.870	0.189	-0.567	-0.064	-1.699	-2.834
-1.460	0.873	0.800	-0.151	1.219	-1.099	-0.168	0.824
2.591	-0.553	-0.072	-1.782	0.201	0.847	0.136	2.270
1.204	-0.565	-0.755	0.378	-0.021	-0.578	-0.092	-2.045
-0.959	-0.960	1.917	-0.904	-0.159	0.775	-1.095	-0.359
0.380	-0.818	0.027	-0.735	-0.779	0.535	0.173	-1.084
1.195	0.162	-0.412	-0.119	9.138	13.559	15.917	12.297
0.524	11.000	11.000	4.699	-6.015	-1.039	-1.330	11.000
-3.102	0.309	0.433	-11.000	3.565	8.210	-1.649	0.143
-5.311	11.000	-11.000	-11.000	8.331	14.265	10.614	3.406
-0.294	0.250	1.048	-0.068	-0.160	-0.694	-0.235	-0.147
1.588	0.582	1.116	0.874	-2.114	-0.274	-0.780	0.640
1.032	1.073	-0.713	1.869	-1.735	-0.667	-1.293	-0.350
-0.597	1.080	0.527	-1.106	-0.304	0.450	1.258	-0.689
0.473	2.098	-0.019	1.352	-0.638	-0.116	-0.128	-11.000
0.570	-0.216	0.219	0.130	-1.418	-2.335	-0.869	-0.988
11.000	11.000	-3.795	4.482	7.350	3.879	11.000	6.089
-11.000	-11.000	3.064	-11.000	-2.190	-3.335	-0.886	0.227
-6.240	11.000	5.258	-6.590	2.896	9.235	2.739	10.992
-0.260	1.292	1.131	-0.137	0.921	1.010	1.436	0.243
0.934	0.969	-0.072	-1.132	-0.434	-0.859	-0.997	0.376
1.264	0.210	-1.153	-1.184	0.529	1.268	-1.097	0.758
-1.528	1.036	1.131	-0.768	0.051	2.197	-0.456	0.277
0.078	1.321	0.406	-0.749	-1.813	0.089	-0.988	0.632
0.450	0.202	1.174	-0.386	-3.033	-0.874	-1.859	-1.435
-1.476	-0.007	0.685	0.513	0.994	0.121	-0.067	-3.130
1.827	0.845	1.253	-0.005	-0.978	0.019	0.795	-0.304
-0.230	0.198	0.029	-0.983	-1.781	-0.429	-2.040	8.610
0.640	2.134	0.322	1.576	1.009	-0.523	-0.509	1.241
1.104	2.239	1.030	-1.642	-2.006	0.253	0.249	-3.381
2.092	1.918	0.540	-0.166	-2.323	-2.147	-1.148	-0.355
1.448	4.827	-0.347	-1.202	-0.650	-1.785	1.412	11.000
-0.089	-2.621	-1.056	-0.360	0.059	-0.753	0.119	2.546
2.812	-0.422	-0.699	-1.344	-0.378	-0.027	0.578	-0.717
-1.055	-1.842	0.111	1.482	1.213	0.241	-0.988	0.215
-0.533	0.221	0.968	-0.864	-1.431	-0.973	2.173	1.190
-0.139	-0.360	-0.252	-0.024	4.168	8.604	-3.657	-1.402
-3.008	-2.879	0.914	-1.109	-1.605	-0.963	4.395	4.958
-0.969	-2.223	-2.939	-2.365	-2.055	-0.403	-1.230	-1.335
4.824	7.362	-0.048	-0.740	-1.167	0.870	-0.119	-0.972
-1.214	1.498	-0.719	-0.088	0.468	0.627	-0.826	1.431
-0.398	1.263	-1.752	-0.851	-0.120	-0.269	-0.463	0.579
0.334	-1.282	-1.231	-0.160	-1.879	1.857	-1.537	-1.590
11.000	11.000	-0.893	-1.817	-2.321	-0.558	2.138	2.065
-0.975	-2.931	-3.829	-5.727	-2.782	-3.370	-0.674	-2.505

Table35.txt

11.000	11.000	-2.903	-2.880	-0.619	-1.196	-0.654	-2.246
-0.474	0.036	1.052	1.152	-0.984	1.048	-0.500	0.262
-0.071	-2.505	-1.398	-1.703	-1.221	-1.438	11.000	11.000
-0.168	-0.110	0.021	-0.888	-1.739	-0.249	-2.841	-2.664
6.832	7.731	1.482	1.593	-4.544	0.934	0.973	7.378
-3.973	-11.000	2.082	-11.000	3.988	11.000	4.126	3.772
-5.715	11.000	3.359	-11.000	-1.196	8.225	5.172	1.323
-1.228	-0.241	-0.012	-1.248	-11.000	-1.509	0.182	0.693
-0.606	2.014	0.790	-0.813	-1.980	-0.755	-0.327	0.505
-0.122	-0.578	0.401	-1.634	-0.816	-1.829	-2.657	-0.396
0.768	0.204	-1.368	-1.825	-0.132	-0.446	-0.566	0.956
-0.292	1.270	-0.181	-0.410	0.745	-0.213	1.004	0.570
1.074	0.615	0.742	-1.520	-0.597	-0.672	-1.418	-2.779
-0.650	0.571	0.420	-1.511	0.683	-0.794	0.606	1.361
0.499	1.419	0.347	-1.241	-1.402	-0.744	0.635	0.509
-0.101	-1.241	-0.188	0.860	-0.206	-0.241	-2.289	-1.430
1.854	2.040	11.000	11.000	0.209	-0.953	-11.000	11.000
-2.713	0.912	-0.489	-1.495	0.563	-0.863	0.473	-1.025
-11.000	-0.210	1.416	-0.966	-1.622	0.517	0.038	-2.579
0.625	0.615	-0.497	-1.782	-0.446	-1.826	1.942	0.835
0.165	0.770	0.565	-0.382	-1.238	-0.407	0.336	0.209
-0.927	1.561	1.736	0.241	-1.704	-1.453	-0.166	12.554
11.000	-3.323	-2.413	-1.968	-0.466	-1.483	-2.674	-3.573
-2.788	-4.808	-2.325	-4.321	-2.830	-3.570	11.000	11.000
-1.849	-3.169	-2.393	-1.706	5.005	6.049	-0.634	-1.343
0.561	1.772	1.417	-0.246	1.744	-1.400	0.698	1.617
0.041	0.777	-0.084	-0.125	0.087	1.026	-0.701	0.204
-0.043	-1.002	-0.070	-0.140	-2.625	0.951	-1.724	-0.097
11.000	4.902	-11.000	5.180	1.307	-1.255	2.665	3.047
1.138	0.996	1.411	1.885	-4.222	4.166	-4.212	5.216
-2.988	11.000	1.051	-11.000	-1.631	12.150	10.673	6.017
11.000	11.000	0.038	2.216	4.131	4.039	11.000	11.000
-11.000	-11.000	6.159	-3.236	6.372	11.000	4.921	-11.000
-11.000	11.000	4.296	-2.841	-2.538	8.731	4.720	12.151
11.000	1.403	-2.126	3.093	-11.000	-5.767	-2.690	6.444
-11.000	-11.000	11.000	-5.365	0.177	-11.000	0.943	11.000
-0.334	11.000	0.812	11.000	1.887	0.016	1.964	7.127
0.349	1.629	-0.798	-0.869	1.647	-0.546	0.442	0.561
-2.132	-0.317	-1.401	-0.977	0.876	0.199	1.145	1.254
-0.842	0.270	0.150	-1.240	-0.711	5.411	-0.103	-1.053
-0.152	0.499	0.369	-0.039	0.731	-1.863	1.335	0.101
-0.747	0.025	0.322	0.215	0.952	0.552	1.102	-0.121
-1.370	-0.468	-2.110	-0.987	-1.444	-1.609	-1.317	-0.910
1.858	7.193	5.949	4.803	2.535	-1.601	4.211	3.988
-3.060	-11.000	11.000	-11.000	4.561	-3.387	3.123	2.041
4.162	6.737	11.000	-11.000	7.491	5.652	8.229	9.621
11.000	1.707	-1.164	-0.510	0.655	-1.866	-1.249	0.126
-2.004	-1.322	-1.677	-0.389	1.251	0.388	-0.913	-0.140

Table35.txt

0.041	0.943	-1.117	0.135	-1.048	-0.532	-2.097	0.880
0.753	-0.242	-0.230	0.161	1.428	0.050	0.019	0.309
1.508	-1.148	-0.469	-2.045	-0.745	2.160	-0.582	0.158
0.757	0.185	-0.528	0.360	-0.962	3.755	-2.663	-3.759
0.407	0.761	0.191	-1.215	-0.633	-1.051	0.455	0.010
-0.241	-1.586	-1.070	-0.451	2.111	-0.280	1.168	0.345
0.703	0.911	-0.840	-0.524	0.571	-0.481	-0.875	-2.599
2.724	-1.830	1.482	3.923	5.155	0.540	-1.545	5.694
1.934	4.260	1.760	-11.000	2.741	4.063	1.898	2.996
-11.000	11.000	0.329	-4.838	5.770	-1.135	-0.841	9.257
11.000	6.013	1.294	2.554	3.012	-3.886	0.575	2.874
-0.495	-3.472	3.592	-4.347	2.664	-11.000	2.404	5.009
-7.034	7.754	-6.780	-1.471	0.146	-0.477	-0.866	0.896
6.998	8.077	-0.931	11.000	-2.166	-1.224	-3.764	7.220
-11.000	-11.000	5.763	-5.961	-2.195	11.000	3.792	-3.365
11.000	4.892	-11.000	5.920	6.053	11.328	10.247	15.142
-0.336	0.587	-0.569	0.594	0.019	-3.579	-0.472	0.571
1.467	1.340	0.169	0.859	1.707	0.197	-3.160	-0.679
-0.576	2.496	-2.106	0.173	-2.130	-1.194	-1.150	-1.835
5.410	11.000	-0.406	11.000	-2.754	0.329	-11.000	11.000
-5.002	-5.328	6.678	-11.000	1.092	4.639	-2.385	-1.597
-5.643	11.000	3.211	-5.318	1.137	10.792	11.681	6.373
0.157	-0.384	-0.869	-1.497	0.396	-1.511	-1.413	-0.716
-1.113	-2.926	-0.825	-0.346	1.406	-0.703	-1.042	-1.499
-1.498	11.000	-0.457	0.383	-1.591	0.410	-0.562	-0.206
-0.338	1.025	2.574	7.283	5.580	-0.248	-4.810	11.000
-5.727	-3.783	7.878	-11.000	7.742	-3.456	5.079	-1.242
-6.081	11.000	-11.000	-11.000	4.101	4.457	-1.099	10.381
4.327	-11.000	1.658	1.099	2.638	0.760	-1.804	11.000
-4.209	-11.000	-4.002	-11.000	-6.476	-11.000	-2.623	2.592
1.789	3.921	-0.760	-0.724	0.192	-0.435	3.947	4.355
1.281	-0.084	0.613	-0.235	0.389	-1.155	-1.179	-0.827
1.012	0.459	0.581	-2.107	-1.122	-0.314	-0.221	-0.764
-0.125	1.667	0.388	0.306	-1.994	-1.586	-1.452	-1.129
1.157	1.245	1.190	0.755	1.309	-1.116	-0.505	1.801
0.702	0.544	-0.382	1.798	0.551	2.735	-0.609	-1.204
-0.578	0.082	0.328	2.210	-2.463	0.437	-1.097	-1.818
0.637	-0.785	1.013	0.056	0.696	-0.589	-1.846	0.269
-2.822	-2.433	-1.233	-0.220	2.233	0.024	-1.077	-0.448
11.000	11.000	0.289	0.488	-0.948	-0.922	-1.304	-1.518
0.560	11.000	2.845	4.336	-11.000	-3.565	8.210	11.000
-11.000	-7.034	-4.667	-1.791	-0.795	-1.642	0.567	-0.856
-11.000	11.000	-11.000	7.633	5.079	5.121	-2.041	-1.712
3.300	11.000	0.634	-0.358	0.262	-1.156	0.073	4.410
6.253	-0.549	11.000	-11.000	5.877	-5.376	1.084	1.041
-11.000	11.000	11.000	7.413	-0.550	4.722	-0.839	11.362
2.944	1.679	11.000	11.000	0.902	3.543	2.747	3.223
1.222	3.148	11.000	-11.000	-6.473	-11.000	11.000	11.000

Table35.txt

11.000	11.000	-6.807	-11.000	-0.971	-0.615	-2.098	4.088
3.377	11.000	-1.047	2.421	-1.861	-4.467	1.329	0.742
-6.880	11.000	4.234	-6.839	11.000	-2.064	-5.685	2.147
-4.780	11.000	-1.093	-5.788	0.912	1.731	8.693	12.790
1.882	1.687	-1.135	-0.300	-5.062	0.040	-1.073	-1.826
-1.648	-2.977	-1.100	-1.956	-0.177	-1.983	-0.438	1.122
-1.388	-0.242	-0.142	0.811	-0.133	6.179	-0.989	-1.817
-0.145	-0.738	-0.969	1.017	1.003	-0.428	-0.132	0.100
-1.574	-2.893	-2.213	0.323	2.122	-0.119	0.127	0.277
-0.798	-0.632	1.221	2.329	-0.112	-1.325	-1.888	-1.044
0.769	-0.004	0.434	-2.119	1.319	0.041	0.226	0.264
-2.487	-2.887	-1.352	-0.019	2.690	0.507	0.217	-0.223
-0.934	1.400	0.306	1.527	-2.269	-1.054	1.494	-1.166
11.000	-6.277	-0.026	6.746	6.598	-2.483	0.230	4.283
-6.058	-11.000	8.210	-11.000	-0.786	-11.000	11.000	4.972
0.521	11.000	-0.498	11.000	3.852	6.677	5.357	6.097
0.471	-1.419	0.621	1.187	1.611	-0.979	0.469	-0.302
-1.717	-2.101	-1.463	-0.481	2.458	-0.585	-0.546	-1.782
-0.766	1.143	0.477	1.700	-1.975	7.636	-1.115	-0.850
-2.098	-3.671	0.066	-1.023	-1.128	-0.851	-2.118	-2.320
-4.082	-5.840	-11.000	-11.000	11.000	7.397	7.187	11.000
1.438	11.000	-1.352	-1.211	-1.579	0.149	3.083	2.674
-1.558	0.816	-0.383	-0.214	-0.186	-0.421	-0.285	-0.433
-1.004	-0.156	0.595	0.187	-0.241	0.584	-0.691	-1.048
-0.478	0.103	0.246	1.354	-0.934	-0.286	-1.325	-0.992
-2.106	-1.957	-1.748	0.057	0.157	-0.367	0.041	0.084
-3.421	11.000	-1.055	-2.422	0.599	-0.853	0.193	-0.703
-1.530	-1.686	-0.681	1.210	0.263	0.450	-1.482	-1.305
-0.396	-1.141	-0.658	0.217	1.539	-0.381	1.159	1.102
-1.698	-2.037	-1.733	0.656	0.919	0.068	0.124	-0.731
0.093	2.077	0.570	0.923	0.627	-2.199	-1.465	-1.117
-0.863	-1.100	0.181	-0.212	0.155	-0.636	-1.084	-0.078
-3.272	-3.506	-2.620	-1.918	-0.562	-0.601	-0.236	-0.829
-1.520	-1.540	0.505	1.019	2.895	8.079	-0.437	-2.588
-0.783	-0.754	-0.417	0.484	0.640	-0.492	-0.670	-0.255
-2.385	-2.153	-1.313	0.044	0.230	-0.248	-2.301	-0.206
-1.850	-0.928	-0.273	1.145	-1.570	5.500	-1.656	-0.456
11.000	11.000	3.329	11.000	2.859	0.066	0.983	6.187
3.147	-1.487	2.476	-11.000	3.561	-6.450	1.578	5.135
11.000	5.240	1.634	-11.000	-0.944	1.344	2.178	9.068
3.358	7.791	11.000	11.000	-2.050	0.108	2.634	11.000
-11.000	-11.000	3.825	-11.000	11.000	-11.000	-1.618	11.000
-11.000	11.000	-11.000	-11.000	-0.668	9.464	0.471	2.210
2.855	3.892	11.000	11.000	-2.230	-3.310	1.173	11.000
-4.079	-11.000	-3.927	-11.000	8.126	-4.363	-0.030	-4.605
-3.008	6.506	-6.215	-5.549	-0.522	0.267	3.424	2.507
11.000	11.000	11.000	5.346	-3.042	-4.417	-1.562	11.000
-11.000	-11.000	6.933	3.996	6.638	-11.000	-0.591	-0.903

Table35.txt

-0.393	-0.351	-11.000	-11.000	2.400	0.683	7.238	-1.185
7.878	-11.000	11.000	1.953	-5.663	-3.920	-1.637	11.000
-6.880	-6.590	11.000	-3.937	11.000	3.984	2.724	0.906
-11.000	11.000	0.549	-11.000	9.541	4.596	-0.697	3.141
3.879	4.427	1.403	0.342	4.965	1.627	1.345	8.210
2.864	1.486	3.669	-5.783	-3.761	-11.000	4.468	4.055
-3.388	11.000	-3.919	-1.287	2.721	1.027	7.067	-2.997
4.199	0.370	0.594	6.490	-0.123	1.256	-2.105	11.000
0.628	-0.103	11.000	0.365	-4.296	-11.000	1.781	0.549
-5.909	11.000	-11.000	0.589	-0.537	-1.716	-0.521	3.796
2.943	2.332	-2.341	11.000	6.023	-4.263	3.681	4.642
-3.268	6.021	1.504	5.175	-0.491	-11.000	-0.122	2.650
-1.095	11.000	-0.207	1.293	9.716	5.759	0.673	4.090
4.210	-0.229	3.940	1.333	0.090	3.003	3.640	11.000
-3.334	-11.000	5.949	-11.000	4.295	-11.000	11.000	11.000
-3.832	11.000	-2.180	-6.880	-2.209	0.417	2.048	3.561
-0.057	0.639	4.547	1.588	11.000	-0.115	11.000	1.668
11.000	-11.000	5.930	-11.000	-4.081	-11.000	11.000	11.000
-5.459	11.000	1.316	1.502	2.697	5.822	-1.138	7.295
5.043	1.001	3.477	2.395	1.036	-4.722	5.970	11.000
-11.000	-11.000	4.042	6.647	-11.000	-11.000	3.930	-11.000
3.668	5.995	4.733	-11.000	1.055	2.298	0.542	0.596
11.000	11.000	11.000	3.399	11.000	-2.759	-5.930	11.000
-1.143	-11.000	-6.880	-11.000	1.925	-0.958	5.751	11.000
-11.000	5.712	-1.856	-6.036	3.215	5.207	1.600	-1.713
-0.080	-0.494	11.000	2.606	0.132	-3.408	1.195	11.000
11.000	2.517	0.446	11.000	2.775	-11.000	-6.549	3.565
-11.000	11.000	-2.081	-0.366	3.379	3.090	4.757	7.196
11.000	-0.832	5.188	5.477	-5.774	-5.309	2.310	11.000
-1.687	-4.309	3.488	-2.370	11.000	-2.007	-1.244	5.750
7.468	11.000	-11.000	-11.000	1.205	6.211	6.076	4.355
-5.636	11.000	4.753	1.237	-0.662	3.659	-1.446	11.000
4.477	11.000	1.132	3.140	-0.911	-5.972	5.969	1.091
-4.186	11.000	-5.544	-11.000	1.826	5.358	2.047	1.629
11.000	6.510	1.354	-0.294	-0.112	-0.199	4.012	11.000
-11.000	-11.000	11.000	-1.560	0.920	-0.623	-2.261	1.020
-11.000	11.000	-0.188	2.108	-1.228	4.527	1.224	6.823
4.983	2.742	1.847	7.742	1.518	-2.222	-3.422	3.027
-11.000	-11.000	1.248	0.971	5.062	-6.525	2.839	11.000
-5.497	11.000	-5.174	-7.034	1.034	-0.987	3.290	0.638
0.662	0.323	2.305	1.731	0.376	1.240	-2.096	-0.499
-0.898	-3.825	-1.300	-0.170	0.211	-0.730	0.204	-1.123
0.457	-0.506	-1.355	1.457	-1.179	-0.738	-0.413	1.321
0.574	0.285	1.732	-0.290	-0.279	-1.529	0.734	-0.262
-2.153	-2.359	-0.688	-0.340	0.949	-0.156	-1.261	-0.035
-0.127	-1.188	-0.967	1.832	-0.007	6.191	-2.166	-0.203
11.000	11.000	-2.672	-2.042	-3.490	-2.195	-5.187	-5.035
-3.870	-7.034	-4.571	-7.034	11.000	-11.000	-4.415	-5.981

Table35.txt

11.000	11.000	-3.735	-3.351	5.471	11.634	-2.045	-1.332
-1.825	5.514	-5.517	11.000	-3.896	2.169	-0.031	11.000
-0.520	-1.736	-0.089	-6.225	4.109	-11.000	-5.050	11.000
-11.000	11.000	-4.921	-4.606	6.730	4.541	6.461	3.208
2.733	4.817	2.008	11.000	-2.805	-2.551	-4.902	11.000
0.349	-11.000	7.176	-4.558	1.297	-0.077	3.149	0.288
-1.912	11.000	0.696	-11.000	0.320	-1.147	-1.167	0.035
1.309	-0.957	1.921	2.904	0.720	1.881	-1.866	-0.291
-2.426	-4.635	11.000	-0.347	1.228	-1.340	0.327	0.719
-5.785	-0.985	-1.744	2.165	-2.895	-0.792	-2.011	-0.965
8.210	11.000	-6.055	-5.681	-6.880	4.247	7.641	11.000
-11.000	-11.000	-11.000	-11.000	6.912	11.000	6.183	7.613
6.125	11.000	5.506	6.283	-0.872	-0.175	-1.221	0.269
0.118	-2.759	0.213	1.038	0.329	3.282	-3.624	-2.548
-1.622	-3.947	-2.321	-2.787	0.563	-3.640	11.000	11.000
0.026	-1.889	-1.706	0.932	2.855	1.297	-2.242	-1.749
7.956	11.000	11.000	11.000	-0.021	-3.974	-11.000	11.000
0.294	-11.000	7.716	-11.000	3.311	1.832	-5.962	0.974
1.726	11.000	-6.480	-6.229	0.172	2.215	10.900	14.966
6.744	-3.277	-1.121	3.031	-0.552	-3.147	-2.381	7.956
-3.166	-11.000	-2.382	2.250	11.000	-11.000	4.811	11.000
-6.043	11.000	-11.000	-6.668	1.596	-0.764	1.660	5.798
0.201	-0.190	1.022	-0.048	0.684	0.949	-1.359	-0.588
-0.518	-1.564	0.494	-1.096	1.596	-0.048	0.273	-1.815
1.372	-0.444	-3.208	0.859	-2.782	5.263	-2.961	-2.891
-6.937	-11.000	-2.778	-2.801	4.652	-1.637	6.569	11.000
-7.034	-11.000	-11.000	-11.000	7.092	11.000	6.745	11.000
7.159	11.000	-6.205	-5.765	6.579	8.621	-0.524	-1.017
-2.401	-4.520	-0.601	-1.998	-1.834	-0.185	-2.586	-2.385
-3.079	-5.692	-3.781	-3.315	-11.000	-3.253	11.000	11.000
1.798	4.673	-2.190	-1.862	-0.077	2.747	-1.327	-1.312
-1.499	-0.697	0.330	0.035	-0.926	0.696	-0.511	-1.952
0.415	-2.281	-0.600	-1.032	-1.403	-0.326	-0.412	0.450
-0.432	0.530	-1.600	-0.409	-2.098	-2.768	-0.354	-2.538
11.000	11.000	6.390	7.208	-2.321	-2.270	-2.117	-2.633
-6.937	-11.000	2.222	-11.000	6.463	4.209	-5.163	-5.025
-5.158	-0.442	2.181	-4.793	1.095	-0.709	1.251	-1.373
5.196	6.330	2.328	1.368	-0.248	2.769	-0.811	-0.693
-2.677	-4.133	-1.899	-0.368	0.344	-1.568	0.532	-1.357
-0.083	-1.346	-0.689	0.896	0.725	-0.432	-0.142	1.713
11.000	6.305	3.544	7.719	-0.252	4.246	5.527	7.804
5.558	6.774	-11.000	-11.000	2.856	-6.348	5.308	5.497
-11.000	11.000	2.854	5.521	-0.685	7.370	3.159	1.636
6.833	4.393	2.307	5.467	1.722	4.771	3.012	11.000
4.921	-11.000	6.998	-11.000	2.268	-0.953	-4.325	-5.538
-6.508	3.650	-11.000	2.598	-1.578	-2.103	-1.932	10.858
3.782	5.948	2.700	2.035	0.864	-5.660	-11.000	11.000
-3.537	-11.000	2.139	0.632	5.946	-11.000	-11.000	11.000

Table35.txt

-4.151	3.409	1.794	3.041	-2.295	6.227	-0.173	-0.845
6.230	4.320	6.745	1.259	1.058	0.952	-11.000	11.000
-11.000	-5.671	2.136	11.000	8.210	-2.868	1.746	2.315
-1.475	11.000	0.988	-0.072	-0.444	-0.508	-0.509	3.504
11.000	11.000	11.000	11.000	-2.293	-2.495	-11.000	-4.105
3.515	-11.000	11.000	-11.000	11.000	-5.531	-0.344	11.000
-3.065	0.472	-6.089	1.347	-1.315	9.580	0.424	4.580
-2.395	-3.178	5.582	3.679	-1.702	-4.923	6.936	11.000
-11.000	-11.000	11.000	-4.599	11.000	11.000	4.166	4.675
4.266	8.077	-11.000	-11.000	1.068	-1.585	-2.259	-0.231
-1.813	1.283	-1.781	1.826	0.061	5.011	-4.429	11.000
1.959	1.177	6.982	-11.000	11.000	11.000	-2.660	-2.058
-6.554	-1.629	1.052	-11.000	3.825	1.976	-1.491	1.250
2.160	-0.514	2.079	1.594	0.466	3.330	-1.096	-0.725
-1.704	-5.088	-1.722	-0.351	1.498	-0.931	2.255	-1.768
1.296	-0.712	0.111	2.035	-0.296	-0.921	-2.528	-1.796
-0.088	-0.822	-0.546	2.374	-4.374	1.156	2.629	11.000
1.284	-11.000	11.000	-5.039	7.420	-6.758	1.456	2.587
-5.463	3.031	3.389	-0.555	-0.488	-0.867	-0.377	-2.380
3.290	2.677	-0.146	1.681	-2.759	-3.311	-0.186	5.948
-0.305	-11.000	3.403	-11.000	7.729	-3.734	-1.711	4.986
-11.000	11.000	-11.000	0.261	0.000	0.000	0.000	0.000
2.081	11.000	-2.702	2.967	1.610	-3.156	-5.221	11.000
-11.000	-11.000	1.579	1.092	4.399	-11.000	7.276	11.000
-11.000	11.000	3.552	-1.261	0.907	-1.131	1.137	-1.143
6.066	0.800	-7.034	11.000	-0.887	6.381	11.000	7.519
1.814	-11.000	1.442	-11.000	0.135	-11.000	4.318	-2.869
-11.000	3.956	3.266	5.416	-0.461	-1.122	-1.661	-1.201
-0.623	-0.556	0.018	0.202	-0.621	0.536	-0.580	0.014
-0.516	-1.759	-0.554	-1.242	-0.717	0.191	-1.992	1.045
0.730	-0.460	-2.396	0.388	-1.701	-2.848	-1.090	-2.451
-1.394	0.667	1.090	-1.453	1.356	-0.294	1.117	0.257
0.069	-0.709	-1.076	0.359	0.924	0.591	-0.335	0.661
-0.361	0.484	-1.457	-0.861	-0.242	-1.103	-1.813	-2.471
0.286	-1.242	-1.189	-0.111	-0.178	-0.512	-0.340	0.795
-1.681	-0.093	-1.401	-0.128	0.327	-0.060	-1.345	-0.183
4.608	7.600	-0.570	1.089	-0.444	-1.339	-2.703	-0.935
-1.482	-0.824	-0.833	0.183	-0.241	-1.126	-1.004	-0.882
-0.938	-0.932	-0.877	-0.398	-0.874	-0.924	-0.326	-0.363
-1.275	0.496	0.289	1.821	3.167	7.227	-0.981	-0.611
-2.224	-1.975	-0.458	-0.031	0.782	-1.034	-1.099	0.558
-0.744	0.292	-0.663	-1.346	-0.290	-0.941	-2.181	-0.528
-0.847	-0.053	-0.308	1.258	1.174	3.361	-2.853	-0.816
-3.509	-3.365	-1.581	-1.922	0.024	-0.675	-2.226	-1.844
11.000	11.000	-1.262	-2.262	-1.855	-2.042	-2.914	-1.071
11.000	11.000	-0.244	-0.191	0.587	-2.225	-0.458	-1.610
-0.319	-0.121	0.517	0.349	0.956	0.532	4.507	-3.136
-2.812	0.528	-0.813	0.124	-0.700	-0.576	-1.434	0.910

Table35.txt

-0.174	1.069	0.329	2.972	-0.354	-1.704	-1.529	-2.138
-0.730	0.203	-0.312	0.170	0.686	0.494	-0.354	-1.867
-0.451	-1.042	-1.108	-0.751	0.595	0.522	-1.229	0.823
-0.524	1.316	0.584	-0.136	-0.694	0.875	-2.694	-0.315
-0.498	5.345	4.054	1.245	-0.314	0.604	1.646	7.754
-2.225	-11.000	-3.235	-6.210	0.248	-4.022	3.230	-2.055
-5.615	11.000	3.720	-5.657	-1.873	-1.571	-1.440	-2.315
-1.629	-2.607	-0.970	-0.779	0.565	-0.807	-1.552	-1.300
-2.099	-4.734	-1.844	-0.095	-1.873	-1.443	-1.640	-0.754
11.000	11.000	0.092	0.008	-0.682	4.945	-2.367	-2.001
-0.810	-0.012	0.720	0.006	0.866	-0.874	0.089	-0.047
-0.489	-0.361	-1.410	0.808	-0.053	-0.315	-0.274	0.290
0.124	0.008	0.707	0.761	-2.486	-0.743	-0.680	-1.958
-3.251	-0.514	-0.199	0.167	2.093	-0.122	1.657	-0.998
-0.930	-1.740	0.012	-1.394	0.608	0.889	-0.851	-1.065
0.100	1.085	0.784	2.373	-1.275	8.969	-1.389	-0.028
3.643	7.052	-1.607	-1.103	-0.322	-0.487	-0.465	-1.715
-0.986	-2.930	0.940	-1.703	-1.518	-0.885	-0.420	0.134
-0.858	-0.202	-0.414	-0.496	-1.043	-2.401	-2.520	-0.311
4.278	7.139	11.000	11.000	-2.425	0.096	-0.153	11.000
-5.845	-11.000	11.000	-0.915	2.430	-0.330	-0.744	-11.000
-4.051	11.000	-0.769	-0.953	8.300	8.824	-1.454	-2.914
-0.444	0.562	-3.567	-2.205	0.106	-4.458	0.634	1.015
0.925	2.212	3.608	2.826	-2.438	2.081	-1.522	1.175
0.164	2.071	1.696	-1.987	-1.120	-0.342	-0.836	-0.888
-4.079	2.571	-5.268	3.418	0.416	-4.185	-11.000	11.000
-11.000	5.213	5.040	-11.000	6.610	-11.000	-0.481	11.000
-11.000	11.000	-5.943	-11.000	0.506	4.062	3.203	3.104
1.277	-0.774	0.009	-0.445	1.711	-1.288	0.261	0.546
-0.680	-1.250	-0.753	-1.158	1.664	-0.607	0.158	-0.481
-1.418	-0.028	-0.364	-0.640	-1.931	-1.119	-0.199	-1.548
5.520	2.466	3.159	6.631	-1.477	1.539	6.473	7.830
-5.616	-11.000	1.786	4.060	-3.071	4.756	2.979	5.075
2.537	5.078	-11.000	-11.000	-0.576	2.450	-1.297	0.028
-0.750	-3.284	-1.235	11.000	-1.144	-1.159	11.000	11.000
-4.318	-5.222	-2.058	-2.156	-0.460	-3.968	-2.002	-3.723
-11.000	11.000	1.747	1.115	-1.973	-1.339	-1.084	-0.835
0.938	2.797	-1.841	6.322	0.594	0.823	0.562	2.578
-2.729	-3.028	0.290	-0.175	-2.517	-6.315	0.726	-0.296
-11.000	11.000	-3.013	-4.035	-0.993	0.044	-0.101	-4.107
-11.000	-11.000	-0.871	2.656	3.332	-5.110	2.140	6.896
-2.086	11.000	8.041	-11.000	5.782	11.000	-2.066	-2.000
-5.488	11.000	-11.000	-11.000	-1.898	-0.223	-1.416	-1.020
-0.136	-0.132	-2.464	0.069	1.698	-1.899	2.059	0.752
-1.495	-0.220	-0.724	-0.312	1.510	-0.154	1.056	0.058
-1.108	1.326	0.432	1.041	-1.343	-1.665	-1.004	-2.499
-2.807	-2.090	-0.597	-1.932	1.847	-3.551	2.733	11.000
-3.123	-5.055	3.366	0.525	5.020	2.477	-5.289	11.000

Table35.txt

-11.000	11.000	-11.000	-6.937	-1.100	-0.210	1.330	1.073
11.000	11.000	-0.118	5.659	8.077	-6.051	11.000	11.000
-2.289	-11.000	-2.789	-11.000	-1.501	-2.521	6.097	11.000
-0.875	-0.637	-6.937	-5.735	-0.444	1.960	1.070	-0.642
-6.657	-0.004	2.356	3.115	0.949	-2.168	1.690	11.000
-4.304	-5.454	4.106	-11.000	-0.001	11.000	-0.688	-3.997
7.600	11.000	11.000	-6.357	6.547	1.073	8.964	10.774
0.932	0.408	0.543	-0.908	0.585	-0.626	0.221	1.686
-0.641	-0.291	-0.403	-0.004	1.378	1.002	-11.000	-0.451
-1.457	-0.075	1.718	0.016	-0.365	-0.336	-0.599	-0.630
0.055	-0.544	0.101	0.663	0.677	-1.484	0.258	1.780
-0.630	-1.494	-1.042	-0.766	2.474	1.028	0.387	-1.327
-1.357	0.100	0.924	0.492	-3.090	-2.749	0.000	0.000
4.360	4.751	2.980	2.409	-2.761	-3.808	1.215	7.515
-5.186	-11.000	1.918	-6.534	6.896	3.475	11.000	2.233
-4.270	11.000	-3.159	-3.875	0.428	3.243	-0.817	1.370
0.253	-0.408	-1.478	-1.555	1.753	-1.034	0.479	1.096
-0.675	0.689	-0.781	-0.035	1.970	1.480	0.376	0.799
-0.515	1.829	0.688	1.126	-2.897	-2.308	-1.896	-3.032
11.000	11.000	-3.270	-1.993	-1.240	-3.542	1.922	2.044
-1.434	-0.036	-1.745	-0.271	0.122	0.957	-1.422	0.193
-1.976	-0.716	-1.291	0.366	-2.202	9.930	-3.090	-0.193
-1.268	-0.706	-1.059	-0.908	0.247	-2.002	-0.555	-0.498
-0.234	-1.227	2.492	6.831	-0.471	0.374	3.831	5.556
-1.356	-0.308	-0.721	-0.754	-1.773	-0.497	-1.156	-2.062
-0.579	0.851	-2.611	-1.071	1.119	-2.119	1.132	1.547
0.446	1.038	-0.226	-0.318	0.822	2.481	-0.023	1.626
-1.743	0.389	0.533	-0.009	-0.765	-2.106	-3.742	-3.550
-0.222	-0.411	0.707	-0.837	0.556	-0.688	0.200	1.374
-0.636	0.635	-0.783	1.343	2.201	0.086	0.460	0.664
-1.485	-0.562	-0.398	0.118	-0.828	1.287	-2.418	-2.708
-0.782	-0.082	0.386	-1.927	1.443	-1.207	0.455	-0.421
0.164	-0.475	-1.658	1.017	0.535	2.466	-2.025	2.541
-0.579	-1.072	-0.410	1.618	0.000	0.974	0.000	-1.002
-1.917	3.395	1.810	4.377	3.733	-0.082	6.929	3.050
-2.170	11.000	0.785	-11.000	8.210	5.249	2.812	11.000
-11.000	6.685	-11.000	-11.000	0.695	-0.432	0.000	0.377
0.533	1.096	-1.908	-0.350	2.641	-0.727	0.661	0.579
0.026	0.535	-1.380	1.525	1.617	1.301	0.055	0.838
-2.266	0.361	-0.281	2.518	-1.547	-0.973	-0.423	-1.109
5.793	8.126	2.143	1.529	-6.937	-2.897	-3.081	11.000
-5.967	-11.000	11.000	-11.000	11.000	11.000	-2.022	-2.536
-2.087	7.128	-11.000	-2.870	3.708	7.883	0.938	3.930
0.279	-2.107	0.181	0.011	-0.559	0.212	0.386	0.405
-1.022	-2.764	-2.188	0.823	1.046	1.258	-0.190	0.878
-1.849	-0.852	-0.760	1.185	-0.922	-0.934	-1.364	-0.484
-1.205	0.301	-0.986	-0.407	0.885	-1.244	0.512	-0.100
-1.097	-1.088	-1.937	-0.460	2.647	1.055	-0.528	0.350

Table35.txt

-1.917	0.268	0.289	1.842	-1.860	-1.652	-0.480	-1.374
-3.591	11.000	1.084	7.567	-0.664	2.711	-6.559	-0.159
2.980	-4.087	3.044	-11.000	11.000	-2.859	2.565	11.000
-6.937	11.000	0.292	-4.792	4.626	7.536	-0.799	1.506
1.541	1.119	-4.971	4.602	0.798	-2.147	3.860	11.000
-2.495	-11.000	11.000	-2.665	11.000	-11.000	0.334	-0.029
-6.758	11.000	-0.002	2.540	-0.219	0.137	0.000	0.527
11.000	11.000	7.941	11.000	1.448	-5.275	-5.585	-4.965
6.698	11.000	-11.000	-11.000	11.000	11.000	-6.937	-7.034
-6.529	-4.946	-0.600	2.503	-1.186	2.346	5.207	8.371
11.000	4.335	-0.128	2.970	11.000	1.610	-0.939	11.000
-6.937	-11.000	3.637	-3.361	6.645	-2.332	11.000	11.000
-11.000	0.989	-5.310	-5.880	-0.256	1.226	5.228	7.311
1.448	1.299	7.536	6.167	11.000	-4.320	-2.651	5.433
-11.000	-11.000	11.000	11.000	-0.396	3.238	2.440	0.645
-3.428	1.108	0.334	-11.000	5.234	8.894	-2.299	-1.505
-0.636	-1.492	1.128	1.522	-0.796	0.162	-1.325	-0.154
-1.367	-0.016	-1.360	-0.744	-1.674	-0.908	-1.426	-0.589
11.000	11.000	0.322	-0.724	-3.853	-4.531	-2.705	-2.739
4.049	11.000	2.292	11.000	-4.709	-3.507	2.888	-11.000
-6.425	-11.000	1.511	-11.000	11.000	-0.333	11.000	4.323
-11.000	3.063	11.000	11.000	-0.998	1.502	0.750	-0.117
2.577	5.745	3.577	3.555	-0.441	-4.426	0.525	4.289
-0.846	-11.000	7.657	-1.206	-1.236	-1.537	11.000	11.000
-6.439	11.000	-5.764	-6.003	1.400	0.087	0.240	0.882
0.693	3.146	0.839	0.887	1.738	-1.216	2.261	2.081
-0.748	1.334	1.367	1.684	-0.318	1.615	-0.147	0.401
0.023	0.675	0.379	0.497	-0.980	-1.629	-0.342	7.879
-0.173	1.994	0.303	0.124	-0.947	0.480	0.713	0.431
-0.928	-0.496	-3.274	0.276	0.161	0.656	-1.648	0.406
-0.577	-1.152	-1.542	1.697	-0.773	-1.341	-0.804	-0.731
11.000	11.000	-0.959	-1.383	0.047	-1.835	-1.716	-1.812
-1.273	-2.660	-4.065	-2.445	-1.020	-2.460	-2.130	-1.513
-1.439	-1.499	-0.019	-0.819	2.553	2.050	-0.193	-2.695
11.000	11.000	3.240	11.000	-1.015	0.827	-1.976	-2.673
5.482	-5.050	-2.719	-11.000	4.579	5.943	3.728	7.459
-11.000	-11.000	7.390	-11.000	-2.673	8.184	8.212	11.316
-1.563	-0.346	0.053	-0.371	-0.805	-0.973	-0.281	-0.273
-0.120	1.177	0.264	-1.182	0.023	-0.294	-0.485	0.367
-0.968	-1.626	-0.520	0.452	0.816	1.273	-1.636	-3.042
0.953	-0.228	0.331	0.012	1.633	-0.021	-0.619	-0.441
-0.395	-0.300	-1.415	-0.278	1.692	0.323	-0.615	0.357
-1.414	-0.895	-0.321	1.935	-0.948	-0.900	-2.118	-0.495
11.000	0.149	3.378	0.378	-0.240	-0.019	0.670	0.293
-1.923	-2.920	11.000	-11.000	0.758	-0.949	11.000	0.739
11.000	11.000	0.950	-11.000	4.483	5.390	-1.267	-3.239
-0.052	-0.008	-0.042	-1.334	-0.592	-0.954	1.209	1.265
0.665	-0.237	0.411	-0.834	1.625	-0.179	1.269	0.260

Table35.txt

-0.315	-0.955	0.276	0.632	-2.210	1.973	-1.102	0.043
-3.185	-1.167	-1.283	-0.630	-1.401	-0.645	-0.917	-1.238
-1.190	-2.094	-0.317	-1.709	-1.496	-0.842	-0.500	-0.917
-1.209	-1.444	-0.668	-0.775	0.847	1.940	0.706	-1.579
0.030	-0.690	-0.017	-1.249	-0.284	-1.954	-0.711	0.920
1.058	0.114	-0.579	-0.194	-0.302	0.941	-0.373	-0.391
-0.842	-1.273	-0.053	1.017	-1.819	-0.236	0.024	-2.652
-0.992	0.725	-0.808	-1.158	1.103	-0.861	-0.912	2.187
-1.612	-2.218	-2.855	-0.002	0.887	0.451	0.843	2.018
2.894	11.000	0.376	1.772	0.447	-1.695	-2.349	-1.945
0.064	-0.601	-1.817	-1.114	-2.585	-1.826	1.593	0.296
-1.546	-4.228	-2.393	-1.956	-0.800	-1.387	-0.007	-1.148
-4.109	11.000	-2.319	-4.852	-0.790	-1.961	0.022	-0.920
11.000	11.000	3.865	1.897	-5.825	-4.163	-1.306	-1.908
-1.817	-4.969	-3.763	-5.898	0.149	-1.655	4.074	5.865
-2.112	-1.100	-6.525	-11.000	0.000	-1.062	0.000	0.000
5.370	5.698	1.658	1.868	3.249	-4.030	-1.494	5.983
-11.000	-11.000	-3.583	6.081	4.183	6.784	-11.000	2.367
-3.557	7.956	-11.000	-11.000	-0.348	-2.038	7.204	4.341
-1.105	0.198	-0.470	-1.137	1.087	-0.908	0.304	-0.266
1.374	-1.280	-1.930	0.739	0.055	0.105	-2.089	1.423
-0.335	1.851	-0.111	0.151	-2.375	1.066	-0.381	-2.181
-5.097	1.524	3.894	4.668	0.783	-1.348	-0.483	11.000
11.000	-3.247	11.000	-6.637	11.000	11.000	-1.004	2.026
11.000	11.000	-4.644	-11.000	1.037	1.435	4.772	3.192
1.607	-1.087	-0.791	-1.138	-0.325	0.139	-0.439	-1.065
-0.955	-0.721	-2.600	0.159	0.656	-0.452	-1.890	-0.352
-1.734	-0.181	-0.462	1.762	4.655	4.874	-1.071	-1.913
2.328	4.339	-0.607	0.087	-1.331	-2.406	3.000	5.263
-3.597	-6.637	1.053	3.845	-2.381	-4.528	-3.844	-11.000
5.716	11.000	-3.244	-2.730	-0.533	-0.400	-0.592	-1.102
11.000	11.000	-3.186	6.312	2.009	-1.428	-0.489	4.122
3.109	-11.000	11.000	1.383	6.532	-4.629	-3.794	0.486
-3.846	3.607	-5.985	-11.000	-1.233	0.347	0.000	-0.246
11.000	11.000	11.000	6.840	-1.895	-1.904	-2.967	-2.416
-1.789	-5.746	-3.613	-2.420	-1.422	-3.633	-2.694	-2.976
11.000	11.000	-1.507	-2.412	-2.448	0.000	1.425	3.486
2.417	1.736	3.744	3.847	3.385	-5.671	7.651	11.000
-11.000	-11.000	-0.132	-5.541	-0.358	-2.706	2.956	11.000
-11.000	11.000	-11.000	-11.000	0.540	-0.902	3.368	2.821
1.863	-3.629	0.114	1.952	1.319	6.371	-5.877	11.000
-11.000	-0.143	6.038	8.210	2.322	-11.000	-0.435	-11.000
-11.000	11.000	1.266	2.150	2.548	-0.932	3.352	4.623
0.412	-0.386	-0.944	-0.020	0.141	-0.110	1.085	1.480
0.497	-0.307	-0.792	1.512	1.628	0.415	0.094	-0.504
-0.918	1.164	0.294	0.420	-2.737	-1.020	-0.566	-1.143
-1.065	-1.814	1.075	2.004	0.845	-0.075	0.159	-0.775
-2.127	-3.020	-3.176	0.501	1.489	-0.677	-0.705	0.573

Table35.txt

-1.388	0.151	-0.006	2.659	-0.548	0.091	-2.359	-0.098
1.728	0.325	-0.878	-1.216	0.464	-1.053	-0.751	-0.596
0.314	0.935	1.545	0.985	0.025	2.003	0.533	0.011
-0.662	1.784	0.368	1.677	-1.607	0.765	-1.916	-0.669
-0.202	0.926	-1.328	-0.366	0.891	-2.366	-0.770	1.035
-0.500	2.103	-0.047	1.697	0.914	2.449	0.070	1.691
-1.271	0.195	0.176	0.383	-1.369	-2.200	-0.794	0.430
-0.385	-1.041	-0.472	0.915	1.471	-0.500	-0.237	0.486
-2.479	-2.460	-1.261	-0.777	2.439	0.646	-0.814	1.539
-0.777	0.270	-0.033	0.745	-1.775	-0.903	-1.576	-1.684
0.401	0.265	-0.152	0.345	-11.000	-1.647	-0.774	2.237
-0.972	-0.893	-2.059	0.293	1.906	2.250	1.004	0.469
-0.566	1.296	1.623	2.608	-1.133	-1.873	0.518	3.001
0.695	0.649	0.344	1.059	1.260	0.671	-2.393	11.000
-11.000	11.000	0.959	0.838	2.083	-0.257	2.910	-0.619
-0.616	0.755	-11.000	-11.000	0.979	-1.004	-1.546	-3.224
4.588	4.262	-1.609	-1.632	0.092	-0.408	-1.376	-2.436
-3.410	-5.101	-4.702	-2.705	-0.188	-0.574	2.681	5.889
7.071	11.000	-0.489	0.040	-0.553	0.460	-2.143	-1.819
4.288	5.683	2.084	3.108	0.321	-6.139	-0.295	4.181
-11.000	-11.000	4.273	4.515	4.218	4.260	2.841	4.460
-11.000	4.601	2.020	-2.052	0.000	0.000	-0.541	-1.697
11.000	-1.062	-0.885	0.373	-1.277	-3.710	-1.672	-0.700
2.905	-0.038	1.961	-0.275	0.600	-4.313	5.043	3.627
-0.890	0.226	-1.358	0.216	-2.265	18.264	-0.009	-1.522
11.000	-1.533	-1.741	0.656	-2.278	-4.176	-2.096	0.070
1.581	-0.521	2.161	-0.792	0.154	-3.132	4.165	3.602
-0.997	0.209	-0.740	-0.291	-0.637	-0.860	0.066	-2.823
0.570	-0.454	-0.151	0.097	-0.671	-2.038	1.191	0.716
2.751	1.133	1.694	0.426	1.361	-2.447	3.748	4.292
-0.682	0.716	1.227	0.733	-2.466	17.407	-0.357	-4.285
0.408	0.392	0.622	0.666	-0.443	-2.362	0.031	1.114
1.958	-1.068	2.190	-1.280	0.720	-1.405	4.585	4.401
-1.505	0.857	-0.138	0.276	-1.552	0.540	1.327	-1.735
0.966	-6.352	-0.326	1.249	0.295	-2.869	-0.498	1.851
3.461	0.653	2.584	1.096	0.092	-3.007	4.176	4.757
-0.269	1.867	0.340	1.345	-0.764	-2.410	-1.818	-1.424
2.417	-7.034	-11.000	-11.000	-11.000	-1.433	-11.000	2.749
3.662	1.763	-6.739	-4.428	-11.000	-11.000	-0.417	-1.671
1.172	2.413	-4.827	1.353	17.356	13.680	10.425	14.068
1.279	0.445	3.783	1.199	-2.400	0.011	0.876	1.167
2.615	-11.000	-5.678	-2.084	6.534	-11.000	3.232	7.066
0.250	-5.929	0.756	-6.590	-1.589	4.855	11.553	5.713
-2.773	-4.386	-4.396	11.000	4.722	-6.066	-1.327	-11.000
4.928	-3.097	-0.817	11.000	11.000	-0.256	4.598	7.241
-0.487	11.000	4.186	2.530	7.460	9.654	11.494	1.172
-4.052	-4.233	11.000	11.000	-3.708	-2.270	4.623	-6.839
-0.109	0.037	-4.826	-2.562	-3.055	-5.096	3.717	2.669

Table35.txt

1.063	2.529	-4.460	-0.247	7.686	14.092	13.320	11.491
2.015	-0.572	0.686	3.907	4.774	-2.028	1.265	0.347
3.143	0.326	2.772	0.811	1.164	-2.421	3.526	4.414
0.193	0.549	1.148	0.961	-0.104	-0.315	-0.051	-2.111
3.761	1.986	-3.121	1.786	-1.884	-11.000	4.233	4.061
-0.052	-2.315	-3.830	11.000	2.917	2.183	3.556	3.397
2.901	2.890	2.719	0.786	0.989	2.328	-0.555	1.735
3.933	0.871	1.301	3.239	3.243	11.000	0.328	-11.000
-2.205	-4.090	-1.780	-3.318	-2.143	-6.839	5.655	6.197
-3.434	-2.399	2.435	-2.493	-1.271	15.144	14.017	18.084
4.237	-4.870	5.323	1.794	-2.162	-1.698	2.625	3.192
-0.019	0.140	0.768	-0.879	1.692	-5.658	4.767	2.379
-0.048	4.331	1.891	-1.296	0.884	2.129	0.526	-1.129
-3.299	-4.230	-7.034	-0.492	7.133	-11.000	-1.467	-11.000
0.265	0.630	4.944	-5.418	6.462	0.146	3.544	3.033
1.014	4.163	-2.470	-2.382	9.836	10.511	6.704	7.834
1.130	-1.162	11.000	0.737	-2.441	-2.301	0.085	0.058
0.890	-7.034	0.662	0.091	8.210	-3.080	2.531	2.244
-1.498	-0.604	-0.121	0.502	-0.730	11.726	-2.138	-2.042
4.313	1.863	-2.451	11.000	3.603	2.698	-2.907	-3.121
-3.257	-3.774	-2.389	-0.515	5.534	-11.000	-1.031	5.930
11.000	4.559	3.140	-3.229	-0.709	9.407	1.534	-1.535
1.214	-0.152	-0.416	1.874	0.307	0.475	-0.358	1.210
-0.535	-0.622	2.082	0.596	-0.315	-2.105	0.784	1.087
-0.601	0.169	0.845	-0.170	-2.050	-1.055	-0.434	-2.532
1.510	-0.524	-0.095	3.040	-0.379	-1.413	0.126	2.005
-0.425	-2.279	0.538	0.508	0.610	-2.106	-0.393	1.061
-0.768	1.076	1.297	0.511	-0.502	4.581	-0.561	-1.738
11.000	-0.942	-0.811	0.520	-1.742	-2.272	-0.157	-0.458
-1.393	-1.085	1.738	0.852	0.502	-4.425	2.615	2.021
-1.420	-1.330	-1.458	-1.029	-2.538	5.294	-1.489	-2.347
1.561	-4.249	-1.892	0.864	-0.686	-2.141	-0.649	0.484
0.932	-0.796	2.344	1.083	0.643	-3.133	1.066	2.150
-0.320	-1.269	0.082	0.053	-2.154	10.799	0.029	-2.745
-4.768	0.621	0.584	7.956	-0.641	-6.464	5.951	-2.610
-3.433	-7.034	3.428	-3.869	0.927	-11.000	0.516	2.993
-3.329	6.383	1.716	5.521	11.329	15.490	10.851	9.733
2.365	-11.000	-11.000	1.878	0.384	-0.260	1.390	1.370
0.382	-0.861	0.730	0.806	1.626	-0.529	1.140	1.804
-0.556	-0.203	2.050	-0.096	14.466	13.404	0.138	-2.326
4.527	4.536	1.149	-0.052	-0.538	-0.485	-1.731	0.897
-0.002	1.839	-4.360	-2.483	2.558	-1.301	2.618	4.261
-0.513	2.097	1.174	-3.446	3.597	4.677	-0.226	7.477
4.388	-1.486	-0.841	1.892	-0.520	-11.000	-1.175	-11.000
-2.014	-6.679	3.093	3.173	11.000	-11.000	11.000	4.530
11.000	-1.192	3.196	-0.987	-2.938	-1.439	0.115	-1.622
4.520	-0.263	-2.355	-1.441	-2.660	-2.370	-0.863	-1.453
-0.708	-1.190	1.606	-1.273	-1.187	-4.815	2.120	1.877

Table35.txt

-1.216	-2.085	-0.930	-1.237	-1.233	7.636	-0.511	-0.486
1.141	0.070	-1.510	2.474	-0.370	-1.528	0.297	0.573
0.303	-0.406	1.326	0.330	1.197	-2.111	2.520	2.215
-0.768	-0.298	0.715	-1.526	-1.273	-0.236	2.230	-0.739
-2.991	-11.000	-11.000	4.081	-4.429	7.386	0.805	-11.000
-6.470	-11.000	7.524	3.042	2.976	4.245	2.200	4.249
1.163	-1.231	-2.087	-3.833	-0.156	12.416	16.948	21.847
-4.496	-11.000	-11.000	-0.001	-4.513	6.041	7.130	-6.058
0.276	-11.000	11.000	4.751	5.108	11.000	1.981	3.505
3.797	0.408	-2.792	-2.868	2.434	13.837	-0.354	19.261
4.755	2.390	-6.309	3.856	2.478	-11.000	-11.000	11.000
0.950	-6.657	-4.360	2.617	2.312	0.638	4.239	3.588
1.385	4.721	2.671	-5.439	-1.291	-1.559	-2.226	-1.765
2.414	4.259	0.880	8.126	1.618	-11.000	3.222	11.000
0.062	3.153	-4.055	-11.000	2.707	2.925	0.947	2.735
-1.691	4.417	2.212	1.528	7.857	3.640	-3.324	-2.153
11.000	-0.798	-0.024	-0.459	-1.474	-0.753	0.092	0.761
-0.013	-1.105	1.053	-0.711	0.206	-3.194	2.691	1.257
-1.444	-0.411	0.748	-0.731	-1.272	0.328	0.714	-0.074
-0.408	-0.036	1.158	-0.559	-0.332	-0.403	-1.147	1.858
-1.966	-1.367	-2.419	-0.685	2.081	0.730	0.747	1.491
-1.227	0.635	0.707	2.087	-1.330	-2.665	-0.530	-0.868
-2.393	-0.552	3.139	4.969	-1.293	-2.679	-11.000	-5.585
0.187	-6.020	-2.408	-3.889	-0.426	-2.672	-0.132	0.468
0.946	11.000	-3.116	-3.468	3.345	10.618	0.849	10.498
-3.124	-0.791	3.698	4.525	-2.243	-1.986	-11.000	-6.253
-0.868	-6.326	-3.593	-5.120	-0.615	-1.960	0.296	0.416
0.251	11.000	-4.001	-4.070	1.527	6.999	2.506	4.946
0.805	-0.666	1.034	1.587	-0.471	-1.540	0.866	1.322
1.937	0.651	3.206	0.948	0.684	-3.236	5.075	5.499
-0.192	1.139	0.693	0.454	-1.298	-0.816	0.029	-0.334
-0.567	0.680	1.026	2.025	0.419	0.630	-0.424	-2.961
-3.116	-1.293	-0.811	-3.307	-0.773	-1.592	-0.663	-1.018
-2.054	-1.234	-0.186	-2.815	-1.178	-2.444	-0.163	-0.847
0.632	-1.226	-0.058	0.313	-2.234	-3.744	0.743	0.796
-0.525	-2.743	0.099	0.121	0.320	-4.107	2.501	1.081
-1.432	-1.215	-0.423	0.071	-0.102	-1.240	4.389	6.009
11.000	-2.779	-1.309	1.268	-0.852	-1.120	-0.364	-0.311
-0.965	-1.635	1.523	-0.960	0.231	-3.355	0.527	0.359
1.188	0.558	0.741	-1.238	-1.462	-0.577	-0.444	-0.562
1.100	-1.472	-0.204	2.431	-0.031	-1.573	0.691	2.517
0.276	-11.000	2.225	1.350	0.949	-3.433	2.617	2.666
0.770	-0.582	0.536	1.014	-0.194	-1.543	0.616	-2.712
1.255	-0.750	0.487	1.954	0.172	-1.050	0.560	1.700
-1.622	-5.545	1.335	0.333	0.659	-1.967	0.986	1.590
-0.299	-1.040	0.994	0.457	-1.139	0.355	-0.994	0.578
1.365	-0.110	-0.527	0.829	0.158	-2.715	-0.264	0.109
1.079	-0.309	2.737	0.247	0.070	-4.505	2.955	3.740

Table35.txt

-0.184	0.015	-0.094	0.883	-0.292	-1.825	3.818	4.313
11.000	11.000	-3.495	11.000	-5.878	-1.666	-2.576	4.645
-11.000	-11.000	0.015	-11.000	3.723	11.000	6.035	11.000
-11.000	11.000	-6.937	-11.000	2.033	8.401	6.792	12.664
3.742	2.194	1.395	7.110	1.077	-2.059	-0.447	1.417
-5.046	-11.000	2.273	1.583	1.993	2.369	-7.034	2.283
-11.000	11.000	-11.000	-3.831	-1.808	8.964	-2.093	2.205
-2.702	-2.348	-0.858	-1.505	-0.536	0.040	-1.899	-2.066
-2.785	-3.674	-2.959	-2.091	0.567	-2.097	11.000	11.000
-1.976	-1.005	-1.277	0.991	4.116	11.922	-0.911	-0.463
-2.787	-0.472	-0.521	0.161	-0.334	1.750	-1.051	-1.452
-2.701	-3.815	-3.697	-1.639	-0.694	-1.410	11.000	11.000
-3.529	-0.758	-1.299	0.771	3.984	10.721	-2.514	-0.430
-1.574	0.083	-2.374	-0.969	0.069	-1.274	0.417	1.213
-0.656	-0.308	-1.318	0.696	0.911	1.444	-0.569	-0.430
4.672	11.000	-6.414	1.047	-3.058	-1.356	-0.827	-0.730
-3.459	-3.080	0.509	-0.784	-0.503	0.322	-2.481	-3.144
-4.313	-4.296	3.627	11.000	-0.302	-1.757	11.000	11.000
-2.560	-2.960	-1.073	0.657	0.345	0.403	-0.710	-0.142
-1.235	-2.133	-0.516	0.334	1.254	-11.000	-0.869	-0.472
-3.535	-4.263	-2.676	-0.152	0.654	-0.400	-0.724	-0.936
0.127	4.799	-0.227	1.213	0.254	6.503	-2.150	-2.417
0.302	-1.312	-0.505	0.294	0.604	-11.000	0.138	11.000
-2.153	-3.569	-2.916	-0.413	1.249	-0.128	-1.627	0.200
-1.603	1.710	-0.500	1.445	-1.370	3.122	-0.228	-1.154
-0.255	-0.190	-1.157	-0.117	1.035	-0.870	-0.089	1.389
-2.157	-1.906	-2.800	0.879	2.344	-0.313	0.151	0.950
-0.833	-0.189	0.731	1.398	-1.250	-2.724	-0.979	-1.885
-0.914	-1.818	-1.582	-1.089	1.277	-1.420	-0.035	-0.322
-3.116	-2.781	-2.435	-0.588	1.310	0.179	11.000	11.000
-1.919	-2.005	-0.647	1.359	-0.828	-1.766	-0.819	-2.222
-1.835	-1.295	0.125	-4.099	-11.000	1.783	-1.456	-3.344
-3.796	-1.117	-3.717	-0.775	3.184	3.961	1.988	11.000
-0.387	0.967	11.000	7.490	3.443	-1.146	3.203	13.351
-11.000	-0.794	-1.310	3.985	0.851	-6.739	1.619	0.711
-2.511	-2.204	-3.277	-0.689	-0.402	-1.800	0.361	-0.687
-1.282	-0.185	5.018	-0.950	0.248	-0.241	1.073	-0.021
-11.000	-11.000	-11.000	2.888	3.040	-7.034	4.012	2.387
-1.840	-1.891	-0.764	-0.259	1.120	2.002	0.710	-0.665
-0.231	0.162	2.723	-1.939	2.336	0.243	13.286	0.221
-11.000	-11.000	-0.492	0.494	-11.000	1.060	3.131	6.213
1.365	4.381	-3.829	-1.255	1.395	0.701	2.504	4.432
0.250	3.029	2.265	3.355	0.368	-0.793	-2.218	-1.412
-0.836	1.792	0.907	2.694	0.764	-1.146	1.978	1.419
-5.205	-11.000	-0.790	0.245	-0.627	-3.770	-1.562	-2.990
-1.324	-1.551	-1.243	-2.101	-1.856	-0.931	-1.357	0.026
-1.248	0.081	0.912	-1.294	0.326	1.190	-0.905	-0.852
-1.626	-1.011	-2.553	-0.326	1.446	1.347	-1.201	0.175

Table35.txt

-0.027	-0.791	-0.153	2.896	-0.173	6.517	-0.740	-2.114
11.000	-3.153	-3.372	1.339	-2.031	-0.499	-1.234	-0.718
-2.215	-3.746	0.843	5.564	-0.371	-3.334	-0.536	-0.393
-1.197	-1.474	-1.439	-1.342	-0.666	13.836	10.258	16.579
0.663	-1.099	-0.224	3.315	-1.522	-0.272	2.412	-0.582
-1.404	-11.000	-0.747	-0.947	0.527	-4.161	1.983	0.694
-2.650	-1.644	-0.616	-0.709	-0.476	2.255	-1.325	-2.001
0.515	1.813	0.184	-0.633	-4.956	4.682	-11.000	4.335
0.242	1.579	0.461	2.984	-2.709	2.519	0.328	1.269
-11.000	1.536	11.000	0.444	-2.413	1.035	-2.032	-1.411
-0.833	0.269	-1.228	-2.313	1.344	-2.264	0.564	1.522
-1.721	-0.905	-2.095	-0.040	1.430	2.644	-0.448	1.053
-1.901	-1.601	0.929	1.976	-0.386	-1.726	-1.444	-0.466
-0.033	0.502	0.651	2.405	-0.942	0.662	1.408	0.375
-2.776	-3.447	-0.187	-1.681	-1.038	-2.360	1.244	-0.763
-2.296	-1.488	-0.308	-1.935	-1.097	15.980	-2.079	-3.666
4.061	0.131	5.116	7.709	-0.409	-1.465	7.145	11.000
-4.530	-11.000	11.000	-11.000	-1.586	-4.682	-3.996	6.200
-2.628	11.000	0.133	6.839	8.710	6.735	1.017	4.445
11.000	-1.256	-0.239	0.390	-1.898	-1.956	0.230	0.267
-0.200	-2.807	0.190	-0.872	-0.702	-2.931	1.311	-0.007
-2.680	-1.067	-0.120	-1.913	-1.281	2.709	0.028	-0.735
2.691	-0.324	-0.025	1.104	-0.736	-2.190	1.068	4.169
2.286	0.722	3.971	2.738	-0.428	-3.779	3.757	5.417
1.171	0.744	0.254	3.261	-3.498	-2.674	-0.324	-2.502
11.000	-1.355	-0.846	-0.780	0.275	-2.705	1.497	0.292
0.634	0.026	2.526	0.218	-0.311	-4.006	1.884	2.723
-0.187	-1.087	0.504	0.711	0.987	-1.890	-0.167	-1.128
11.000	-2.840	-0.225	0.370	-1.002	-2.264	1.463	0.952
-0.823	-0.471	2.126	0.330	-0.246	-4.068	1.132	1.241
0.715	-0.156	-0.337	-0.147	-4.451	-0.642	-0.532	-2.827
-3.555	11.000	11.000	-2.416	-4.849	-6.780	-4.654	-3.215
7.455	5.868	-0.485	-1.807	-1.705	-6.032	0.253	0.190
-2.584	-2.455	-2.979	-0.824	6.462	6.308	6.593	8.942
0.928	-0.980	0.269	1.026	-0.366	-1.222	1.698	2.027
-0.391	-0.866	1.951	0.123	1.110	-4.049	1.430	1.837
0.170	-1.227	-0.539	-0.185	-2.111	12.376	-1.680	-2.806
1.989	-0.144	-0.184	0.795	-1.153	-3.109	0.809	2.741
1.873	-0.979	3.055	2.394	-0.548	-4.281	1.735	3.767
-1.199	0.141	1.455	1.075	-2.300	-1.175	-1.455	-5.307
2.177	-1.033	-2.029	1.491	-0.785	-2.283	0.058	1.318
2.215	0.243	4.621	1.580	-0.470	-2.990	2.407	2.991
-0.449	0.157	1.509	1.168	0.072	17.251	0.707	-1.178
-11.000	-2.422	-1.640	-6.434	-11.000	1.139	11.000	-11.000
4.196	-1.897	-5.900	4.612	3.234	-4.317	4.105	5.157
2.887	3.807	-1.454	-5.338	15.908	19.843	-0.604	2.920
11.000	-0.619	-0.198	0.719	-0.674	-2.860	0.347	1.485
0.981	-1.007	1.501	-1.726	-0.052	-3.652	4.287	2.676

Table35.txt

-1.159	0.581	-0.294	-0.079	-2.801	-1.120	-0.238	-2.170
-11.000	0.206	0.672	0.534	-0.137	-0.318	1.002	-0.103
0.554	0.402	1.174	0.068	0.441	-1.729	3.332	2.495
0.340	1.072	0.245	0.483	15.861	13.903	-0.835	0.311
11.000	-11.000	11.000	6.698	11.000	-11.000	0.057	-11.000
7.928	0.106	-3.177	8.126	-4.145	-11.000	-1.393	-3.373
-0.650	-0.013	-6.308	-4.174	17.343	-0.680	-0.588	-2.019
11.000	-5.468	-0.548	0.800	-0.296	-11.000	-3.107	-4.805
2.671	-1.830	-0.517	0.830	-2.034	-11.000	1.541	-0.338
-2.195	-0.730	-3.699	-2.445	12.739	22.228	16.001	23.387
11.000	-2.713	-2.400	0.937	-1.500	-2.799	-1.642	-1.000
-0.018	-1.297	2.005	-0.199	0.118	-4.260	1.369	1.947
-0.599	-1.024	0.183	-0.871	-0.777	18.504	-0.319	-1.179
-0.937	-11.000	-11.000	5.797	3.232	4.452	0.630	-2.214
3.002	1.309	11.000	1.762	2.761	-11.000	-0.916	5.025
3.340	2.964	3.459	-1.578	-1.237	0.199	1.517	-1.527
0.978	-2.132	-1.114	1.960	-1.085	-1.623	0.128	0.906
0.533	-0.514	0.414	0.380	0.573	-3.141	1.465	1.383
0.265	-0.694	0.584	-0.687	-2.381	14.246	-1.526	-1.638
0.621	-0.623	-0.440	1.162	-0.743	-1.502	0.416	1.339
1.939	-0.406	2.235	-0.034	0.094	-3.247	4.696	3.104
-0.480	0.900	-0.618	1.046	-1.602	-1.951	0.172	-1.686
1.711	11.000	-0.493	-1.179	1.141	-0.315	-2.941	4.885
-11.000	1.219	-0.277	-3.825	7.587	-0.224	-1.474	2.551
-0.328	6.604	-11.000	-11.000	-0.858	-1.118	1.012	2.766
-0.694	-1.098	-1.231	0.448	0.807	0.974	0.117	1.191
-1.677	-2.834	-2.834	0.719	2.881	1.680	0.441	-0.321
-0.042	1.896	1.022	1.622	0.862	-1.296	-1.255	-0.155
0.521	-3.520	-1.889	-1.003	0.563	-0.353	0.419	-1.490
-1.909	-2.584	-2.101	-2.170	0.592	-0.163	-0.622	-0.938
6.414	11.000	-1.611	0.164	0.000	-2.338	0.050	-0.841
3.258	3.005	11.000	7.473	2.057	-2.079	-1.013	11.000
-5.210	1.763	0.613	-7.034	11.000	-0.836	3.792	0.472
-5.899	0.805	-4.955	-5.280	0.000	0.000	0.000	0.000
-0.331	-2.381	-0.538	0.941	0.640	-0.097	-0.463	0.688
-0.568	-1.587	-1.730	-1.345	2.779	-0.004	-0.330	-1.030
-1.825	-1.739	-1.355	1.379	0.000	0.000	0.000	0.000
-2.851	0.867	5.083	0.960	3.373	-1.140	11.000	11.000
2.449	3.057	0.758	-2.336	11.000	4.809	11.000	-4.535
-11.000	11.000	-11.000	-11.000	1.053	7.324	2.946	6.837

-0.929	-0.365	-0.059	-1.771	-0.194	-0.102	0.022	-0.164
-1.921	-1.942	-3.807	-0.823	1.958	1.677	-1.287	0.404
-1.267	-1.246	-0.185	0.785	0.083	0.000	-2.022	-2.504
-1.334	-0.992	1.263	-1.442	1.121	-0.208	-0.215	-0.158
-1.809	0.061	-2.313	0.602	1.928	1.927	0.000	0.496
-3.741	-0.095	0.488	2.678	-0.783	-2.827	-2.133	-1.056
4.841	-6.260	3.600	3.576	-3.236	-2.183	-0.708	11.000

Table35.txt

-5.733	-11.000	-4.484	-11.000	1.825	-2.439	11.000	11.000
-11.000	11.000	2.169	-4.309	4.610	4.918	5.534	10.915
-1.114	0.457	-0.856	-0.561	-0.228	-0.268	0.471	-0.006
-3.258	-0.139	-1.543	1.147	1.884	0.854	-1.628	0.761
-1.590	-0.148	0.216	1.517	-0.951	-3.275	0.503	-2.468
5.502	3.087	3.679	11.000	-2.922	1.299	5.479	6.413
-1.201	-0.045	-4.661	-3.171	1.631	7.323	-11.000	-11.000
2.254	11.000	-11.000	-11.000	1.932	3.470	4.744	-0.256
-2.050	-0.914	0.259	-0.199	-0.416	-0.454	0.942	0.957
-1.773	0.179	-2.576	0.504	1.235	1.098	-0.187	1.025
-0.806	0.201	0.345	1.900	0.019	-0.918	-0.271	-4.899
11.000	11.000	-2.986	-4.361	-3.229	-3.170	11.000	11.000
-6.637	-11.000	-5.660	-5.606	11.000	11.000	8.077	11.000
-5.551	-6.470	-3.831	-3.546	-1.115	2.194	-2.606	-0.288
-0.878	11.000	4.218	11.000	0.671	2.600	-11.000	-11.000
4.225	-6.286	0.586	3.221	-0.732	0.824	-3.654	-11.000
-1.598	11.000	-11.000	-6.807	-1.009	4.243	-2.032	-0.980
-2.080	0.267	-0.915	-1.054	0.355	-0.595	0.739	0.911
-3.046	0.067	-2.222	1.498	0.749	3.050	-0.336	-0.031
-2.481	0.202	-0.902	-0.176	-2.522	8.426	-0.758	-1.178
-0.840	0.843	-1.339	-0.922	0.052	-0.276	1.028	-0.466
-1.055	-1.050	-1.800	0.796	1.583	2.281	-0.960	0.275
-1.225	1.039	0.164	2.675	-0.579	-2.172	-1.947	-0.527
-3.236	-2.559	-0.703	-0.904	-1.319	0.299	-2.035	-0.329
-2.902	-2.190	-3.800	-1.567	0.557	-1.305	11.000	11.000
-1.928	-1.870	-1.165	0.374	0.163	-1.793	-1.102	-0.726
6.947	7.848	3.280	3.126	-0.034	-4.052	-11.000	-7.034
-1.502	-1.620	1.138	5.687	5.419	-11.000	2.655	4.146
11.000	11.000	-1.248	-6.571	9.916	9.998	3.521	-0.823
-1.072	0.692	0.155	-0.874	0.491	1.066	-0.816	0.409
-2.193	-0.392	-2.226	0.563	2.358	1.816	-0.616	1.414
-0.978	0.154	-0.284	1.549	-2.454	-0.909	-1.646	-2.196
-1.296	0.692	-2.117	-2.249	-0.242	-2.458	-0.773	1.038
-0.283	2.663	-1.246	0.873	1.090	3.610	-1.913	-0.513
-3.847	-0.428	0.061	1.670	-0.634	-0.576	-1.917	-1.302
5.083	6.113	11.000	4.605	-11.000	-0.041	0.175	11.000
-11.000	-11.000	6.171	-11.000	7.737	0.598	-0.682	-3.893
-1.665	11.000	-11.000	-11.000	-0.896	1.909	4.400	2.915
-0.323	0.301	-1.048	-1.130	1.904	-2.343	0.366	-0.295
-0.371	1.355	-0.189	0.434	1.389	2.048	-0.300	0.469
-3.229	1.173	0.616	0.610	-1.740	-2.335	-1.644	0.046
0.402	-0.434	-0.513	-2.376	1.134	-1.372	0.289	-0.211
-1.491	-0.361	-1.140	1.069	-0.109	1.056	-0.905	1.510
-1.703	0.481	-0.008	1.132	-0.182	0.820	-0.771	-1.750
7.941	-1.183	3.786	2.545	1.039	-1.790	-11.000	11.000
-4.935	-11.000	-3.965	-6.126	1.430	-0.672	-3.422	1.117
-11.000	11.000	-11.000	-11.000	4.847	-0.247	-0.345	8.577
1.830	-11.000	2.927	3.862	2.163	-2.717	-5.389	11.000

Table35.txt

-11.000	-11.000	11.000	-3.093	11.000	-6.937	1.868	3.534
-4.282	7.009	-4.667	-11.000	6.314	6.123	6.465	4.889
2.362	4.030	0.106	1.584	-5.306	-0.582	1.479	11.000
-0.042	0.278	3.240	-11.000	5.122	-4.306	-2.460	3.269
-2.575	7.614	-5.783	1.848	-1.139	2.424	0.281	0.612
-3.369	7.332	11.000	11.000	0.760	-4.265	-2.780	-3.485
5.021	-11.000	-4.691	-11.000	11.000	11.000	11.000	11.000
-4.840	1.937	-0.362	-4.787	0.566	-1.446	6.622	11.255
-0.681	1.628	0.269	11.000	0.614	-0.750	1.375	11.000
-1.903	-0.717	-1.561	-1.487	0.978	1.290	-11.000	-11.000
-0.251	1.227	-0.032	2.025	-3.838	-1.056	3.963	-2.442
-2.017	-0.547	-0.048	-1.219	-0.151	-0.071	-0.283	0.105
-2.509	-3.225	-3.549	-1.177	0.499	0.489	-1.506	-0.246
-1.311	11.000	-0.174	1.904	-0.683	-0.560	-1.490	-3.925
-0.490	1.268	2.620	2.762	1.798	-3.720	2.459	11.000
-11.000	-11.000	4.043	11.000	-0.649	-11.000	-1.468	-1.263
3.911	11.000	-1.090	-0.651	-1.322	-0.477	-0.661	-1.060
-0.984	0.627	-0.817	-0.306	-11.000	-1.605	0.181	1.611
-1.605	0.721	-1.241	1.287	0.891	1.140	-0.693	0.100
-0.048	0.665	0.490	0.415	-0.264	-0.284	-2.821	0.086
0.072	-0.564	0.024	-0.365	1.216	-5.589	0.529	0.239
-1.458	-0.879	-1.811	-0.229	0.544	0.744	-0.042	-0.464
11.000	11.000	0.329	1.075	-1.962	-1.161	-1.236	-1.208
11.000	-11.000	-0.505	1.902	-5.669	-4.298	-11.000	11.000
-3.440	-2.569	7.251	-11.000	3.470	-3.999	0.398	11.000
-0.197	7.135	-11.000	-2.523	2.572	-0.556	9.653	11.593
-0.950	1.739	-1.037	0.989	0.570	-0.292	-0.627	0.658
-2.664	-0.905	-2.805	-0.572	1.079	1.909	-0.669	0.592
-0.700	0.181	0.067	3.366	-1.830	4.341	6.847	-1.056
0.895	0.817	1.047	2.068	-1.794	-2.163	0.345	0.133
-6.512	-11.000	-5.344	-6.432	0.493	-3.424	11.000	7.685
11.000	11.000	-3.296	-2.963	-0.458	-1.340	-0.929	0.181
3.924	5.390	1.512	11.000	2.573	-4.770	4.286	4.265
1.425	-11.000	2.316	5.021	-4.282	-11.000	-6.839	0.845
2.052	11.000	2.041	4.281	-1.174	1.067	2.082	1.601
-3.230	-2.053	-0.658	-0.405	-0.567	-1.940	0.916	1.673
-1.547	-2.709	-2.877	-2.244	-0.290	-0.816	0.379	1.739
-1.765	-1.650	-0.892	-0.133	2.697	-1.152	-1.659	-1.989
0.501	1.585	2.166	1.467	-1.985	-3.030	0.078	11.000
-11.000	-11.000	11.000	-11.000	7.516	-0.873	-11.000	11.000
-3.912	4.955	-3.170	3.348	7.923	4.793	-0.113	13.772
-1.633	-2.844	1.303	1.653	0.125	2.332	-2.342	-2.201
-2.990	-6.577	-2.407	-1.530	0.351	-2.861	-0.385	-1.079
11.000	11.000	-2.440	-0.257	0.879	-0.628	-1.746	0.279
-1.073	0.167	-0.335	-0.642	-0.179	0.280	-0.095	0.960
-1.000	-0.002	-1.318	-0.769	2.375	1.395	0.284	2.532
-1.352	-0.116	-1.198	2.308	-1.097	-1.034	-0.651	-2.042
-1.917	-2.348	-0.182	0.315	-0.484	-1.046	-1.731	-1.061

Table35.txt

-2.098	-3.351	-2.592	-0.993	0.306	-0.815	11.000	11.000
-1.183	-1.245	0.218	1.209	-1.322	-0.402	-3.253	-1.268
-0.469	-0.053	0.331	-0.600	0.389	-0.055	-0.529	0.820
-1.134	-1.582	-2.913	0.661	0.822	-0.325	-0.784	0.173
-1.206	0.675	0.872	1.631	0.822	11.854	-1.718	-2.136
-0.957	-11.000	0.594	1.390	2.242	-3.285	-1.370	11.000
11.000	-11.000	1.336	-1.555	-1.055	1.679	1.779	1.014
-2.723	11.000	-2.027	-11.000	6.998	-0.868	-0.554	-1.242
0.187	1.763	1.672	3.221	-1.956	0.450	-2.615	-0.404
-11.000	-11.000	5.438	-2.955	4.009	-4.463	3.323	5.423
-11.000	11.000	11.000	2.714	-0.287	4.559	-1.260	1.422
0.279	1.044	2.289	-0.715	0.287	-5.078	0.721	0.879
-1.436	-0.996	-2.682	1.235	1.498	0.453	-0.137	0.099
-1.301	-1.456	-0.876	3.096	-0.555	-1.213	-1.002	-2.464
2.855	4.008	3.238	3.298	2.295	-3.452	11.000	3.515
8.126	-11.000	1.627	3.129	3.183	-6.839	-5.041	11.000
-4.181	7.140	-6.937	4.552	1.149	0.000	0.226	0.267
0.858	1.294	0.610	0.182	0.933	0.745	-2.133	0.034
-11.000	-11.000	0.540	1.420	11.000	0.281	0.670	0.958
-11.000	11.000	0.189	1.966	3.963	6.946	0.135	-0.544
11.000	11.000	11.000	11.000	-11.000	-2.592	0.088	7.151
-0.990	-6.880	4.836	-11.000	-1.876	-11.000	-6.056	-5.255
3.753	5.044	2.160	2.334	1.825	0.263	-0.627	-0.483
0.715	1.233	0.633	11.000	1.774	0.541	2.054	-0.646
-0.957	1.543	-2.221	-1.173	1.391	2.032	-4.533	-1.544
-2.005	1.841	1.068	2.571	4.155	-1.908	-1.252	-1.934
-0.146	11.000	6.966	6.105	0.457	0.814	-1.647	11.000
-2.815	-11.000	5.741	-5.047	5.109	-0.705	-6.188	-5.064
-11.000	11.000	11.000	11.000	-0.066	7.679	0.000	4.291
-4.224	2.052	-2.107	2.636	-1.505	1.506	-1.437	11.000
-0.990	-0.233	11.000	-6.706	6.728	-1.848	2.480	3.806
-2.901	11.000	-2.907	6.610	1.207	4.578	1.064	1.201
1.209	3.218	0.850	1.228	1.846	-0.005	1.700	11.000
1.475	-6.807	0.478	-6.399	1.817	-11.000	1.078	11.000
-2.532	11.000	1.242	2.384	1.517	5.592	0.052	-2.244
-1.715	-0.808	1.002	0.419	1.192	1.061	-0.458	0.056
-3.512	-2.688	-2.425	-0.855	1.647	-1.016	-0.051	0.219
-0.059	11.000	-0.607	-11.000	-0.764	0.560	-1.069	-3.330
-0.238	-0.470	4.923	11.000	0.829	1.105	-0.220	-0.542
-2.146	-1.523	-2.658	-0.662	0.531	-1.405	-0.581	-0.385
-11.000	11.000	-1.412	2.583	-1.318	-1.606	-0.583	-0.035
-1.385	-0.515	0.875	1.132	0.326	-11.000	0.164	0.337
-3.033	-3.142	-2.408	0.099	1.591	0.436	0.259	1.496
-0.291	-0.718	0.531	2.196	-2.645	-2.554	-1.212	2.199
-2.305	0.015	-2.855	-3.421	0.846	-3.665	-0.634	-0.544
-1.039	1.400	-1.112	-1.058	-0.507	2.261	6.967	11.000
-3.716	0.125	0.481	-0.216	0.319	5.044	-2.483	0.833
-0.594	0.457	-3.049	-1.303	-0.222	-4.075	1.030	1.748

Table35.txt

0.327	2.410	-1.286	1.548	1.792	4.055	-0.870	-0.169
-2.659	1.534	0.061	2.837	-0.115	4.271	-1.958	-1.752
-1.438	2.010	-2.896	-2.484	-0.410	-3.117	1.195	2.296
0.599	4.614	0.738	0.853	0.679	4.435	-2.170	-1.313
-1.721	1.529	0.266	0.069	-0.516	9.883	-1.946	9.009
-1.562	0.793	-1.907	-2.775	0.764	-2.081	0.589	1.623
-0.225	1.527	-1.130	2.341	1.385	3.735	-0.709	0.328
-1.380	1.120	-0.690	1.760	-1.417	-1.512	-1.945	-2.157
11.000	11.000	-2.761	-2.918	-0.606	-4.179	-3.029	-1.816
-1.695	-2.391	-1.754	-3.022	0.050	0.134	-2.601	-2.873
11.000	11.000	-2.046	-1.080	0.317	5.834	-0.995	-1.813
-1.798	1.682	-2.549	-2.961	2.457	-2.435	0.563	2.272
-1.237	2.118	-0.484	2.720	0.181	2.635	-0.302	0.000
-1.116	2.702	0.637	2.495	0.433	11.098	0.506	0.367
1.905	4.201	-2.827	-3.208	0.572	-3.664	-0.192	-0.316
-2.184	2.051	-1.165	1.090	-0.567	1.212	-0.448	-1.363
-2.377	-1.122	0.640	-1.301	7.037	6.875	-1.684	-1.602
-0.578	0.760	-0.950	-1.080	0.764	-3.796	1.087	0.593
1.051	2.448	-0.192	1.949	1.384	3.551	-0.861	0.000
-2.482	1.948	0.150	1.363	-0.629	0.813	-1.048	-2.350
6.123	5.791	-2.703	4.979	-3.556	-1.485	-4.348	11.000
-11.000	-6.230	-11.000	5.624	4.883	-6.501	-3.366	3.482
-3.563	5.012	6.031	-4.689	-1.066	0.893	2.097	10.578
11.000	5.542	1.067	1.669	-3.196	-1.016	-11.000	7.694
-6.807	-11.000	5.640	-11.000	6.093	3.206	0.366	11.000
-11.000	8.210	-11.000	-0.943	4.563	2.758	-1.255	7.399
0.480	0.740	-2.722	-2.244	0.696	-2.102	0.917	1.800
-0.157	3.237	-2.183	1.686	1.792	2.004	-0.379	0.487
-4.187	-0.782	-0.449	0.724	-2.052	-1.969	-2.593	0.882
-3.420	-3.702	11.000	7.862	-1.522	-4.309	11.000	11.000
-3.050	-2.607	-3.398	-3.158	-1.150	-0.204	-2.383	-1.930
11.000	11.000	-1.727	-0.628	0.039	-1.239	-2.277	-1.599
11.000	6.877	11.000	11.000	6.331	0.302	-11.000	8.077
-3.993	-0.481	-2.949	-0.310	1.684	0.897	8.210	-0.403
-0.743	-0.830	-11.000	-11.000	-2.262	9.393	6.688	10.056
-0.689	0.942	-3.063	-2.781	1.045	-3.704	-0.622	3.112
-0.949	3.040	-1.669	1.581	0.877	3.555	-0.690	0.731
-0.361	3.076	0.624	0.433	0.172	-0.578	-2.824	-1.854
11.000	11.000	2.361	2.332	-3.435	-3.889	0.318	3.721
-0.380	-11.000	11.000	-11.000	-2.602	3.278	3.870	-11.000
-5.286	11.000	-7.034	5.364	-1.450	7.585	7.784	4.957
11.000	2.267	5.082	11.000	1.353	-6.425	-11.000	1.676
-11.000	-11.000	-11.000	-11.000	-0.457	2.172	0.916	2.150
11.000	11.000	-3.693	-5.965	1.647	5.547	0.235	1.026
-2.849	0.308	-1.649	-2.284	-1.164	-1.940	-1.668	-1.718
-0.980	-0.731	-3.025	0.011	1.214	1.431	11.000	11.000
-2.822	-1.283	-1.911	0.460	1.593	2.767	-1.463	-1.188
1.049	0.309	-0.575	-1.730	0.663	-1.212	0.305	0.546

Table35.txt

-0.638	-2.512	-0.490	0.681	0.745	0.393	1.356	0.855
-0.319	-1.336	0.516	2.173	-0.005	-0.007	-2.546	-1.352
2.919	3.177	-2.832	-2.761	-11.000	-4.611	-1.488	3.241
-1.549	0.762	-1.741	1.474	2.751	3.946	0.398	0.256
-2.890	0.984	0.326	-0.809	3.529	1.473	-1.314	-0.434
-2.971	0.337	-2.284	-3.574	0.155	-4.166	-1.601	0.597
-11.000	-0.251	-2.485	-0.144	1.856	2.170	11.000	11.000
-3.050	0.180	0.121	-0.062	-1.615	0.645	-1.577	-1.980
-0.305	0.775	-2.032	-5.095	1.213	-4.667	0.395	3.130
0.835	2.701	0.891	2.671	1.802	4.614	0.993	-0.527
-2.582	0.929	1.952	1.668	-2.816	-1.340	-0.987	-1.150
2.560	5.209	-3.411	-4.163	0.670	-4.105	1.070	2.756
-1.132	3.036	-0.464	2.420	2.304	4.164	-0.792	0.914
-2.375	0.318	1.087	0.713	1.095	-1.831	-0.954	-0.912
-2.066	-1.426	2.944	3.694	4.718	-5.959	11.000	11.000
1.520	-11.000	5.329	7.536	-6.453	6.864	5.216	-11.000
3.990	11.000	4.913	6.362	2.722	0.000	-1.516	-0.184
1.195	1.515	-1.983	-0.369	0.668	0.196	-0.768	0.436
-0.852	-0.655	0.390	-1.448	1.185	0.674	0.195	0.768
-0.834	0.905	-0.183	0.355	0.327	-1.238	-2.206	-1.543
4.389	1.807	1.221	2.158	2.530	-6.401	3.242	11.000
-11.000	-4.456	1.314	-4.775	11.000	-2.339	2.525	11.000
-4.697	11.000	-11.000	-11.000	0.455	-0.595	0.062	-2.427
0.590	1.193	-1.932	-0.733	0.412	-1.860	0.072	1.242
-0.368	2.567	-1.244	-0.941	1.993	2.965	0.639	1.251
-1.124	-1.021	0.571	2.329	-0.730	1.525	-1.600	-0.953
0.185	0.951	-2.769	-3.160	0.338	-3.541	0.075	-0.198
-0.115	1.199	-1.346	-0.693	0.418	3.821	-2.124	-0.082
-2.688	0.601	1.511	0.136	-0.726	-2.767	-0.601	-2.487
0.019	0.483	-2.727	-2.815	1.468	-3.703	-0.046	1.394
1.137	3.703	-0.131	0.266	0.397	2.854	-1.451	1.681
-1.186	2.288	1.219	1.588	-1.101	-1.701	-3.423	-1.325
-0.259	0.303	-1.576	-2.582	1.537	-2.501	-0.541	1.380
1.037	2.196	0.723	-1.350	2.433	3.292	-0.043	1.168
-2.296	0.998	-1.219	-1.008	-2.170	-0.569	-1.340	-0.739
-0.404	0.957	-2.227	0.007	1.234	0.139	-0.786	-0.429
-0.946	-0.580	-0.919	0.180	2.014	1.760	-0.886	0.476
-1.222	0.207	0.987	1.674	-1.289	-0.761	-1.013	-1.959
5.183	7.417	1.292	-0.015	11.000	-5.648	-1.339	11.000
-2.697	-5.179	3.157	-11.000	6.690	5.111	-5.313	2.711
-6.937	11.000	11.000	-2.115	5.694	1.495	3.526	3.262
4.489	1.665	2.311	2.828	-11.000	-5.317	-4.919	11.000
-11.000	-11.000	5.372	-11.000	4.006	5.336	-2.673	11.000
-6.706	11.000	-6.604	4.875	-2.309	-2.134	6.232	-0.302
-0.237	0.133	-0.665	-0.801	1.071	-0.277	-0.540	-0.055
-0.952	0.245	-2.009	-0.869	1.808	2.055	-0.061	1.249
-1.815	-1.943	0.397	2.903	-0.737	1.136	-1.386	-0.922

Table35.txt

11.000	-0.070	7.352	6.821	0.215	-0.165	-3.462	2.337
1.363	1.626	2.524	-4.385	-1.794	0.238	1.685	6.158
0.617	11.000	-11.000	-5.585	-0.351	2.830	6.882	13.713
7.277	11.000	3.410	3.309	-2.338	-0.003	2.785	3.250
-0.537	-5.249	-1.075	-11.000	0.001	-3.892	-4.677	-4.783
-6.104	11.000	-3.355	-5.551	-1.483	-1.652	-2.094	-0.743
-2.262	-1.955	-2.569	-1.578	-0.029	-1.477	11.000	11.000
-1.408	-3.059	-2.640	-2.978	-0.443	1.285	-3.015	-1.789
11.000	11.000	-1.152	-1.572	0.334	7.421	-1.306	-1.863
-0.434	0.342	-1.502	-0.594	0.695	-1.313	-1.899	-0.576
-0.947	-0.263	-1.263	-0.294	1.347	0.623	-1.467	-0.697
-1.003	0.748	0.349	0.206	-0.563	4.802	-2.102	-3.167
0.472	0.338	-2.741	-2.481	-0.595	-4.601	0.175	0.638
-0.290	0.525	-0.177	0.446	1.026	-11.000	0.574	0.267
6.869	11.000	1.220	0.411	-0.447	-1.477	-1.538	-1.122
-11.000	11.000	1.654	2.367	0.271	-0.004	5.470	11.000
3.951	-3.840	3.209	-11.000	-1.147	-11.000	-11.000	1.657
-6.739	11.000	11.000	4.216	-0.800	0.758	0.179	-1.414
0.847	1.566	-3.368	-1.488	2.292	-1.775	-0.168	1.769
-0.853	0.043	-0.167	1.519	0.473	3.221	1.477	0.839
-0.914	0.883	2.198	0.171	-0.902	-1.558	-2.093	-4.054
4.184	-3.934	0.701	-0.443	0.079	-1.912	-11.000	11.000
-7.034	-2.649	11.000	-1.108	5.626	0.241	4.409	0.977
-3.775	5.628	3.679	-3.637	-1.820	1.921	1.939	0.770
6.559	11.000	2.925	2.672	-1.600	-2.774	-1.335	11.000
-11.000	-6.937	-4.378	-3.780	5.894	8.210	4.686	-5.392
4.109	11.000	-11.000	-11.000	-1.102	0.000	-0.378	0.762
2.039	3.391	-0.245	-3.381	7.276	-11.000	3.539	6.983
-2.831	1.117	6.503	-0.225	4.643	4.694	0.959	4.043
-11.000	11.000	5.062	-0.590	0.705	-1.696	0.295	6.505
0.729	-0.970	4.025	3.833	-1.047	-3.791	6.498	11.000
-11.000	-11.000	-0.488	-11.000	11.000	11.000	-1.726	7.416
-2.116	11.000	-11.000	-11.000	-0.053	-1.865	2.061	4.844
0.641	1.788	-2.402	-1.141	2.296	-2.490	0.441	1.181
-0.132	2.002	-0.282	0.249	2.234	3.973	-0.181	0.088
-1.122	0.231	-0.751	0.286	0.168	-0.294	-2.827	-2.232
7.956	2.568	11.000	6.084	-1.821	-6.418	8.077	11.000
-11.000	-11.000	11.000	-0.959	6.984	-4.476	-11.000	-2.642
1.263	11.000	-1.052	-1.904	3.148	2.592	1.419	3.429
0.227	1.282	-0.804	-1.838	0.421	-2.318	0.904	0.479
-0.638	1.737	-0.405	0.433	3.301	1.241	-0.311	1.323
-1.932	1.541	0.044	1.304	-1.669	-0.309	1.528	-2.554
0.427	11.000	11.000	-2.721	-1.042	-0.845	1.800	11.000
-11.000	-3.847	2.968	-11.000	3.487	-2.081	-5.638	-6.807
-6.501	11.000	1.551	3.965	-0.206	-0.781	-2.767	4.248
2.030	11.000	-5.804	0.447	1.494	-3.267	-2.990	11.000
-2.485	-11.000	6.582	-11.000	-1.620	-2.214	-3.540	4.348
-11.000	2.765	11.000	-7.034	1.669	1.901	0.041	6.297

Table35.txt

-0.022	0.588	-1.590	-1.653	1.443	-2.168	0.336	1.364
-1.138	0.667	-2.047	0.632	1.024	2.955	0.428	0.718
-1.168	-1.394	-11.000	-11.000	0.604	-1.815	-1.088	-1.224
11.000	11.000	-2.699	2.889	-11.000	-11.000	-1.104	11.000
-6.379	-11.000	3.794	-11.000	1.470	1.747	11.000	1.324
-0.983	1.253	11.000	0.364	-0.087	0.780	-1.086	-0.911
5.914	11.000	4.045	2.625	-1.964	-0.247	-3.722	11.000
-11.000	-11.000	4.612	11.000	-0.581	-1.774	-1.870	-11.000
3.312	7.973	-11.000	-11.000	-0.683	-1.105	-0.498	0.038
-0.149	1.147	-0.515	-2.918	0.426	-3.385	0.504	2.042
0.139	1.598	-2.644	2.750	2.182	2.487	-0.529	0.093
-1.114	-0.164	0.970	0.994	0.000	0.000	0.000	0.000
-0.739	1.591	-2.442	-0.631	1.110	-3.247	0.015	1.747
-1.777	0.566	0.539	0.261	2.506	3.881	0.768	0.900
-2.532	2.166	1.841	0.767	-1.964	-0.740	-1.636	-2.342
-0.239	0.428	-1.643	-2.185	-1.228	-2.812	-1.702	1.016
-1.189	-0.306	-1.438	0.078	1.300	2.467	0.162	-0.518
11.000	11.000	0.925	-1.469	-1.387	-1.214	-0.583	-2.778
4.159	7.654	-0.732	-1.439	-2.289	-1.883	3.003	4.505
-4.801	-11.000	3.178	6.164	2.431	-1.947	3.694	7.259
5.940	11.000	-2.914	-4.509	0.000	0.000	0.000	0.000
0.875	1.746	-2.511	-2.347	0.585	-2.755	-1.529	1.350
0.122	2.502	-0.857	1.383	1.062	3.258	0.189	0.676
-1.711	1.646	0.792	-0.229	0.275	-1.063	-4.125	-2.645
-1.533	1.902	-1.612	-0.639	1.126	-2.565	-0.802	1.110
-0.761	1.561	-1.532	0.270	1.076	2.874	-0.452	0.463
-2.381	0.364	-0.115	-11.000	0.472	6.469	-0.664	-0.108
1.750	1.220	-2.678	-1.976	1.057	-3.047	-0.168	0.972
-1.858	2.829	-1.956	1.782	3.166	3.702	-1.384	-0.092
-3.030	-0.010	1.204	1.444	-0.570	0.994	-0.151	0.598
-0.594	0.286	-2.432	-2.752	2.159	-3.262	-0.391	3.620
1.223	1.094	-1.029	1.342	2.782	3.504	0.383	0.430
-1.263	-0.265	0.509	-0.828	-0.803	1.738	-0.709	-0.338
2.295	3.579	-3.500	2.755	4.002	-4.657	5.715	11.000
-11.000	4.155	4.289	-11.000	6.672	-2.440	6.162	11.000
-11.000	11.000	-6.246	-11.000	-1.306	-2.069	4.150	3.578
-3.679	1.621	11.000	11.000	2.074	-5.510	3.643	4.736
-11.000	-11.000	11.000	11.000	-2.297	-3.250	-2.115	5.406
-2.069	11.000	-11.000	-11.000	3.540	1.968	2.694	2.436
-0.072	1.810	-2.279	-3.160	-0.199	-2.946	1.420	2.136
-2.313	1.507	-0.007	0.240	3.891	1.295	-0.688	1.231
-2.431	5.093	0.352	0.511	-0.430	0.121	-0.445	-1.615
-1.592	-1.696	-2.190	-1.987	0.819	-2.707	-0.650	0.220
-1.885	-3.250	-2.551	-0.531	0.409	0.506	-2.002	-1.583
-3.074	-0.674	-0.162	0.595	-0.821	0.232	-1.190	-2.638
0.404	0.627	-1.307	-2.955	0.005	-2.259	0.678	2.441
0.328	0.181	0.737	0.027	-0.252	1.188	-1.635	0.290
-2.157	-0.399	0.298	-0.364	0.000	0.000	0.000	0.000

Table35.txt

3.667	3.726	11.000	7.060	-11.000	-2.616	-11.000	4.208
-11.000	-11.000	0.764	3.775	3.540	4.715	1.676	2.970
0.023	2.796	-11.000	-11.000	4.635	6.664	-4.117	-0.953
11.000	4.942	0.590	0.494	1.749	-11.000	2.309	3.926
1.622	4.268	0.565	4.132	2.322	-11.000	1.644	2.605
-11.000	1.802	1.665	-0.405	-2.131	-2.549	-1.164	-0.913
-0.952	1.229	11.000	7.374	-0.190	-4.647	-1.379	1.650
-1.056	1.127	-3.327	0.126	1.284	2.411	-1.935	0.828
-3.721	-0.445	0.079	-1.209	5.430	2.656	-3.170	-3.102
11.000	2.122	0.739	3.273	-1.034	-3.668	2.490	11.000
-6.379	-11.000	11.000	-0.932	2.479	-1.744	4.604	0.615
-2.886	3.102	-4.993	-4.329	0.605	-1.482	-0.555	0.405
-1.115	2.347	-2.101	-2.767	-1.566	-3.096	-0.414	0.069
-1.412	0.267	-1.785	-1.445	2.320	2.615	-0.462	0.138
-1.985	0.028	1.054	-0.219	-1.663	-0.985	-2.500	-2.387
-2.205	3.777	0.992	2.675	1.329	-2.589	4.555	5.953
5.438	5.070	6.242	-11.000	-5.246	-11.000	-4.242	11.000
-1.724	11.000	0.821	-5.715	2.388	3.956	0.000	3.090
-2.138	5.100	0.019	11.000	4.656	-6.880	11.000	11.000
-1.268	-11.000	-2.666	-0.854	5.256	-1.011	11.000	11.000
-11.000	11.000	-0.958	-11.000	0.287	4.746	8.893	-3.241
-1.503	0.746	-4.503	-0.782	0.147	-1.224	-0.472	1.784
-0.523	2.932	-1.447	0.537	0.162	2.480	7.036	11.000
-2.149	-0.952	1.256	-0.094	-2.549	-0.554	-1.506	-0.942
-0.487	-1.233	-1.001	-1.948	-0.695	-1.420	-0.575	0.144
-1.458	-0.527	-1.894	0.385	0.575	0.860	0.279	-0.622
-1.564	0.005	0.658	1.437	-0.218	1.036	-0.514	-0.994
-0.943	1.922	-2.557	-2.122	1.009	-3.571	-0.070	0.862
0.085	2.260	0.277	1.548	1.931	3.958	-0.641	-0.003
-1.865	1.976	2.439	-1.026	-0.080	2.009	-2.967	-1.596
0.146	1.105	-1.574	-3.294	0.883	-3.414	3.124	3.703
0.971	0.945	-1.822	-0.050	2.799	-1.148	-0.759	0.424
-1.804	0.994	0.514	-0.751	0.163	3.167	0.063	-1.812
-2.324	-0.468	-1.554	-2.302	0.246	-2.424	1.397	-1.090
-1.907	1.586	0.896	0.149	2.317	3.135	-0.410	2.618
-1.889	1.391	0.584	0.623	0.437	-0.870	-3.090	-1.900
11.000	-2.256	-0.021	3.561	0.517	-1.286	-6.172	11.000
-6.352	3.906	11.000	-11.000	7.035	-0.215	-4.354	1.955
-11.000	11.000	-11.000	1.460	-1.609	-0.790	8.332	12.306
7.434	0.373	-0.340	2.836	-2.002	-3.253	0.369	11.000
-4.291	-11.000	7.433	-6.839	5.720	2.338	-2.009	11.000
-6.604	11.000	-3.163	-6.458	2.246	-1.511	7.439	1.063
7.019	11.000	-3.499	3.492	6.781	-5.370	-11.000	4.661
-11.000	-11.000	11.000	-3.202	6.753	3.103	2.761	2.025
-4.657	11.000	-3.581	-6.880	1.428	3.601	2.906	6.491
-0.006	1.233	-2.296	-2.074	1.533	-2.655	-1.035	0.750
-1.707	1.940	-0.872	-0.167	-0.030	2.755	-2.270	1.736

Table35.txt

-2.529	0.597	0.031	1.789	-0.985	-0.070	-1.908	-1.486
11.000	11.000	2.697	1.734	-3.452	-6.100	-5.666	-4.926
-5.703	-11.000	7.088	11.000	-5.413	-7.034	6.018	11.000
6.244	11.000	-4.077	-5.615	0.790	2.420	-2.655	-1.176
1.982	-0.169	-0.688	1.168	-0.489	0.059	1.559	0.972
2.246	-0.230	1.709	-0.154	0.407	0.056	-0.751	1.469
1.551	1.479	1.584	1.356	-1.839	0.085	-2.639	0.844
11.000	0.700	11.000	0.587	1.247	0.132	1.008	2.402
3.834	0.605	1.637	1.435	0.423	1.557	0.023	1.039
2.888	2.191	1.247	1.951	1.904	8.214	-0.471	-0.775
-4.073	-4.684	-5.026	4.334	5.309	3.767	11.000	-0.440
0.068	-2.739	5.053	4.275	-2.266	-3.624	-1.213	-2.366
5.775	4.003	-2.370	-0.718	-1.144	-0.485	0.657	-0.285
-6.368	-3.825	-4.882	6.181	8.041	11.000	11.000	6.880
-2.763	-4.366	0.350	1.959	-3.146	-5.070	-1.328	-3.745
4.937	3.929	-4.050	-2.407	-1.120	-0.711	-1.865	-0.510
0.582	2.243	1.912	-1.727	1.324	-0.880	0.068	-0.121
-0.788	-0.749	-0.986	0.655	-1.565	1.102	-0.629	-2.271
0.183	-0.525	-1.143	0.004	-1.259	-0.863	-1.360	-0.852
-0.431	0.537	0.531	-0.781	0.884	-1.703	-0.306	-0.828
-0.764	-1.629	-1.491	-1.156	-1.149	1.013	-1.591	-1.301
-0.660	-2.292	0.035	-1.508	-1.551	-0.756	-0.924	-1.074
-4.460	-2.386	-2.520	11.000	11.000	11.000	-3.115	-4.835
-2.814	-3.371	-2.724	-3.142	-2.283	-1.805	-2.097	-2.542
-1.897	-2.713	-2.107	-2.221	-0.979	-1.227	0.200	-0.630
-0.248	0.492	-0.464	-0.281	0.835	0.541	0.360	0.535
-0.095	-2.327	-1.021	-0.373	-1.691	11.000	-0.993	-0.836
2.231	-1.283	0.716	-0.814	-1.094	9.377	-1.593	-1.564
-5.887	-4.133	-5.806	3.571	7.783	6.881	6.575	-5.183
3.276	2.311	-3.093	3.480	-3.478	-4.420	-2.167	-3.639
4.401	2.219	-3.706	-2.813	6.763	6.513	-1.424	0.011
0.738	0.410	0.663	-0.288	-0.741	0.020	0.376	0.571
0.807	-1.395	6.272	11.000	-1.456	0.507	-1.029	0.143
0.610	-1.431	0.177	1.776	-0.167	1.062	-1.237	-2.329
-1.562	-1.036	-1.241	-3.243	-3.124	11.000	8.210	-3.365
-0.779	-3.311	-2.860	-2.208	-2.872	-2.014	-1.945	-2.554
11.000	5.791	11.000	-1.487	0.052	-0.562	-1.500	-1.410
-5.748	2.937	1.706	-3.575	-5.016	1.153	1.259	0.421
0.645	-0.724	11.000	0.833	-1.085	1.204	-0.786	-1.130
1.616	-1.414	0.615	11.000	-0.889	0.017	-0.269	-0.070
-0.365	1.865	0.748	-0.970	1.804	0.718	1.318	-1.109
-1.605	-0.888	-2.133	-0.675	-1.308	1.201	-0.051	-1.172
-0.520	-0.257	0.224	-0.912	-0.833	-3.644	-0.842	-1.141
0.688	2.354	1.914	-0.602	-0.390	-0.342	0.649	-0.360
-1.179	-1.255	-1.173	-1.365	-0.781	0.363	-0.762	-0.864
-0.277	-0.723	-0.010	-0.189	0.553	-1.588	-0.736	0.188
-0.595	0.765	-0.227	-1.234	0.058	-1.446	-0.214	-0.877
-0.818	-2.336	-1.298	-1.209	-1.262	0.689	-0.710	-1.378

Table35.txt

-1.233	0.024	-0.743	0.420	-0.190	0.154	-1.591	-1.208
2.370	2.555	2.707	-0.021	1.521	11.000	1.976	11.000
1.272	0.277	0.198	1.199	11.000	11.000	0.354	0.028
11.000	11.000	0.364	0.444	9.912	12.054	-2.245	-1.452
0.319	11.000	11.000	3.767	6.253	-4.389	5.003	-5.980
-1.337	-3.008	-4.731	-6.620	1.188	3.284	-0.875	-0.013
-1.098	-1.889	-5.698	-4.741	-0.740	0.126	1.266	2.115
-0.834	-0.105	1.885	-2.414	0.024	5.796	-0.665	2.976
-0.637	-1.741	-1.397	-1.199	-0.125	-0.924	-0.904	-2.126
1.411	0.010	-1.373	-1.190	-1.375	-0.319	-1.003	-1.233
0.970	0.964	0.891	-1.147	0.816	-0.380	0.562	-0.232
1.091	-1.843	-0.276	-1.024	-0.888	0.769	-2.095	-0.922
0.911	-0.233	-0.927	0.136	-1.596	-0.990	-1.600	-1.494
-3.028	1.411	-0.156	0.479	2.109	1.482	3.310	-0.201
1.657	-1.196	-1.689	-1.403	-0.403	0.006	0.167	0.081
1.950	-0.385	0.007	-0.272	-1.535	-0.146	-1.981	-0.158
0.599	2.303	1.422	-1.442	0.826	-0.670	0.677	0.119
0.002	-1.289	-2.617	-0.474	0.227	1.030	-1.205	-2.412
1.347	-1.856	0.026	-0.003	0.145	-2.035	-0.189	-2.227
2.469	3.880	11.000	-3.211	-4.380	2.779	-3.318	-1.624
1.902	0.049	11.000	2.100	11.000	11.000	0.413	-0.031
11.000	5.877	-2.605	-5.070	0.806	3.007	-1.259	-1.378
-0.860	1.208	0.079	-2.666	-0.204	-0.256	0.455	-0.792
-1.487	-2.287	-2.130	-1.341	-1.989	1.836	-2.293	-3.514
-0.010	-1.663	0.348	-1.395	-2.131	-1.539	-0.887	-0.502
0.312	2.130	0.672	-0.743	0.465	0.946	1.350	11.000
-0.015	-0.144	-0.774	0.269	-1.889	0.683	-0.097	0.256
1.405	-0.426	-0.303	-0.637	-0.045	-1.515	-2.393	-1.526
-1.603	-0.078	-0.062	-1.857	-0.890	-2.121	-0.842	-1.814
11.000	11.000	-1.655	-1.512	-2.341	0.260	-1.773	-2.174
0.610	-1.464	-1.284	-0.792	-0.236	-1.962	0.238	-1.918
0.696	3.681	0.569	0.637	0.503	0.057	-0.191	-0.130
0.033	-1.748	-1.713	-0.180	-3.285	-2.829	0.096	-0.584
-4.035	1.683	1.003	0.144	-0.749	0.632	-1.528	-0.647
1.049	-0.420	-0.237	0.058	0.531	-0.319	0.710	0.903
0.645	-4.491	0.521	0.421	-0.393	1.269	-1.033	-1.624
1.470	-0.117	0.952	1.425	-0.319	-0.772	-0.916	-0.860
1.985	-2.228	0.372	2.214	1.079	0.255	1.104	-2.318
1.832	1.399	-5.886	-5.396	-0.724	11.000	1.693	2.614
2.397	0.728	-0.179	1.825	-2.602	-0.467	-1.335	-0.807
1.502	1.789	-0.093	-1.528	0.762	-1.198	1.864	1.083
0.655	-1.669	0.054	-0.345	-1.039	1.313	-1.135	-0.329
0.383	-0.067	0.897	0.694	1.518	0.007	-0.694	0.124
0.233	-0.603	-1.559	-0.184	-1.454	-1.512	-0.018	0.546
-0.348	-1.190	-0.055	0.551	-0.755	-0.493	-0.654	6.103
8.210	6.432	0.500	0.927	0.523	0.302	0.631	0.632
1.140	-0.401	-1.644	-0.189	-0.234	-0.136	1.261	1.476
1.388	0.616	1.327	1.537	-0.102	0.124	-0.451	-1.079

Table35.txt

2.573	-0.317	2.261	1.265	0.080	0.724	0.508	-1.290
-5.350	2.275	1.177	-1.103	0.866	0.760	1.532	-0.210
-0.549	-1.725	-0.769	0.815	11.000	11.000	-0.590	-1.799
11.000	8.210	0.709	-0.697	0.146	-0.937	-2.009	0.910

chr3p_AI	chr3q_AI	chr4p_AI	chr4q_AI	chr5p_AI	chr5q_AI	chr6p_AI	chr6q_AI
chr7p_AI	chr7q_AI	chr8p_AI	chr8q_AI	chr9p_AI	chr9q_AI	chr10p_AI	chr10q_AI
chr11p_AI	chr11q_AI	chr12p_AI	chr12q_AI	chr13q_AI	chr14q_AI	chr15q_AI	chr16p_AI
16.359	13.449	4.441	25.039	11.377	24.836	14.713	23.035
8.661	9.198	8.920	14.971	13.932	16.283	8.664	16.263
14.451	15.168	9.182	10.723	18.041	15.705	-1.959	4.833
-2.473	-0.697	-0.257	-0.569	-1.141	-0.445	-0.106	-1.037
-1.064	-1.387	-0.251	-1.793	2.854	0.482	0.638	-1.771
-1.101	-0.861	-1.472	-0.773	-1.163	0.831	-1.291	0.467
-1.014	-0.275	-1.485	0.841	-0.043	-0.778	11.784	20.229
-1.387	-0.085	10.507	21.177	14.786	15.424	0.675	-0.492
-0.485	-1.764	-1.132	-1.469	18.758	-0.636	15.136	-1.724
8.913	21.371	13.347	24.827	12.950	1.134	11.690	12.982
3.254	-0.417	10.451	20.292	12.905	12.844	10.465	11.461
16.125	19.033	7.933	9.090	23.336	15.868	14.545	10.081
13.043	17.374	6.460	14.360	8.618	13.339	-0.109	-0.826
13.938	17.593	12.439	0.637	3.436	3.359	1.050	-1.505
-0.860	-1.793	7.399	5.323	19.574	14.825	14.823	9.769
-0.998	-1.098	-0.852	-1.467	-1.095	-0.246	0.974	0.123
0.364	0.766	0.739	-1.267	-0.912	1.226	0.699	-0.329
-0.754	0.569	1.384	-1.012	0.927	-1.983	-1.959	0.419
-1.813	3.986	-0.157	18.843	14.022	25.367	0.044	1.807
4.278	5.406	2.504	18.859	-0.533	1.311	-0.061	18.095
-0.723	7.098	13.716	8.453	-1.641	9.197	-0.161	-1.417
-0.793	-3.307	-0.144	19.823	10.629	23.230	-1.282	-1.260
-1.356	-1.512	11.651	19.873	0.613	-0.412	-2.036	-0.876
14.626	17.955	-0.654	-1.454	-2.647	-0.402	1.374	7.549
17.854	20.314	13.164	21.185	-0.858	21.106	10.822	18.078
13.976	17.231	-1.861	-1.510	-1.564	-0.098	-0.936	8.389
-0.164	0.529	0.102	0.204	22.055	13.861	14.289	7.621
-2.328	-2.505	-3.438	-1.528	-1.124	3.414	-1.386	-0.584
-0.274	-1.749	-0.419	-2.472	-0.360	-1.409	-1.939	-0.418
-2.989	-2.102	-0.960	-1.613	-1.225	-0.531	-1.163	-0.493
-0.844	0.046	-0.574	-2.544	1.751	-0.834	0.046	-1.461
-1.249	-1.629	-1.289	-0.992	-0.763	-1.072	-1.268	-0.392
-0.976	-2.603	-0.194	-0.996	-1.346	-0.328	15.055	-1.396
-0.698	-1.676	-2.321	26.270	-1.587	-1.251	5.086	-5.054
-1.041	-0.366	0.967	-1.368	0.344	-0.292	-0.026	-1.237
0.950	0.047	-0.769	-2.191	21.580	17.799	2.629	-1.518
-2.408	-1.821	7.762	12.889	0.058	-2.579	-0.903	-1.922

Table35.txt

7.234	19.385	7.881	20.541	-1.352	0.579	-0.943	-2.226
1.692	-0.129	0.247	-2.476	13.999	0.251	-1.911	4.359
-0.875	-0.584	-1.939	-2.135	0.427	1.445	-1.876	-2.518
-2.270	-1.455	4.175	17.473	-1.668	0.688	-1.983	-2.107
-0.183	0.089	-1.959	0.433	-0.642	1.088	9.793	-0.572
19.656	23.897	-0.443	-1.459	-1.889	-1.144	-0.743	-0.932
-0.122	-0.070	10.630	11.476	12.724	14.602	14.167	14.742
-1.835	-1.287	10.640	21.803	14.915	17.744	13.069	1.624
19.077	19.837	0.287	5.478	12.700	-0.478	12.796	0.368
13.504	18.196	14.365	20.242	16.575	0.979	0.072	-2.003
15.886	-0.183	10.760	-1.416	21.567	-1.005	-1.739	-1.683
-1.004	-1.495	0.173	-1.198	2.087	9.518	8.362	-0.256
-1.243	-0.138	6.905	9.635	-1.500	-1.768	1.666	-1.295
-0.977	14.011	-0.884	8.564	14.852	13.501	-0.371	-0.301
10.351	10.166	15.188	26.434	-1.774	17.978	5.779	10.778
-1.456	8.889	8.353	19.972	8.741	0.000	5.958	4.955
-1.781	-2.737	5.012	9.557	19.530	-0.388	-1.953	4.694
11.362	14.361	15.070	8.865	1.813	19.073	3.408	3.116
-1.384	0.324	8.697	21.181	11.816	15.545	8.455	-1.008
7.356	3.218	8.831	11.303	22.349	15.952	15.314	-0.559
17.305	9.814	-0.408	0.782	6.589	21.169	14.287	22.330
4.803	5.535	11.078	23.347	13.882	-1.802	7.053	7.658
8.785	11.221	1.762	-0.829	22.740	15.125	7.139	6.141
2.327	0.232	-2.647	-3.221	-0.362	0.357	4.649	6.454
2.910	2.092	-0.675	-0.277	4.210	3.789	0.149	0.127
0.601	-0.049	2.533	0.396	7.438	-0.654	2.876	-1.891
19.611	23.516	10.542	14.465	11.771	19.656	6.465	13.519
12.079	9.979	9.603	5.959	12.423	7.739	7.267	6.532
1.055	11.701	6.476	13.468	-0.865	16.276	11.524	0.530
-1.981	-2.343	-0.780	-2.708	4.266	7.135	3.968	3.516
3.888	-1.507	1.030	-0.316	2.557	-0.591	-2.641	-0.260
-1.173	-0.665	0.067	4.387	0.463	2.279	-0.369	-0.504
-1.991	-1.094	11.784	19.840	8.216	11.025	-0.593	0.237
-0.739	1.510	8.920	1.539	11.868	9.659	9.928	11.535
5.616	2.227	-0.208	11.380	21.445	11.884	-0.429	-0.193
2.114	-1.999	12.917	24.792	11.915	20.571	10.924	10.520
8.253	16.578	12.767	3.967	10.601	-0.826	-1.089	-0.141
-0.135	6.041	0.671	0.146	1.236	0.270	0.617	-0.616
-0.709	-0.419	15.201	24.730	-0.366	12.096	5.185	9.691
10.639	13.526	11.450	22.664	1.238	-0.837	0.359	0.302
5.496	8.405	-0.020	14.052	20.772	6.098	15.509	5.543
12.884	19.061	12.511	21.997	14.156	22.324	11.898	20.391
7.650	4.620	12.806	-2.674	14.474	14.815	12.644	15.890
10.749	14.166	8.432	15.679	22.833	15.925	14.551	6.200
17.236	21.357	13.439	20.253	4.831	16.344	11.181	2.701
12.510	13.811	11.614	13.856	10.160	11.135	9.506	12.440
-0.268	-0.548	2.511	14.191	20.668	7.339	14.563	7.455
-2.356	-2.399	-2.699	-3.172	-0.773	-1.906	-0.273	-1.722

Table35.txt

13.729	18.970	-0.124	9.842	-0.278	-0.967	-1.234	-1.126
-0.664	-0.395	-0.708	-0.383	20.365	-0.230	-0.370	-1.547
0.121	-1.564	-0.630	-2.037	-1.024	17.893	-0.610	-0.518
9.115	10.651	5.534	18.323	11.145	9.720	-1.154	-0.396
-1.340	-1.045	6.990	-1.451	19.692	-2.252	0.694	-0.891
16.016	18.571	15.528	27.737	10.838	15.680	10.767	14.479
-2.732	5.634	8.539	18.537	9.733	9.138	7.650	10.335
13.742	11.410	7.216	5.804	20.321	18.280	15.701	10.027
-1.189	-0.175	-0.658	-1.892	-1.889	15.073	0.387	-1.449
-0.387	-1.778	0.398	-2.081	-0.196	-0.107	-0.301	-0.236
-2.530	-1.313	11.159	17.032	21.817	-0.844	1.545	-1.235
0.730	-1.697	-1.659	0.194	-0.056	18.751	1.279	-0.481
10.288	11.098	-0.346	0.702	9.732	7.247	-2.269	0.055
-1.040	-1.406	1.219	-2.097	-1.592	-0.340	-0.150	0.622
-2.614	-1.053	14.768	25.454	10.775	1.161	-1.836	24.060
8.199	-0.110	12.528	-0.611	-0.419	0.999	-1.269	-0.766
11.406	18.052	0.282	-1.393	24.820	16.367	-0.468	-2.183
16.359	16.573	14.870	23.392	12.933	-0.799	1.115	-1.875
12.613	18.190	9.910	14.209	3.185	2.143	-1.758	-0.345
0.820	-0.021	-0.796	-0.094	18.433	17.923	13.513	2.025
-0.255	-0.393	-1.160	7.951	-1.385	2.265	0.040	3.097
5.189	8.109	-1.696	8.397	4.485	-0.452	-0.468	-0.183
-1.059	-0.665	-2.137	-0.312	8.119	-1.183	0.860	-0.762
15.528	19.307	6.074	22.969	-0.152	11.815	3.045	2.779
6.033	6.253	8.972	21.177	15.606	13.560	4.448	2.052
4.392	2.811	2.284	9.118	9.271	6.064	2.490	-1.042
0.393	-1.885	2.464	4.290	-0.089	5.190	0.445	0.165
1.174	-0.254	0.655	1.995	1.863	-1.504	1.003	-0.662
-0.269	2.376	0.126	7.770	-0.405	-1.010	5.729	1.570
1.865	-2.842	1.331	7.499	6.166	8.617	-1.867	-3.178
-0.236	-0.958	10.090	18.124	7.835	2.858	10.157	10.049
10.939	10.770	1.063	-2.509	7.640	5.258	13.384	-0.007
16.056	17.655	8.125	15.876	-1.691	-0.693	7.141	15.594
12.900	14.142	-1.026	-1.506	-1.351	-1.516	9.783	9.633
7.002	9.399	9.086	17.766	14.138	-1.218	0.514	-0.162
9.941	10.707	14.543	22.525	0.064	-0.620	5.958	5.597
0.760	-0.990	3.283	21.559	6.021	6.224	0.037	-0.320
6.360	8.459	6.204	9.522	6.251	-1.615	-2.184	1.233
-0.718	-0.855	0.599	-1.384	0.042	-0.834	2.877	-3.513
0.370	-1.356	0.747	0.086	-0.046	-1.395	-1.199	0.366
-0.639	0.101	-1.560	0.039	3.386	-0.886	-0.262	-1.029
-0.949	-0.501	-0.694	-0.821	-0.312	-1.696	-0.293	-0.946
6.676	7.061	1.421	-0.263	-0.191	-0.350	0.296	-1.440
0.074	3.790	1.190	0.102	18.238	-2.139	-0.876	-0.286
-1.662	-0.450	4.604	9.697	-1.405	8.360	-1.401	-0.853
0.378	10.548	-0.639	1.138	-1.113	-2.130	-1.917	-0.482
4.168	2.950	1.315	-2.330	5.525	-0.709	0.361	-0.665
11.119	15.042	11.325	20.431	6.770	2.945	-0.383	-0.809

Table35.txt

1.698	2.980	6.477	18.026	3.207	5.945	0.997	1.013
9.192	10.935	-1.979	-1.972	9.421	11.758	8.694	-0.258
0.629	-2.692	-2.519	-1.168	0.233	-2.140	0.524	-2.198
-0.408	-1.792	-0.917	-2.506	12.616	-0.845	-0.234	-0.671
-1.087	-2.199	-2.915	-1.411	11.113	-0.806	-1.259	-0.332
-0.541	-0.574	1.712	5.849	-0.747	0.761	2.145	4.918
-0.591	-3.114	1.482	-0.204	-1.467	-2.446	0.306	-0.368
-0.778	0.276	0.050	-4.070	-1.711	4.160	1.640	-1.153
10.645	12.627	5.939	7.079	9.108	18.550	7.035	10.122
-1.332	6.962	5.283	8.009	12.194	9.677	-1.686	-3.274
9.598	7.822	0.072	-0.318	7.137	-0.446	-1.789	-0.166
-1.346	-0.628	-0.803	-1.453	-2.033	-2.285	-0.707	-1.443
11.081	14.100	0.005	-1.058	-1.335	-0.593	0.680	4.435
-0.219	-3.242	-0.850	-2.114	-0.183	-0.540	-2.235	-0.815
-1.100	-2.249	-1.157	-3.051	4.001	2.745	-1.431	1.856
12.556	4.328	0.993	3.736	-1.174	-2.148	3.474	2.755
-1.618	-2.335	-1.705	-0.725	2.384	2.492	6.116	5.972
8.435	3.229	1.397	-0.887	-0.546	2.431	6.909	-0.501
1.402	6.098	4.048	20.466	0.786	2.162	0.239	1.474
0.360	0.288	-3.236	1.627	15.460	11.849	-0.680	-1.247
-1.223	0.226	-1.243	-0.515	1.330	-0.827	0.660	0.061
-1.505	-1.567	5.008	13.538	-0.841	-1.005	-0.720	0.055
0.515	10.417	9.059	15.013	0.207	-0.491	-1.600	0.974
1.900	-0.949	2.192	2.463	0.556	-1.514	1.806	0.847
0.536	-1.716	0.522	-0.736	0.347	-1.388	-2.753	0.576
-1.162	-0.125	1.559	-0.346	-2.000	0.444	3.718	-2.723
12.446	20.702	6.645	12.058	4.224	8.649	-2.204	-0.359
12.452	18.252	9.355	20.724	12.799	13.451	-0.987	-0.482
14.861	16.701	8.135	16.706	18.207	0.729	10.861	11.054
-1.919	-1.691	-1.457	-0.975	0.044	-2.168	-1.524	-2.058
-1.075	-1.312	-0.825	-1.013	-2.885	0.362	-1.090	-0.559
-1.635	-1.579	-1.038	16.120	-2.478	0.164	-0.141	-0.529
0.069	-0.853	-0.943	-1.057	-2.774	-2.479	-0.404	-3.684
-0.126	-2.497	-1.614	-2.734	-0.731	-1.930	-3.113	-1.638
-0.835	-1.358	-1.246	-0.587	-1.456	-1.146	-0.536	0.514
-1.914	1.416	-2.050	0.612	-2.295	-0.664	0.850	-0.902
-1.276	-1.282	8.295	5.659	0.041	1.663	1.017	-0.995
-1.088	-1.467	0.286	1.221	-0.148	-1.480	-0.110	-0.440
-1.654	-2.295	-0.898	-0.058	-0.776	-0.328	-0.328	-1.987
-0.692	-0.387	0.028	-1.401	-3.834	-0.042	-1.021	-1.216
-0.281	-0.752	-0.213	-0.934	-3.119	-1.183	-0.771	0.092
-0.671	-2.610	2.433	10.375	12.654	18.515	3.663	-0.604
-0.423	-0.574	9.103	-1.348	-1.596	-0.815	10.064	13.565
-1.003	0.100	0.198	-2.195	-2.165	9.447	11.234	2.670
4.570	-2.446	-0.329	-2.229	-1.670	-0.057	-0.011	-1.026
-1.146	-0.112	-1.352	-0.532	-2.170	-0.543	-1.989	-1.218
-1.382	-2.026	1.784	-3.056	2.696	-0.596	-1.027	-0.824
-0.141	-2.177	7.191	13.930	-0.324	-1.922	8.495	16.731

Table35.txt

1.207	3.979	2.316	1.737	7.181	7.909	-1.061	-1.397
0.184	-1.613	0.726	-1.179	4.718	-2.149	-0.790	0.494
-1.566	-0.937	-0.614	4.583	1.951	11.304	0.392	0.876
0.170	-1.913	4.549	13.586	-1.970	0.532	-1.165	-0.875
0.472	-1.696	-1.914	0.873	7.203	-1.024	1.453	0.984
6.551	8.783	2.299	2.584	10.071	8.733	6.182	9.548
6.661	8.731	4.823	22.284	6.150	1.974	4.396	6.889
5.652	7.459	4.036	8.080	4.599	12.107	13.403	-1.556
-0.234	-1.275	-3.691	-1.891	-0.546	-1.234	-0.750	-1.671
1.382	-1.288	-1.290	-1.596	-0.274	-2.001	-1.885	-1.701
-1.181	1.417	-0.509	-2.889	-3.263	-1.658	10.452	-0.028
16.375	19.502	14.429	24.209	9.592	15.644	7.907	12.214
12.813	19.214	6.687	14.430	7.378	10.526	-2.082	0.838
1.289	-1.325	9.777	16.369	10.061	15.955	-0.916	7.455
0.040	-2.489	-2.203	-1.633	-1.366	-0.395	-3.767	-1.548
-0.551	-3.247	-0.828	-1.968	-2.295	-1.832	-1.336	-0.191
-0.019	-1.570	-3.267	-2.242	-0.268	-0.556	-1.336	-0.608
-1.416	-1.699	5.107	16.287	0.580	-1.441	0.295	-1.603
2.133	0.551	6.765	14.287	12.949	12.848	-0.499	1.613
-2.569	0.463	0.366	-0.930	4.285	1.056	-0.522	-1.122
1.568	-3.089	4.860	13.457	-0.387	10.857	11.049	19.732
8.025	20.325	1.231	18.167	-1.652	0.282	6.368	7.759
-0.134	11.310	-0.911	6.208	8.727	8.032	12.148	0.484
-0.243	-1.613	-1.044	-3.299	-2.167	10.202	-1.096	-1.669
0.038	3.991	3.016	6.133	8.899	11.941	-1.588	-3.545
-0.834	-2.967	4.707	3.158	-1.114	-3.712	0.896	-0.582
0.341	-1.581	-1.523	-2.772	-2.682	-2.269	0.258	-2.651
0.164	-2.803	-0.577	-2.114	0.134	-2.053	-0.937	0.448
-1.736	-1.851	-0.730	8.022	0.439	-1.603	0.594	-0.533
-2.032	-2.365	-1.099	0.013	-0.245	-1.842	-2.911	-1.230
-0.843	-1.215	0.168	-0.935	-1.739	-2.437	0.307	-2.617
-1.001	-1.558	-0.607	-1.285	-1.675	-2.507	-0.265	-1.849
-2.092	-1.479	-0.686	-2.539	2.707	6.407	-1.050	-1.352
5.256	-0.295	-0.629	-1.871	-1.553	-0.937	-0.430	-1.912
-0.173	-0.249	-1.762	15.332	-1.398	-2.599	-2.732	-1.199
3.396	5.378	4.072	15.965	7.190	7.003	3.616	0.626
-0.800	-2.099	3.590	3.444	0.034	-0.321	0.984	6.136
4.176	5.579	5.451	12.018	2.002	-0.363	7.542	-0.692
1.735	17.347	7.062	3.104	2.769	8.780	4.224	4.588
7.786	14.557	9.295	20.217	6.217	8.192	8.776	14.781
0.641	3.187	-0.207	3.997	-0.494	2.875	1.722	4.219
-1.927	-1.988	-0.810	-0.742	-1.351	-0.684	0.260	-0.077
-1.634	0.081	-0.467	-0.718	0.031	-0.120	-0.508	0.296
2.519	-1.378	0.862	10.524	-1.125	-0.852	-0.838	-2.180
1.702	-1.783	1.431	0.873	0.062	6.742	0.445	-1.274
0.423	0.188	3.582	-1.336	4.273	-0.882	-0.817	0.502
0.638	1.454	1.989	-0.170	-0.468	1.556	-0.106	0.587
3.139	-1.582	-1.304	-2.328	-0.229	10.127	-1.410	-0.813

Table35.txt

-0.910	1.469	4.558	-1.153	5.536	-0.594	2.287	1.804
1.282	2.459	2.219	2.397	3.250	3.728	0.981	-0.995
-1.871	-0.914	-3.406	0.651	0.173	-0.671	7.732	3.565
-0.732	-0.316	1.510	-0.328	0.438	0.469	0.154	-0.702
-0.363	-0.110	-0.395	-1.711	-2.802	-0.355	-0.567	0.058
0.794	-2.342	-2.132	-1.622	-0.416	-1.804	-0.067	-0.304
-1.250	-1.011	0.659	-1.949	8.057	9.434	-1.225	-3.512
-1.635	-2.759	-2.242	-1.099	22.392	9.815	14.086	2.046
-2.367	-0.992	-2.322	0.392	-1.895	-1.946	0.628	-1.260
-3.485	-1.870	2.194	3.797	2.385	2.894	-0.257	-1.278
0.459	-0.529	-1.474	-0.136	5.799	-0.735	-1.189	-1.096
-0.516	-3.437	2.207	8.754	3.654	8.106	9.366	14.408
4.007	1.283	3.116	10.295	3.731	7.341	4.133	7.159
-1.418	-1.892	2.719	7.275	-0.755	8.111	-0.231	4.710
1.785	3.768	2.979	4.065	1.796	7.497	3.640	4.996
0.339	-0.516	3.199	7.723	12.467	8.776	6.648	7.542
5.705	5.372	3.881	4.946	5.281	9.018	-0.971	0.130
-0.160	0.099	2.051	7.186	6.699	20.512	0.495	0.918
14.054	10.972	4.036	10.836	1.945	3.220	5.075	5.676
8.646	11.430	0.286	-1.107	18.241	16.379	3.948	2.391
0.291	-0.304	1.653	3.660	-0.037	2.421	0.087	-0.239
3.343	1.647	0.066	0.213	0.172	-0.230	-0.386	0.473
0.298	2.149	-0.083	-2.108	8.177	-1.953	-0.429	0.636
-1.141	-0.249	0.461	1.369	1.534	-1.883	0.130	-1.591
9.490	12.751	8.935	19.696	-2.461	-0.585	1.759	-2.913
-1.447	-1.768	0.512	0.139	10.798	-0.048	9.879	-0.826
1.860	1.702	0.002	0.007	1.558	2.881	1.042	2.833
10.981	15.293	8.485	18.954	2.582	1.145	1.514	0.675
-0.297	1.328	0.821	3.777	15.406	1.104	9.902	3.988
-1.541	-0.695	-2.218	-1.211	7.863	12.023	7.471	-0.818
0.033	-0.070	7.011	19.380	0.704	-1.912	-0.252	-1.207
0.158	-0.157	-2.854	0.850	0.731	15.986	-0.590	4.436
0.356	2.893	-0.782	4.781	8.985	17.402	7.174	4.437
0.170	5.594	7.870	20.631	-0.005	2.325	3.592	0.837
1.579	3.544	4.227	2.580	5.274	15.972	2.837	2.413
-1.434	-0.930	-0.101	-0.117	-0.411	-0.274	-1.770	1.181
1.631	-0.245	-2.376	-1.516	1.905	-1.466	-0.130	0.706
-1.452	-0.246	-0.340	-1.173	-0.805	0.259	-2.680	-0.786
11.247	14.871	10.122	22.020	1.843	20.278	12.658	22.742
0.749	2.300	7.570	3.617	6.768	6.415	4.229	8.374
-1.424	-0.790	8.270	10.974	4.873	8.386	-1.574	-0.258
1.986	0.090	2.012	3.688	2.217	15.784	1.561	3.061
11.104	19.207	7.067	17.175	1.239	0.608	4.051	5.070
1.128	0.321	8.208	16.278	19.274	16.394	14.933	-0.871
-0.149	-2.150	-0.416	-2.882	-0.759	-1.378	0.152	-3.033
-0.102	-2.073	-0.445	1.629	-2.741	0.090	0.693	-2.700
-0.136	-2.084	-0.572	-0.433	-1.409	-1.225	-0.618	-0.516
0.118	-1.748	-0.543	0.546	-0.178	0.108	0.826	-0.845

Table35.txt

-0.094	-0.079	-0.540	-0.416	-0.755	1.605	-0.094	0.351
-0.430	-1.295	0.005	-1.026	1.130	-2.701	-0.245	-0.303
1.855	0.062	-1.807	-0.207	0.816	2.638	0.619	1.101
2.211	2.481	-0.219	1.902	0.606	-0.937	-0.775	2.509
1.555	-0.486	1.570	1.261	2.939	-0.639	0.706	-0.575
5.200	3.151	0.584	1.430	1.993	3.420	3.181	2.899
5.012	2.107	0.426	6.212	-0.897	0.319	0.953	1.681
3.620	1.664	3.447	2.739	7.424	0.901	2.464	-0.005
4.060	4.463	0.595	3.991	1.732	4.629	4.557	2.754
3.439	3.184	0.686	5.424	2.351	0.914	0.662	1.701
2.607	3.559	5.942	1.712	6.249	1.138	1.519	-0.254
-0.913	-0.345	-0.726	-0.740	-0.133	-0.015	2.414	0.840
0.832	-1.358	-1.078	0.015	-1.025	0.871	0.582	-0.967
-0.835	-0.243	1.519	-0.249	11.207	-1.053	-0.002	-1.702
-2.242	-1.399	-1.354	-1.676	-1.173	-1.613	-1.171	-2.548
0.386	-0.515	2.671	6.284	-2.290	-1.471	-0.399	-1.046
-0.341	-2.123	0.009	-0.712	-0.204	0.324	-1.488	1.771
-2.274	0.228	-1.874	-1.908	-1.077	-1.947	-1.597	-1.457
2.396	3.406	-0.902	-2.002	-1.192	-1.129	-1.576	-0.238
0.024	-4.591	-0.628	0.156	-2.488	-1.102	-2.022	0.131
5.053	8.221	3.306	2.662	1.026	1.518	1.660	1.968
1.015	0.707	1.892	-0.030	1.067	1.715	0.850	2.117
1.990	-0.660	0.306	-1.353	0.996	10.840	1.978	1.133
1.395	-0.060	0.684	-2.414	-1.741	-3.308	-2.092	-0.994
0.164	-2.029	-2.648	-0.273	0.275	-0.159	-0.449	-0.624
0.149	-1.191	1.848	-1.238	0.362	-1.784	10.178	0.030
6.052	5.043	1.134	4.876	1.799	4.863	-0.810	4.732
10.146	14.673	9.331	4.950	12.563	13.708	3.913	4.741
2.927	6.066	2.979	1.847	9.953	2.353	0.829	0.559
-0.692	-3.331	8.869	14.858	0.107	-1.057	10.199	-1.047
-0.495	-2.943	3.595	11.200	14.531	0.022	8.975	5.908
2.949	13.046	5.678	-0.026	-1.307	2.375	15.026	0.853
3.694	2.816	1.789	1.570	2.837	0.132	1.525	5.573
13.117	15.664	9.061	15.574	12.896	12.866	6.505	2.503
1.266	3.877	0.449	4.542	7.404	16.772	12.963	2.484
1.006	1.029	0.110	-0.001	0.836	0.243	-1.086	-0.553
13.924	17.442	9.976	13.485	14.954	13.081	4.850	4.367
-0.622	-1.383	1.475	-0.112	0.185	16.941	12.922	-1.212
-0.254	-1.500	1.807	-0.184	-1.300	-1.305	-1.730	0.076
-2.660	-1.454	-0.474	0.203	-0.135	-0.322	-0.491	-2.308
-2.712	-0.530	0.009	-0.550	-0.404	-0.142	-1.707	-1.585
9.004	4.221	8.662	16.222	3.960	7.896	10.707	5.870
2.076	5.430	5.794	15.498	0.245	1.875	2.281	1.384
4.052	2.284	4.621	5.330	5.008	1.370	1.890	3.703
11.117	0.241	3.828	4.686	1.109	2.664	0.124	1.636
3.455	3.143	10.616	20.565	0.869	1.266	0.747	1.573
13.599	17.901	-0.510	1.687	21.387	5.805	14.945	0.451
0.110	-0.344	8.703	9.462	-1.238	-2.713	0.467	1.420

Table35.txt

1.026	0.629	5.312	15.184	-1.312	-1.169	-1.464	-0.497
0.268	-2.781	1.196	6.579	13.710	6.497	8.452	2.225
6.713	-1.220	15.155	17.266	4.566	-1.333	-0.881	-0.889
0.703	1.488	-0.381	-1.057	0.066	-0.486	0.545	-1.693
1.805	-1.525	0.689	0.120	14.164	-1.927	13.121	0.826
6.171	5.652	0.467	-1.169	0.041	-0.460	3.312	6.622
-2.454	-1.224	-1.854	-1.976	2.042	3.014	-0.590	-1.190
2.400	4.157	7.085	11.267	0.551	0.481	-1.547	-2.000
0.085	-0.389	-2.073	-0.679	-1.034	-0.645	0.139	1.988
12.146	17.952	-1.136	-0.856	14.644	13.318	-2.099	-0.289
1.082	-0.694	8.241	15.878	16.762	-1.340	-1.545	2.102
0.654	-0.663	7.624	13.485	-0.211	-0.027	7.236	8.807
2.151	2.211	2.117	-0.229	11.054	9.255	7.794	6.513
9.211	11.186	3.947	7.468	16.260	8.457	-0.298	-1.691
15.930	17.962	10.420	21.588	10.221	18.744	-0.983	-2.118
12.739	16.268	1.301	-0.858	13.666	13.890	10.614	3.160
10.960	13.526	6.452	16.636	20.589	13.661	12.667	9.178
-1.886	1.442	-0.268	1.132	-1.108	1.310	6.415	14.654
6.297	14.712	9.197	21.200	9.130	11.063	6.736	-0.808
8.638	9.616	8.541	19.741	20.468	6.718	-0.870	6.294
13.758	17.788	13.065	22.462	-0.430	17.910	12.034	2.778
12.358	15.570	9.178	17.600	11.633	9.952	11.121	12.588
11.759	15.445	-0.104	-0.378	18.443	1.135	-0.313	1.719
-2.115	-2.371	-1.045	23.277	-0.168	16.419	-2.637	1.800
13.389	16.276	-0.224	-1.378	-1.108	-0.801	0.585	0.339
15.273	16.874	9.013	16.302	18.985	-1.769	0.079	-0.382
18.946	22.502	2.337	4.634	0.344	2.671	8.439	10.799
12.661	17.572	10.197	19.560	1.424	1.095	-0.081	0.160
3.229	-1.011	-0.901	-0.603	20.941	2.470	6.066	2.349
-0.707	-0.194	12.435	17.214	10.831	21.710	0.663	-1.009
-0.021	-0.353	9.590	20.984	-0.047	0.328	-0.862	-0.238
5.964	1.494	-0.150	-1.237	14.905	-1.804	-2.924	1.199
16.567	19.862	11.923	19.715	8.465	20.904	12.602	19.760
3.517	4.173	8.954	20.091	15.880	14.549	7.348	6.793
-0.245	-0.621	10.459	13.344	18.740	12.806	12.138	2.343
6.835	9.116	-0.890	0.247	0.468	-0.324	-0.492	1.715
4.830	1.944	0.190	-1.349	-0.929	-1.754	1.000	-0.418
12.504	14.384	0.856	-2.232	19.736	16.132	0.757	1.857
-1.553	-0.134	16.380	24.728	-1.733	-1.036	-0.267	-0.107
-2.136	1.136	7.766	11.720	-2.038	2.043	-0.523	-0.856
0.177	-0.804	5.053	9.397	7.235	1.321	1.457	-0.308
-1.281	-0.660	0.186	-2.369	-1.098	0.610	-1.329	-1.272
-2.649	-1.335	-0.529	-3.125	-0.707	0.425	-1.197	-2.040
-1.154	-0.129	0.273	-0.795	-0.627	0.062	-0.210	-0.412
14.507	21.092	-0.722	-1.684	10.546	23.586	-0.488	0.042
11.991	17.628	9.203	18.366	-0.251	-0.830	5.235	2.562
11.227	14.242	8.981	19.042	15.102	10.082	-0.375	7.986
-0.040	-1.431	0.323	0.225	0.073	-1.620	0.423	1.600

Table35.txt

-0.052	0.656	-0.556	4.478	-1.130	0.344	1.303	-1.074
-0.529	0.723	0.186	1.777	-0.241	-0.461	0.215	0.347
-1.289	-0.287	-1.138	0.568	-3.461	5.101	-1.691	6.506
0.258	-0.556	6.844	19.296	-2.689	-0.314	-1.017	-0.807
-0.929	1.631	-1.714	-1.786	20.429	-1.207	11.828	5.831
6.986	0.028	-0.834	-1.118	-0.185	-0.298	-0.426	-0.105
12.395	14.129	10.214	18.425	-0.914	0.810	-0.107	0.727
-0.885	1.032	-0.604	0.963	18.192	0.005	14.167	0.555
-0.166	3.165	4.114	1.064	2.581	13.161	9.848	6.104
3.778	13.090	7.939	14.293	1.128	2.210	-0.035	4.517
0.831	2.214	11.910	3.456	20.018	13.472	14.810	-2.651
-1.221	-0.770	11.063	15.255	-0.820	16.061	12.501	21.608
-0.513	-1.695	11.292	20.128	11.131	9.368	9.911	12.229
-1.684	-2.219	-0.924	0.105	-1.146	12.664	15.112	3.584
11.726	12.236	-1.509	1.534	-0.570	8.155	10.546	18.190
-1.233	1.407	9.014	18.928	13.487	14.923	0.416	-1.197
12.047	4.080	10.564	3.022	16.186	14.350	0.298	8.341
-2.435	-0.534	-0.426	-2.020	0.700	14.893	0.621	-0.455
0.039	-1.618	1.452	6.932	3.779	5.452	-0.291	-0.804
0.138	-1.892	-0.380	-0.590	0.018	-0.697	-0.218	0.762
13.478	12.570	3.749	19.928	7.195	16.651	9.642	14.936
10.580	17.248	8.806	15.505	8.865	8.638	11.185	15.027
12.900	12.384	4.766	8.026	9.249	5.308	11.186	3.424
-1.380	-1.358	-0.483	7.466	3.538	9.204	2.872	-0.438
12.110	1.026	9.534	19.530	-0.125	-0.518	0.200	0.860
1.840	-0.780	-0.452	0.003	17.155	14.702	-1.512	1.737
3.440	1.823	0.911	0.298	1.842	1.605	0.506	1.722
3.069	5.653	-0.143	4.561	0.199	0.203	2.945	2.421
1.620	1.188	3.680	-0.781	2.603	-0.206	3.107	0.243
0.482	2.410	3.029	1.596	2.651	2.927	2.102	2.609
8.026	7.472	4.617	0.341	4.479	-2.262	8.057	11.873
0.870	0.758	1.319	2.393	11.031	0.178	-0.176	1.336
15.813	17.886	13.480	25.252	10.511	20.744	0.884	0.171
2.535	3.627	8.325	16.668	0.896	-0.573	1.835	-1.339
0.031	1.620	1.735	1.039	7.779	13.411	0.159	-0.339
0.057	-2.360	-0.171	-3.199	-2.800	-2.910	-0.356	0.813
-0.409	-1.750	-0.962	4.005	-3.259	-0.752	-2.318	-2.208
-1.594	-1.269	3.297	8.123	-1.934	-0.461	-0.964	-1.012
15.059	20.737	12.494	21.044	9.759	15.595	1.807	-0.139
6.892	11.860	8.569	18.507	11.455	8.230	-0.390	0.606
12.665	10.494	8.717	16.420	4.107	-0.906	0.073	8.175
0.085	1.376	10.151	17.095	12.042	17.044	1.904	10.790
-0.594	-0.239	0.252	5.236	-0.380	0.185	0.971	5.238
3.397	1.269	0.997	1.156	2.299	13.239	0.327	1.700
0.448	-1.334	-0.536	0.644	0.463	-1.759	1.084	-0.468
1.451	1.265	11.659	2.573	-3.024	0.042	1.641	0.393
15.140	0.101	0.976	1.164	1.833	-0.982	-1.127	-0.062
-1.141	-0.959	-3.908	-2.931	-0.409	-1.732	0.830	0.920

Table35.txt

-1.848	-0.088	0.525	-1.415	-0.690	-2.110	1.317	-0.268
-1.086	-2.080	0.359	-1.362	-0.758	0.128	0.370	-0.168
-0.676	0.462	-0.184	13.881	13.427	13.817	1.569	3.520
-1.314	-3.313	6.479	15.730	0.456	8.734	-1.369	2.114
-0.015	-2.212	3.079	3.130	3.214	0.636	0.440	2.020
1.089	-2.481	0.886	0.813	-0.523	4.574	10.180	-0.726
12.703	14.489	11.210	-1.635	12.704	14.883	0.506	-1.841
1.285	-0.216	0.343	1.085	-1.974	-2.096	13.597	-0.596
0.494	0.930	1.827	8.204	3.649	15.760	1.519	5.823
4.858	3.998	5.639	6.524	6.389	3.122	7.160	11.408
1.851	14.089	1.526	6.690	17.333	11.542	9.467	0.827
-1.470	-1.940	-1.268	0.492	-1.454	5.020	0.138	-1.257
-0.517	-0.015	-0.176	1.748	1.798	-0.612	-0.742	1.608
-0.756	1.753	4.091	0.353	-0.119	3.941	-0.503	1.801
15.696	22.079	-0.302	18.451	7.582	16.255	12.418	20.573
13.194	16.137	9.476	4.825	16.676	15.784	-0.422	1.467
15.052	17.604	1.370	-0.475	15.062	0.917	12.542	4.254
-1.093	-0.561	-0.505	0.000	0.000	0.000	0.000	0.000
-0.307	0.000	0.000	0.000	0.000	0.000	-0.445	0.000
0.000	0.000	0.000	-0.378	-1.819	0.000	0.000	0.000
-0.505	-2.268	-0.084	-2.246	-1.446	0.000	-0.505	-0.027
-0.272	-1.937	-0.868	-0.217	0.000	-1.281	-0.692	0.000
0.000	0.000	-0.790	-2.141	-1.325	-1.525	-2.842	0.000
-0.423	-1.687	1.597	-1.060	0.000	0.000	0.526	0.000
-2.340	0.000	1.852	0.000	0.000	-2.345	-1.247	-1.440
1.207	-0.261	0.000	-2.351	-1.521	-0.176	-0.571	0.823
0.762	1.153	1.886	-1.333	-0.591	0.000	0.000	0.000
-0.615	0.218	1.153	0.000	0.000	0.797	-3.842	1.820
0.000	-0.730	-0.736	-1.096	1.562	-1.063	-2.169	-1.892
0.070	-0.942	2.612	-0.965	-1.493	-1.763	-0.391	0.000
-0.854	0.529	0.362	-0.592	-0.691	-0.399	1.733	1.523
1.637	0.000	0.969	1.382	4.509	0.720	-0.529	0.068
0.569	0.474	-0.697	-0.939	-0.189	0.000	0.000	0.000
0.651	0.000	0.000	0.000	0.000	-0.887	-0.329	-2.269
0.000	0.000	-3.090	0.744	1.418	0.762	2.427	1.330
-0.498	-1.578	-1.658	-1.622	-1.459	-0.525	-1.122	-1.627
-1.608	0.366	-0.446	0.553	-0.499	-1.053	-1.499	-3.064
-2.912	0.487	-0.283	0.018	0.139	5.516	-2.886	-0.586
-1.158	-1.588	-1.889	0.479	-1.439	3.679	2.555	0.676
0.802	1.800	4.777	-0.391	0.618	-0.826	-2.068	1.731
4.349	4.975	-0.440	-0.809	-2.745	-2.264	-3.521	3.927
-2.625	-2.180	-1.035	-0.064	1.084	-0.755	-0.650	0.000
1.934	0.717	1.603	-1.688	1.001	-1.729	0.377	2.618
2.705	0.826	0.356	0.846	-1.811	-1.713	-1.860	0.015
0.000	0.000	-1.137	1.738	3.376	0.000	0.000	0.000
0.000	-0.790	-1.364	-1.683	0.226	-0.748	1.289	-1.253
0.083	-1.341	0.000	0.218	2.720	-3.229	-1.821	0.000
1.829	-1.256	-1.476	-0.668	-2.310	-0.426	-0.541	0.000

Table35.txt

0.000	0.000	0.000	-0.002	0.000	-0.759	-1.581	0.000
-0.790	-1.457	0.000	-1.312	-2.926	-2.214	-1.863	-0.569
-1.839	-1.610	0.000	-2.447	0.717	-0.990	-0.258	0.000
0.384	0.000	1.526	-1.277	0.000	-1.195	-1.790	-0.376
-1.772	0.487	0.000	-0.529	-1.730	-0.848	-1.005	-2.357
-0.159	0.964	-2.013	0.000	-0.361	0.099	1.950	0.000
-0.411	-0.100	0.000	0.000	0.000	-0.009	0.105	0.000
1.607	0.000	0.000	0.000	3.090	0.050	0.178	0.000
-1.855	-1.472	-0.109	-1.690	2.831	0.741	-2.722	2.587
0.602	3.265	4.245	-0.381	-0.188	2.043	-1.919	-0.104
0.600	-1.199	2.840	-0.507	-1.964	-0.886	-1.628	-2.749
1.671	5.314	7.641	2.623	3.044	-1.592	1.224	0.000
0.000	-0.851	-1.181	1.867	1.826	4.186	6.699	-1.365
-0.071	-1.209	0.000	-0.720	3.059	0.997	-0.482	-1.776
0.307	-0.407	0.669	2.970	5.491	2.896	5.319	3.090
-0.031	0.000	5.492	-0.057	-1.378	5.053	-1.655	1.152
5.481	0.594	3.181	0.043	-2.271	0.390	-1.589	3.317
-2.144	-0.262	7.336	1.261	0.104	-0.445	-1.039	0.000
0.000	-0.910	-0.137	0.000	-1.455	-0.065	0.280	-3.090
0.865	-1.334	0.000	-1.132	0.055	-0.271	-0.834	-0.489
-0.970	0.146	2.938	0.000	0.000	-0.013	0.525	0.000
-1.650	0.000	0.000	0.163	-1.144	1.008	0.031	0.000
0.243	0.694	0.000	-0.340	0.000	0.067	-1.933	0.309
0.076	4.241	10.008	7.187	0.707	-0.620	-0.466	0.000
-1.556	0.000	1.736	-0.505	0.270	-0.882	0.088	3.489
4.499	-1.567	-1.388	-0.355	-2.018	1.001	0.096	-0.407
-2.076	-3.668	-0.526	-2.239	-1.177	-1.355	-1.738	-0.395
-0.634	-1.649	-2.768	0.324	-0.682	-1.562	-0.699	0.351
-0.092	-1.949	0.718	-2.176	-2.971	-2.349	-3.079	-0.561
0.000	0.000	-0.512	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	-0.654	0.000	0.000	0.000
0.000	0.547	2.257	-0.445	0.000	0.050	0.556	0.000
-0.110	0.000	0.333	0.000	0.000	0.309	-0.414	0.384
-0.862	-0.074	0.000	0.478	-1.589	0.000	-0.362	0.000
1.046	-0.169	1.939	0.762	-1.203	0.716	-1.185	-0.700
-0.909	0.595	2.211	0.000	0.000	-2.139	-0.930	0.000
4.042	-2.487	0.000	0.193	-1.283	0.647	-1.307	1.333
-1.969	-0.855	2.066	-1.903	0.566	-0.800	-0.563	4.342
-0.493	3.090	5.333	-1.519	-1.096	-1.428	-1.205	0.240
4.146	-2.269	4.326	-1.021	-0.513	11.205	-1.585	-0.753
1.664	4.378	-0.710	4.261	2.180	0.297	-1.540	-0.137
-0.204	-1.529	-0.704	-0.790	-0.976	0.820	-1.390	-1.389
-0.002	-2.040	0.202	-1.450	-4.294	0.258	-2.921	-2.010
-1.535	-1.662	6.265	-0.956	0.514	-0.092	-0.654	-2.179
1.380	-1.223	-2.706	0.012	0.537	0.151	1.046	-2.175
-1.165	-0.329	0.914	10.299	11.012	-2.844	-0.789	0.662
2.818	7.444	2.515	1.367	1.326	-2.687	-1.248	0.000

Table35.txt

4.166	-0.171	-0.490	0.163	-1.902	0.990	1.495	0.000
4.004	-0.702	1.338	-1.592	1.376	1.582	2.239	2.148
-0.077	-1.607	-1.444	-1.188	-1.060	-0.445	0.368	0.000
-0.877	-0.654	-1.123	-0.790	0.487	-3.346	-2.612	-0.863
0.362	-1.002	-0.135	-2.060	-1.378	-1.786	-3.775	-1.690
0.487	0.884	-0.790	1.170	-1.984	-0.010	-3.798	-0.001
0.240	-1.058	-0.969	1.402	0.090	-0.363	-4.545	0.747
-1.138	-1.398	-2.407	-0.793	-0.543	-1.527	-1.876	-2.315
-0.486	-1.546	4.160	0.000	-1.879	-0.525	-2.294	0.000
-0.550	0.000	0.000	-1.894	1.204	0.078	-2.345	2.623
-0.094	0.000	0.000	2.664	5.401	-1.343	-2.525	-2.227
1.596	2.382	2.598	-0.136	-0.373	-1.038	0.710	-0.427
-1.056	-3.090	-1.684	2.176	0.473	-1.990	-1.274	-1.288
-0.197	-1.740	-0.104	-1.304	-2.208	-1.445	-2.753	-0.384
0.842	-1.126	-1.120	-0.966	-0.217	-0.170	-1.281	0.000
-0.375	0.000	0.000	0.000	0.000	0.000	0.531	0.000
0.000	0.651	0.000	0.284	0.518	0.083	0.430	-0.895
1.854	3.655	-2.805	7.805	-1.026	-1.153	1.262	0.000
1.765	0.000	1.172	2.772	-0.807	2.935	5.875	3.688
6.839	3.691	1.582	1.967	1.211	3.103	3.824	6.084
1.594	2.291	-0.792	1.466	-1.301	-1.370	-1.829	0.000
0.972	0.000	0.561	-0.619	-1.575	1.875	2.539	0.000
0.342	-1.108	-0.700	4.913	4.411	0.271	-1.399	-1.537
-0.770	3.114	7.225	0.000	0.000	-0.029	-2.743	0.000
-2.292	0.000	0.000	3.455	0.864	-1.047	1.997	2.229
2.634	1.346	1.081	-0.928	1.712	1.335	1.794	0.578
-1.390	-1.562	-2.482	-1.720	-1.183	0.110	-4.381	3.090
5.409	-1.212	-3.315	-0.199	-0.403	-2.085	-0.778	-3.368
0.166	-2.288	-0.740	-0.932	-2.904	-1.354	-3.417	-0.272
-0.694	-0.140	2.452	-2.433	-1.262	-1.483	-2.779	0.000
0.000	0.000	1.153	-0.113	-1.169	-0.536	2.144	0.000
5.168	1.742	-0.395	0.774	1.264	-1.056	-1.602	-0.406
-0.590	-0.560	18.587	14.872	10.405	-1.434	-2.157	3.710
0.737	5.711	11.648	-1.272	-2.148	-0.520	1.184	0.171
7.224	8.399	-0.668	-1.892	-1.238	-2.655	-1.901	-1.510
0.006	-1.922	-0.429	-0.719	-1.003	-0.420	0.755	3.166
-1.316	2.277	-0.613	0.290	-0.761	-0.299	0.427	-2.581
-0.511	-0.265	-0.975	-0.053	11.617	-3.013	-1.733	-0.416
-1.418	0.741	-2.092	-0.343	-0.856	-0.163	-3.767	0.000
-0.378	0.169	-0.707	0.914	0.404	-1.627	-1.071	2.015
2.903	-1.077	-0.763	-3.048	-0.219	-1.097	0.906	-0.468
-1.671	-2.048	-1.527	-2.258	-0.051	-0.617	-3.688	-1.215
-2.696	0.819	2.490	-0.729	-0.420	0.270	-2.436	0.053
-0.032	-2.475	-1.357	-0.750	-1.402	-2.200	0.467	-0.178
2.269	1.959	12.964	-3.436	0.670	1.681	-0.558	0.000
0.363	0.000	0.000	-3.090	0.504	-0.381	-2.755	1.402
-0.217	3.297	0.000	-1.218	-3.095	-1.513	-1.296	0.060
-0.036	-2.854	2.483	3.108	-0.469	-1.284	-0.380	0.000

Table35.txt

-1.808	-2.088	-0.882	0.975	-1.047	-0.253	0.890	5.797
4.590	1.526	0.120	-1.841	-1.125	-0.303	-0.959	-3.144
1.760	3.210	0.210	-2.192	-0.448	0.776	2.692	0.000
1.611	3.090	6.175	3.017	1.130	-1.526	1.154	3.154
4.192	3.721	2.516	2.717	2.497	1.464	-1.259	1.781
-1.596	-0.385	4.072	-1.407	0.000	2.348	-1.209	0.000
0.000	-0.557	0.690	1.418	-3.079	-1.711	-0.398	-0.788
0.079	-1.693	0.000	-2.517	-4.039	-0.557	-1.295	-2.249
1.528	3.232	4.489	-0.410	0.637	1.672	-0.248	0.000
0.210	1.371	0.000	0.000	0.922	0.118	-0.812	3.281
3.916	2.477	1.323	-1.882	0.953	1.904	4.451	0.000
-2.363	-1.104	-1.397	-3.471	-0.771	-1.555	-0.775	-0.340
-2.001	0.060	0.599	-0.177	0.359	-1.261	-0.898	-0.924
-0.808	-0.226	-2.460	-0.048	-2.384	-0.376	-0.672	-0.565
-1.373	-0.235	-3.953	-2.186	-1.240	-0.751	-2.316	-0.736
-0.999	-3.090	1.093	-0.780	-0.527	-3.628	-1.520	-0.610
0.000	-1.029	-0.261	-0.984	-2.620	-0.651	-1.035	-1.741
0.778	0.745	4.204	4.115	-1.090	-1.323	-1.508	0.969
-0.850	-1.738	-0.161	-0.051	0.928	-0.948	-1.476	0.506
-0.412	0.610	-0.487	0.926	-1.708	2.013	1.215	-0.487
3.627	5.453	2.620	10.277	9.835	-0.762	-0.147	2.450
7.175	5.559	8.460	0.451	1.806	13.513	13.883	1.769
-0.181	9.115	8.563	-0.099	-1.096	1.673	-1.783	8.890
-0.603	0.902	5.191	4.900	6.419	0.969	-2.393	3.113
-0.606	2.875	4.256	0.458	-0.336	0.725	0.304	1.027
6.153	-0.590	0.000	-0.527	-0.855	-1.821	-0.073	2.005
0.060	-2.164	-2.620	-0.307	-1.013	-1.304	0.160	-1.202
-1.816	0.303	-1.642	0.127	1.295	-2.324	-2.551	-1.027
-1.201	0.232	-0.756	-1.354	-1.232	0.520	-0.127	-1.948
1.829	8.247	15.962	10.677	7.142	1.676	2.775	5.542
5.120	7.648	10.667	-1.471	0.885	1.474	3.113	2.776
7.422	3.918	4.834	0.953	0.820	10.842	12.927	6.935
0.940	1.144	-1.861	0.000	-1.457	0.175	0.338	0.000
0.000	0.540	1.173	0.660	2.593	2.842	0.935	3.068
4.264	-1.423	0.769	3.453	5.636	-1.665	-1.570	3.319
-0.315	2.276	2.274	-1.395	-0.170	5.431	4.226	2.742
4.704	0.670	3.825	3.420	2.544	3.528	3.940	2.739
2.788	3.081	-3.628	-0.306	-2.004	0.309	0.818	-2.380
0.000	0.000	-3.169	-0.328	-1.770	-0.369	0.320	-0.027
-0.241	-2.206	-0.049	-0.145	-1.997	-0.344	2.574	1.592
0.771	-0.766	0.000	2.594	2.933	-0.703	-2.224	0.572
5.794	6.008	-3.452	-2.369	0.116	0.403	-1.327	0.000
-1.434	2.864	0.039	2.091	1.446	-1.916	-3.491	-1.607
-2.188	-1.596	-1.856	1.714	-0.511	1.023	-1.533	-0.321
-0.541	-2.728	1.142	0.266	-0.914	0.309	0.025	0.000
0.717	-0.204	0.560	0.000	-1.316	-0.217	-1.817	-0.378
-3.090	-1.629	-0.515	0.142	-0.058	0.138	-1.290	-0.940
-1.548	-1.969	5.572	-1.060	2.436	4.104	2.200	0.000

Table35.txt

1.598	-1.622	2.366	0.089	2.145	-0.336	-1.355	-1.616
-0.210	3.422	0.944	4.258	6.108	-0.250	-1.026	-0.951
-3.674	-2.280	-0.863	-0.758	-0.664	-1.441	-0.299	-0.878
-1.585	-0.298	-0.826	1.250	-0.777	-1.923	-0.892	0.034
-1.067	1.061	-0.470	-1.800	-0.985	-2.458	-0.289	-1.643
-0.588	-0.677	-1.662	-0.411	0.000	-0.161	0.050	0.000
-0.971	0.000	-0.144	0.000	0.309	-1.233	0.621	0.000
0.000	-1.256	-2.377	-0.861	-2.679	-0.144	-0.403	0.000
-0.434	-3.695	-1.302	1.287	-0.331	-0.002	-1.035	-1.214
0.362	0.595	-0.412	-0.736	-0.975	-0.034	-2.308	0.210
-1.434	-1.483	-1.546	-2.869	0.574	-3.478	-0.769	-0.820
7.820	2.704	-0.207	-0.338	-0.870	-1.382	-1.818	-0.271
2.293	-0.968	-0.454	-1.134	-0.477	-0.701	-2.897	-1.345
-0.083	1.066	0.180	0.938	2.127	-0.870	-2.732	0.207
-2.378	-3.078	-1.837	-1.863	-1.484	-3.548	-0.335	-0.573
2.960	-1.029	-1.409	-0.186	-0.173	-0.493	-1.751	-3.090
-1.274	1.330	-0.954	-2.052	-1.608	-1.855	-1.406	-0.842
0.441	-0.707	0.464	0.000	0.000	-1.316	0.865	0.000
1.235	0.000	0.000	0.000	-0.445	0.309	-0.157	-0.368
-1.371	-1.120	0.000	0.481	-0.879	-1.644	-0.773	-0.202
4.487	6.307	-3.857	0.000	-1.833	-0.595	-1.469	0.000
0.000	0.000	0.000	1.423	-0.868	0.000	0.000	0.955
0.821	0.000	-0.155	0.000	2.567	1.983	3.493	0.000
1.338	8.803	-2.142	5.487	3.090	0.000	1.598	2.439
1.897	1.883	3.024	-0.499	-3.886	3.288	5.818	0.994
1.064	3.090	1.961	0.000	6.529	-0.320	5.696	2.516
-0.210	-1.327	13.567	22.839	3.866	7.728	11.776	8.032
2.873	5.616	10.465	0.411	3.355	0.743	-2.850	-0.817
10.989	13.081	5.766	7.462	0.880	15.015	-0.147	2.574
-0.052	-2.096	11.548	19.475	4.000	5.851	10.745	6.395
3.784	6.265	9.860	1.862	4.688	-0.628	0.715	-1.268
10.225	10.405	6.638	5.182	-0.634	14.158	-0.912	4.949
7.658	9.120	11.521	17.666	12.471	20.514	5.727	15.067
8.144	14.144	1.043	7.580	13.861	13.239	10.871	15.130
11.876	12.598	12.020	16.834	20.436	10.313	13.672	8.322
-0.591	6.096	-0.742	1.671	10.023	0.445	0.330	16.516
10.347	-0.398	3.109	12.745	9.827	-1.895	8.875	7.852
2.328	11.664	-2.202	8.559	16.362	11.126	11.259	-1.234
-2.232	0.008	-0.053	-2.000	-1.600	-0.584	-3.518	-2.411
0.689	-2.057	3.714	5.464	-1.611	-1.027	-1.012	-2.716
-1.049	-2.699	-0.217	-0.466	0.526	1.437	4.178	0.382
3.998	0.493	0.581	-1.089	9.620	14.439	-1.281	4.441
-0.314	0.275	3.747	11.885	7.595	-0.881	0.458	1.161
-0.928	1.596	-0.963	-1.834	-0.002	-1.721	-0.663	0.750
6.826	6.174	5.159	0.199	0.536	1.119	7.410	10.732
7.261	10.142	6.333	-0.522	4.057	-0.703	-1.558	-1.617
-1.882	0.499	-0.840	-1.392	5.074	-0.377	9.164	-1.758
8.650	11.604	5.154	0.154	0.632	0.344	7.589	15.000

Table35.txt

8.627	11.330	6.874	-0.219	4.204	-1.038	-1.078	-0.729
-0.681	-1.499	1.494	-2.248	7.003	-0.736	10.201	-1.458
2.112	7.010	-2.190	-0.308	-0.521	6.193	11.755	15.989
-0.859	-1.467	5.488	11.370	-0.872	-0.506	-1.224	0.098
-0.874	-0.739	7.150	17.140	-1.293	0.054	-1.147	5.136
3.216	7.521	-0.412	-1.908	0.773	6.398	8.409	12.913
0.560	-2.620	5.099	11.209	-0.083	-0.231	-1.081	0.716
-0.706	1.751	3.979	12.310	0.921	-1.069	-1.593	4.333
6.497	13.755	3.941	20.076	4.597	4.467	8.384	-0.734
12.091	10.998	10.800	4.553	10.371	12.250	9.046	9.415
11.600	14.172	4.607	5.387	8.650	5.418	3.223	-1.664
9.389	14.305	10.568	21.400	11.188	20.955	4.087	2.826
0.413	11.932	11.627	16.315	-2.135	-0.021	8.424	10.324
4.669	12.382	10.787	18.902	20.352	14.432	8.922	7.262
9.392	12.357	8.104	17.893	8.525	15.735	2.862	3.987
1.194	11.019	9.832	13.917	-1.413	-0.794	6.972	8.329
4.864	12.571	8.901	16.333	16.306	11.288	9.901	6.485
5.406	-1.342	1.093	1.623	10.685	-0.103	9.306	7.959
7.164	8.011	9.879	13.056	-0.734	2.836	11.811	15.045
2.612	8.138	9.057	14.919	20.399	12.895	6.392	1.385
11.651	16.978	8.512	13.091	0.534	8.108	6.153	-1.329
12.578	18.960	9.109	-0.588	13.436	15.799	8.248	0.773
-0.938	0.208	5.879	13.061	12.772	6.295	15.128	6.632
11.840	18.197	9.275	9.011	-1.725	1.801	5.498	0.441
3.703	14.201	9.220	15.209	9.794	11.366	7.885	5.976
5.404	5.752	7.912	8.179	8.231	11.032	12.009	2.790
-0.074	-0.939	-1.067	-1.061	-0.210	2.638	4.991	-0.208
0.790	20.434	-1.640	0.409	-1.386	-0.958	1.220	10.185
0.366	1.058	-1.388	0.810	-2.003	0.355	-1.377	-1.981
5.479	16.774	7.714	10.995	-0.636	17.107	4.516	7.074
-1.002	5.600	7.823	12.128	-1.477	8.358	0.227	8.139
1.598	8.388	4.112	1.304	8.985	13.831	-2.396	3.600
-0.775	2.176	-1.909	-1.630	-0.620	-0.592	-1.557	-0.781
0.236	-2.714	-0.133	-0.528	-0.400	-1.895	1.096	-0.687
2.537	-0.121	-0.883	-0.573	-0.546	-0.820	-0.306	-0.090
-0.040	-1.358	-1.249	-0.878	-1.196	-0.580	-0.647	-2.196
-0.235	-0.082	1.969	2.258	1.047	1.353	-1.463	-1.678
-1.377	0.575	-1.348	-0.909	10.240	-1.421	-1.187	-1.320
-2.255	1.663	3.369	-1.897	-0.549	0.060	-1.859	-1.070
-0.353	-2.131	11.986	19.351	0.460	-2.363	0.033	-1.709
-1.763	-1.953	-3.659	-1.377	11.523	-2.577	-1.753	-0.184
18.261	21.911	14.140	25.276	11.958	20.637	13.340	22.542
8.673	19.158	11.463	19.709	5.706	14.642	-0.633	1.569
16.233	15.622	3.514	16.996	13.135	13.053	14.099	8.390
-1.068	-1.896	-1.213	-0.838	-0.744	-1.605	10.775	19.153
0.036	-0.402	11.867	12.785	-1.961	-0.232	-0.461	-0.926
-0.091	-0.807	-0.244	-1.442	-0.473	-1.023	10.177	0.689
-1.213	-1.297	-1.353	-0.057	-0.960	-1.073	11.495	-1.195

Table35.txt

1.161	-0.545	12.699	16.631	-0.466	0.544	-1.652	-3.521
0.330	-1.968	1.437	-1.498	-0.877	-1.758	-1.683	-2.481
-0.677	-0.930	7.958	14.577	-1.937	1.256	10.429	13.844
-0.361	-0.956	6.660	13.416	-0.361	-0.550	-0.699	-1.488
-1.891	-0.731	0.323	-0.686	1.102	0.614	-2.282	0.561
0.087	-1.818	0.988	6.421	8.185	10.403	-0.150	-0.422
-0.718	0.472	9.526	13.828	1.146	-0.906	-1.486	11.442
1.749	-0.256	-0.972	-1.124	-1.730	0.504	-0.327	-1.819
14.762	-0.180	11.904	19.889	11.132	16.040	-1.126	1.069
1.376	-0.426	9.088	2.545	9.119	-0.502	1.357	0.321
-0.661	11.344	0.549	-1.576	17.932	-1.728	9.470	-1.143
11.326	10.057	-1.192	-0.072	0.500	9.029	7.891	13.375
0.282	1.052	7.486	14.221	-0.926	0.396	-0.265	-0.498
-0.670	-1.192	0.946	1.611	0.284	-2.085	2.908	1.165
13.302	17.220	0.007	-1.519	1.235	-0.532	6.765	5.010
-0.246	-0.048	-0.730	2.317	6.783	9.223	5.242	-1.220
4.574	4.308	10.266	20.326	4.318	0.234	-1.005	0.025
18.482	-1.502	13.920	-0.393	0.163	17.251	13.413	1.920
0.051	-1.450	0.310	-2.834	13.361	14.923	1.349	12.976
11.428	12.025	1.450	12.132	16.139	17.723	8.792	6.263
20.465	14.260	13.800	29.916	0.510	25.804	12.379	21.212
2.002	3.238	13.065	21.040	16.710	16.977	-0.835	-1.170
1.151	-0.114	1.149	14.060	23.392	2.877	3.926	1.461
-0.692	3.103	0.454	-0.940	-0.716	-1.070	9.244	-0.497
-1.299	0.282	-0.671	0.664	-0.853	4.473	-0.460	3.540
-1.624	3.968	-0.974	0.069	-2.186	14.649	0.164	-1.021
16.930	12.050	15.124	23.383	10.912	11.825	5.130	22.031
13.101	7.811	10.147	20.559	11.800	15.076	10.886	12.669
13.480	4.339	10.281	17.742	22.274	16.248	12.635	10.553
12.537	9.395	10.745	15.795	6.743	7.695	3.889	15.723
9.508	6.155	7.243	14.322	9.184	7.162	6.602	8.736
6.555	4.749	6.868	12.803	16.711	11.420	7.824	7.605
-1.410	0.400	-0.968	-1.771	-1.302	-1.331	-0.316	-0.247
0.547	-1.511	-0.692	-1.217	-0.585	0.327	-0.642	-1.239
0.061	-1.171	-0.009	-1.178	-0.672	0.137	0.264	-1.656
9.808	16.989	7.887	-0.033	7.176	-1.109	6.226	10.746
11.979	0.918	10.966	10.027	12.819	4.515	1.992	7.768
9.156	5.616	-0.277	4.169	18.386	16.282	-0.585	-0.409
3.835	0.200	-0.396	-0.977	-0.200	9.950	-1.408	-2.089
1.107	-0.774	-0.984	-1.156	7.392	9.792	-0.440	-0.118
-1.374	-0.146	-1.602	1.413	0.761	-0.940	-1.030	2.021
14.531	22.779	15.559	22.788	-1.710	0.673	8.921	-0.194
-0.123	0.778	14.739	21.123	0.126	1.118	10.269	12.592
1.220	0.209	9.151	18.747	0.007	14.187	11.791	-0.544
15.523	14.848	13.067	4.184	8.599	-1.141	14.802	17.232
7.996	12.494	3.141	-0.249	4.154	15.834	-0.921	-1.939
5.562	11.036	-0.672	-0.469	16.582	1.269	-1.995	5.585
-2.564	-1.341	-1.249	-1.212	-2.036	-1.261	0.435	14.318

Table35.txt

-0.990	-1.317	-2.415	8.076	9.360	-0.141	-0.363	-1.103
0.521	-1.189	0.170	-1.161	-2.280	-1.601	-0.826	-0.397
4.907	18.365	-1.234	-0.953	2.194	13.672	-0.775	-2.882
3.291	3.544	2.239	4.555	1.180	2.434	2.977	5.686
0.591	-0.177	-1.532	0.859	1.432	4.155	1.892	1.416
-0.584	2.385	-0.839	-1.530	-2.279	-0.901	4.609	9.169
0.860	1.927	0.234	-0.339	12.462	0.940	-0.677	-2.590
-2.244	-1.151	1.233	0.517	1.477	3.456	-0.740	-1.246
-0.388	-1.960	10.330	-0.561	9.026	2.781	12.014	19.647
-0.109	0.077	4.562	7.331	7.127	-0.715	0.843	9.333
-2.336	-1.557	0.464	-1.478	3.919	7.507	1.598	8.429
1.140	3.248	0.229	-0.566	-1.774	1.324	0.526	3.596
-0.700	-0.315	-0.437	-0.112	1.054	1.252	1.520	-1.183
-0.771	-0.478	-0.561	0.305	6.852	-0.280	-1.457	1.059
15.656	0.767	14.471	8.354	8.107	20.933	7.836	13.991
-0.387	-0.763	-1.667	6.368	13.023	5.696	12.279	8.605
-0.453	-0.492	4.188	7.690	20.599	-0.323	12.732	5.576
-1.133	-2.547	-0.164	-4.064	-2.023	-1.835	8.758	-0.942
-0.532	0.080	1.936	6.887	1.758	0.697	-1.114	-1.685
-0.947	-4.338	1.668	-1.087	-1.462	7.731	1.215	-0.449
15.620	20.486	11.999	22.514	4.336	16.093	7.808	18.046
2.467	15.824	4.470	12.323	8.337	14.407	9.815	12.724
9.397	12.537	7.335	17.139	16.832	11.924	11.391	4.596
-1.656	7.195	-0.932	-2.074	5.446	-3.714	-1.196	-0.740
-0.032	1.572	-1.643	-3.735	0.355	-2.045	-1.028	-3.145
-1.673	7.650	-0.850	-0.948	7.163	3.113	12.649	-1.155
0.613	11.469	-1.772	2.403	-1.222	0.578	-0.769	6.087
-1.563	-0.912	-0.003	0.236	-1.602	-0.350	-1.088	-0.235
0.595	14.195	-2.938	-2.460	-4.039	4.186	2.890	6.812
11.184	11.847	10.615	17.816	0.990	15.063	8.004	14.293
2.864	7.079	0.004	13.111	8.055	7.499	4.064	8.365
9.003	-0.248	0.833	1.490	16.963	-2.684	9.989	6.112
11.131	15.295	3.064	5.656	-0.396	0.240	8.155	6.428
1.058	2.535	0.585	-2.674	-1.511	-1.314	2.616	-1.880
-1.587	13.354	-0.626	0.637	2.537	-1.657	7.311	0.116
16.780	21.836	14.675	15.947	5.316	25.250	4.397	13.934
15.180	16.480	5.155	14.235	11.992	13.697	8.772	2.549
5.666	5.139	-0.495	6.479	20.807	6.640	-0.525	3.813
15.996	7.765	-0.346	-0.335	1.779	1.264	-0.119	3.107
-0.948	2.092	5.882	0.794	7.223	0.402	9.088	6.786
0.357	0.102	3.429	9.457	0.043	2.191	-0.754	0.002
13.678	21.486	14.124	21.510	-0.766	23.026	2.332	0.048
0.801	-0.294	8.400	-0.067	14.366	6.649	2.419	1.976
0.242	-1.928	4.781	0.725	-1.541	12.712	-1.168	3.843
13.150	-0.552	-0.350	23.897	-1.076	-1.422	-1.342	-0.334
9.215	1.275	8.875	18.850	15.076	0.454	6.660	9.393
3.485	4.521	0.661	-1.750	10.357	-2.901	6.502	1.281
19.013	21.157	14.362	24.976	1.337	0.687	13.033	22.548

Table35.txt

12.785	19.365	10.130	3.960	15.678	1.896	13.813	16.584
11.440	12.782	1.713	1.280	16.519	-0.008	12.327	-1.533
0.783	-1.346	-2.543	-1.057	0.146	-0.771	-1.863	-1.672
9.071	11.428	8.542	16.202	14.497	0.365	0.033	-0.861
-0.887	15.497	0.974	0.709	10.324	1.275	-0.457	-0.509
0.029	-1.124	0.425	-1.127	-0.511	-1.881	-0.016	-3.450
-1.392	-1.289	7.057	16.899	-0.670	-0.274	-1.091	-1.319
-0.363	-0.227	2.656	14.945	-2.157	3.293	-0.483	0.554
-1.589	-0.755	-0.193	-0.114	-2.086	-1.353	-1.576	-1.735
0.169	-0.984	-2.928	0.402	-2.218	-0.809	-0.234	-0.959
-3.440	-1.386	0.309	-0.175	0.136	-0.471	-2.298	-0.416
14.825	2.210	-0.526	8.234	-2.310	15.150	0.293	0.340
1.248	0.188	8.573	6.103	12.482	8.087	8.737	0.262
9.908	11.047	-0.785	-0.208	12.526	-2.934	-0.388	0.870
18.921	2.361	15.167	24.590	3.820	23.812	7.883	10.801
0.062	12.359	5.455	10.545	15.324	14.512	8.398	7.854
15.246	18.996	7.501	12.539	19.772	1.786	9.189	-0.173
-1.945	-2.957	-1.216	-1.021	-1.895	-1.006	-0.699	-1.912
-0.020	-0.323	-0.283	-0.560	-1.240	-0.329	0.131	-2.090
0.393	0.323	-1.427	-1.664	-2.921	-1.742	-3.492	-1.789
1.106	1.666	-2.206	-3.820	3.988	2.861	0.000	-0.106
-2.787	1.009	6.521	-1.113	-0.446	4.820	-1.295	3.238
0.249	5.683	-1.157	-1.436	-1.596	-3.729	-2.579	-3.104
0.001	-0.151	-1.439	-2.222	0.548	-1.752	-1.492	0.362
1.009	-0.444	0.368	0.218	3.238	-0.233	2.172	-0.408
-1.416	-0.018	0.000	-1.562	-3.485	-2.314	-1.094	-1.934
-1.641	-2.399	-1.088	-0.010	-1.193	-1.310	-1.016	-2.032
0.555	-0.741	-1.017	0.504	-0.916	-1.941	-0.784	-1.658
-2.621	-1.313	0.812	-0.027	-2.690	-1.559	-1.780	-1.129
-0.169	-0.803	-1.900	-1.321	4.835	4.211	2.294	-0.855
0.619	1.016	-2.768	-0.218	-0.688	-1.792	-1.342	1.716
0.928	-2.053	2.114	-1.118	-1.545	-0.576	-1.419	-1.523
-2.299	-2.385	-0.886	-0.477	9.843	0.109	-2.347	-1.772
-0.829	3.024	5.291	2.407	5.863	-2.260	-0.591	-1.440
-1.422	-2.264	-1.390	-1.960	-2.599	-3.197	-2.663	-1.429
-0.504	-1.738	-2.616	-0.458	-0.392	-0.718	0.601	-0.185
-0.106	-0.204	6.122	0.091	0.350	-0.584	-2.035	-0.498
0.461	-1.361	-3.302	-0.997	-1.769	-1.210	-2.575	-0.530
-1.715	1.744	-1.934	-1.869	-0.769	0.615	-0.036	-2.728
-0.127	0.188	-0.976	0.020	0.284	0.048	-0.258	-0.631
-1.091	0.155	-0.263	0.362	-1.679	-1.146	-2.099	-1.531
-1.179	-2.955	0.212	-0.195	0.017	-2.225	-0.845	0.208
-3.207	-1.038	-1.614	-1.608	-0.210	-1.969	-0.985	0.009
-1.302	-0.442	0.413	-2.521	-1.583	0.029	-3.030	0.238
-2.515	-2.563	-2.593	-0.644	-2.645	-1.892	-0.356	-1.195
-1.226	-2.617	-2.028	1.281	-2.828	-2.872	-1.712	-0.659
-1.087	-1.101	0.853	-0.378	-4.176	-3.115	-2.251	-2.046
0.580	-3.302	-3.566	-1.127	-0.899	-0.896	-1.866	-1.148

Table35.txt

-0.072	-2.478	-0.707	0.927	-0.379	-1.394	-2.188	0.837
-0.915	-0.740	1.095	0.405	-0.262	-1.289	-2.404	-0.484
-0.230	-2.727	-3.023	-0.449	-2.194	1.071	1.289	-0.871
-0.249	0.373	-0.792	-1.066	-1.674	-0.649	-0.137	-3.277
0.243	-0.125	-2.981	-0.813	-2.345	-1.799	-1.054	-0.114
-0.032	-1.679	-1.727	-0.198	0.532	0.690	-1.828	-0.479
-2.348	-2.786	-0.781	0.252	-1.043	-1.229	-0.510	0.196
-0.196	-1.566	2.822	-0.007	-0.962	-2.139	-0.225	-3.316
-1.442	0.784	0.095	-2.748	-0.495	-0.300	-0.944	0.000
6.450	-1.724	0.692	-1.436	-1.714	-2.307	-1.507	-0.103
-0.092	-1.694	0.023	-1.230	-1.974	-2.534	-2.997	-2.024
0.108	-0.829	-3.348	-1.126	0.358	-1.216	0.349	-1.191
-0.426	-1.546	0.046	-0.691	-1.241	-1.764	-0.856	0.464
-0.938	-0.524	-0.153	0.543	-0.675	-2.820	-2.711	-1.831
-0.900	-0.929	-2.282	-0.884	-0.488	-1.236	-1.565	-0.759
-0.512	-0.213	-1.213	0.851	-0.080	-0.863	-2.150	-1.279
0.343	-0.732	-1.157	-1.746	-1.662	-1.952	-0.020	-0.756
-1.233	-0.971	-2.349	-1.555	-1.870	-2.183	-0.877	-1.644
-0.677	0.005	-3.441	-2.483	-0.031	-1.199	-2.381	-0.636
-3.115	-1.837	-0.934	-1.610	-0.982	-2.991	-1.847	-2.025
-2.477	-0.483	-1.797	-0.211	-2.675	-0.479	-0.544	-2.111
-2.947	0.452	-2.761	-1.800	-0.710	-1.894	-1.658	-0.645
-1.004	-0.246	4.650	-1.157	-2.240	-4.212	-1.217	-0.714
-2.847	0.066	-1.069	-4.041	1.067	-1.360	-0.994	-3.469
0.458	0.041	-0.598	0.400	0.443	-2.084	-0.511	-0.233
-1.136	-0.652	-1.625	-0.015	-2.076	0.900	-1.946	-1.881
-0.534	-1.663	-2.757	-2.166	1.040	-0.915	-2.282	-1.278
-0.110	-0.258	-2.164	-0.247	-1.148	-3.474	-1.337	-0.250
0.053	-1.110	-0.241	-1.570	-1.370	-0.172	-2.319	-0.980
-1.564	-1.229	-0.695	-2.352	-1.547	-1.713	0.780	-0.105
-0.101	-2.146	-2.046	-0.346	-1.108	-1.940	-1.080	-0.792
-0.053	0.780	-0.292	-3.225	-2.775	-0.988	-2.199	-1.071
-3.003	0.103	-2.779	-2.794	-1.434	3.597	7.982	2.439
3.920	0.990	-1.557	-2.846	-1.743	-2.372	-3.162	-1.688
-0.149	-1.468	-1.554	-1.520	-1.490	-1.522	-3.802	-2.962
-0.390	-0.526	-1.724	-1.723	-0.228	1.412	-2.124	-1.465
-0.175	-1.632	0.127	0.288	-0.211	-1.786	-1.350	-0.580
-0.180	-0.148	-2.156	0.352	-0.397	-1.838	-1.469	-2.631
2.762	5.549	6.243	1.323	8.794	3.940	1.358	5.328
7.807	0.090	10.063	2.373	4.105	6.869	7.002	-0.448
-1.306	6.755	-0.432	12.664	18.837	13.062	4.652	12.797
14.496	14.878	7.283	23.295	-1.901	0.498	1.134	5.551
10.945	11.963	8.980	0.651	10.593	6.116	2.927	9.108
0.247	14.203	-1.315	11.980	2.367	9.716	8.957	5.643
-0.864	2.615	-0.800	1.625	1.740	0.185	2.019	3.540
0.108	0.446	0.732	1.799	0.818	2.156	0.774	-2.229
-0.733	6.364	-0.211	1.231	3.225	8.363	5.688	1.225
-0.584	0.715	-1.592	1.713	-1.624	-0.999	-0.411	-0.959

Table35.txt

0.373	2.224	8.552	-1.594	-0.649	-1.199	-1.506	-2.237
-0.951	3.090	0.684	-1.290	0.415	-0.023	-1.369	-0.393
0.294	1.178	9.585	12.698	-1.694	-0.085	-1.881	4.644
3.282	5.084	-2.112	0.309	-1.505	3.539	3.299	1.666
0.057	4.571	-0.934	11.141	16.314	8.422	1.925	6.611
-0.863	0.640	2.949	0.663	-1.155	1.533	-3.132	-0.489
0.475	1.147	1.363	0.188	0.517	-0.922	0.037	0.427
2.301	1.678	0.670	-0.456	0.670	0.550	-2.328	0.657
0.060	-0.522	14.996	13.565	1.712	0.962	3.047	4.776
3.270	1.218	3.291	0.489	-2.244	7.664	13.025	4.173
3.780	-0.986	-0.064	-2.264	-1.990	12.054	0.299	8.801
1.934	3.929	14.132	-2.051	-2.221	0.136	-1.896	5.574
0.376	0.551	7.977	0.286	0.932	5.481	8.294	-0.363
2.994	1.514	1.230	1.730	6.757	-1.706	2.930	3.221
-0.452	-1.352	-1.846	-1.999	-0.034	0.044	-1.394	0.315
-1.527	1.409	1.557	-2.242	-0.733	-1.329	-1.699	4.329
-1.240	-0.993	-0.667	-0.540	-1.441	3.310	-0.800	0.092
4.284	1.136	14.416	10.540	-0.138	8.884	3.803	0.788
5.611	7.294	7.988	2.079	0.707	11.129	5.658	10.013
1.623	3.934	2.580	1.878	3.548	7.101	-0.820	-0.184
-1.451	-0.349	0.900	0.353	-1.305	0.849	-1.601	1.672
0.162	5.124	7.734	2.938	-0.190	-2.226	14.939	7.678
1.752	1.681	0.804	-0.376	5.688	13.875	6.493	-1.046
2.482	-0.861	5.044	3.069	3.311	3.378	10.798	5.596
1.961	-1.327	3.175	1.234	0.854	2.119	5.980	-1.234
-1.340	0.549	0.212	0.109	-0.690	11.629	1.895	-0.268
-0.086	-1.083	15.463	6.657	2.689	-0.497	-0.575	6.319
0.786	0.150	8.767	2.945	-1.005	2.916	5.756	0.440
-1.486	2.416	-1.964	-1.643	-0.012	11.312	-1.414	-0.495
0.336	-0.673	15.366	0.164	0.892	-1.102	0.044	5.120
-0.708	-0.785	5.749	1.049	1.711	2.163	-0.485	1.408
-1.131	0.336	1.095	-0.804	2.258	6.622	0.378	-1.539
14.313	12.823	0.770	-1.905	0.117	-2.392	-1.597	-0.421
-1.006	0.742	8.165	17.722	10.324	12.170	-0.959	-0.617
-1.792	10.930	-0.033	0.508	-0.108	11.802	-2.228	0.015
0.917	-0.228	0.282	10.319	0.042	0.680	-0.368	7.574
2.310	-0.835	-0.625	0.021	2.443	-0.718	-1.796	0.973
-0.795	3.780	3.529	0.624	-1.831	12.700	14.659	-0.106
0.485	2.534	-1.294	-3.678	0.367	-1.153	0.186	0.045
-0.308	-0.426	-0.672	-0.107	-0.306	-1.474	1.306	2.158
-0.645	-0.146	0.332	-1.117	-0.975	-1.515	-1.562	-0.974
13.487	12.197	0.572	1.536	1.714	-1.545	-0.995	15.470
9.501	0.248	6.814	15.538	1.080	12.940	0.944	-0.265
-0.725	11.766	-0.726	-0.107	0.863	11.211	-1.096	-1.464
-1.069	-0.946	-2.813	5.417	-0.413	-1.184	9.444	-0.359
-1.498	1.934	4.986	0.948	-0.468	-0.832	-0.417	1.422
-2.952	-1.237	0.543	-1.757	-0.820	5.787	4.178	-1.987
4.643	18.117	22.117	2.925	11.250	-0.179	-1.111	8.180

Table35.txt

10.299	6.117	13.401	3.901	-0.920	3.158	3.512	9.153
2.048	7.231	1.462	13.257	14.817	17.098	13.008	2.367
-0.787	-1.664	-0.534	-0.265	-1.531	-2.202	-0.115	0.948
0.911	-1.449	-1.131	1.259	-1.633	-0.823	-1.546	-0.190
-0.110	0.920	0.371	-0.175	-0.298	3.340	3.842	0.533
0.609	5.868	-2.345	-0.416	-0.465	-1.693	-1.739	5.995
7.975	0.736	5.216	2.135	-0.771	-0.889	3.060	-0.767
0.136	7.588	-0.172	-0.942	-2.252	12.359	5.826	-1.948
-1.517	10.007	11.144	0.772	11.814	3.658	2.528	6.655
8.668	1.012	0.869	6.092	6.399	7.478	7.289	-0.521
-0.897	-1.143	5.872	-0.991	-0.211	15.786	19.942	-0.140
6.492	14.138	3.278	16.801	11.864	5.229	10.882	0.000
7.398	6.072	10.770	3.879	0.867	4.885	2.665	-1.529
-1.416	0.085	1.215	-1.809	-1.909	-0.794	17.696	0.922
5.921	0.370	17.998	-0.614	9.547	7.051	12.132	6.141
1.817	-1.600	10.418	3.202	5.116	-0.018	17.601	3.977
3.199	7.833	5.097	0.158	16.394	17.546	14.482	11.653
0.236	-0.808	-0.715	-0.158	-0.455	0.198	-0.790	-0.023
1.246	0.819	0.072	1.726	1.342	-0.475	0.296	1.972
1.143	-1.029	1.105	0.148	-0.832	1.390	-1.014	-1.009
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.588	-0.575	3.374	-1.731	-0.125	0.954	-1.556	3.415
5.230	1.732	0.675	1.260	-0.101	1.751	2.817	0.099
-0.837	2.013	0.286	-0.122	1.132	3.898	7.128	-1.635
-0.350	-0.938	0.589	-1.684	-0.483	-1.270	-1.152	0.335
-1.228	0.395	-1.054	-1.917	0.805	-1.194	-2.266	-0.505
-2.341	-2.056	-0.704	-3.636	-2.244	-2.424	-2.429	-4.770
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-0.508	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	-1.034	0.000
-1.679	-0.305	-0.590	-1.430	0.561	0.000	-0.445	0.000
0.000	0.000	0.266	-0.144	0.000	-0.914	-1.717	0.000
0.000	-0.378	0.000	-1.214	-0.563	-1.114	0.218	-3.090
-2.487	-2.156	0.000	0.729	1.692	0.091	0.919	0.000
-0.100	1.412	0.662	0.218	0.077	-1.381	2.059	-0.602
0.675	-0.265	0.000	-0.133	-4.061	-1.327	8.099	-1.056
-1.075	-1.711	1.004	-1.424	1.520	-0.877	-0.713	-0.005
0.451	-2.278	-1.741	-3.082	-0.305	-0.061	-1.014	-0.966
1.329	-0.563	-3.306	-3.979	-1.360	-2.046	0.325	0.743
-0.878	-3.568	-1.374	-2.869	2.442	-0.690	-0.947	-1.028
-1.210	-1.363	-0.317	-0.999	-0.815	0.419	-2.251	-2.193
-0.297	-2.142	-1.550	-2.076	-2.047	0.000	-2.931	-1.263
1.335	2.381	2.213	-1.010	-0.355	1.713	-1.122	1.240
-0.388	0.326	0.204	0.108	-1.561	-2.531	-2.109	5.524
6.438	1.108	1.132	-1.593	4.119	10.153	8.752	1.328
-1.436	-1.410	0.874	-1.751	-2.189	-0.523	0.359	-0.384

Table35.txt

-0.165	0.858	-0.556	1.257	-2.232	-2.377	-0.582	-0.292
-0.179	-1.294	1.402	-1.366	0.442	1.792	0.377	2.107
-1.823	-2.494	-0.562	0.386	0.698	-0.090	5.008	2.666
-2.251	4.719	5.059	-0.789	-1.189	-0.156	-0.071	1.958
2.225	-3.175	1.009	-2.250	-1.804	-2.031	-1.557	-1.826
-0.090	-1.769	4.198	-0.966	-0.986	-0.485	-0.142	2.630
0.702	0.580	-1.591	0.735	-0.377	-2.839	-2.346	1.970
1.336	1.612	0.105	-0.443	-1.957	3.218	4.084	-2.292
-0.543	1.191	-2.160	0.001	-1.930	-0.086	-0.942	-0.318
-0.107	0.526	-0.599	1.417	-0.264	-0.176	-0.161	-0.890
-0.162	0.221	-0.081	-0.847	-1.821	4.805	0.854	-0.154
3.992	-1.724	5.391	9.706	0.703	8.000	0.010	-1.203
5.131	9.029	1.868	15.588	7.090	6.327	5.452	2.534
0.000	3.090	1.270	-1.903	9.606	3.090	3.744	8.357
4.148	5.252	3.955	6.645	3.490	3.344	10.778	9.733
4.918	6.843	6.037	12.195	0.658	-1.671	2.113	6.863
9.776	10.066	3.083	3.662	3.362	3.608	-2.846	3.551
-0.138	-1.584	0.105	-1.897	-1.726	11.686	-2.412	2.325
2.466	4.480	2.536	5.592	-0.173	-0.835	-0.839	-2.027
-1.906	-1.516	-0.109	-2.136	6.572	-0.790	-1.692	-1.691
-2.374	16.029	-1.563	-1.950	-0.577	6.009	8.640	16.303
-0.482	5.763	1.383	16.228	9.930	7.619	5.904	9.079
5.339	7.384	-2.623	-2.551	12.520	-0.257	0.207	3.234
9.263	4.441	2.453	4.300	0.118	-1.475	5.241	3.095
1.610	2.781	0.608	3.015	0.116	1.955	2.793	2.460
3.683	3.499	1.654	1.518	-1.073	3.550	11.969	4.874
-1.245	-2.495	-1.202	-1.765	0.249	5.680	-0.299	-3.033
-1.799	-2.398	1.082	2.449	0.160	-2.360	-0.797	-1.449
-0.853	-1.252	-0.229	-1.817	17.022	4.490	-1.665	-0.558
6.933	5.418	2.457	5.576	5.892	13.154	8.560	18.111
2.672	1.890	-0.908	1.035	1.856	1.415	-0.082	-1.271
4.657	3.363	5.455	13.187	9.726	8.486	3.106	2.443
-0.643	-0.795	5.351	13.151	3.196	2.243	9.234	15.534
-0.506	0.093	1.567	12.042	1.224	0.649	-2.513	-0.952
4.837	5.888	3.868	5.343	19.308	7.402	7.159	-0.533
0.959	-0.407	-1.571	-2.785	0.522	-0.980	-1.966	-2.947
-0.339	-0.393	-0.254	-2.515	-1.086	-0.965	-0.252	1.198
-1.768	-0.767	-0.168	-0.335	7.162	-0.637	0.048	-0.530
-1.413	-1.510	-1.010	-2.658	-0.487	-1.783	-1.162	-2.509
0.590	-1.140	0.746	-0.464	-1.329	-0.760	0.892	-2.923
-1.609	-2.480	-0.063	-0.042	-1.055	-1.726	0.351	0.000
-1.060	-0.136	-2.295	-3.328	-0.203	-1.236	-0.796	-1.973
-0.139	-1.791	-1.915	-1.252	-4.153	-1.716	-2.511	-2.702
-0.299	-2.340	-1.660	-0.712	-3.641	-2.304	5.010	-1.808
-0.617	-1.145	-1.312	-1.888	-1.106	-2.372	-0.929	-2.362
-0.356	-2.131	-0.501	-1.573	-1.239	-1.619	-0.762	0.262
-1.045	0.370	-0.835	-2.569	-1.875	-0.434	-1.639	-0.426
-0.320	-2.670	-0.378	0.000	-0.251	1.748	1.526	3.090

Table35.txt

-0.046	-0.652	-1.567	-1.236	-0.151	-1.746	0.872	-2.647
0.963	0.388	0.708	-0.552	-1.163	-0.894	-3.709	0.000
-0.510	-3.334	-0.620	-1.848	0.971	-2.194	-2.706	-1.538
-2.096	-1.472	0.000	-1.050	-0.098	0.000	-0.592	-1.903
-1.657	-2.719	-1.201	-0.874	-1.041	0.000	-1.063	0.000
-1.468	-1.643	-2.061	-1.930	-0.566	-1.973	-1.071	-2.356
1.898	3.309	1.526	11.010	0.425	0.218	-0.359	-0.948
-0.462	1.339	-0.136	-2.754	-1.697	-1.261	-0.754	0.131
0.573	1.960	-2.016	-2.097	-1.126	-0.070	1.362	-2.837
1.861	1.799	-0.307	-1.924	-2.203	-0.304	-0.286	-2.216
-1.281	-2.763	-1.116	-1.257	3.628	0.865	-2.167	0.000
-1.536	-3.008	-2.229	-1.472	-2.385	-1.686	-1.746	-1.688
3.974	4.281	2.668	-1.610	-1.305	1.787	-2.997	1.177
-2.562	-1.857	-0.305	0.229	15.696	4.095	1.442	-1.867
0.419	-2.555	-2.465	-0.651	-1.273	-0.027	-1.522	-0.082
-0.449	0.420	0.036	-2.287	-0.776	-1.146	-1.308	1.040
-1.153	-3.164	-1.612	0.418	-2.387	-1.789	-0.929	3.337
-0.340	-2.333	-2.291	1.291	0.000	-1.860	-0.642	-0.284
0.374	0.701	-0.520	-1.955	-0.766	-0.405	0.200	-0.784
-1.699	-0.907	0.000	-0.912	-1.162	0.365	0.000	1.239
-1.040	-0.930	4.520	7.018	4.090	-1.660	-0.939	0.936
-2.438	0.058	1.194	8.261	-1.781	-1.581	0.684	5.443
5.077	5.797	-0.386	-0.640	-1.206	-1.192	-1.250	0.520
-0.627	0.985	5.529	5.502	0.804	3.271	-0.677	-0.894
-1.223	-1.034	-0.911	2.116	4.741	3.226	-0.099	-2.025
-0.757	-3.312	0.029	0.313	0.613	-1.966	1.498	0.208
0.000	2.614	0.000	0.362	1.365	0.000	1.064	3.103
0.584	0.000	0.000	2.179	0.000	0.000	2.654	1.887
1.198	2.638	1.151	-1.574	2.102	-1.650	-2.498	-1.256
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.161
0.000	-0.961	0.000	0.000	0.000	0.000	0.000	-0.823
-0.020	-2.231	4.022	9.870	8.909	12.463	-0.373	-0.125
9.411	12.904	5.324	6.925	8.732	9.195	4.033	5.250
4.906	12.321	3.737	3.401	6.127	3.537	-2.518	-0.269
-1.445	-2.306	-2.541	-1.085	5.063	6.570	-3.244	-2.130
2.189	6.511	-1.591	-1.178	6.068	6.040	-1.516	-0.766
-2.173	-1.322	0.218	-2.352	-0.175	0.272	6.056	4.721
-2.229	-1.724	-1.617	0.140	-0.171	-0.009	-1.082	-0.988
0.132	-1.077	0.000	-1.567	-0.713	-1.281	0.000	-0.717
-1.169	-0.772	0.000	-1.073	0.000	0.309	0.529	0.204
-1.383	-3.274	1.634	3.982	3.507	1.842	2.750	-0.707
2.679	-2.098	-1.793	1.813	0.110	-1.827	-0.470	0.921
-0.893	0.623	3.763	1.605	-0.877	-1.990	1.096	1.040
0.646	3.237	5.078	4.649	0.000	0.000	-1.786	-2.642
8.072	10.364	-0.791	-0.640	2.593	0.751	0.424	-0.960
1.579	3.143	1.894	4.233	5.260	-2.278	-0.738	0.303
1.423	0.406	0.000	-3.693	0.382	-1.444	2.969	0.098

Table35.txt

7.629	4.874	0.022	-1.576	0.731	0.010	-1.461	-0.347
-1.310	2.083	-2.009	-3.903	2.036	0.614	1.064	-1.397
-0.328	-3.308	0.103	-0.256	3.975	5.255	5.107	5.013
7.601	8.509	-0.318	-2.871	2.114	1.400	-1.565	-1.837
-1.215	-2.373	0.699	-2.059	5.826	3.797	1.702	1.296
2.782	5.028	-0.697	-1.072	-0.732	1.440	2.199	-0.242
0.281	2.975	2.483	8.426	-2.178	0.459	-1.256	-2.486
-0.124	-2.558	-0.115	-3.316	3.559	2.055	-0.105	0.651
-3.118	-3.878	3.731	1.960	0.333	-2.099	-1.456	-1.638
3.083	7.106	-1.292	-1.923	-2.215	-0.887	-1.198	-1.112
-2.103	-0.860	-1.747	-1.043	13.550	5.081	0.075	0.000
-0.955	-1.915	-0.026	-1.782	-2.905	-2.231	-1.523	-2.095
0.474	2.654	-1.309	-2.583	-1.285	-1.135	3.945	-1.964
1.423	-0.849	1.210	5.656	1.700	-0.888	-1.836	-0.343
-2.065	-1.650	-0.881	0.007	-0.888	-1.933	1.405	-0.709
-0.462	-1.267	-0.314	-1.144	0.014	-1.557	0.977	-1.987
-1.893	-1.382	-0.542	-1.866	6.114	-1.647	0.231	0.909
0.000	0.000	0.000	0.000	-0.059	0.000	-0.505	-0.005
-0.589	-0.829	0.000	0.000	0.000	-0.790	0.000	-1.787
0.000	-0.736	0.000	-2.419	3.104	0.000	0.000	0.000
0.826	-4.032	3.263	2.738	1.860	12.603	5.680	11.279
1.070	3.474	2.825	3.956	-1.113	-1.690	-0.673	-1.040
0.179	-1.956	2.840	2.497	10.899	5.987	1.131	-2.393
1.164	-1.826	-1.489	-0.938	-1.876	-1.215	-0.334	-1.977
-0.199	-2.109	-0.449	2.131	-0.163	-0.078	-2.414	-1.952
-0.622	-4.437	-0.927	-2.043	-2.423	-1.848	-0.391	-0.598
-0.297	0.921	0.000	-0.527	0.566	-0.060	-1.096	-0.418
3.733	6.068	2.327	12.992	-3.063	0.955	-1.799	-0.985
-1.146	-2.618	-0.798	-0.531	13.906	-1.460	-0.490	0.000
0.000	0.107	-0.217	0.696	0.000	-0.203	-0.144	-0.739
0.000	0.000	0.000	-0.827	0.000	0.000	0.000	-2.642
0.000	-0.651	0.000	0.969	1.197	0.000	0.000	0.000
-1.272	-1.244	1.347	3.243	0.000	-1.994	-0.983	-0.727
-1.323	-1.012	0.643	0.007	0.000	-0.792	-0.257	-0.168
0.228	0.524	-2.640	-0.283	-0.026	-0.530	-0.683	-0.442
0.234	-4.058	0.038	-2.076	1.009	-1.404	3.936	-4.150
-1.901	-1.199	-2.429	-0.889	-0.896	-1.696	-2.138	-1.782
-0.147	-0.743	0.531	-1.391	0.438	2.396	-2.475	0.000
0.042	-0.125	0.905	5.887	0.320	5.663	0.237	-1.740
-0.147	-1.480	-0.663	13.713	-0.863	-1.755	-1.690	-2.580
-0.769	-0.432	0.951	-2.740	7.044	0.733	-0.053	-1.183
0.000	0.000	0.137	-0.248	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.004	0.000	0.000	0.000	0.000	0.000	0.000
2.700	-0.824	0.163	1.379	-0.716	4.069	-0.270	-0.625
2.282	2.979	0.917	4.466	-0.805	-1.168	-0.278	-0.793
0.721	0.002	-1.268	-0.945	-2.176	0.238	1.161	1.897
-0.265	7.194	-2.491	-2.841	-2.105	7.381	-0.114	2.653

Table35.txt

5.772	7.496	4.549	6.591	3.090	5.251	0.213	0.356
4.693	6.727	-1.670	-0.715	6.997	3.864	0.000	0.440
1.047	0.113	1.423	1.677	2.542	0.647	1.862	-0.114
0.000	1.519	0.000	0.174	-1.703	1.262	0.382	2.272
0.083	-0.840	-0.144	0.143	0.952	-1.934	0.083	0.000
0.000	-0.484	0.265	-1.292	0.137	1.616	0.610	-1.138
-0.826	0.534	0.000	-0.411	-1.080	-0.071	0.000	2.772
-1.393	0.360	-1.169	-0.206	-0.599	-2.649	-0.914	0.000
-1.695	-1.247	-1.433	-1.553	0.819	-2.374	-1.179	-1.729
1.964	-2.403	-0.009	3.868	-3.382	0.763	-0.171	-0.421
-0.669	-1.952	-0.814	-0.073	5.728	4.106	1.853	-0.166
-0.448	-0.598	-1.937	-1.705	-0.632	-1.174	-0.208	-1.395
-0.323	-3.399	-1.399	-1.413	-1.213	-0.418	-0.236	-0.948
-1.303	-0.673	-1.812	0.644	-1.610	-0.136	-1.306	-0.302
1.627	8.642	2.338	6.254	-1.056	2.149	3.023	2.830
-0.422	1.896	-0.180	2.196	2.887	2.512	2.368	-2.900
1.566	2.604	1.226	0.492	0.738	5.939	3.066	-0.596
-3.263	-0.736	-2.081	0.101	-0.493	-0.447	10.492	-0.936
-0.092	-1.297	-0.859	-1.641	0.466	0.297	-1.139	-1.648
-0.103	-0.984	-1.113	-1.740	-2.100	0.505	0.328	-1.872
0.000	-2.340	2.144	0.006	0.000	0.491	-0.315	-0.541
-0.197	-0.677	0.000	-1.544	-1.427	-1.214	-2.798	-1.723
-1.009	-0.669	-1.139	0.547	-1.359	-0.467	-2.998	0.000
0.977	2.613	0.000	0.000	0.163	1.475	0.375	0.000
2.949	2.011	4.354	5.654	2.679	-1.074	0.007	-2.444
2.771	1.099	0.587	1.332	-0.954	1.146	0.935	0.000
-1.091	7.272	-0.770	-2.128	-0.384	-0.934	2.100	1.390
-0.936	1.353	4.002	14.802	5.939	6.776	4.489	1.487
7.422	6.266	0.019	3.838	8.178	8.611	-0.128	0.184
5.984	-0.894	-1.430	-2.717	-0.869	-1.922	-0.165	-4.147
-0.166	-0.197	-1.510	-1.700	-1.552	0.712	-3.275	-1.426
-0.761	-2.878	1.192	-0.198	-1.386	-3.078	-1.596	-1.826
0.000	0.000	0.000	3.090	10.345	4.365	3.090	3.090
0.000	3.090	0.000	3.090	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	3.090	0.000	3.090	0.000
-0.940	-1.518	-0.828	-1.467	-0.030	-3.383	10.054	18.161
-1.351	-1.232	0.725	-0.763	4.953	4.155	0.478	0.299
-2.643	-2.497	0.847	-0.575	-2.440	-0.705	-2.004	-2.060
-1.330	-1.539	-0.080	-2.937	1.364	0.832	0.331	-1.802
-1.079	-1.413	0.309	4.162	-2.003	0.350	1.575	-0.254
0.493	2.709	0.873	4.309	-0.338	-2.402	0.644	-0.267
-0.923	-1.620	6.790	8.972	-1.237	-0.900	10.384	17.002
-2.934	-1.601	4.055	13.948	10.027	9.497	-0.637	-2.938
0.852	-1.946	0.190	-0.950	13.848	-3.884	-1.336	-1.127
-1.518	3.277	16.582	-0.671	8.392	-0.952	-2.533	4.069
3.172	5.627	10.009	3.090	6.083	-0.841	0.806	3.881
3.779	-0.325	2.192	12.482	14.790	-0.172	-1.791	7.631
0.661	-2.181	0.935	-0.726	0.653	0.904	-0.232	2.968

Table35.txt

1.288	-1.872	1.329	1.450	1.691	-1.897	2.491	2.716
3.832	-0.137	0.336	0.776	1.183	-1.109	2.004	6.480
-1.740	-1.827	-0.856	-2.868	-0.900	-0.636	2.486	-2.517
2.183	4.147	-0.542	1.136	4.655	1.530	-0.508	2.067
-1.042	-0.705	2.749	-1.499	-1.679	1.740	3.090	-1.049
2.536	4.994	-2.314	6.933	2.999	4.414	1.911	7.225
-1.860	-3.437	4.250	10.445	2.646	-1.561	-0.091	6.659
-0.281	-0.856	6.660	5.959	10.281	0.349	0.038	-0.319
-1.512	-2.981	-0.794	-2.676	1.000	-2.858	2.529	-1.145
0.213	-1.435	-0.949	-0.186	0.958	-1.045	-0.596	-0.869
-2.088	-0.521	0.353	-3.032	-1.826	-0.764	-1.863	-0.314
-2.055	-1.634	9.397	14.209	6.769	8.912	3.744	-2.797
9.143	11.074	3.866	9.181	4.130	0.615	-0.864	-1.709
-0.143	0.382	1.170	3.052	-1.089	-1.751	9.410	0.928
-0.804	-1.850	-0.395	-0.358	0.000	0.000	-0.027	-1.464
4.324	6.376	0.000	0.000	0.000	0.000	-0.433	-1.665
-0.372	-0.265	0.481	-0.925	7.555	0.257	0.000	0.366
1.572	3.577	13.558	7.541	-2.087	-0.790	5.229	1.591
6.046	3.342	6.286	1.676	1.433	-4.378	-1.153	4.524
3.794	2.775	0.961	-1.339	-2.114	8.067	6.273	-0.302
0.000	-0.823	0.069	-2.190	0.000	0.000	0.000	-1.389
-0.028	-3.090	-0.736	0.000	-0.445	-1.717	0.665	0.000
0.000	-1.281	0.000	0.000	-1.272	-0.204	-0.394	-1.148
-0.209	-1.021	3.826	3.773	0.282	-0.594	-2.217	0.527
-1.484	1.064	1.374	-0.610	-0.066	-0.965	-0.244	4.868
-0.002	-1.006	-0.571	-1.171	-3.311	-2.083	-3.037	-3.176
-2.077	-0.873	-1.359	-2.376	-1.229	-1.236	-1.330	0.083
-0.213	-1.968	-2.280	-0.971	-0.188	-2.164	-2.395	-1.159
-0.269	-1.052	0.142	0.652	-1.510	-2.979	-2.074	-3.994
-0.215	0.217	0.136	0.000	0.000	0.000	-1.378	0.000
0.309	0.000	0.000	0.000	-0.352	1.173	-0.555	-0.831
0.000	0.114	0.000	-1.413	-0.642	-0.700	-1.843	-0.799
-0.898	3.514	0.438	1.724	2.704	0.620	0.541	0.000
4.679	0.000	1.989	0.093	-1.382	-0.716	1.565	1.419
2.789	1.707	0.000	2.604	1.453	1.113	2.374	2.228
1.579	3.283	5.548	8.733	5.279	1.446	7.506	0.553
-0.870	4.279	5.869	0.000	3.090	-0.033	-1.542	1.713
3.342	3.652	0.000	-1.357	1.431	4.536	6.098	3.687
-0.959	-1.346	6.822	-0.081	2.780	-0.716	-1.222	0.794
-1.261	0.802	1.588	0.557	-0.332	-2.164	-1.226	-0.173
0.661	-0.341	-0.606	-0.015	-3.579	-1.675	-1.619	-0.877
-0.648	-2.113	-0.805	-1.039	0.151	-0.912	1.093	-1.814
-1.047	-0.843	1.326	0.114	-0.102	-1.004	0.631	-1.266
-1.042	-0.436	0.893	-0.645	-1.493	-1.548	-0.961	0.820
6.429	7.690	7.481	1.875	5.870	2.990	4.294	3.524
3.147	5.167	3.663	1.272	3.399	7.921	6.124	6.615
3.562	1.816	1.844	7.294	9.388	4.669	8.630	4.762
1.228	0.123	-2.910	5.414	-0.707	1.972	0.299	1.039

Table35.txt

-0.766	-0.606	-0.359	-1.256	-0.127	-1.740	0.261	-0.941
0.116	-0.977	-1.091	2.778	4.062	-0.944	0.014	2.542
-0.293	-0.504	0.363	0.180	1.538	-1.067	-1.479	1.825
1.318	-0.447	-1.918	-3.897	-1.470	-1.844	-3.079	-2.084
1.011	-2.156	-2.295	1.168	-0.530	0.821	-1.414	0.367
0.209	2.831	-2.392	1.128	0.651	-0.371	3.486	2.771
-0.284	0.546	5.146	0.526	-1.198	2.472	3.024	0.758
0.494	-2.182	-1.951	4.876	-1.927	0.728	0.489	0.636
-1.038	-1.779	-0.829	-1.015	0.475	-0.964	0.230	-0.423
-0.470	-2.631	-0.628	-1.645	0.117	-2.660	-2.649	0.044
-1.075	-0.092	-2.546	-2.419	0.238	-2.070	-1.114	-2.345
-1.014	0.909	0.527	0.951	5.226	-0.496	-0.426	0.648
0.690	1.510	1.310	1.621	3.955	-0.606	1.255	-0.644
0.697	0.099	3.070	0.212	0.518	0.191	-2.117	-1.185
0.407	-0.870	-2.404	-2.307	-0.391	-0.532	-2.679	2.134
-0.133	1.067	-0.973	-1.884	-0.601	-2.920	-1.320	-0.083
0.516	-1.866	-1.652	-1.173	0.039	-3.387	-0.655	-0.066
1.140	0.437	2.886	7.501	-0.048	0.336	0.730	7.094
-0.203	-0.133	8.837	-0.713	-1.791	9.337	5.376	2.590
-0.962	2.118	-1.952	0.010	4.804	5.131	6.183	0.965
-4.187	-1.143	0.270	5.501	-1.942	-0.302	-2.605	0.832
-3.212	0.150	-1.146	-0.850	1.182	-0.104	0.495	-1.227
-1.434	-1.817	3.972	0.113	-3.974	-0.776	-1.355	6.846
-2.078	11.949	9.560	4.783	-1.631	-0.183	-0.084	5.042
4.904	4.847	-1.886	-0.422	1.167	6.477	0.758	2.912
-1.280	5.622	-2.048	4.489	2.097	6.504	5.367	5.763
-0.325	-2.294	9.138	-1.854	2.520	-0.187	2.011	1.153
1.942	1.282	2.510	-0.810	-2.150	-0.224	1.677	0.137
1.899	0.494	-0.113	0.032	-1.308	0.397	3.678	3.761
-0.013	1.097	7.208	9.548	-0.216	2.623	10.289	4.939
-0.026	1.142	-0.021	2.736	-0.268	12.220	11.796	-1.552
1.568	6.625	0.662	7.639	-0.102	9.834	-0.394	4.095
-1.797	-1.813	1.833	3.456	4.399	5.108	-0.673	0.144
-0.442	3.971	5.491	-0.545	-4.284	1.306	-0.122	5.000
5.221	0.375	-2.102	-0.936	-2.925	-1.375	-1.415	2.838
0.690	-2.634	5.705	7.664	4.530	4.180	5.312	4.445
1.679	-2.410	-2.299	4.135	6.787	11.890	2.420	3.578
4.055	-0.101	1.793	-1.195	-1.598	5.914	6.887	4.161
0.571	2.483	-1.315	-0.168	-2.759	-1.388	1.251	-1.214
-0.795	1.533	0.086	0.000	-0.043	0.809	1.741	1.147
0.690	-1.482	0.215	-1.386	-1.584	2.235	3.066	5.504
7.487	10.605	-1.984	-1.480	-0.714	0.059	-0.759	-1.003
-0.211	-1.843	-1.083	-1.006	-1.462	-0.795	-2.300	-1.118
-1.495	4.686	-1.327	-0.471	-0.501	7.855	-2.315	-1.462
1.319	-2.567	-1.542	0.780	-1.432	-0.665	4.170	-0.431
0.314	0.525	-0.004	-0.580	-0.787	-1.168	-1.560	0.632
-2.421	-0.642	-1.934	-0.684	-2.487	-1.312	0.416	-1.711
-0.850	-1.299	3.931	-0.446	2.976	-0.060	-0.746	-0.381

Table35.txt

6.760	0.100	-1.180	-1.249	-1.982	-1.500	-0.033	-1.074
0.560	-0.173	-0.415	1.467	-1.804	-1.186	-3.785	-2.499
2.200	8.425	0.000	-1.166	3.474	1.147	0.904	0.000
2.240	-1.890	-2.194	2.688	1.937	0.115	-0.672	5.793
6.136	-0.218	1.879	-0.710	3.943	3.394	8.325	0.182
-0.453	-1.915	-0.802	-2.353	-0.427	-0.893	-0.445	-0.592
0.730	-0.375	-1.918	0.000	0.000	-0.316	0.003	-0.340
0.000	0.000	-0.866	-1.588	3.407	0.153	0.156	-1.715
0.222	0.223	-3.338	-1.319	-1.341	-0.233	-3.541	0.024
-1.647	4.609	6.771	0.000	0.653	-2.152	-1.754	0.157
-0.645	-0.953	1.628	-2.281	-0.651	-1.112	-0.654	-0.518
1.302	-2.345	7.091	-0.839	-1.087	-0.573	-0.907	-0.261
0.719	-0.958	-2.771	-0.221	1.135	-0.627	0.117	-1.884
0.407	-1.668	-2.054	-1.584	-1.344	5.193	-1.613	0.315
-2.575	-2.078	4.076	-1.326	-2.458	-1.035	6.449	0.491
-0.608	-0.771	-3.014	0.382	-2.639	-1.003	-1.988	-1.747
-1.828	-1.792	1.136	-1.035	-0.404	-1.707	-2.604	0.626
0.308	-0.219	0.308	-2.103	0.124	0.307	-0.132	0.000
-0.856	-0.416	2.121	-0.849	-0.270	1.129	0.505	1.148
1.893	3.042	0.139	-1.049	-1.706	-1.410	0.371	-1.239
1.543	2.469	8.032	8.101	3.752	0.479	3.891	3.879
4.361	5.073	6.753	1.241	2.749	1.028	9.054	-0.594
2.037	6.138	0.000	4.442	4.815	5.335	0.385	7.751
0.833	-2.834	-2.230	7.787	2.123	-1.525	-2.620	1.163
1.225	1.883	0.466	0.034	1.849	-1.290	-1.362	-1.080
0.809	-0.748	-1.925	1.229	-2.626	0.037	-0.357	2.555
3.550	4.565	8.967	-2.273	-1.578	1.280	0.469	1.700
3.861	4.365	6.849	-0.867	-0.467	3.971	-0.174	1.526
-1.989	3.778	0.000	2.964	3.319	2.691	6.165	-0.913
0.005	2.268	9.895	1.859	0.983	0.011	0.000	0.218
-1.179	3.956	8.839	0.000	-0.387	-1.189	8.004	-3.252
-0.767	-0.343	1.346	0.375	-1.384	-0.510	0.561	-2.292
-3.090	-0.150	-0.913	-0.340	-0.823	-2.214	-0.790	0.000
0.717	-0.790	0.000	0.000	0.000	-0.445	0.445	-1.281
0.000	0.000	0.000	-0.378	-0.737	-0.545	-3.763	-0.688
-1.169	0.865	-1.652	0.000	0.000	-1.169	-0.074	0.000
0.000	0.000	0.000	0.000	0.000	0.050	0.632	-3.090
-0.378	0.000	0.000	0.000	-0.219	-1.120	-0.137	0.137
0.000	-2.767	0.000	0.000	-0.211	0.000	0.000	0.000
-0.074	0.595	0.460	0.000	0.000	0.000	-0.492	0.000
0.000	0.000	0.000	-1.331	-2.785	0.137	-1.439	0.685
-1.495	-1.612	-0.588	-1.466	-0.517	-2.090	-1.744	-1.371
-1.149	-4.869	3.335	-2.662	-1.720	-1.692	-0.311	-0.399
-1.174	-4.080	4.952	3.115	5.010	-0.125	-1.877	-0.242
-0.201	-0.249	-0.405	-4.892	-2.361	2.074	1.925	2.145
-1.508	-0.551	-0.941	1.133	-1.790	0.888	1.922	2.080
2.125	2.174	-0.737	1.344	4.113	-1.016	-1.292	1.169
-2.126	1.661	1.816	0.187	-1.099	0.980	-0.180	0.228

Table35.txt

0.874	2.570	0.065	0.718	-0.775	0.144	0.566	-3.063
-0.691	-0.887	-0.357	-0.495	-2.156	-2.238	-1.642	-0.241
-2.384	-1.226	-0.356	1.162	1.181	-1.834	-0.962	-2.901
-2.756	-0.795	-3.383	-1.592	-0.425	-3.744	-0.638	-0.325
-0.445	-0.190	-1.409	-2.051	-2.440	-1.799	-1.630	-2.759
0.195	-1.619	9.413	15.815	-0.945	13.048	-0.966	0.750
-0.425	-1.692	3.471	6.274	-1.650	-0.596	-1.513	-0.944
3.269	2.249	-0.254	-0.446	5.725	7.625	1.594	1.638
-0.874	-1.768	-0.372	-2.941	-1.613	-1.113	3.265	-0.700
-1.483	-1.688	-0.500	-1.923	-1.857	-0.954	-0.591	-1.726
-0.792	-1.488	-2.208	-0.584	-1.899	1.121	6.186	-0.113
-1.848	0.394	-2.281	-1.757	3.243	1.515	-3.123	-3.824
-3.027	-3.176	-0.896	-0.430	-1.195	-0.804	0.380	-3.538
-1.113	0.949	-0.941	0.334	-0.592	-1.646	-1.707	-0.592
2.778	3.106	5.638	13.322	-1.754	-1.554	-1.638	3.273
3.032	-2.674	4.543	0.764	6.607	6.488	6.418	9.000
11.267	10.630	1.685	2.472	11.994	2.547	-1.444	0.889
4.946	5.244	-1.439	-4.775	0.809	5.951	5.421	8.849
0.823	5.386	3.762	6.082	1.411	0.000	-1.717	-1.043
4.035	3.165	4.201	5.941	4.317	-2.746	6.679	2.718
-0.737	-1.574	1.734	4.204	-0.843	13.897	-0.363	-0.837
4.723	6.903	-2.240	-1.256	9.617	11.056	-0.621	8.795
7.770	12.145	7.716	14.906	1.029	8.490	7.353	-1.221
0.272	3.717	-0.359	0.451	1.390	1.266	-2.316	-2.149
-0.835	-0.278	-1.833	14.091	0.309	0.080	3.728	-0.736
0.782	1.264	0.979	0.781	-1.888	1.890	4.324	0.002
5.791	6.782	0.271	0.242	0.081	1.655	-1.906	-1.653
1.240	3.826	-0.474	-0.540	-2.103	-1.047	-1.769	5.376
-0.560	-2.466	-0.982	1.997	6.269	-1.032	-0.864	-0.984
-0.937	-0.607	-1.979	-2.977	-2.245	-2.884	-4.403	3.333
2.277	-0.030	-2.199	6.874	-0.089	-0.208	-2.126	-1.087
-1.624	-3.216	4.865	13.532	-1.424	-1.063	-1.309	-1.513
-2.170	-2.700	-1.585	-2.769	-0.693	-1.731	-1.327	-0.866
-2.807	-3.045	-2.708	-1.868	-2.451	1.381	-1.512	-1.072
-2.019	-3.711	-2.590	-2.227	6.003	-0.094	-1.225	-0.158
-0.637	-3.581	-1.704	-2.984	-1.837	-2.805	3.922	0.000
10.878	17.887	0.000	8.490	-0.581	-0.874	-0.887	-1.272
-2.555	-2.633	0.486	-2.150	-1.736	-1.485	-1.393	0.357
-1.009	-1.968	-0.934	1.165	-2.915	-2.364	3.090	-2.983
2.913	2.415	-0.720	-2.829	-1.207	-0.026	-1.018	-0.293
-2.112	-0.439	-2.238	1.890	-1.312	-0.631	-0.953	-0.285
-3.133	-3.815	-0.759	-2.754	-1.446	5.386	-0.042	-2.209
-0.611	-1.371	0.309	8.157	-1.982	-1.161	-3.855	-3.309
-1.380	-1.653	-1.163	-0.745	-1.580	-2.660	-0.705	-0.355
-0.622	-1.536	0.317	-1.475	-0.915	-0.678	-1.889	-1.125
-2.901	-0.325	1.648	4.763	-1.243	-0.286	-0.067	-2.348
-1.143	-0.215	-0.853	-0.669	-2.712	-1.813	-0.428	-0.538
5.137	0.333	-1.600	7.089	-0.222	3.054	3.530	3.123

Table35.txt

-1.264	0.048	-1.378	-1.112	-0.600	-1.920	-2.262	3.885
0.626	5.290	-1.358	1.105	0.169	3.550	3.444	2.792
8.410	4.352	6.680	17.337	-0.618	-2.134	10.647	19.653
-1.028	3.440	6.436	6.477	0.684	2.640	1.702	2.825
-0.866	-2.882	1.238	3.410	8.430	-0.381	3.407	5.114
-0.879	-3.023	-4.567	-1.479	-2.909	-2.064	-0.889	-1.745
-0.482	-0.973	3.606	6.552	-0.934	-2.468	-1.357	5.266
-1.866	-1.379	-1.800	-0.768	14.466	3.004	1.745	-0.729
-2.587	2.325	0.269	-1.877	-0.380	-1.507	4.452	-2.594
-1.759	-2.695	3.600	-1.667	-0.836	0.270	-2.140	-0.300
-1.703	-0.129	-1.649	-2.344	-0.581	-1.045	-2.569	-0.997
-0.010	0.050	-0.997	-1.689	-0.586	-1.644	2.828	0.405
-1.617	0.183	1.343	0.709	-0.550	-0.530	0.190	-0.002
-0.776	-0.856	-2.008	-1.348	-0.225	-0.342	-3.419	-1.185
-1.772	-0.841	-2.117	-0.083	-0.184	-2.046	4.424	2.371
-0.569	-0.555	-0.574	-0.943	-1.154	-1.772	-0.852	-2.117
-2.345	-0.533	-0.219	-0.484	-1.273	-1.195	-0.129	-0.934
-5.752	-1.565	1.186	1.271	-1.802	-2.164	2.411	2.795
0.059	3.643	2.040	0.032	-1.454	-1.871	-0.093	0.148
0.194	1.230	-0.777	0.151	-1.338	-1.390	-2.231	-1.162
1.320	1.065	-1.877	5.747	1.888	12.190	0.611	2.122
-1.263	-1.984	-1.469	2.055	5.862	1.989	2.139	2.539
3.461	4.096	0.774	5.216	9.094	-0.861	7.143	0.927
11.812	12.071	5.861	1.423	6.080	14.572	10.244	3.088
-1.283	1.162	7.844	10.059	-1.905	-0.402	3.898	-1.399
5.319	5.664	5.073	9.134	6.728	-1.664	0.237	3.489
-0.902	-3.554	2.956	2.901	-2.720	12.100	-1.766	-1.997
0.508	3.390	4.734	17.501	0.619	2.436	1.340	4.553
-1.523	-0.700	0.107	4.426	2.314	2.448	2.669	-1.047
4.102	-2.136	18.474	2.981	2.072	0.045	-0.340	-1.102
-0.754	2.987	-0.943	-2.280	-0.684	2.279	2.229	0.743
-0.518	0.826	0.662	3.036	3.771	4.067	-1.606	3.824
-1.364	-1.462	7.842	1.375	-2.011	-1.603	-0.629	-0.623
1.121	2.447	3.522	-0.580	4.704	0.056	0.454	2.061
1.881	-0.444	-2.604	1.547	2.848	-0.583	-0.229	-0.841
3.931	3.499	1.569	5.249	2.228	1.959	3.971	0.000
-0.794	0.000	2.208	-0.779	-1.535	4.145	-1.716	4.259
5.869	-0.612	-0.297	-2.493	5.140	3.038	5.906	4.737
0.167	0.054	-2.470	3.090	5.281	2.016	2.325	0.000
4.812	0.000	5.695	1.412	0.715	5.321	4.818	4.572
6.475	4.234	-1.928	-1.123	-1.430	5.271	6.545	-0.559
-1.002	-2.899	1.236	7.361	-1.133	-0.952	0.080	1.433
-1.026	3.884	3.667	-0.925	-0.443	-2.788	-0.644	2.023
4.089	3.742	0.528	-2.598	-2.300	0.670	-2.990	-1.395
-1.750	11.866	-2.958	-2.238	-2.612	-1.255	-1.378	0.356
-0.717	1.233	-2.493	-1.144	-0.251	-2.039	-1.704	-0.413
-1.068	0.774	0.043	-0.749	-1.843	5.324	-0.945	-0.099
-0.550	5.640	7.336	8.731	3.011	2.166	-0.725	0.000

Table35.txt

-0.163	6.831	9.041	2.692	3.809	1.073	4.741	0.104
-1.385	7.383	2.881	4.694	5.209	4.018	4.140	8.829
2.097	4.747	-0.790	6.503	3.232	0.230	-0.609	1.236
3.169	1.509	0.093	0.102	0.920	4.240	0.009	2.832
-1.408	0.431	2.751	1.024	2.856	3.046	5.637	-1.439
0.826	5.558	-0.297	13.690	1.991	5.589	7.753	5.465
1.195	2.944	9.078	0.923	-1.918	3.010	5.957	2.241
2.749	1.695	0.682	-0.519	-2.747	2.835	17.214	2.536
0.000	0.000	-0.987	0.000	0.000	0.000	-1.169	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.163	0.000	0.366	0.000
1.031	-3.780	1.163	-1.067	0.478	1.426	6.393	-0.955
-0.349	-1.459	-1.529	3.145	3.877	8.101	-1.036	-2.204
1.484	-1.221	0.558	-1.506	-0.961	-1.229	-1.137	-2.079
3.082	3.715	0.560	0.250	5.962	4.116	4.226	2.218
1.071	-0.014	-1.317	1.528	1.668	2.754	2.031	0.708
-0.802	-0.039	0.362	6.890	6.422	0.243	3.568	3.826
1.526	-1.361	-0.243	-2.145	-1.830	-0.255	-0.538	-0.442
-1.343	-0.647	-2.483	-0.317	-0.512	-0.408	0.488	-1.145
0.061	-0.330	0.229	-0.943	-0.307	-1.324	1.354	-2.943
-2.447	0.382	5.958	-1.966	5.025	-1.488	-1.394	4.879
-0.946	6.451	7.770	-3.211	-2.186	7.355	-0.482	1.312
1.575	-0.810	3.632	-1.793	-0.959	11.519	12.845	9.962
5.649	8.109	12.274	7.458	9.571	0.254	-0.706	4.369
6.506	5.029	4.162	0.959	2.390	0.373	1.641	-1.852
0.058	2.154	-0.561	2.933	6.837	8.096	-1.800	9.804
-1.312	-1.381	-0.924	-2.883	-2.618	1.079	-1.662	-2.221
-0.410	1.361	-0.697	-0.910	-0.285	-1.688	-1.027	-0.745
0.207	-0.660	0.344	0.115	-2.971	-0.272	-2.271	0.708
-2.663	-1.379	-3.027	-3.039	-2.042	-0.130	-1.371	-1.366
-0.480	-0.305	-1.666	0.636	-1.200	-0.754	-0.031	-0.768
-2.369	-0.866	0.163	-1.867	-1.709	-0.673	-0.708	-1.696
2.212	-0.990	6.063	0.155	5.533	-0.851	-0.503	2.827
-0.335	-1.584	4.402	2.912	-0.895	-2.206	-0.633	-0.652
-0.938	3.004	-0.095	-0.388	-2.276	-0.403	-0.604	5.802
-1.666	0.053	18.694	-2.641	4.784	-1.734	-0.685	5.313
7.466	2.456	4.230	1.084	0.579	-0.176	-2.585	3.876
4.672	0.399	-0.194	-3.118	-3.587	-2.524	-2.208	-0.568
0.838	7.467	7.353	10.975	10.672	1.047	-1.594	5.282
0.544	4.756	9.998	-0.985	-1.757	-0.656	6.095	2.723
2.394	8.614	6.122	-0.389	-1.757	-1.254	-0.284	0.305
-0.467	-1.775	0.604	1.687	1.851	1.620	0.116	0.000
-0.540	-0.274	0.000	0.529	1.451	-0.124	-0.923	4.365
2.941	-1.398	0.000	-0.890	-1.788	1.879	4.470	0.897
0.353	-0.851	-3.210	-0.593	-0.149	-0.753	-0.899	-0.897
-1.804	-0.038	0.544	-1.588	-1.119	-1.650	-0.745	-1.227
-1.745	0.665	0.021	-1.981	-2.800	-2.588	-1.250	-1.577
-0.557	-2.932	2.234	-0.685	-0.263	-0.898	-2.487	0.000

Table35.txt

-0.525	2.433	2.572	0.000	-0.317	-0.177	2.693	-1.319
-1.856	0.533	2.428	6.628	-0.299	2.426	-1.410	2.405
-1.324	-1.203	-1.964	-0.330	-0.193	-0.351	-2.276	0.050
0.391	0.000	-1.415	0.595	-0.505	-1.592	2.760	0.309
0.994	0.578	-0.933	-0.693	-1.437	-1.435	-1.010	-0.517
1.203	4.366	4.928	3.339	7.399	-0.259	-2.017	3.090
0.375	2.703	5.272	4.073	3.090	9.227	10.882	1.682
3.824	4.763	1.729	-2.248	3.255	2.660	2.515	7.652
-1.543	-2.387	-2.238	-2.273	-0.329	0.242	-0.508	0.000
-0.777	-2.367	-1.970	-1.389	-1.364	-0.939	-2.072	0.178
-0.727	-0.900	-0.662	-3.301	-1.378	-0.143	-3.054	-0.861
-0.350	-0.543	-0.016	-1.202	-2.211	-1.914	-1.035	0.307
-0.986	0.149	1.253	0.635	-2.529	-0.718	-2.063	-0.379
1.023	-0.045	-0.224	-1.795	-2.121	-1.289	-1.540	-0.073
6.727	-1.503	-1.712	8.048	-0.295	-1.981	-2.092	5.618
7.722	4.005	7.113	-0.877	-0.177	-2.082	-0.757	4.390
3.009	0.129	0.030	-0.012	-1.022	-0.396	-1.881	-2.634
2.588	1.728	0.219	4.316	-0.368	1.151	0.675	1.932
3.727	0.973	0.488	0.498	-1.528	3.733	2.126	-0.344
3.456	4.212	2.085	-0.277	1.593	5.245	0.900	-1.599
0.998	-1.948	2.168	-0.426	2.063	-0.445	-1.105	4.608
-0.831	2.278	-1.764	-1.832	-1.819	-0.611	0.225	0.352
-2.356	-0.286	-1.092	-1.657	-0.356	2.466	0.315	1.080
-0.447	-1.336	-1.119	-2.257	-1.205	0.173	-1.052	0.455
-1.866	-0.622	0.598	-3.006	-0.171	-0.952	2.424	-1.656
-1.339	-0.509	-0.315	0.793	-2.727	-1.481	-0.248	-0.481
-0.993	-0.885	-1.639	-0.492	-0.173	-1.049	-1.521	0.366
-0.181	-0.144	-1.508	0.373	0.000	1.926	-1.691	0.476
-3.187	0.223	-0.981	-0.518	0.570	3.176	-1.104	-1.708
-0.086	-0.220	2.319	-1.667	0.503	-1.890	0.787	1.338
0.646	-2.433	-0.482	-0.064	-0.803	-2.393	-1.235	3.840
3.588	0.280	-0.747	6.854	11.542	-0.800	-2.136	-3.653
-0.339	2.366	0.098	6.078	3.819	-0.798	-0.644	1.404
3.003	4.567	3.023	1.546	1.823	-2.161	-2.481	-1.272
1.208	1.288	-1.907	11.319	14.215	0.623	0.569	-0.500
-0.338	-1.206	-0.689	-3.379	-1.594	0.613	-1.410	0.586
-0.877	-1.450	0.083	-0.498	-0.105	0.590	11.083	-2.345
-1.550	-0.643	0.134	-2.197	-0.614	-0.957	-1.612	-0.829
-1.133	-3.274	3.651	0.043	-0.937	-0.876	-0.626	-0.694
0.139	-2.536	-2.455	1.924	-1.000	-0.298	2.433	1.580
0.187	-0.655	-1.768	-0.386	-0.583	-1.423	-1.276	-1.542
1.541	3.911	13.311	7.501	6.473	5.206	2.675	3.680
4.785	3.353	5.183	0.061	2.640	0.523	4.678	3.684
0.506	2.157	1.127	4.032	3.624	2.194	0.528	-1.323
0.340	-0.817	-1.946	0.750	-1.952	-2.094	-0.638	0.000
0.283	-0.178	0.333	-0.868	0.471	-1.311	-1.449	-1.245
0.042	-1.381	-1.069	-1.688	-3.509	-2.075	-2.176	0.556
-0.907	-2.482	-2.495	-2.054	-0.273	0.137	0.412	1.866

Table35.txt

3.721	4.086	7.107	-1.074	-1.155	-1.310	-0.752	4.016
3.188	0.285	1.503	1.572	2.853	-0.715	-2.351	-0.992
4.228	10.686	4.102	5.740	6.666	1.169	-0.727	0.000
2.543	4.192	3.654	2.706	4.766	7.940	9.863	2.452
5.357	2.947	6.108	3.464	5.151	7.510	10.170	1.959
-0.812	-1.881	5.855	7.389	-0.141	-1.639	-0.652	-1.989
5.624	-0.954	5.804	-0.443	-0.668	-1.679	-2.369	2.797
2.878	5.950	0.246	-3.953	0.756	-0.621	-2.005	0.546
-0.402	0.635	6.220	-0.553	-1.040	-1.181	-1.768	2.197
0.670	0.996	1.493	0.146	-0.797	-1.201	-0.396	2.382
2.074	0.692	-1.182	0.792	-0.220	-1.353	-2.940	0.405
-0.015	-1.329	13.936	8.170	-1.603	-2.017	-1.077	0.595
5.288	1.809	4.730	-0.105	-1.534	-3.632	10.111	2.323
4.458	4.114	0.099	1.394	2.739	4.522	-1.053	-0.930
-0.394	-1.853	6.093	-1.150	-3.388	-0.034	-0.644	0.441
2.544	0.163	3.008	0.000	2.072	-1.744	-1.711	-0.168
8.460	-1.378	-2.247	-1.615	-0.554	-2.426	-0.599	0.016
-2.827	-1.076	-0.794	-0.631	-0.438	0.535	-1.665	-1.489
-1.223	-0.769	-0.479	1.217	-1.286	-1.507	-2.805	-1.347
-2.315	-2.073	-0.433	0.839	-1.926	-0.274	-1.231	-2.507
9.439	14.045	-1.469	1.629	-1.394	4.283	7.919	2.838
-1.641	5.322	7.387	0.295	-1.631	-0.910	-1.450	1.494
0.519	-0.833	-0.152	-2.319	-0.589	-0.322	-2.282	7.417
0.859	0.624	12.655	11.085	2.623	1.803	0.136	6.036
-1.242	0.873	6.956	-1.067	0.277	-0.690	5.631	5.389
1.777	0.054	2.333	5.125	6.438	13.385	6.173	0.052
0.311	0.646	2.075	3.380	5.758	1.662	5.248	3.109
2.949	3.669	2.399	-0.642	0.456	1.856	-1.015	0.010
-0.405	1.629	0.272	-2.968	0.461	-0.813	-0.615	1.159
-0.464	0.142	12.954	0.286	7.031	3.090	6.383	0.000
3.090	4.164	4.365	-1.069	-0.928	-1.554	0.773	-0.490
-1.876	-0.779	0.000	6.501	-2.371	-1.777	-0.623	5.343
-0.206	-2.815	-0.359	-1.440	0.379	-0.646	0.348	-1.477
-1.726	0.453	-3.404	-0.082	-0.299	-2.073	-0.766	-0.431
1.128	-0.224	-0.631	-0.770	-1.228	-1.310	-1.268	-0.963
-0.573	-1.197	2.145	-4.455	4.054	-1.231	0.175	1.690
-0.028	2.761	3.555	-2.341	-0.241	6.039	0.616	0.418
-0.094	0.138	0.906	-0.439	1.876	0.351	1.202	5.141
0.989	1.184	4.908	2.925	5.016	0.443	1.585	0.000
5.433	-0.207	-0.545	-0.445	0.075	0.246	2.591	2.429
0.648	-0.653	1.910	-2.563	-3.898	0.546	1.900	2.010
2.946	-2.285	12.696	0.000	0.487	5.333	6.119	0.000
-0.141	0.000	1.236	-0.752	-0.785	-1.458	-0.536	0.322
-0.653	0.000	0.323	-0.935	-1.801	-1.052	-1.673	-2.577
-0.930	-2.115	6.842	1.255	-2.213	-1.449	-0.673	-0.144
3.864	0.553	0.438	0.460	-1.420	-0.800	0.092	4.588
7.302	0.877	-0.939	-0.530	-1.868	-0.331	-2.918	3.718
3.663	2.272	4.799	5.949	8.024	1.871	-0.100	1.608

Table35.txt

2.320	4.363	6.059	-0.541	1.351	-1.075	-0.429	4.714
-1.159	4.219	1.484	2.724	5.331	6.097	6.031	4.827
4.869	2.506	12.808	-3.175	-1.982	-0.837	1.047	2.229
-2.186	-0.254	3.523	0.000	1.533	1.681	2.765	2.119
-2.092	-0.024	3.065	2.042	3.619	5.766	-1.322	8.762
1.975	5.357	10.059	8.128	0.950	2.521	3.403	3.211
1.130	4.669	4.896	-0.197	-0.082	1.892	-0.283	2.512
-0.066	3.335	3.090	-1.550	-1.858	2.590	3.099	-2.478
5.480	13.734	17.695	3.876	4.043	0.083	6.326	3.715
-0.182	5.179	8.425	2.356	1.247	3.115	3.398	4.024
7.271	2.375	1.877	10.804	16.245	0.218	0.100	2.146
4.370	11.794	1.921	4.356	3.795	-0.909	-2.221	-0.515
3.948	1.731	-0.868	-0.641	-0.378	4.581	15.624	3.324
5.353	2.669	1.965	-2.082	-2.124	7.612	7.421	4.846
3.504	4.863	1.606	5.227	-1.815	0.034	-2.826	0.969
0.841	5.092	1.829	-0.039	0.401	0.140	5.386	1.347
-0.885	-0.397	0.073	1.276	0.026	0.187	1.098	-1.890
3.269	-1.800	11.341	10.526	8.522	7.151	7.306	-1.212
3.204	6.751	5.892	-0.519	-2.330	9.059	13.783	3.219
-0.838	7.132	3.489	-0.264	-1.256	8.858	13.618	7.981
-0.371	-0.903	-1.191	-1.171	-1.022	-1.487	-1.373	2.096
-0.308	-0.407	0.573	-0.089	0.149	-2.068	1.367	-0.767
-0.104	-0.348	-0.227	-0.787	-3.236	-2.641	-3.033	-0.329
1.162	4.994	12.248	5.738	5.946	-1.675	0.576	0.000
1.834	1.547	0.000	-0.775	0.947	2.936	7.398	-0.440
6.895	-1.025	3.064	-0.912	-1.259	-1.604	-0.624	3.836
0.479	-1.078	3.957	1.273	5.341	0.031	-2.313	0.000
-1.494	4.246	0.000	-1.277	-1.903	-2.041	-0.543	0.000
7.558	0.117	-0.009	-1.071	-1.748	-0.910	-3.440	-0.436
-1.826	0.369	-0.786	-3.292	-1.076	0.434	-2.117	0.000
-3.090	0.000	3.573	-0.843	-0.432	3.437	2.558	-0.341
2.010	-1.010	0.000	0.667	0.891	-1.108	-1.327	0.000
3.254	2.585	9.004	6.015	4.369	-0.576	-0.600	0.000
2.219	3.761	0.000	1.901	0.395	1.891	2.957	-0.276
0.662	0.000	-1.197	-1.214	-1.476	3.090	2.864	5.341
0.956	1.673	-2.172	-0.330	-2.390	-2.574	-0.586	-0.314
0.321	1.229	0.629	1.394	-1.178	-0.614	3.956	-2.485
-0.177	-1.856	-1.450	-1.994	-3.666	-1.836	-1.713	-2.140
4.512	7.704	5.048	5.409	8.427	2.887	1.631	4.967
2.964	5.467	6.317	-0.427	-0.667	4.092	5.757	1.718
7.447	2.381	-0.241	2.789	5.320	6.583	4.216	4.213
-1.027	1.535	12.287	6.507	-1.782	1.672	-0.020	0.000
2.797	4.862	2.465	0.674	-1.672	-0.735	9.750	2.700
6.284	2.868	0.000	1.710	1.704	-3.917	1.992	1.932
-1.275	-0.359	10.512	-1.495	6.480	-0.606	4.299	2.397
-0.847	4.731	3.559	-1.761	0.011	-1.258	-0.624	2.203
3.052	-2.866	0.625	0.372	-1.770	-1.481	-2.279	5.694
-0.907	-2.320	6.532	-0.909	-2.342	-0.144	-1.565	-0.123

Table35.txt

-0.089	3.090	3.158	-0.490	0.000	-1.435	-0.839	-0.899
-1.925	4.036	2.181	-1.489	-0.574	4.893	4.816	6.181
-1.732	3.366	9.120	-2.437	1.180	0.025	4.242	2.859
3.818	4.215	0.404	-0.698	0.636	3.057	-1.460	3.381
-0.180	1.313	2.391	2.031	4.202	8.315	13.313	9.902
2.066	3.652	16.356	-0.961	3.384	0.806	1.662	2.911
6.879	3.373	4.442	-2.351	-1.833	-1.133	0.753	-0.998
-0.620	-1.595	0.000	4.983	6.617	7.591	6.305	-1.953
4.733	-1.821	-1.713	-1.932	3.148	-0.807	0.758	-1.346
1.334	-1.427	0.682	-1.110	0.000	-0.935	-1.975	-0.230
0.959	-1.186	-1.439	-0.373	-1.038	-0.189	-1.874	-0.813
0.174	-0.342	1.312	1.414	-1.117	0.999	0.266	0.000
0.313	0.651	1.144	0.000	0.000	0.710	-1.002	0.000
1.565	-1.522	-0.097	-0.026	2.145	1.124	2.200	-0.281
0.374	1.785	-2.437	-1.363	5.121	1.651	-1.378	3.619
0.585	4.520	3.485	0.000	-1.582	1.922	4.617	0.140
3.898	2.636	4.817	1.072	4.587	3.919	3.013	-1.084
0.133	-1.623	-0.130	5.544	0.040	-1.283	-1.185	0.000
0.844	1.582	4.720	1.591	-1.046	3.849	4.129	0.000
-1.254	6.619	2.499	0.978	-2.340	2.715	0.430	4.548
-2.206	-1.199	11.220	3.912	3.571	4.773	-1.214	2.671
3.134	2.941	7.151	-2.090	-0.761	9.130	8.127	2.596
3.024	3.826	4.155	3.252	5.030	2.411	12.426	7.242
3.118	2.567	-2.472	-1.013	2.710	0.047	1.025	0.826
0.000	0.000	3.282	0.000	-0.136	-0.718	0.706	-0.181
-0.621	1.042	-0.297	-1.773	-0.763	0.120	-0.716	4.542
1.838	-1.648	13.086	0.836	-1.895	0.886	-0.675	4.021
6.097	1.340	12.123	-0.519	-1.343	0.331	-1.956	-0.240
0.288	2.118	1.382	-0.780	-0.687	-1.245	-0.409	0.471
2.059	3.162	4.537	2.396	1.290	1.022	0.156	0.000
1.553	2.539	0.891	2.330	0.218	2.592	3.595	0.382
0.000	-1.650	0.561	2.740	4.779	1.011	7.350	2.408
1.938	2.499	13.092	0.955	-1.020	1.000	-2.152	3.343
0.110	4.864	9.996	-1.480	-0.270	-0.172	1.728	5.164
5.684	-0.622	-0.001	-2.065	-1.481	0.238	0.528	4.698
0.000	-0.490	-1.074	-1.223	0.099	0.453	-0.921	0.000
0.000	0.000	3.090	0.415	-0.798	0.366	-0.646	-0.145
-1.006	-0.402	0.000	-0.997	-2.249	-1.381	-1.211	-0.270
-0.217	0.334	8.877	4.226	-1.257	-1.616	6.339	-0.517
0.652	-0.304	-1.232	1.170	0.000	6.741	-0.475	-0.387
-1.668	0.937	0.000	-0.523	7.999	-1.230	0.498	-3.104
-0.506	-0.739	-1.141	1.873	9.759	-1.782	8.145	4.687
0.787	5.876	10.159	-0.504	6.336	-2.963	1.631	0.786
-1.133	0.439	1.508	-3.006	-3.197	8.111	7.932	0.465
-1.109	-0.326	-0.449	0.759	2.423	-1.756	-0.172	1.886
1.648	2.975	1.924	-0.908	1.383	2.303	1.274	-0.097
0.276	0.674	1.248	-2.109	-0.154	-0.152	1.379	3.465
4.154	6.878	-1.665	6.351	11.117	6.297	4.707	5.224

Table35.txt

6.427	3.175	8.914	0.285	-2.132	11.781	2.965	6.285
4.250	3.573	4.369	8.668	11.158	11.652	5.852	4.895
-2.447	-2.376	11.018	9.296	6.148	-0.240	-0.661	0.266
3.490	-0.693	5.275	-0.807	-0.813	7.689	14.265	-0.341
-1.497	-0.375	0.010	4.274	10.241	0.288	-2.090	2.694
3.184	5.940	6.627	4.893	2.082	-0.031	0.564	1.367
1.399	6.838	7.613	3.007	2.968	3.289	5.123	7.549
4.667	6.778	2.041	-0.552	-2.836	2.728	6.325	-1.212
-0.970	2.361	7.087	9.491	9.831	1.175	0.557	2.903
7.689	-1.034	0.418	1.746	2.187	-0.667	11.766	-0.555
4.989	4.546	6.043	3.236	3.961	5.344	7.307	9.665
4.591	3.015	-2.407	0.610	-0.637	2.237	-1.446	7.148
0.546	0.097	-1.581	0.000	-0.337	-1.020	-2.573	1.784
0.162	0.417	1.125	-0.719	-2.636	10.094	11.130	-1.968
-1.645	-1.576	9.326	0.640	-1.186	2.822	-3.196	1.095
-0.262	0.000	0.926	0.000	2.481	4.279	7.710	1.237
-0.325	0.611	1.598	7.252	8.822	-1.134	-0.771	2.485
2.176	-0.187	-0.279	-0.626	7.211	0.134	-0.901	-0.696
-0.191	-0.168	-0.126	-1.364	-3.774	-1.423	-1.075	0.776
-0.580	-2.365	-0.733	-2.951	-0.957	-1.251	-0.953	-2.870
2.609	12.330	0.514	-2.948	-1.167	0.272	1.873	2.376
-1.068	3.044	4.010	1.056	1.361	7.080	-0.012	3.512
4.187	1.253	0.140	1.275	2.082	-0.290	-1.263	7.184
0.052	-1.139	12.728	-0.717	-0.214	0.745	-0.929	0.000
-0.906	0.000	0.000	0.256	-3.268	-1.298	-0.895	3.533
3.853	0.690	0.000	-0.964	-2.860	-0.679	-0.549	-1.837
-0.530	-1.912	-1.149	0.310	-1.034	-1.048	-0.794	0.237
-0.293	0.574	-0.947	-0.881	-0.488	-1.829	-0.599	-1.346
-0.133	-2.292	-1.499	-1.757	-1.930	-3.262	-2.419	-1.604
-2.599	2.185	10.031	6.792	6.828	4.350	6.732	0.000
0.142	2.595	4.432	0.801	-1.506	1.995	1.468	4.001
1.374	1.595	0.000	4.835	3.566	-2.600	15.390	-1.865
1.658	7.115	7.564	5.469	5.307	4.922	7.037	3.199
0.925	2.741	8.665	4.127	2.659	7.294	7.669	6.037
6.730	6.505	3.655	6.992	13.007	-3.038	-2.863	9.995
2.144	1.192	18.468	13.477	5.075	-1.332	-0.473	5.446
4.034	6.654	13.595	-1.246	0.616	8.785	4.653	6.706
3.063	8.354	4.907	0.794	-1.170	-1.616	18.807	-2.396
0.000	1.526	7.771	-0.701	0.937	-1.817	-4.424	0.000
2.913	-0.040	-2.424	-3.090	-0.940	-0.489	-2.346	0.333
0.866	0.000	-0.823	-0.598	0.031	-0.217	-3.721	-2.293
-0.280	-2.439	5.218	-2.034	-0.728	-0.975	-0.916	-1.316
0.226	2.005	3.607	-0.736	-0.671	3.197	-1.474	2.955
5.110	0.303	1.070	-0.966	-1.814	1.135	-2.094	-0.452
1.307	2.410	15.029	0.975	5.654	-0.244	-1.636	0.787
-1.960	2.144	6.157	0.742	-1.637	0.415	5.975	3.837
5.748	8.647	1.263	0.469	1.484	1.303	0.772	3.236
-0.856	-0.317	3.965	2.678	-1.237	2.226	1.789	0.255

Table35.txt

4.601	4.237	9.412	-1.235	-1.943	3.061	5.241	5.658
4.889	2.113	1.858	7.093	12.781	-1.112	-1.811	5.830
-1.645	-1.288	1.173	-1.783	0.349	-0.190	-1.689	-1.514
2.243	-1.542	-2.358	-0.443	7.334	-1.782	4.562	0.650
0.561	-0.873	1.148	-0.610	-2.701	-2.678	-2.054	-3.279
13.465	12.481	-2.983	-1.801	11.159	11.112	6.771	15.180
1.422	12.179	8.690	6.394	9.000	11.116	1.301	1.490
0.553	1.798	-1.608	1.957	1.565	-1.488	0.793	3.463
-1.041	-1.267	19.392	-0.721	12.650	-0.711	-0.631	7.223
-0.671	7.304	11.826	-0.054	0.077	-0.252	1.064	7.719
6.726	0.840	0.699	-0.120	-1.271	-0.325	-1.944	-1.417
5.629	7.719	6.200	12.495	7.288	2.816	2.668	5.620
3.617	6.743	12.128	4.422	5.104	5.483	6.262	4.705
4.353	-0.457	-1.073	4.894	8.964	4.200	5.525	-1.803
-1.425	-2.072	-2.005	-2.717	-2.111	-3.993	-1.890	12.042
-1.821	-3.538	2.861	2.465	-2.146	-1.870	-2.524	0.681
-1.932	-1.796	-0.418	-0.675	-1.121	-0.896	-2.682	-1.172
7.473	15.166	5.053	11.481	4.916	5.821	6.621	0.159
5.584	-2.425	2.551	2.191	-0.039	-1.527	8.985	3.570
6.567	7.361	3.737	8.976	18.035	7.615	6.988	9.995
1.976	8.605	17.018	7.095	6.953	0.178	-1.093	5.464
0.848	6.924	13.680	2.191	4.608	8.406	6.283	-0.239
8.698	3.435	1.125	12.207	16.883	7.779	10.055	5.164
0.337	-2.040	17.169	0.574	-2.361	0.417	-0.021	-1.595
-1.273	-2.586	-0.359	-0.207	0.809	-2.011	-0.427	-0.756
-1.238	-2.245	-0.149	13.007	6.609	-1.520	-0.934	-2.079
3.580	8.381	16.489	1.256	-0.516	-0.111	0.503	4.879
1.289	0.815	10.017	1.888	3.534	-0.834	11.907	1.205
8.557	-1.330	1.109	5.169	8.076	2.477	10.663	10.640
0.307	-1.425	-1.633	-1.248	0.000	0.000	-0.465	-3.090
0.266	0.000	0.000	-0.762	-0.541	-0.088	1.561	0.000
0.000	0.000	0.000	0.597	0.524	-1.067	-1.529	0.163
1.357	2.961	17.018	3.557	-1.584	0.520	-1.115	2.856
1.076	5.361	11.170	4.701	5.077	0.457	2.889	3.901
6.499	-1.204	-0.869	-1.402	-1.159	6.893	19.761	6.081
0.771	0.812	17.852	0.622	6.019	4.299	7.921	5.586
6.124	7.250	12.974	2.051	0.259	10.328	9.276	7.518
6.554	3.557	5.683	5.018	8.966	-2.521	1.125	5.681
2.642	5.024	-1.958	3.688	2.215	1.261	-0.759	4.876
2.063	4.851	8.708	-0.092	4.518	4.583	2.970	5.828
6.201	-0.563	1.059	-0.888	-0.687	-2.746	-1.953	2.773
3.540	3.374	13.808	1.696	3.497	0.242	-0.836	-0.571
1.857	2.501	8.697	2.505	2.308	7.377	6.070	-0.095
1.205	-0.479	2.374	2.679	4.150	8.181	12.790	7.217
3.743	14.734	7.554	-2.376	2.536	0.270	-1.117	0.000
-3.972	1.991	4.352	-0.694	-0.398	3.833	5.295	-0.099
-0.748	-0.340	-2.056	-1.268	-3.067	4.558	5.737	5.220
1.056	-0.274	-1.899	-1.943	-3.268	-1.724	-0.389	0.472

Table35.txt

-0.308	-1.196	0.327	1.266	0.529	-0.123	2.193	-1.235
-0.155	-1.500	1.534	-0.428	-1.521	-2.264	-2.142	-0.506
-1.168	1.961	-2.526	-1.135	1.657	-3.029	-1.275	0.441
4.292	-0.119	-0.980	-0.445	4.601	-2.333	-0.899	-1.258
-0.936	-2.103	-0.976	-1.503	-0.118	-1.130	-0.638	-3.769
2.539	1.697	2.612	0.615	0.441	6.384	2.891	-0.794
-0.243	1.651	-0.705	1.397	1.174	0.452	1.083	-1.159
-1.574	-1.599	-0.945	-1.592	-1.214	2.890	1.431	2.570
-0.153	-1.488	-1.209	-1.750	-0.199	-1.578	0.498	-0.467
-1.729	-0.813	-1.065	-1.564	0.066	-1.027	-1.883	1.483
0.419	-0.005	-1.175	-1.384	-2.628	-2.982	-1.514	-1.379
2.669	7.520	8.959	7.382	-0.596	-2.355	0.102	0.000
-0.855	-0.027	3.461	0.752	-1.395	-1.608	2.722	1.151
1.904	-1.856	0.498	1.180	-1.938	9.405	-0.641	0.560
-1.879	-1.261	-1.205	-2.247	-1.441	-0.628	-1.831	-0.770
0.827	-1.432	-0.596	-0.413	-1.261	-2.642	-1.220	-0.231
1.271	-2.163	-0.119	0.699	0.069	5.132	1.021	-0.920
0.473	-0.387	12.073	-1.891	-0.815	-1.276	-2.355	-1.196
4.076	-1.389	-0.885	-0.151	-1.680	0.545	0.965	-1.373
-0.489	-1.259	-1.042	-1.297	-3.311	2.923	-1.484	-1.538
-2.074	1.033	11.213	2.341	2.528	-0.730	-0.342	1.971
3.389	2.959	6.929	-3.304	1.158	0.450	10.410	-0.279
1.227	0.724	2.630	1.035	0.931	1.575	-2.404	0.129
-0.316	1.556	1.648	-0.788	-1.726	-1.411	-0.012	0.000
0.455	0.000	-2.058	0.812	-1.214	-0.922	-0.903	1.872
1.872	0.017	1.503	-0.811	-0.648	-0.405	-2.657	-0.843
-0.583	-0.144	4.939	-2.677	-1.004	-3.088	-1.187	0.000
4.598	0.167	-1.615	-0.378	-0.692	-2.150	8.824	-1.268
2.202	-0.858	0.184	0.275	-0.993	-1.733	-1.068	-0.072
1.763	2.945	1.706	-2.295	2.063	-0.344	-1.520	-0.040
0.853	1.772	0.296	0.153	-1.080	-0.397	-0.763	2.991
4.046	-0.008	-0.012	7.953	9.380	-1.290	-1.986	-1.523
3.986	-1.575	-1.427	-0.923	-0.185	-0.144	-0.827	1.406
4.936	2.481	3.722	0.309	0.732	0.508	-1.173	0.415
-3.090	-0.978	-1.486	-2.670	-1.738	-1.471	0.641	-0.214
0.757	-1.845	-1.364	0.010	-0.256	-2.179	-0.239	-1.989
-0.547	-1.199	-1.748	0.378	-1.448	-1.854	-1.218	-0.593
0.021	-1.462	-0.654	2.289	4.030	-1.591	-2.697	0.074
-0.389	-0.678	1.458	-1.639	0.865	0.000	-0.445	0.000
0.922	2.948	0.000	0.000	0.000	0.000	0.276	0.000
0.000	-0.144	0.000	0.000	3.090	0.000	2.732	-0.700
-1.113	-4.513	-0.987	-0.223	-1.174	-0.660	-0.330	-1.820
-0.870	-1.291	-1.786	-2.122	-1.990	-1.238	-0.097	-2.666
-2.267	-1.422	-0.829	-1.904	-0.375	-2.178	0.000	0.000
-0.719	-1.643	-0.662	-0.307	4.093	2.064	4.509	5.922
0.628	0.590	0.436	-1.066	-0.310	-0.863	-0.281	-0.974
-1.418	-1.223	-0.259	-1.802	6.126	2.292	-1.218	0.504
0.079	0.421	1.213	1.961	-2.205	5.245	-0.729	5.282

Table35.txt

-2.268	-2.184	-0.343	-0.772	2.195	2.021	0.916	-0.453
-0.052	1.215	-1.174	2.326	-2.152	1.080	1.202	-1.980
-1.105	-0.691	1.903	-2.977	-0.500	-0.251	-1.614	0.592
0.658	-2.203	2.644	0.806	0.259	0.723	0.614	-1.864
1.334	0.698	2.543	2.462	-2.067	1.142	-1.338	3.471
-2.289	-1.426	7.280	8.119	-2.170	-2.055	-2.034	-0.596
-1.474	-2.815	-1.004	-1.124	-1.509	-0.720	-0.455	-1.338
-1.914	-1.719	-2.531	-1.069	3.473	-1.478	-1.163	-0.928
0.000	0.000	0.000	-0.064	0.000	-3.090	0.000	0.158
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	1.236	0.000	-0.736	-0.144	-0.823	0.000	0.000
0.000	-0.736	-3.090	1.251	0.000	0.000	0.000	-0.541
0.000	0.000	0.000	-0.712	0.000	0.000	0.000	1.071
0.000	-0.376	1.950	-3.090	0.217	0.000	0.000	0.000
-1.764	-2.819	-2.023	-2.514	0.214	-2.361	-1.342	-0.836
-2.307	0.058	-0.736	-1.005	0.000	-1.346	-0.040	0.015
-2.409	-0.076	1.142	-1.150	-2.864	-2.392	0.631	-0.961
0.000	0.000	0.000	-0.265	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.676	0.000	0.000	-0.002	0.000	0.000	0.000
0.144	-1.780	-0.217	1.371	-0.824	1.454	-1.254	-1.478
-0.520	-2.347	0.000	-0.139	0.000	2.692	0.000	0.317
-0.507	-0.627	-3.090	-0.348	0.163	-0.658	0.331	-0.326
0.000	0.000	0.000	0.000	1.505	-0.144	1.194	-0.321
0.000	-0.066	0.000	0.000	0.000	0.000	0.000	0.000
0.000	1.011	0.000	-1.934	-0.598	0.629	0.050	0.595
1.531	2.376	-1.574	-0.720	0.503	0.019	-2.125	1.121
2.148	-0.154	0.224	8.099	-0.746	0.104	0.676	-0.353
0.916	1.366	5.462	-1.724	1.343	2.979	4.549	3.328
-1.875	-2.109	-0.843	-2.768	-0.420	-2.904	0.528	-1.757
0.542	-0.868	-0.775	-2.566	-1.350	-0.612	-1.548	-1.286
-2.033	-2.355	0.001	-0.651	0.700	-0.977	1.735	-0.714
0.000	-0.074	-2.489	-0.160	-0.393	0.487	0.352	-2.069
0.000	-0.693	-0.610	5.262	0.000	0.000	0.000	0.309
0.000	-0.422	-0.778	0.095	1.875	-1.672	-1.327	0.000
-1.470	1.013	1.695	1.157	1.329	1.429	-2.076	0.403
1.132	11.206	2.702	3.986	4.428	3.081	-1.308	0.898
-1.495	2.328	-1.222	-0.451	7.351	4.817	2.358	1.542
4.383	8.788	9.017	7.543	5.664	9.637	5.610	6.978
-1.624	-2.150	6.307	8.457	6.434	4.110	3.083	8.744
5.817	9.282	4.633	6.583	10.689	7.799	1.185	3.475
0.000	0.000	0.000	-0.551	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-0.074	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.505
-0.541	-1.256	0.000	0.000	0.000	0.000	0.000	0.000
0.000	2.636	0.000	0.000	0.000	-0.823	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.736

Table35.txt

0.000	0.000	0.000	0.959	0.000	0.000	0.000	2.365
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.005	-2.515	-1.214	2.079	0.137	0.000	-1.705	-1.692
-2.501	-0.461	-1.587	-0.608	0.000	0.000	-0.302	-1.114
0.000	1.029	0.289	-1.026	-0.393	-1.172	0.000	0.380
1.701	2.753	2.515	-0.114	4.356	3.631	1.310	-1.756
-0.760	-0.930	2.842	15.030	5.354	4.249	4.985	4.932
-1.532	0.268	3.063	2.578	5.458	5.876	3.437	1.013
-2.101	0.731	-1.071	-0.046	2.334	0.480	0.739	0.530
2.084	-0.166	-2.420	0.426	0.790	-1.009	0.422	0.042
-1.778	-2.314	0.000	-0.731	3.450	0.649	-0.221	0.005
1.147	-0.110	8.039	8.269	5.417	2.991	0.171	1.957
2.263	5.659	5.229	0.833	-0.179	-0.431	0.273	0.359
5.278	2.701	3.090	-1.230	-0.628	0.158	-0.140	3.417
2.356	3.913	11.869	8.975	2.890	0.389	1.984	3.030
0.590	2.616	5.655	-1.341	-2.268	1.820	3.967	3.751
0.068	1.450	4.364	4.158	-2.046	2.101	1.204	1.935
-1.696	-2.220	1.844	0.206	0.231	-1.447	-2.672	0.694
0.328	1.745	0.779	-3.324	-0.009	0.018	-0.096	3.033
-1.521	-1.769	0.957	-0.250	-0.760	-0.661	-1.041	-1.791
-2.281	-2.453	0.441	-1.702	-1.579	-1.154	0.349	-2.434
-2.123	-1.369	-1.380	-3.511	-4.066	-0.089	-1.619	-0.882
-1.679	-1.281	-0.339	1.442	-1.877	-1.442	-2.417	-1.281
3.873	1.030	-0.358	-0.537	1.903	5.871	4.399	2.876
7.995	-0.402	-0.850	-1.113	0.331	-0.154	-1.456	-1.871
-1.748	-2.527	-0.058	-1.338	0.452	1.197	3.621	-0.823
3.342	2.124	-0.384	5.990	0.652	-1.611	-2.617	8.957
-1.575	-0.635	7.226	-4.522	11.374	-1.235	-1.242	-2.926
-1.662	10.658	-0.305	8.881	11.158	0.248	4.097	4.070
-0.395	-1.820	0.028	-1.281	0.223	0.381	0.000	-0.236
-0.541	0.105	0.000	-0.350	0.770	0.561	0.000	0.118
-2.379	-1.047	-1.316	0.387	-1.426	-1.093	-0.493	0.000
-0.168	-0.888	0.366	5.040	0.638	-0.950	-0.222	0.459
0.518	0.944	0.765	0.571	-1.246	-0.710	1.084	-0.032
0.000	1.225	2.938	-0.541	6.206	0.000	-1.813	0.000
-1.129	-1.154	-1.115	-2.728	2.438	3.639	1.065	-2.190
-0.278	-1.645	-0.441	-1.256	-0.521	-1.178	-2.462	-2.156
-0.396	-0.808	0.281	-1.445	-1.286	0.097	-0.781	-1.939
0.366	1.141	-2.600	-1.746	0.721	-1.490	0.108	-0.891
0.271	-0.561	-1.305	-1.484	-0.507	-0.331	0.000	-3.090
0.000	0.000	-1.214	-1.183	-1.891	-2.033	-0.570	0.000
-2.224	-0.655	-3.446	-0.915	-2.275	-0.148	3.773	6.148
3.812	5.744	-0.472	7.899	-1.540	-3.459	-2.115	-0.243
-1.216	-0.673	2.916	2.656	6.689	1.265	-1.105	-2.372
-2.896	-2.033	0.311	-1.580	-0.687	6.384	1.518	5.349
-1.664	0.424	4.000	-1.505	-0.855	-2.495	0.873	-0.318
-1.444	-0.290	0.629	-2.192	-1.696	1.689	-1.617	-2.311
0.000	0.194	0.233	2.035	2.186	0.000	0.000	-0.422

Table35.txt

0.218	-1.339	0.000	-0.445	-0.996	0.309	-0.868	0.000
0.278	-1.833	0.000	-0.025	2.032	0.000	0.000	0.000
-3.338	-2.446	-3.471	-3.344	-0.651	-0.542	6.311	11.670
3.607	-2.729	3.630	16.838	-0.454	-2.808	0.523	-0.968
-2.375	-2.527	0.000	4.595	2.060	-1.848	-2.132	0.114
-0.807	1.380	0.000	0.000	-0.445	0.000	0.163	4.593
1.253	-0.293	-2.227	4.189	0.000	-0.736	0.402	-3.090
0.000	0.190	4.081	0.785	0.137	0.000	0.000	-0.633
-0.793	0.529	-0.311	-0.217	0.000	0.000	0.266	-1.198
-0.246	-0.244	0.000	-2.673	-0.445	0.000	-0.790	0.000
-0.130	-1.733	0.000	-0.677	0.000	-1.629	0.000	-3.067
-1.561	-0.692	2.010	1.865	-0.852	0.129	-0.201	-1.770
-0.481	-1.399	-0.256	-0.280	6.672	-0.408	-1.746	0.167
-0.793	0.823	0.669	1.195	4.541	1.090	-1.164	0.959
-0.369	0.529	0.000	2.084	1.153	1.653	-0.977	-2.922
-1.134	0.074	-1.202	-3.615	-2.508	-1.010	0.095	-0.837
-1.474	0.630	0.032	-0.515	0.127	-0.489	-2.064	0.000
1.950	0.737	-0.592	-0.506	0.441	-2.260	0.000	-0.255
0.000	-0.775	0.000	4.432	-0.137	0.529	-0.910	0.000
-3.090	-3.974	-1.169	-0.009	-1.190	0.250	-1.256	0.515
0.000	0.560	1.088	-0.383	0.000	-1.122	-0.790	-1.687
-0.144	-0.342	-0.554	-1.135	-0.515	0.684	-1.112	-2.671
-1.051	-1.185	-1.501	-0.320	-1.804	0.241	-1.278	0.218
-2.697	-1.478	-0.247	1.927	0.000	-0.804	-3.498	-1.214
-2.110	0.978	0.000	3.121	-1.410	-0.756	1.451	1.069
-0.413	-0.096	0.474	1.014	0.000	0.684	0.137	-0.479
-0.268	-0.336	-0.727	0.787	-0.058	-1.730	0.000	-1.085
-1.183	-1.330	-0.736	-1.656	-3.281	-0.321	-0.790	-0.611
-0.823	0.166	-0.694	-0.512	-0.736	0.167	-0.097	0.959
0.737	-2.820	1.327	3.132	-1.122	-1.875	2.910	1.701
7.065	6.939	0.651	11.361	3.628	-2.651	-1.233	-0.734
-0.322	-1.755	-3.271	-3.060	-2.308	0.636	4.292	-1.708
0.000	0.163	0.000	0.634	-0.272	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-0.929	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.042	-1.369	-1.131	-1.600	2.782	-0.042	-0.702	-2.200
0.350	8.297	0.000	6.522	0.000	-1.881	0.000	0.000
1.711	1.366	-0.997	-2.733	1.140	0.000	0.000	-1.862
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.403	-1.663	-1.403	0.193	-0.866	0.013	0.074	-1.025
-0.263	-0.642	-2.246	0.747	1.068	-1.059	-1.055	-1.690
-1.422	0.502	-2.080	-1.396	-0.250	0.050	1.073	0.687
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table35.txt

0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.790	-1.359	-1.309	-1.039	0.000	0.439	0.474	0.000
0.682	0.620	0.489	5.108	0.651	-0.261	-0.378	0.460
-0.317	1.034	0.000	0.917	1.511	-2.969	0.000	0.000
-0.131	-3.467	-0.844	-2.092	-2.603	-1.983	-2.241	-2.583
-0.760	-0.315	-1.189	-2.983	-1.290	-0.501	-1.046	-0.098
-3.722	-1.167	-0.770	-5.100	-0.102	-1.475	-0.297	-2.216
1.556	-1.396	3.919	-0.795	-1.075	-0.678	-0.136	-1.559
8.136	-0.553	1.929	6.080	-0.509	-1.346	-1.790	-0.061
3.180	-2.931	2.316	5.382	2.130	4.890	3.664	0.598
1.442	-1.149	0.000	0.000	0.023	0.000	-0.300	-0.498
-0.028	-3.327	0.000	3.032	-0.166	0.000	0.000	1.325
0.050	0.458	-0.378	-0.549	0.000	0.000	0.000	0.000
0.000	0.000	0.000	-0.445	0.000	0.000	-0.541	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-1.599	-0.363	-0.608	-1.373	-0.231	-0.827	-1.351	-3.666
-1.732	-2.623	-0.387	-3.227	-1.987	-0.754	-0.973	-2.016
-0.965	0.364	-0.249	-1.302	-2.375	-0.922	-3.672	-1.927
-1.328	-1.623	-0.541	-0.404	-2.032	-2.188	6.366	-1.985
-1.549	-2.195	3.554	-1.272	-0.779	-1.863	-1.540	-1.234
-0.841	-1.198	0.132	-0.023	-0.326	-1.056	0.307	-0.164
0.877	-3.666	-2.826	-2.746	-0.816	-0.950	0.578	-2.543
-1.443	-3.809	-1.599	-0.547	-2.888	-1.017	-0.371	-0.201
-0.724	-1.508	-1.303	-0.153	-0.476	-1.123	-2.105	-1.111
-1.725	-0.796	-2.224	-1.804	-1.526	-2.977	-2.602	-2.835
-2.242	-1.940	-0.552	-0.524	-1.738	-0.543	-2.189	-2.367
-0.602	-2.933	0.212	-1.836	-1.483	-1.247	-1.136	-1.103
0.000	1.677	0.218	2.033	-0.122	-0.505	0.000	-2.668
-0.667	-0.910	0.000	-0.208	0.000	0.000	0.000	1.406
0.199	-0.481	0.000	-0.257	4.299	-0.378	0.000	0.000
-1.726	0.096	2.284	4.343	-2.659	-2.878	-0.349	-0.370
0.463	0.148	2.349	7.651	-1.800	-0.284	1.871	2.014
-0.837	1.198	1.267	0.399	0.041	0.470	3.211	1.654
-1.555	-0.624	2.037	-2.840	-0.343	0.529	3.877	-2.077
0.045	-0.279	-0.074	-1.610	3.667	-0.042	-1.235	0.898
0.567	0.912	0.000	-0.313	-2.121	0.321	-1.120	-1.239
-2.697	-3.132	0.000	2.988	-1.191	-1.921	-0.355	-0.822
-1.751	0.346	-1.851	3.001	-0.461	0.708	-0.118	-1.981
8.172	1.288	-1.620	-2.365	0.000	-0.751	-0.616	-1.489
-0.843	-3.217	-3.512	-2.375	-1.893	-1.569	-0.442	-0.419
-0.782	-1.941	-1.290	-1.827	0.715	-1.159	-0.251	-1.733
-1.453	-1.022	-0.296	-1.792	-0.750	-1.247	-0.637	-0.465
-0.611	0.601	-1.002	-0.361	0.320	-2.338	0.629	-1.356
1.468	-2.954	0.000	-1.596	-0.074	-0.262	-0.148	-0.420
-0.327	-0.865	-1.256	-0.920	0.255	0.936	-0.528	1.194
0.000	-1.092	-2.180	-0.799	1.533	-0.302	-1.276	-0.081

Table35.txt

-0.729	-1.534	0.000	-1.298	-0.203	-2.678	0.451	0.239
-3.090	1.352	-0.495	-0.143	-1.923	-1.412	-0.207	-0.144
1.193	6.373	4.186	5.028	-0.056	1.681	1.236	-1.272
-0.652	0.196	-0.842	1.742	2.763	1.469	0.000	-2.201
0.000	5.087	2.898	-3.596	2.288	4.213	2.503	-0.127
5.311	0.000	2.961	1.473	4.183	3.588	-0.378	5.595
-0.366	-3.160	0.460	3.180	-0.495	-1.163	-2.138	2.820
8.443	1.062	0.457	2.009	4.637	-0.374	4.393	-2.244
0.140	-2.102	7.163	1.820	-0.829	-1.386	-1.966	0.396
-1.803	-1.798	0.218	-1.905	0.053	-0.936	-0.929	2.981
0.994	0.542	1.370	5.422	-2.595	1.425	1.564	0.851
-0.506	-1.382	1.655	0.852	-2.215	-2.419	-1.150	4.098
-2.522	-2.977	-1.385	-2.567	4.807	1.903	8.072	2.823
1.932	4.502	2.630	2.435	5.649	-1.823	2.120	2.215
1.304	1.491	-1.629	-2.435	-0.027	-2.974	2.998	-3.071
8.702	10.106	1.281	2.792	0.221	1.972	-2.380	2.940
-1.720	0.162	-0.852	-2.523	2.061	0.317	-1.436	-0.278
1.187	-0.401	0.820	0.472	1.983	3.920	-1.366	2.677
0.041	-2.358	8.357	6.116	-1.803	-2.580	-1.273	-0.123
3.955	2.382	2.464	5.091	20.285	6.056	13.022	2.600
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	-1.169	0.000	0.000	0.000	0.000
1.141	-1.618	-1.829	-2.880	-1.041	-2.199	-0.706	-1.355
5.218	3.197	-0.027	0.491	-2.222	-4.871	0.712	-1.424
-3.099	-2.971	-1.128	4.339	-1.647	0.194	-3.261	2.517
-1.570	-0.535	2.208	3.400	1.416	2.409	-2.163	-0.696
0.024	-1.215	-0.314	2.654	-2.709	-0.774	0.625	0.798
-0.848	-0.999	1.352	-0.191	15.834	2.286	0.542	1.282
-2.034	-1.221	-1.575	-0.478	-1.304	-2.046	0.033	-1.204
-0.914	2.225	0.029	3.146	-0.652	-1.179	-1.619	-2.015
-2.813	-3.816	2.087	0.789	-0.459	-2.745	1.898	0.065
0.176	-2.758	3.521	8.314	-0.944	-1.744	5.087	3.149
-1.298	-2.004	0.636	-0.278	-2.412	-1.220	-1.525	-3.667
1.528	-0.352	-1.591	4.060	12.459	3.090	4.863	5.452
-1.673	-1.738	-0.874	-2.725	-0.140	-2.073	-1.436	-0.368
-0.133	-2.577	0.141	0.363	0.027	-0.991	0.497	-0.934
-0.898	-1.457	0.082	1.510	1.754	-0.122	-1.832	-0.509
2.246	1.474	1.997	7.963	-1.746	1.406	1.027	2.072
12.436	0.833	6.013	13.330	-1.233	0.937	0.923	2.438
-2.272	0.116	2.581	2.549	9.170	4.044	2.362	2.678
3.417	3.369	-2.337	-2.847	4.146	6.936	0.229	1.926
-0.011	0.993	2.809	5.322	3.715	2.648	3.248	3.351
-1.199	-1.095	5.861	6.194	7.710	-0.733	-0.056	1.508
-3.055	-1.733	-1.001	-2.765	-1.850	-2.093	-2.757	-1.510
2.943	3.507	1.763	14.627	-1.276	-1.097	-2.713	-0.535
-4.302	-2.135	-3.199	-0.528	0.890	-0.280	2.235	-0.618
-1.453	-1.744	6.091	13.991	-1.340	-1.577	10.086	11.838

Table35.txt

12.682	17.628	6.096	12.719	8.931	8.552	7.428	10.554
-2.129	-0.485	11.466	0.069	5.856	-1.686	0.294	5.859
-2.950	-0.750	6.563	7.900	-0.017	-2.791	-1.638	2.290
1.578	-3.334	1.824	0.256	-2.407	-0.061	-1.188	-1.101
-1.626	3.160	-1.860	7.558	5.389	-0.434	2.281	6.343
-0.674	-0.014	-1.003	-2.318	-0.812	-1.602	0.079	-2.497
-0.597	0.390	0.000	-2.120	-2.433	-1.543	-1.452	-1.145
-1.926	-0.363	0.354	-4.016	-2.836	-3.121	-2.139	-0.505
-1.703	-1.747	5.491	9.719	-1.374	-1.609	-1.427	-3.470
-1.618	-2.182	-1.326	-3.361	-1.251	0.769	0.293	1.251
0.465	0.456	-1.518	-3.418	-0.994	-0.277	-2.890	2.152
-1.864	-4.968	-1.604	-1.481	-0.852	-1.274	1.431	-2.618
-1.344	-1.977	-0.712	-2.396	-1.765	-0.398	-1.300	-1.903
-3.315	-1.014	0.026	-0.437	-2.225	-2.663	-0.797	-1.288
-3.133	-3.669	-1.171	-1.658	-1.753	-1.297	-1.415	0.566
-2.607	-0.254	-0.302	-2.306	-0.919	-0.704	-0.766	-0.585
-0.768	-1.500	-0.749	-1.594	1.737	-0.990	-4.049	-0.389
-0.253	-1.244	-1.350	-1.432	0.772	-0.991	-0.767	-1.123
6.920	6.630	2.193	8.875	-0.321	-2.386	-1.061	-0.505
0.211	-0.683	-2.030	-1.528	9.484	-1.079	6.261	1.534
-1.666	-1.659	-3.009	-2.711	0.109	-3.709	-1.067	-1.341
0.751	-1.026	-0.349	-2.791	-0.262	-0.377	-0.889	-0.378
-3.835	-3.872	0.879	-2.149	-1.522	0.324	-0.922	-0.120
7.991	8.615	-1.830	-2.076	-1.148	-1.995	3.064	5.391
4.513	6.570	-1.126	2.587	3.977	3.670	-1.112	-1.689
-1.236	-1.506	-2.601	-2.326	6.618	-4.618	4.314	0.347
2.749	-0.289	-0.786	3.055	3.117	-0.313	-0.301	-1.952
1.089	4.816	-1.881	9.125	1.222	0.396	0.955	1.608
-0.752	5.774	-3.444	-0.483	1.075	1.436	-1.346	-0.448
-0.801	-0.410	-0.243	-1.161	-0.811	-3.484	-0.107	-1.571
-4.647	-1.104	0.548	-1.061	-1.415	0.122	0.532	-0.358
-1.308	-2.385	1.930	-2.688	1.493	-0.412	-0.542	-0.422
-2.089	1.455	0.796	-1.332	-0.278	0.529	-1.155	-1.169
0.029	-0.919	-0.279	0.313	-0.523	0.599	-0.576	1.144
0.495	-0.285	-1.750	-2.041	-0.608	-0.087	-0.519	-0.131
-2.159	-2.530	2.911	5.556	5.513	4.260	-0.243	1.304
3.026	5.479	-0.588	6.759	-0.940	2.777	-0.753	3.158
-1.433	-2.133	0.065	5.755	3.901	0.942	1.363	0.951
-1.106	-1.069	-0.272	-3.565	-1.262	-1.759	-1.730	3.361
-2.325	-2.101	2.959	-0.288	-0.552	-1.811	1.512	2.386
-0.739	0.954	-0.092	-2.589	-3.104	-0.539	-1.516	-1.819
-2.956	-0.814	-1.628	-2.562	-0.496	-1.601	-1.123	-1.603
0.572	-1.785	-3.256	12.449	-0.716	-0.414	0.074	-3.039
-2.202	-1.179	-3.239	-2.423	-0.679	-1.392	-1.366	-0.010
-3.487	-3.184	-1.652	-2.760	2.018	4.122	1.061	2.161
-1.858	-0.751	-1.031	-0.160	-1.010	-3.055	2.168	3.046
-1.058	-3.197	0.346	2.654	4.742	-1.436	-2.650	0.793
-1.642	-2.214	-1.015	-2.251	-2.394	-3.348	-0.643	-1.024

Table35.txt

-0.187	-0.682	-2.978	-2.991	-1.235	-0.100	0.056	0.006
2.541	0.107	-0.867	1.053	2.407	-0.555	-1.985	-0.320
-1.370	-3.686	-1.125	-4.068	-1.738	6.706	-2.159	-2.157
-2.126	-1.684	0.255	-1.542	-2.825	-1.938	-0.652	-1.937
-1.767	-2.367	0.034	-2.109	-1.383	-2.608	-1.984	-1.002
-0.848	-3.301	-1.783	-3.709	-1.653	-2.753	-0.187	-1.280
-0.583	-1.119	-0.513	-0.323	-0.213	-0.083	-1.070	-1.180
-0.926	-1.448	-1.672	-2.602	0.000	2.916	2.248	3.206
-1.029	-0.651	2.918	5.934	0.876	-2.097	-2.428	3.738
-1.223	-2.827	2.709	-1.313	1.010	-0.200	2.529	2.697
0.717	0.396	0.024	-3.009	1.564	3.619	2.952	3.583
1.080	0.844	0.341	1.722	0.137	0.401	-1.145	-0.730
-1.323	-0.065	0.000	3.613	-2.241	-1.166	0.951	0.561
-1.547	-2.417	0.676	1.890	0.973	-1.964	2.083	-0.626
2.376	2.168	1.899	2.150	2.157	-2.871	0.384	2.254
-1.490	-0.107	4.883	10.465	1.220	2.530	1.045	1.952
-0.827	0.961	0.000	2.543	-1.920	-1.009	0.000	0.136
-1.947	-0.667	-2.664	-1.845	1.696	4.510	1.487	-0.980
-1.623	-3.376	2.524	4.005	2.771	0.523	1.482	4.943
1.995	4.931	2.569	5.613	1.711	-0.746	2.694	-1.125
-1.641	-1.747	-2.209	-1.188	0.861	-2.293	-1.349	-1.449
-1.441	-4.121	1.559	17.014	-2.541	-0.876	-1.823	-0.940
-0.959	-1.795	-0.381	-2.475	-2.425	-1.147	-1.746	0.413
-1.726	-3.270	-2.525	-2.187	-1.792	-2.273	-0.005	-2.452
-2.528	-1.418	-0.249	-3.238	-1.008	-1.840	-2.180	-1.489
-0.745	-0.697	0.031	-1.907	-1.380	-2.772	-2.115	-0.752
-0.903	-1.525	-2.456	-2.429	-1.310	-1.856	-1.934	-1.298
-0.490	-2.009	-1.192	-0.649	-2.203	-0.866	-0.794	-2.988
-1.529	-1.643	-1.192	-3.122	-1.750	-0.344	-0.655	-1.277
0.000	0.000	-1.169	0.000	0.752	0.000	0.000	-1.169
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.257	1.125	-0.736	0.460	-1.802	0.000	0.000	0.000
0.508	1.371	1.109	3.334	1.560	0.000	-1.545	-0.581
1.658	0.279	-0.823	-3.370	-0.044	1.210	0.011	1.467
-3.409	-0.355	-0.137	-0.742	8.339	0.000	0.000	0.224
-0.290	0.460	0.089	-0.598	-1.233	-0.288	-0.589	-0.855
2.160	1.053	0.169	-1.060	-1.620	-0.453	-0.217	0.000
1.344	0.156	0.595	-1.331	1.822	-0.082	-1.425	0.000
0.000	0.000	0.000	-3.090	0.000	0.000	0.000	0.137
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.366	0.000	0.000	0.000	0.000
10.140	12.962	-1.081	10.105	3.950	6.263	-1.344	-3.449
-1.503	0.138	5.241	16.111	-1.432	-2.264	-1.182	-3.130
9.581	8.572	-0.871	-1.476	11.520	-1.230	9.157	0.535
0.000	3.153	-0.445	0.000	-3.090	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
1.614	7.475	5.567	10.829	-0.997	-1.966	3.786	4.831

Table35.txt

0.346	2.712	6.215	-2.015	6.911	7.448	2.567	2.360
2.222	1.898	1.401	5.898	-0.551	5.801	2.723	1.273
1.406	0.104	-0.321	3.123	-1.054	0.000	-0.183	-0.137
0.840	4.289	-0.633	-0.880	0.000	0.441	0.000	2.105
0.000	-0.499	-1.247	0.387	0.000	-1.430	-0.273	-0.610
2.044	3.561	1.546	6.763	-1.555	-4.511	-1.123	3.107
2.603	4.336	7.194	12.976	-1.126	-0.791	4.531	4.000
2.800	1.618	1.928	3.040	5.295	-0.869	3.029	4.890
0.496	2.209	0.423	1.096	1.169	-0.899	-1.515	-0.468
-1.683	-2.415	1.843	-0.684	0.820	2.465	-0.549	-1.090
1.258	0.045	-2.351	0.920	-0.997	1.319	0.737	1.547
-0.828	0.495	-0.849	-1.941	0.066	-1.539	4.916	-3.038
-2.269	-1.433	5.341	-2.150	4.410	-1.600	-1.525	-3.263
-1.881	-2.427	7.467	12.363	6.491	-0.298	-1.257	0.058
1.950	-2.700	-0.473	-2.211	-4.047	-0.375	2.166	1.419
0.046	-1.235	3.459	-1.529	1.309	0.362	0.000	0.688
-0.361	2.154	-0.640	-0.224	0.000	2.343	-1.545	0.600
-1.672	-2.733	-3.119	-3.082	2.222	2.190	0.247	-2.122
-2.813	-1.567	2.447	4.100	0.302	-2.180	-0.901	1.218
-1.048	1.299	0.954	3.161	3.391	0.881	-1.826	-1.013
0.000	4.354	-2.155	-1.768	-0.563	0.145	5.225	3.090
4.542	11.029	3.090	17.819	-0.446	-2.047	3.090	3.090
0.000	0.000	-3.031	-1.233	3.090	-2.035	-1.042	-3.041
5.789	-0.883	6.504	-2.083	10.288	7.638	-1.135	-1.670
0.080	3.966	0.593	-1.341	6.460	6.373	-0.363	-0.540
1.368	6.891	9.467	-2.630	9.867	5.139	0.061	6.468
3.088	1.292	-0.317	2.490	7.885	7.751	-0.557	-0.566
-1.410	-2.032	2.885	-1.181	8.073	2.891	7.471	1.346
4.808	10.012	-0.775	0.050	4.348	8.760	4.730	2.633
6.674	4.070	-1.241	4.643	2.987	2.385	3.394	4.418
2.154	5.144	2.085	2.157	1.831	1.899	3.697	5.346
2.539	-1.593	3.325	5.915	1.368	-1.246	2.927	1.613
0.000	0.930	-3.090	-0.616	0.000	0.000	-1.169	0.000
0.137	0.000	0.000	0.000	0.000	0.000	-1.189	0.323
0.000	-0.647	0.000	0.218	-1.569	0.317	-2.835	-0.079
-1.886	-0.435	0.921	-0.683	1.980	0.550	2.491	2.356
0.951	0.010	0.627	-3.051	-0.769	0.757	5.985	-1.008
0.721	0.733	3.583	-0.456	2.362	-1.494	-2.406	-1.496
0.508	0.263	0.000	1.330	-0.487	-1.504	-1.345	-0.810
1.132	3.967	0.000	4.504	2.320	0.000	-0.220	-2.053
-0.130	-1.723	0.244	0.899	3.247	-0.778	0.000	-0.411
0.050	-1.787	-0.581	-0.608	-0.378	0.050	-3.090	-0.736
0.000	0.131	-3.090	-1.281	-0.321	0.000	0.000	0.050
-0.074	-2.214	-3.090	-0.914	0.000	0.297	-0.261	0.000
-1.169	-0.690	-1.432	-1.435	0.000	0.000	0.497	-3.084
2.964	3.999	0.000	5.069	-0.629	-0.027	0.717	-0.914
0.546	-0.115	0.000	0.000	5.453	0.000	-0.380	0.717
0.460	0.865	-0.217	1.529	1.843	-1.256	0.000	0.000

Table35.txt

-1.694	-2.575	-1.169	-2.123	0.000	0.000	-0.144	-1.448
-1.586	-1.645	0.000	-0.191	-1.379	0.412	0.000	0.000
0.000	0.041	-0.541	0.000	1.236	0.000	-0.644	-2.557
-0.144	-0.144	0.000	0.000	0.000	0.000	-3.090	-0.027
0.000	-1.008	0.000	0.023	0.138	-0.217	0.000	0.000
0.000	0.000	0.000	-0.375	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.179	0.465	-1.127	-1.624	-0.339	-1.148	-2.730	-1.090
-0.578	-0.839	0.000	-1.141	-1.280	0.051	1.233	-0.509
0.095	-1.017	-1.215	-0.106	2.625	-2.993	-0.797	-1.169
0.000	4.019	0.295	-1.687	-0.535	-0.960	-0.233	-3.090
-3.090	-0.714	-0.775	0.000	-0.610	-1.470	-0.296	-1.850
0.309	0.000	0.394	-0.298	-0.879	-1.871	0.830	-1.539
0.150	-0.290	0.000	-0.146	0.687	0.000	0.000	0.000
0.000	0.137	-0.971	0.000	2.763	-0.349	0.108	0.382
0.050	-0.180	0.000	-0.942	0.143	0.144	-0.338	-0.519
-0.911	2.985	5.313	-1.806	0.575	0.503	0.913	0.000
0.000	-0.436	-0.125	0.527	-0.170	2.552	-0.115	-0.663
0.309	0.000	0.922	-0.527	4.716	2.144	5.634	3.543
-0.919	-1.679	14.750	5.525	7.201	3.310	5.443	3.090
3.140	3.152	7.603	2.055	-0.183	5.173	7.632	5.763
3.972	6.616	2.313	2.420	4.513	-2.140	-1.427	6.972
0.714	-3.814	-1.506	0.033	3.108	-0.415	0.363	1.043
-1.392	4.339	4.026	1.225	0.190	-0.480	-1.236	2.350
0.322	0.920	-1.709	-1.256	-1.278	-0.626	-1.036	-1.669
-2.222	-0.045	-2.104	-0.912	1.157	-0.637	-1.322	0.000
1.622	0.000	0.000	-0.119	0.000	0.956	-0.468	0.000
2.826	-1.298	0.000	-2.324	-0.627	0.878	-0.759	-0.247
0.044	-1.431	-1.868	0.656	-2.540	-0.142	0.492	0.000
-0.473	0.654	2.849	0.658	-0.694	0.098	-2.691	0.865
2.563	1.370	0.000	-0.659	-2.598	-2.035	-3.120	2.560
-0.701	-1.672	-1.244	0.421	-2.433	-0.734	-2.101	-0.592
1.960	-1.549	-0.671	-0.259	-1.217	-2.681	-2.128	-1.188
-0.159	-0.535	-0.381	-0.135	-0.707	-1.414	-0.584	-0.298
-0.892	-1.652	-1.868	10.663	8.004	-2.915	0.884	-3.142
-1.521	-0.525	-2.760	-1.015	-1.250	-2.843	-2.183	-1.107
-1.985	-1.293	3.450	-1.784	-2.533	-1.073	-2.646	-2.447
-2.408	-3.502	0.827	-0.448	-0.892	7.151	2.898	3.844
1.379	4.330	-1.704	-2.475	-0.794	-0.952	-1.359	1.235
-0.263	-2.075	-2.056	-3.044	2.394	-1.519	3.803	4.000
-1.606	-2.205	-0.031	-3.467	-0.887	9.019	-1.140	-1.809
-2.666	-1.145	-0.228	-1.369	-0.342	-0.378	-1.837	-0.897
-1.971	-0.918	0.004	-2.386	-2.548	-0.263	-1.305	-0.686
-3.228	-3.352	-0.346	-2.544	-0.798	-2.133	-2.473	-1.594
-1.119	-2.179	-1.290	-4.352	-0.679	-0.541	-1.507	0.309
-2.419	-1.844	-2.375	-0.778	-2.727	-1.142	-2.253	-0.766
-3.428	-1.749	-1.312	-2.705	-0.751	0.125	1.170	-1.454

Table35.txt

-0.952	-0.477	-0.535	-2.276	0.952	0.099	-0.139	-0.274
0.000	0.140	-2.856	-1.277	3.101	0.000	1.683	0.317
-1.415	-3.423	-0.439	-1.090	-0.805	-1.528	-0.578	-1.374
2.338	0.770	-1.791	1.828	-4.859	-1.468	-0.811	2.414
-1.149	1.285	-0.895	-1.411	0.134	-5.161	-1.289	1.122
-1.414	-4.272	1.438	-1.216	-0.487	3.769	-1.411	3.276
-0.901	-3.749	0.000	8.216	-0.345	1.236	1.205	-2.440
1.899	4.231	-0.304	-2.003	0.000	-2.638	4.875	1.296
-3.504	-1.546	-2.250	-3.073	-0.845	-2.334	-1.662	-0.796
-1.081	-4.998	-1.318	-3.091	-1.623	-3.403	-0.532	2.529
-0.101	-1.171	-3.527	-0.260	-2.318	-0.783	-0.651	0.622
4.790	5.537	-1.132	-3.638	-1.643	0.272	-2.265	-3.160
-1.077	-0.194	0.000	2.257	-1.815	-0.477	-2.378	-2.094
-0.767	-1.055	0.000	3.886	-2.708	-1.571	5.410	0.663
-2.278	-2.711	-1.029	-2.228	3.446	8.717	9.426	-3.116
3.560	-0.201	-2.396	1.124	-1.931	-0.834	-0.397	0.158
-1.490	-0.941	-1.060	-4.296	-0.820	-0.269	-1.205	-2.697
-0.434	12.027	-1.122	-3.575	-1.552	-1.161	-0.250	1.265
-0.061	-3.192	-1.271	-1.835	-0.512	3.023	-1.929	-0.783
-0.079	-0.678	-0.221	-2.723	3.967	-0.007	-0.698	-1.468
-3.480	-2.392	-0.040	-2.559	-1.070	-1.377	0.066	-0.539
-0.692	-0.613	-0.318	-2.252	-0.027	0.786	-1.754	-0.198
0.043	-1.439	-1.719	-2.593	7.551	2.676	-0.975	-2.557
0.341	-0.754	1.787	1.592	-0.200	-1.460	0.348	0.965
-1.633	0.062	-0.239	4.972	0.875	-0.682	0.031	0.552
1.005	1.171	3.802	5.171	-0.743	-2.514	2.383	0.297
0.021	2.225	3.281	1.651	0.130	-0.656	2.417	3.399
-1.047	-1.686	0.089	1.587	1.112	-1.672	1.540	1.931
3.320	3.783	2.048	0.844	4.858	3.780	1.795	-0.370
-0.550	1.668	0.994	-2.277	2.638	-0.875	0.653	-0.042
-2.280	4.317	6.619	10.117	0.527	-2.922	-0.197	-0.653
-1.130	2.159	4.571	-0.999	0.055	0.141	3.948	3.014
-2.661	-2.919	-2.273	-3.263	3.090	7.472	-1.811	-2.854
6.205	9.563	-1.086	-1.564	5.309	-1.265	0.153	-1.918
-0.748	-1.875	-0.215	-0.589	17.362	5.094	5.148	1.014
-1.800	-2.558	-2.288	-2.489	-2.346	7.929	-0.179	-2.459
-1.413	-2.744	4.284	9.981	-2.227	-1.216	-4.252	-2.419
-1.086	-0.696	0.473	-3.896	2.296	4.936	-0.066	0.247
-2.196	-1.626	-0.179	-1.899	3.301	-2.509	-1.891	-1.268
-1.095	-3.115	-0.727	-3.041	2.329	3.066	-0.896	-3.022
-3.568	-1.026	-1.287	-2.071	-2.102	-1.536	-1.281	-0.803
-1.281	-0.940	0.000	0.000	0.000	0.000	0.000	-0.416
0.000	0.000	0.000	-0.512	0.000	-0.790	0.000	0.000
0.000	-1.667	0.000	0.000	-0.089	-1.934	0.000	0.000
0.830	-1.465	-1.387	-3.545	-0.380	-1.225	-1.970	-1.946
-1.004	-0.488	-1.825	10.994	-0.824	-0.855	-0.349	-1.530
-0.386	-1.157	-0.327	-2.961	3.368	1.934	2.656	0.125
0.223	-1.765	-1.226	-3.138	-0.373	-2.632	-0.165	-2.505

Table35.txt

-2.606	-2.301	0.299	-0.791	-1.660	-0.980	-1.175	-2.520
0.046	-2.212	-0.820	-2.193	-1.277	0.002	-0.821	-0.534
-0.159	-1.839	-0.964	-2.331	-0.099	-2.803	0.000	-2.368
0.321	-1.165	0.000	6.079	-0.629	-1.080	-1.317	-1.134
-0.861	-1.952	-0.170	-2.894	0.560	-2.299	-0.737	0.000
-0.802	-3.971	-0.380	-1.792	-0.339	-1.792	-2.215	-2.831
-2.154	-1.609	-1.548	-0.355	-1.412	-0.038	-1.351	-1.030
-2.969	-2.235	-1.154	-2.008	-3.185	-0.722	0.608	0.955
-0.845	-2.675	-2.155	-0.814	-3.116	-3.082	-0.233	1.891
3.085	1.815	-1.534	-1.155	-1.365	-0.836	-0.948	-0.482
-2.840	-0.406	-1.127	-0.790	-0.824	-0.765	-1.571	0.559
1.430	-1.592	-2.345	-2.093	0.653	-1.488	-0.734	0.728
-0.035	-0.638	-0.720	1.966	-0.179	-1.263	-0.261	-0.450
-0.756	-1.593	-0.054	3.985	4.162	1.618	0.282	-1.857
-1.723	0.861	-1.909	-0.142	-1.564	2.486	-0.927	1.806
7.803	0.674	0.000	0.000	0.000	-2.788	1.492	-0.409
-3.072	-1.410	-0.159	1.928	9.239	-2.041	-0.330	-0.796
-0.355	-2.133	-2.634	0.150	-1.918	-1.452	-1.716	-1.868
-1.055	-0.301	1.142	-1.239	0.717	0.000	-0.877	-2.129
-0.194	7.096	-0.244	-3.045	-3.328	-1.761	2.694	0.000
-1.193	-1.778	2.609	5.910	-0.018	-3.296	-1.561	-3.028
3.279	3.025	-0.829	-0.558	-0.217	0.100	-2.228	0.096
0.100	-1.018	-0.495	-1.607	15.265	4.956	-2.471	-0.865
-1.357	-2.999	-1.151	0.567	-0.979	-2.114	0.396	-1.583
-2.831	6.564	3.609	18.701	-2.660	-1.160	-1.191	-0.186
-1.805	-1.402	-1.512	-2.655	10.063	-0.623	2.793	-1.768
-0.219	-2.770	-4.350	-2.668	-0.174	-2.033	-1.417	0.822
8.741	11.321	-0.096	-2.086	-2.168	0.424	-1.633	-0.925
-1.309	-1.144	2.536	12.985	5.248	-2.087	-3.607	-1.334
-1.326	-1.382	0.462	4.914	-1.032	-1.832	-0.468	-1.800
2.270	-1.488	0.700	5.510	-2.154	-0.724	-2.476	-1.876
-1.583	-1.608	-0.996	-2.047	3.525	-0.844	3.412	-0.475
0.340	-1.040	0.214	-0.357	-1.769	3.295	-0.058	-0.425
0.487	1.938	1.393	-0.052	2.024	2.123	-1.347	5.173
3.665	3.082	-0.536	1.535	0.950	4.436	1.023	-0.891
2.209	-2.258	-0.696	1.132	1.610	1.123	0.403	-0.104
0.056	-1.928	-0.509	7.172	-0.050	0.764	-2.651	2.228
-0.465	-2.113	0.028	1.541	1.414	1.179	-0.487	-1.362
-4.136	-2.753	-0.876	-3.814	-2.255	-2.766	-0.287	-3.302
-2.366	-0.706	-0.862	-2.257	-2.224	-1.122	-1.147	-1.980
-1.166	-2.607	-2.169	-3.357	-2.204	-2.888	-1.199	-1.581
0.519	0.131	-0.355	-1.983	-1.994	-1.890	-1.560	2.093
-1.995	-2.773	1.073	3.403	-1.441	-0.489	-0.052	-1.825
-0.287	-1.591	-0.262	-1.546	-0.132	-0.335	-1.557	-1.479
0.595	-0.098	0.000	-1.532	0.441	-0.436	0.137	0.176
-0.847	0.000	0.000	-0.557	-0.974	0.000	-0.823	0.000
-0.995	0.098	-1.164	0.865	-0.152	0.460	0.137	0.000
-3.269	-3.337	-2.254	-1.276	-0.329	-1.978	-2.473	-2.142

Table35.txt

-1.542	0.676	-0.396	2.860	-1.068	-1.316	-0.796	-1.055
1.443	-2.072	-2.884	-0.032	-3.748	-1.871	-1.097	-0.930
-2.605	0.393	7.606	-0.463	7.807	12.059	1.619	3.976
9.135	6.447	2.564	12.557	9.116	1.347	-1.586	0.758
-0.245	-0.599	2.163	6.379	9.340	9.825	4.010	2.111
0.587	-0.976	3.556	1.599	4.422	1.438	-1.922	-3.354
1.570	0.374	-0.897	-0.439	-0.024	-1.343	2.419	0.332
0.769	-0.878	0.514	0.371	0.288	4.333	1.060	0.128
6.469	-2.026	2.124	2.140	5.362	3.672	3.199	-1.500
-0.097	-1.280	-0.292	1.194	4.059	6.775	-2.024	5.349
1.476	6.363	-0.018	1.068	10.450	8.844	-0.289	-0.716
1.849	1.271	1.763	1.932	0.852	1.795	0.149	-0.419
2.866	3.159	-1.947	0.196	-0.474	-2.581	2.925	1.228
-1.065	-0.142	-0.055	-0.624	2.909	-0.121	0.000	-0.317
5.770	-1.002	13.899	12.314	3.702	-1.859	-1.247	2.252
0.318	4.415	8.679	-2.091	-2.500	0.012	10.077	4.942
3.481	1.176	-1.913	-0.966	9.335	-0.135	0.678	-0.271
-1.161	-3.146	10.580	-0.662	4.444	-0.790	0.172	-0.730
1.039	-2.883	-2.205	-1.272	1.170	0.000	14.221	-0.331
0.589	-1.078	2.397	0.000	-2.006	-1.607	5.138	-0.884
-0.467	-0.412	-0.379	-0.288	-2.834	1.676	-0.069	0.512
-1.209	-2.786	-0.956	0.621	0.006	-1.962	-0.418	-0.323
0.037	-0.816	-0.455	-2.295	-2.201	-2.119	-2.366	-0.427
5.853	7.682	6.304	5.691	0.672	2.385	1.288	0.000
1.538	3.064	3.188	0.158	0.062	0.000	2.436	0.140
0.705	4.908	2.383	-1.299	-2.234	1.406	5.164	5.444
0.000	-1.802	3.090	-0.440	4.236	-0.811	0.000	0.000
0.000	5.264	6.386	-1.243	-1.316	-0.914	-0.686	2.231
-0.823	3.090	0.000	-0.310	-1.169	0.000	12.325	1.082
0.175	-1.552	-3.181	0.200	-1.312	0.051	-1.824	-0.292
0.266	-0.753	-1.686	0.648	-0.045	0.055	-2.447	-1.656
1.258	-0.504	1.364	-3.375	-0.043	1.239	-1.418	2.006
10.260	13.320	1.909	13.287	8.810	7.663	6.793	0.511
3.530	0.789	5.618	3.782	5.642	10.306	13.011	1.704
3.387	6.213	1.035	8.917	1.552	10.479	0.789	-0.505
-0.154	-1.204	4.194	-0.524	0.417	0.184	-1.193	-2.261
-0.064	0.338	-0.004	1.220	-0.058	-0.240	7.051	0.777
2.479	-2.688	-0.797	-1.551	-1.030	-0.553	-0.418	-0.676
-0.694	-0.291	-2.073	10.322	0.610	0.009	-2.159	4.525
-0.753	7.140	8.096	-1.224	-0.935	9.771	0.377	4.572
5.965	1.381	3.090	-1.600	-1.537	-0.820	2.514	0.655
-0.409	0.186	1.937	-2.610	-1.559	0.173	0.000	0.000
0.000	-0.337	1.694	1.835	-1.329	-1.591	-1.335	0.000
-0.582	0.051	0.000	-0.562	-5.284	-2.168	-2.342	-1.252
0.681	10.866	5.844	0.752	0.654	0.210	4.332	1.924
4.228	-0.065	-0.581	-1.115	-0.700	-1.623	4.963	1.002
-1.062	5.483	-1.922	4.057	0.275	5.159	0.867	-1.659
-0.906	0.027	8.232	2.514	-1.084	0.716	0.000	1.573

Table35.txt

5.147	0.314	1.265	-0.317	0.409	-1.603	1.437	-0.911
-0.817	7.645	-1.165	7.109	11.031	-1.506	-1.057	-1.363
2.007	0.170	4.820	3.229	1.971	0.118	-0.287	1.295
5.433	-0.375	-1.064	0.000	1.874	-2.779	0.731	0.849
2.822	0.131	0.549	6.400	8.411	-3.974	-2.561	0.366
1.062	5.939	0.902	1.885	3.437	-1.532	1.262	1.976
1.593	-1.266	-1.028	-0.304	0.728	2.107	4.853	-0.803
0.908	-0.491	4.187	-0.455	-1.202	4.278	8.992	-1.032
-1.778	-1.207	-2.560	-1.122	-0.641	-0.943	-2.075	0.000
-0.235	-0.108	-1.320	-0.032	-1.380	-1.785	12.734	0.376
0.077	-1.472	-0.518	-1.536	-2.261	-0.900	2.420	-1.173
-1.150	3.817	3.107	-2.332	0.499	0.204	2.459	0.000
1.966	2.621	0.623	-1.342	-0.823	2.755	1.039	3.213
2.551	4.101	0.000	-0.081	-0.842	1.296	1.261	-1.531
-1.155	-1.093	3.023	1.481	-0.849	-1.524	1.324	-0.259
-0.790	1.527	2.273	1.095	0.994	2.663	4.185	-0.553
2.576	0.000	1.821	-1.527	-1.487	-2.915	-1.593	5.405
0.467	-1.260	-1.203	2.854	0.412	-1.747	2.245	1.153
3.133	1.888	6.034	0.000	0.462	-1.572	-2.104	-2.258
1.584	-1.666	-0.101	0.170	0.757	0.127	-0.400	-2.560
6.276	1.220	13.122	6.519	4.080	0.355	0.382	4.280
3.853	3.178	3.553	-1.294	1.657	-2.681	2.678	2.904
0.750	7.185	0.000	2.830	6.535	8.188	14.094	-2.986
-0.440	-2.164	9.506	5.190	5.340	-0.509	5.844	1.428
1.591	0.743	7.625	-2.212	1.375	-1.447	7.415	5.319
0.330	-0.889	0.362	-0.461	4.208	-0.349	-0.055	-1.298
-0.290	0.261	16.623	-0.035	2.593	-0.539	-1.216	1.467
1.989	1.107	2.559	3.824	5.190	1.510	-3.745	5.082
3.813	-1.656	0.156	-3.574	-3.263	0.449	3.529	3.489
-0.248	3.135	-0.114	-0.475	1.345	-2.436	0.534	-1.694
-0.663	0.388	0.210	2.750	0.684	0.911	-2.652	-0.382
1.069	2.132	-0.155	1.932	2.870	2.492	0.520	-1.642
0.000	-0.505	0.000	0.000	0.000	0.000	-0.505	-0.144
0.000	-3.090	-1.169	0.366	0.000	0.000	-0.823	0.000
0.000	0.000	-0.144	-0.217	0.302	0.362	0.000	0.000
11.312	13.018	11.140	17.288	10.474	16.829	10.709	18.816
9.759	11.836	8.520	20.039	6.705	9.373	0.473	1.098
10.547	13.277	7.446	10.146	13.520	7.202	4.834	-0.336
-0.638	-1.550	0.588	0.354	0.088	-1.599	0.677	1.402
-0.203	2.805	2.469	-0.722	-0.937	2.442	-0.641	-1.186
-0.804	-1.849	2.906	0.837	0.729	-2.537	-2.694	3.709
3.852	5.805	14.992	11.869	4.851	-2.038	7.591	3.663
3.121	3.118	6.308	1.120	2.682	8.925	5.464	0.333
-0.747	4.882	5.101	13.250	15.418	-1.132	-0.542	3.668
0.342	-1.267	7.658	0.390	-1.509	-0.533	-0.365	0.000
0.606	2.703	-2.779	-2.203	-1.237	0.638	0.303	5.613
3.359	-1.066	-1.550	-4.155	-1.630	-0.031	-1.315	-2.253
-0.646	0.216	-0.759	2.411	3.404	0.788	0.131	1.627

Table35.txt

6.086	1.932	-0.235	-0.964	1.791	9.872	11.001	-0.172
0.167	2.872	1.382	-2.040	-3.402	3.718	5.522	3.027
-0.616	-0.144	-2.490	0.509	0.000	0.000	0.139	0.000
0.000	-2.491	0.000	-0.027	0.000	1.320	2.850	-1.176
2.730	-1.169	-0.705	-0.859	0.904	0.775	0.955	0.309
0.014	-2.138	-0.112	3.467	0.530	0.783	1.973	0.116
2.207	-0.490	-0.671	-0.045	-1.389	0.446	2.632	-1.096
-1.220	-0.051	-0.349	2.173	-1.046	1.147	-1.846	-0.263
-1.555	6.729	-1.830	-0.092	2.164	-1.181	-1.784	-0.236
-0.941	-1.987	-1.951	0.599	-2.948	0.594	11.067	1.440
-0.485	-0.841	0.101	-1.904	-2.158	-0.486	5.463	-1.939
-0.881	-2.423	1.819	-0.517	1.439	4.004	-0.027	0.000
-2.303	-0.118	-1.284	-0.350	0.000	1.738	7.938	0.000
0.000	-1.281	0.000	1.143	0.711	-0.674	-2.305	-0.409
5.129	9.262	13.227	-1.446	6.732	1.793	3.836	-1.092
5.692	3.090	6.038	3.090	5.033	-2.376	14.959	4.565
5.749	4.349	2.117	5.640	10.642	5.048	8.410	4.791
-1.492	0.382	17.344	15.033	11.237	-0.042	11.152	3.996
0.171	0.272	-1.004	-0.552	-0.249	14.838	17.091	0.028
1.065	9.260	0.609	4.763	-0.722	4.571	21.032	-0.986
2.667	5.273	-1.134	-0.790	0.000	0.471	0.000	0.000
0.000	0.000	-0.288	-3.151	-0.189	-0.469	-0.147	0.000
-1.957	-0.421	2.590	0.281	6.654	0.000	0.000	-1.227
-0.588	-0.040	0.818	-0.561	0.216	0.218	0.132	0.000
0.362	0.000	1.478	-0.088	0.000	0.989	0.055	0.000
-0.823	0.480	0.000	-2.487	-0.620	-0.378	-0.135	0.000
-1.581	-1.577	2.586	0.217	3.227	-0.236	0.823	-0.297
2.989	2.059	1.058	-0.784	-0.767	-0.020	-0.300	2.288
1.576	-0.254	-0.699	0.097	-0.546	1.137	-3.025	-0.659
-0.709	-1.392	-1.574	-1.528	-0.666	-0.348	-1.857	0.000
-1.185	0.000	0.000	0.139	-0.074	-0.399	0.528	-1.583
0.677	-1.218	0.000	-0.860	-0.041	0.000	-1.260	-0.161
-0.166	0.523	0.000	-1.519	1.166	-1.316	-1.508	0.000
0.000	0.308	6.057	-0.143	-0.645	-2.187	0.900	-0.761
-0.788	0.000	0.469	-1.627	-1.113	0.000	4.672	1.873
3.957	1.083	1.348	3.990	3.090	0.000	0.000	0.000
1.387	0.000	0.388	1.809	0.204	2.450	0.000	0.485
2.592	0.000	0.000	2.911	-0.021	0.000	6.208	0.000
-1.607	-2.006	-0.208	1.034	-0.432	-1.488	0.818	0.229
-0.297	0.221	-0.378	-0.117	-2.050	-1.271	3.757	-0.199
-0.901	0.228	0.345	0.086	-0.004	-0.388	5.715	-2.187
3.584	5.824	11.396	6.096	10.887	-3.726	-2.029	4.711
6.596	0.479	4.823	1.385	0.774	6.067	1.684	-3.305
0.221	6.583	-2.166	3.303	3.234	7.095	-0.300	8.375
1.628	-1.787	4.030	4.329	5.687	1.653	0.911	0.366
3.086	0.000	2.760	0.000	1.273	0.958	0.399	0.134
-2.151	-0.364	-0.727	1.258	4.876	2.996	-1.571	6.062
0.895	5.115	7.212	5.317	8.082	2.075	3.343	2.102

Table35.txt

3.090	3.445	5.610	0.742	-0.400	2.120	2.341	-1.573
-2.231	-0.910	-1.340	1.907	-0.131	2.271	-3.077	7.822
1.568	10.777	3.274	9.220	1.876	0.872	5.109	0.000
6.174	4.911	5.738	1.175	0.000	5.233	3.754	1.575
-0.575	4.743	0.836	3.295	-0.737	7.355	4.040	0.578
-0.184	-1.432	0.486	2.759	3.378	-1.040	-0.244	1.838
0.526	2.359	2.960	1.043	-0.350	-2.106	0.072	0.431
2.227	1.185	0.557	3.407	-0.082	1.680	7.187	-1.005
0.459	4.509	12.134	0.629	0.253	2.729	-1.209	3.090
-0.008	1.138	10.663	3.037	4.163	5.476	0.024	5.028
3.141	9.163	1.486	0.487	6.181	11.623	11.042	1.866
-0.413	-1.446	0.000	2.366	-0.983	0.000	0.388	0.000
-0.957	-0.830	-1.346	-1.171	-0.512	-1.402	-2.634	-0.514
0.000	-0.398	-0.260	-1.102	-0.385	0.000	4.149	0.000
-1.097	-2.492	4.368	-0.959	11.435	2.030	0.000	0.000
1.580	-0.747	7.044	3.658	-0.122	0.000	4.922	4.261
-0.203	2.852	2.853	-1.290	-0.405	0.000	1.304	0.000
-0.060	-1.139	-0.594	-2.171	-1.740	0.009	-0.137	1.978
4.260	-1.489	-2.475	0.852	-0.552	-2.052	4.283	-0.731
-0.648	-1.475	3.299	-2.940	-2.162	-1.315	-1.254	-2.998
-0.080	0.833	2.695	1.039	2.749	-1.772	-0.467	4.358
3.837	0.184	-0.683	2.831	1.919	-0.120	1.038	0.470
0.434	-0.747	0.178	4.124	5.779	-0.221	-1.870	-0.800
-1.762	-0.789	-1.754	-3.139	-0.995	-1.486	-1.479	2.327
4.301	-0.639	-0.249	2.089	2.675	0.542	19.986	-0.417
-1.357	6.183	-3.373	-0.982	-2.107	-1.102	-2.811	-1.326
0.284	-2.658	-1.725	-0.658	-0.475	-2.039	-1.594	0.244
-2.643	1.383	0.157	0.080	6.285	-1.369	0.782	2.879
1.624	-0.006	-0.515	7.601	9.555	4.869	0.514	-0.733
0.282	-3.829	3.090	0.000	0.000	3.090	0.000	0.000
0.000	3.090	1.582	3.090	4.526	3.769	4.355	0.000
0.000	0.000	1.405	0.000	0.000	5.162	13.371	0.000
5.692	-3.415	11.448	9.835	4.801	-0.747	4.792	0.000
2.206	6.519	7.102	0.000	3.003	-2.428	14.727	3.035
4.338	5.082	3.090	6.258	-0.711	5.543	10.481	2.721
7.874	10.542	16.051	2.467	8.634	-0.840	1.757	3.785
4.006	2.030	-2.626	0.736	0.925	-1.795	1.135	2.595
3.747	-0.164	1.466	5.145	6.658	5.899	-0.188	-3.030
4.797	-0.008	8.670	0.515	2.216	0.679	-1.107	0.000
0.000	0.212	4.169	0.000	-3.090	11.082	2.754	0.163
2.976	4.974	0.000	1.790	10.777	0.717	-1.009	-0.663
3.548	-1.408	-2.014	4.812	5.411	-1.362	-1.244	2.888
2.485	-0.386	-0.302	4.882	6.237	2.145	1.165	-0.947
1.369	0.037	-1.058	-1.322	-2.036	2.198	3.626	2.047
9.129	11.660	13.594	1.899	4.075	-1.419	-0.618	1.194
5.874	3.175	1.521	3.090	0.815	15.605	13.283	0.576
2.140	7.319	2.135	9.043	15.329	2.257	17.470	8.407
2.898	-2.342	3.071	-1.127	10.411	4.612	0.241	1.925

Table35.txt

7.267	2.932	9.094	0.092	-0.170	-1.301	4.912	0.041
-0.493	6.328	3.395	-1.788	4.500	12.609	3.220	3.904
0.942	-1.759	-0.467	1.348	-0.945	0.430	0.618	0.000
0.208	-0.823	1.824	0.997	-1.246	0.911	-1.557	-1.342
-1.114	-0.091	0.670	-2.859	-0.409	-1.432	-3.077	-2.767
1.948	2.167	0.060	5.793	0.237	-1.404	-2.015	0.000
0.475	0.000	-0.961	-0.376	0.139	1.489	0.782	0.468
-0.558	1.482	0.839	-0.163	-1.910	-1.109	-2.872	-1.063
0.000	0.000	-0.736	0.000	0.000	0.000	0.000	0.000
0.000	-0.914	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.309	-3.122	0.501	-2.214	-0.610	0.000	0.000
0.050	0.000	-0.736	0.000	0.000	-0.217	0.345	0.000
0.000	0.137	0.000	-0.911	-2.648	-0.660	-3.374	-0.357
10.759	9.535	6.230	10.731	-1.876	-1.968	2.432	18.263
-1.347	-1.579	0.320	9.986	-1.936	-0.899	-0.066	-0.683
-0.939	11.811	-1.296	-1.542	5.644	12.440	-0.499	-0.771
4.365	4.509	-0.441	-2.940	3.732	6.594	12.002	22.270
-1.096	-0.403	9.586	8.982	11.198	5.201	3.974	3.530
6.407	5.871	-0.200	0.210	-1.154	0.491	-0.218	8.896
-0.885	-2.062	14.070	24.611	-0.528	0.620	-2.176	-1.246
-0.364	0.786	8.419	18.178	9.421	-1.088	1.197	2.555
-0.836	-1.638	0.210	-1.342	-0.781	0.850	-1.993	9.232
7.913	9.531	-0.670	-1.230	-0.291	0.460	-0.961	-1.696
-1.481	6.497	-0.983	-1.037	-0.090	-0.711	-0.966	-1.683
4.229	7.289	-0.600	5.615	4.543	5.901	-0.480	1.167
-3.166	-3.011	-0.252	-1.960	-1.607	-3.437	-1.273	-1.755
-1.435	-1.528	-2.420	-2.880	-1.609	-0.676	-2.404	0.149
-2.054	-0.221	-1.173	-2.762	-1.892	-1.961	-0.216	-1.870
-2.221	-2.640	-2.082	-3.021	-2.700	-1.842	1.793	2.120
0.649	-1.104	0.000	5.953	-0.926	-0.598	-0.925	-2.775
-1.120	-1.289	-1.286	-1.221	-3.046	-0.894	-1.214	-0.654
2.351	-1.573	-2.990	-2.615	-1.284	-2.892	4.760	-2.062
4.735	4.963	-2.173	-0.624	1.733	0.107	-0.495	-3.321
-2.310	-0.144	0.722	-1.375	0.043	-2.911	0.330	-2.668
0.296	-1.669	-0.647	-0.860	-1.604	-1.162	0.226	-2.736
0.574	-1.856	-0.879	0.609	0.529	-1.675	0.518	-2.080
2.851	-3.061	1.177	-1.361	-1.457	-1.459	0.800	-0.545
-3.295	-1.044	-3.237	-1.767	-2.794	-4.069	0.098	2.854
0.071	-2.607	-1.647	-3.545	1.553	-1.824	0.903	2.997
-2.078	-0.794	1.025	-1.278	-2.560	-2.308	2.294	-0.963
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-3.090	0.651	0.000	0.000	0.000	0.000	0.000
0.000	-1.169	0.000	0.000	0.000	-0.378	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	-1.214	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.309	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table35.txt

0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.748	5.710	0.725	-1.679	1.644	4.406	2.283	-0.323
-2.292	-1.810	-1.967	-3.047	0.000	1.934	0.000	0.442
-1.613	-0.693	0.152	0.405	7.569	0.095	1.223	-2.135
-0.534	0.000	0.000	0.000	-3.090	0.000	0.000	0.000
0.000	0.460	0.000	0.529	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-2.312	-0.608	-0.897	-3.228	-0.409	-2.270	-1.002	-0.717
-0.931	-1.434	-2.673	-0.097	-0.341	-0.445	-0.377	-1.785
-1.198	-1.356	-0.382	-1.757	-2.296	-1.345	0.380	-3.090
-0.854	-0.677	-1.052	-1.281	-1.348	-2.341	-1.457	-4.455
-1.137	-0.923	-0.868	-0.031	0.618	-0.610	-0.183	-0.981
0.483	-0.635	0.088	-2.101	-0.461	0.000	-0.815	-0.059
-0.281	-2.278	-1.683	-2.742	-0.764	-3.283	-0.448	-0.253
-3.963	-2.035	0.439	0.298	-0.875	-2.217	-1.032	-1.030
-0.904	-2.392	0.484	-0.387	-0.540	0.310	-1.017	-0.384
0.825	-0.352	-0.588	-3.581	-1.344	0.002	-1.018	0.769
-1.035	-1.903	2.385	-2.274	-0.125	2.644	-0.678	-0.525
-1.533	2.012	-0.840	-1.233	-3.541	-1.636	1.479	0.437
-0.388	-3.625	-2.838	-2.388	-1.695	-2.345	-1.060	-1.953
-1.323	-2.278	-1.264	-2.604	-1.393	0.304	-1.530	-0.785
-2.067	-2.361	-2.400	-2.878	-0.841	-1.130	-1.945	-3.339
0.125	-1.433	-1.358	-3.270	-2.065	-3.101	-0.867	-2.365
-0.167	-1.535	-2.629	-2.129	-0.364	-1.567	-1.473	0.538
-2.720	-1.371	-0.554	-1.458	-3.040	-3.692	-1.789	0.359
-2.569	0.948	2.667	6.901	2.197	2.087	-1.508	-1.161
-2.477	-1.672	-0.207	6.545	4.260	2.220	-0.757	-0.155
1.326	-0.699	0.467	4.310	1.571	-1.863	-0.721	-0.097
-0.910	-0.224	0.460	-0.654	-3.090	0.201	-0.054	-1.560
-4.333	-0.708	0.137	-0.595	-0.378	0.186	0.000	-0.741
1.090	-3.814	0.000	0.000	-1.967	-0.705	0.163	-0.583
-2.478	-3.222	-0.385	-1.711	-2.683	-2.542	-2.973	-1.420
-1.541	-0.944	1.059	-2.069	-0.778	-1.243	-2.502	0.322
-2.742	-3.100	-2.006	-1.835	-2.350	-1.432	-1.767	-1.652
3.019	-0.375	-0.528	-1.844	-0.363	-1.219	-1.756	-2.523
-0.497	-0.839	2.358	1.824	3.193	-0.222	0.623	0.015
-1.128	-2.242	-0.371	6.541	-0.845	-1.161	1.031	-1.388
0.000	0.317	0.000	-0.823	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.089	-0.736	0.000	0.000	0.137	0.000	0.000	0.000
-2.669	-1.598	-1.593	-0.424	-0.956	-1.088	-0.654	2.236
-1.010	0.089	-0.753	-2.861	0.545	-1.798	-1.193	-1.983
-2.061	-2.287	1.486	-0.871	-1.742	0.226	-2.369	-0.783
0.000	0.000	0.000	-3.090	0.000	0.000	0.000	0.000
0.000	0.000	0.000	-0.144	0.000	0.000	0.717	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-3.074	-3.744	-1.681	-4.254	-2.530	-2.115	-2.251	-1.222

Table35.txt

-1.999	-2.896	-1.167	-0.597	-0.823	-1.609	-3.479	-1.549
-0.184	-2.090	-1.517	-2.434	-1.355	-2.765	-2.048	-2.146
-1.834	-1.673	-1.947	-0.521	0.463	0.230	0.054	-0.042
-0.897	-1.997	-0.212	-1.226	2.500	-0.161	-2.066	-1.687
-2.008	-2.721	-1.276	-0.679	-1.693	-2.312	-0.686	-1.068
8.118	9.269	0.000	6.259	-0.468	-2.022	4.334	6.848
3.784	2.644	0.000	3.090	9.150	9.117	3.090	0.000
5.339	4.322	0.000	3.090	6.140	3.090	0.000	0.000
5.438	7.865	3.704	4.678	-1.184	-2.667	0.546	2.976
0.087	-2.679	1.682	11.820	3.787	7.523	-0.967	-0.474
3.190	-2.138	5.179	7.054	12.164	6.318	-1.744	1.406
2.425	4.092	-2.572	-1.510	1.137	-1.724	-0.013	1.776
-1.340	-0.875	0.000	0.922	0.000	0.000	-1.111	0.988
5.727	3.055	0.000	1.577	-0.260	-0.170	-0.006	0.010
6.215	-1.424	-2.562	-2.436	-0.583	-2.714	9.531	13.450
-1.968	3.874	2.154	-0.598	3.790	6.537	-1.452	-0.878
-0.590	-1.665	3.771	0.078	-1.795	-0.031	-2.396	-2.658
3.943	5.207	-0.078	-3.843	3.829	-2.809	7.538	7.026
4.397	6.040	2.766	6.421	-3.743	-0.169	4.305	6.504
3.760	-0.999	10.377	0.650	10.507	6.234	-1.343	-0.522
-0.480	-4.027	-3.332	-2.498	0.195	0.210	-2.655	-2.362
-1.399	-0.699	0.134	-2.461	-1.335	-1.488	-1.053	-1.353
-0.973	-3.096	-0.756	-1.786	-3.693	-0.785	-2.084	-1.631
1.988	1.822	-1.367	-1.457	3.297	6.962	1.247	5.179
-0.242	3.991	-2.225	-1.476	15.180	11.958	5.168	2.939
1.149	3.880	5.092	7.063	0.917	5.938	2.195	-0.880
1.179	1.806	2.439	1.746	5.738	5.690	5.264	8.670
-1.310	-1.084	3.468	-0.425	-1.742	-2.046	1.980	2.348
1.717	1.675	4.281	7.099	1.536	0.755	5.929	2.026
-2.869	-2.854	-0.432	-2.302	-1.261	0.006	-1.161	-2.439
-1.519	-1.467	3.418	-2.242	-2.175	-3.444	-0.305	-0.266
-1.520	-3.134	-1.379	5.247	-0.074	3.573	2.444	-0.308
1.996	-0.326	-1.057	-0.881	-1.150	-2.386	1.355	6.148
-0.743	-0.075	-0.497	0.060	4.970	2.928	-1.917	-2.014
-1.243	-1.412	0.088	-1.313	-1.416	-0.179	-0.987	-2.112
3.928	4.235	-2.605	-1.268	-3.236	-1.675	-3.185	-1.744
-3.438	-2.321	0.464	4.629	0.975	-0.132	-0.566	-1.691
3.167	-0.331	2.396	-3.176	-0.837	-1.179	-1.048	2.446
7.600	7.769	0.467	-2.618	0.034	1.673	4.123	2.175
0.862	1.855	2.723	3.265	4.431	-0.673	-2.122	0.237
1.383	5.182	-0.292	8.712	0.302	-0.061	-0.401	-2.682
0.366	0.524	-0.198	-1.232	-2.563	-0.723	-1.382	0.134
4.244	7.902	0.710	-0.478	7.961	1.778	0.822	0.658
-0.412	1.318	2.518	1.157	1.825	-0.114	-0.434	-0.848
2.971	-0.781	-2.934	-0.836	0.844	-2.548	-1.412	-1.753
1.178	-0.574	1.122	0.225	0.827	1.473	1.366	-0.364
2.605	0.986	-0.988	0.058	-2.066	-1.052	-0.532	-0.853
1.539	-0.697	-2.354	-2.073	-1.016	0.323	-1.455	1.812

Table35.txt

-1.399	-0.735	-0.670	10.509	9.717	10.676	0.550	1.994
-1.202	0.423	1.356	3.772	3.469	-0.872	-1.799	2.313
-1.528	0.654	-2.446	-2.710	-1.058	-1.403	-0.785	1.265
-2.068	-0.026	1.205	4.236	8.220	8.294	-0.385	-1.261
-2.319	-0.807	1.161	0.101	3.151	-0.891	0.241	0.399
-0.007	-0.717	1.336	2.850	-1.395	10.211	4.452	11.614
-1.412	1.071	4.860	7.356	4.877	9.833	6.301	6.844
0.870	0.281	5.543	8.114	0.968	7.417	-0.514	0.640
-0.048	-0.927	6.457	10.967	5.851	18.459	11.942	18.330
-2.124	0.311	10.335	6.009	9.297	12.006	12.636	13.993
-1.607	-0.856	10.079	17.670	-0.354	14.555	-0.674	3.380
-2.274	-2.644	-0.482	-3.817	-1.209	-1.842	-1.403	-2.678
-1.435	-3.228	-1.031	-0.972	-2.720	-2.382	0.384	-1.642
-1.914	-1.762	-0.619	-0.803	-2.530	-0.923	-2.468	-0.389
1.034	-2.590	-1.081	0.048	0.845	-0.246	0.006	1.321
-0.858	-0.699	2.639	-0.907	0.031	-1.188	-0.593	-2.840
-1.577	-1.866	-0.253	0.148	-2.570	-1.740	-0.138	-0.654
-1.169	-0.978	-1.328	-0.817	0.000	0.000	0.000	0.232
0.647	-0.234	0.000	0.000	-0.736	0.000	0.000	-2.557
-3.090	-0.345	-4.351	0.460	-0.513	-1.851	-2.464	0.000
8.311	1.913	1.983	-2.233	-0.846	4.494	-0.862	1.608
-0.308	0.566	-2.541	1.918	2.810	-0.571	-1.050	-0.392
-1.966	-2.236	-0.311	-1.759	3.834	4.319	-0.048	0.980
0.153	-1.049	-1.026	-0.675	0.467	5.554	-1.420	-2.431
2.159	3.441	0.494	11.116	1.602	3.163	0.619	-1.276
-2.168	-0.886	-0.471	0.624	-2.201	8.904	2.306	-2.985
0.000	-1.385	0.137	-2.586	0.089	0.000	-0.790	-2.341
-0.730	-0.736	0.000	0.000	0.000	0.000	-0.219	0.000
0.309	0.000	-0.790	-0.505	-0.868	-2.129	-0.736	0.000
0.000	0.000	0.000	0.309	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2.104	-1.234	-1.247	-3.211	2.065	-1.704	-1.410	-0.953
2.275	0.561	-1.336	1.168	2.587	-1.374	-0.317	-1.317
0.156	-1.160	2.268	3.685	-2.207	0.224	0.404	-3.614
-1.728	-1.183	-4.416	-2.990	-1.150	-1.539	0.029	-1.994
-0.454	-0.924	1.435	-2.613	0.997	0.110	-2.643	-1.194
-2.820	-1.772	0.425	-2.501	0.174	-0.940	-2.166	-2.482
1.275	-0.530	-0.140	-0.718	-1.430	-2.212	3.529	-3.072
-0.189	-1.355	0.444	-0.705	3.509	0.435	-1.689	0.133
-1.840	-1.363	4.748	7.071	-0.717	2.145	4.341	-2.610
1.804	-0.532	1.849	0.510	-0.686	5.226	2.127	3.639
-0.171	-1.425	-0.524	-1.130	2.534	2.578	-1.032	-1.653
-0.600	0.466	-1.712	-0.120	-0.646	-1.421	-0.062	-1.598
-0.790	-1.477	-0.360	-0.477	-4.328	-1.392	-1.484	-0.983
-3.190	-1.468	-1.630	-0.457	1.027	-3.041	-2.259	-0.215
-0.681	-1.426	-1.405	-0.339	0.475	-0.488	-1.650	-0.231
-0.884	-1.601	-0.882	-2.669	-0.169	-2.411	-2.544	-0.570

Table35.txt

-0.233	-0.327	1.440	0.174	1.406	-1.237	-1.299	-1.718
-0.947	-0.043	-0.521	-0.995	-0.693	0.386	-0.874	-0.060
0.428	-2.176	-1.382	-2.754	-0.005	-1.984	-1.522	1.299
-0.410	-1.356	-0.336	-0.781	5.611	0.809	0.786	0.369
-0.524	-2.191	-0.655	-1.442	-2.054	0.192	-0.221	-1.204
0.691	2.176	0.043	1.564	0.616	0.392	-2.346	-1.560
-0.085	-1.440	-0.059	-4.564	-0.831	1.931	-1.342	-0.931
-1.427	-0.148	-0.125	-1.358	-1.343	-1.170	3.578	0.969
-0.662	-1.203	0.613	-1.954	-0.754	-1.682	-1.350	-0.096
-1.372	-2.156	-0.558	-1.844	-0.737	-1.151	-2.320	-1.122
-2.516	-1.629	-1.140	-2.404	-0.928	-2.576	-0.460	0.240
1.297	-0.685	-0.001	-3.760	3.004	5.166	-0.119	-1.932
-0.680	0.808	-1.156	1.279	-0.720	0.390	-0.285	0.166
-2.131	-1.651	2.719	-0.107	2.238	0.702	0.918	-1.848
0.409	-0.513	0.678	-2.470	-1.020	-1.769	-0.781	-2.444
-1.763	-0.524	0.913	-1.316	-0.206	-0.803	-1.652	-2.479
-0.830	0.756	-0.581	-1.417	-2.965	-0.857	-0.769	0.218
1.207	-4.115	1.503	-1.400	0.964	-2.678	-1.700	4.533
-0.959	-0.700	1.700	1.955	1.987	3.648	0.729	1.748
-0.479	-2.512	5.051	-0.567	-1.734	-2.326	-0.757	-0.505
0.133	-3.983	-1.314	-1.293	0.431	-2.173	3.265	3.185
5.352	2.518	3.591	-2.851	5.589	1.581	4.969	0.979
-0.646	6.489	-1.130	-0.376	-0.534	2.044	-1.938	-0.733
-1.655	-1.079	-1.617	-2.006	-1.697	-3.032	-2.694	-2.080
-2.077	-1.095	-0.529	-2.843	0.892	-1.729	-1.118	-0.074
-0.924	-1.747	-1.293	-0.811	-1.896	-1.450	-0.880	-0.017
-0.495	-0.978	-0.926	-1.739	0.347	-2.116	-0.535	-0.155
-1.814	-1.436	-0.250	-0.908	3.529	-0.900	-1.886	-1.758
-2.245	-0.094	1.495	-0.448	-1.676	1.760	0.615	-0.233
-0.465	-1.984	-0.857	-2.465	-1.533	-1.594	-1.171	-0.124
0.388	-1.440	-0.162	-1.892	0.155	0.508	0.591	0.059
-0.060	-0.803	-0.964	0.754	-1.965	-1.521	-0.101	-0.259
6.293	-0.641	-0.169	-1.333	-0.828	-3.240	6.420	1.270
-0.952	3.971	-0.509	-2.291	5.457	2.390	0.274	-1.636
-0.888	2.973	-0.204	-2.691	-0.901	-1.932	7.886	0.127
-1.220	-2.387	-0.796	-2.788	-0.486	1.077	-1.632	-1.014
-1.791	-1.660	-1.527	-0.305	-2.550	-2.275	0.266	-0.630
-0.442	-1.616	2.093	-0.113	1.655	-0.557	-2.178	-0.382
-0.642	-1.416	-0.900	-1.699	-0.724	0.284	-0.558	-2.698
3.646	5.495	2.373	0.560	-1.764	-1.179	-0.961	-1.875
-1.496	-0.892	-0.225	0.067	-2.119	3.575	0.780	-0.064
1.934	-0.792	-0.206	-1.757	1.077	-1.924	-0.124	-0.111
0.414	0.417	-1.370	0.492	2.512	-0.629	-1.220	-0.630
-1.329	-1.509	-0.114	-2.526	-1.296	-2.221	-1.034	-0.834
3.173	1.918	-0.067	-0.402	0.787	5.187	-1.022	2.572
-2.983	-2.174	-0.259	0.251	-0.046	2.789	-0.139	-0.276
-0.711	4.105	0.593	-0.734	0.973	0.163	-0.427	-1.089
-0.767	-2.145	-0.015	-1.193	5.165	7.553	-2.687	-1.097

Table35.txt

8.085	10.988	5.061	9.996	-1.095	-0.591	1.362	-0.557
0.557	0.106	0.428	-0.580	-0.321	0.865	6.499	-0.639
-2.916	-4.707	-3.659	-2.089	-1.257	-2.090	-0.855	-3.425
-0.045	-3.801	-0.628	-2.154	-1.165	-1.939	-1.361	-0.943
0.538	-1.104	-0.614	-1.316	-1.903	-1.806	-0.830	-0.339
-2.085	-1.583	0.939	-0.781	5.989	0.499	1.319	-0.738
-1.316	-0.759	-0.378	6.291	2.208	2.134	-0.159	-1.615
-1.764	0.985	-1.669	1.034	-2.086	3.353	0.857	-0.278
0.000	-0.378	-0.217	0.595	0.000	0.000	0.460	1.273
-1.214	0.000	0.000	0.050	0.000	0.000	0.000	-3.090
0.000	-1.354	0.000	-0.152	-1.169	0.000	-1.169	0.000
-1.588	-1.132	-2.554	4.407	3.593	7.688	4.525	6.948
0.383	3.024	3.177	-2.784	3.318	-1.777	2.466	3.539
2.837	4.889	8.795	4.716	-1.346	4.665	-0.443	-0.697
-2.080	0.517	2.157	0.946	-0.958	-0.062	-1.980	-0.538
2.130	-0.483	5.467	8.253	-2.746	-1.527	-0.853	-0.726
4.241	1.593	3.813	-0.788	-1.492	4.037	-0.976	-1.461
-0.937	-2.236	0.412	-0.417	-0.123	-2.120	-0.277	-2.031
-0.402	0.298	-0.332	-0.970	1.082	0.371	-0.397	-1.682
-1.998	-2.177	0.687	-2.098	-1.980	-0.791	-1.962	0.335
1.164	-0.660	-0.882	-1.194	-2.762	0.014	-0.825	-0.533
-0.121	-2.003	-0.285	-1.989	-0.486	-2.894	0.407	-0.413
-0.009	0.357	-0.511	-1.093	-2.187	-1.231	0.189	-0.262
-1.578	-2.349	-2.406	-1.660	-1.811	-1.291	-0.926	2.474
0.958	-0.973	-3.231	-1.595	0.153	-0.196	-0.327	-0.807
-1.833	-0.065	0.455	1.444	-1.528	-0.828	-0.318	-1.124
-1.078	-2.460	-2.310	-2.182	-0.660	0.103	-1.205	-0.972
-2.021	0.152	4.285	8.651	8.011	4.037	0.209	1.129
-0.824	-1.711	-1.822	-0.924	9.498	-0.810	-2.172	-1.528
-0.510	-1.050	5.728	6.247	1.925	5.391	1.030	4.355
-0.481	8.678	2.304	0.586	6.922	7.113	2.384	5.419
-1.166	6.612	2.190	4.963	5.557	6.320	2.906	1.093
-0.549	-1.421	4.755	6.449	0.940	-2.345	-0.485	-1.580
-1.074	3.140	-0.882	0.696	6.309	5.755	-1.729	-2.342
0.568	1.305	-0.104	0.688	0.422	-1.335	-0.518	-1.803
-2.780	-2.361	-1.243	-2.521	-0.414	-0.617	6.700	13.872
-1.521	1.013	-1.610	-1.474	6.869	6.973	4.342	0.112
0.014	-2.254	0.439	10.830	-2.213	-1.428	5.162	-1.323
-0.484	-2.143	-0.774	-1.754	-1.013	-1.240	-0.201	-4.646
-2.252	-0.637	-1.444	-1.543	-1.033	-0.168	-1.851	-2.852
-1.281	-1.088	1.849	-2.160	0.481	-2.283	-0.887	-0.635
-0.972	-0.788	-1.063	-0.619	-1.713	-0.890	-0.407	-0.083
-0.101	-0.865	-1.497	-1.276	0.406	-0.059	-1.647	0.536
-1.209	-0.552	-0.203	-1.689	-0.369	-2.862	-2.067	-0.424
-0.956	-3.695	-0.448	-3.744	-3.256	-0.787	-1.307	-2.488
-1.673	-1.421	0.645	-2.463	0.338	-1.781	-1.392	-1.228
-0.454	-1.962	4.048	1.729	-1.245	-0.606	-1.104	-2.007
-1.418	0.685	-2.451	-4.503	-1.273	-1.463	-0.186	-2.501

Table35.txt

0.283	-2.345	-0.020	-1.207	-1.478	1.866	-1.993	-1.917
-1.588	-1.174	-0.797	-3.210	-1.457	-0.646	-0.421	-1.322
-1.120	-2.614	0.044	-3.250	-1.654	-1.698	-2.431	-0.614
-0.919	-1.216	-1.436	-1.856	0.239	2.751	-1.274	1.811
-1.288	-2.124	0.211	3.250	2.904	-2.801	-1.286	-0.837
-1.627	-2.248	-1.974	-0.893	-1.977	-1.661	-1.420	-0.832
0.271	-2.550	-1.213	-2.928	1.146	1.117	0.461	-0.275
-1.097	-1.905	0.313	0.556	1.128	-0.738	-0.820	-0.217
0.527	-1.549	0.975	0.255	1.569	5.573	-0.385	6.622
-0.224	2.784	2.337	-0.349	6.255	3.552	1.309	-0.183
1.561	2.467	-0.094	5.462	4.704	-1.272	-1.044	-1.564
-1.162	0.270	-1.280	-0.474	0.498	1.429	3.529	0.718
0.400	-0.075	-0.627	-0.683	9.692	-0.989	-0.077	-0.915
0.471	-0.649	5.424	-0.041	-0.756	-2.936	-1.139	1.297
2.014	-1.787	-3.721	-1.872	-0.778	-0.268	0.062	-1.530
0.078	-1.319	0.484	2.642	-0.677	-0.816	0.961	1.373
-2.340	-1.486	0.381	2.627	0.784	1.959	-0.601	-0.057
-0.715	-2.222	-1.318	-1.371	-1.270	-2.992	-3.846	-2.042
-3.150	-2.126	-0.398	-2.156	-1.134	-0.521	-1.958	-2.188
-0.764	-1.130	-0.454	-3.826	-0.139	-1.868	-1.268	-0.547
-0.457	-1.970	-0.604	-0.220	0.820	-0.335	-1.518	2.575
-1.404	-2.723	1.460	0.109	-2.783	-0.587	-0.454	-2.125
-1.389	-1.263	0.129	-0.259	-1.540	-2.425	-1.493	-0.717
-1.993	-2.116	0.156	-1.247	0.144	-2.255	-0.450	-3.493
-0.020	-2.434	0.000	-1.804	-1.833	0.000	-0.427	-0.899
-1.781	-2.998	0.076	-2.803	-0.043	-0.858	-1.313	0.000
-1.214	-0.822	-0.345	-0.817	-1.355	-1.813	-0.378	-1.344
-1.256	-2.159	-1.826	-0.160	-0.027	0.000	0.460	0.595
-1.165	-0.170	-3.802	-2.050	-1.150	0.080	-0.902	0.000
-1.377	-3.616	-1.652	-3.929	-0.554	-1.443	-1.101	-2.677
-0.258	-0.196	-2.510	-0.287	-1.895	-1.183	-2.710	0.933
0.998	-2.278	-1.958	-1.463	-1.551	-0.465	-0.577	-0.849
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.413	-0.506	-0.692	-0.947	-0.413	-0.170	0.218	-1.083
-0.009	-3.090	0.000	-0.042	0.366	-1.173	-0.638	-0.927
-0.144	-0.491	-0.113	-0.261	0.136	-1.139	0.062	0.137
-2.219	0.486	-0.711	-1.259	0.292	-0.373	-1.472	0.553
-0.098	0.115	-1.684	-2.740	0.463	-0.154	-0.584	-1.270
-1.083	-2.283	-0.828	0.033	-0.553	-1.616	-0.422	-0.505
-1.168	-0.637	-3.149	-2.248	-1.240	-1.334	0.056	-1.041
-2.954	-2.559	-1.105	-0.967	0.053	0.000	0.923	0.029
-1.126	-0.276	-1.227	-0.814	0.221	-0.241	-1.436	-1.416
-1.309	-1.885	-2.137	-0.900	-1.057	-1.786	-1.720	-0.742
-0.983	-2.711	0.685	0.066	1.456	0.535	-1.253	-0.861
0.876	-3.534	1.608	-1.637	-3.682	-0.648	-0.857	0.309
-1.199	-2.461	-3.123	-0.811	-1.227	-1.953	1.579	-1.727

Table35.txt

-3.102	-2.573	-1.632	-1.817	-1.233	-0.692	-1.454	-2.329
-2.215	-3.220	-0.812	-2.091	-1.967	-1.206	0.107	-0.882
-2.081	-0.990	0.540	-1.130	-1.748	-3.616	-0.202	-1.419
-2.112	-1.779	-2.855	-0.828	0.324	-0.083	-1.838	-0.700
-0.943	-3.622	-1.888	-3.363	-2.673	-3.277	-0.692	-1.742
-2.639	-3.554	-1.627	-2.912	-1.206	-2.565	-0.968	-1.980
-0.776	-2.924	-1.895	-3.767	-1.332	-1.699	-2.363	-0.899
-0.644	-2.898	-0.788	-3.779	-1.962	-1.037	-2.465	-0.626
-1.934	-2.140	-1.441	-1.418	-0.585	-0.095	-2.536	1.435
-1.513	-1.216	-0.169	-0.553	0.402	0.898	-1.855	-1.441
-0.683	-2.915	-0.078	-2.317	-3.185	-2.935	-1.731	-0.761
-2.414	0.115	0.369	0.217	-0.668	-3.337	-1.545	-3.260
-1.670	-1.902	-0.893	-1.262	-1.528	-1.544	0.376	-2.286
-1.770	-1.041	-1.756	0.371	-0.878	-1.363	-2.889	-2.568
-2.861	-1.839	-1.657	-3.187	-1.709	-2.121	-0.982	-1.674
-1.407	-1.937	-0.473	-0.303	-0.498	-2.552	-1.607	-1.448
-0.836	-2.195	-1.169	-0.366	-1.988	-2.920	-1.080	-0.591
-3.910	-3.867	-0.179	-1.454	-0.907	-3.087	0.586	-0.087
0.370	-3.813	-0.515	-2.649	3.158	0.858	-3.582	-2.411
-3.237	-3.319	-0.861	-2.306	-0.790	0.850	-1.594	-0.137
0.030	-2.972	-0.639	-1.328	-0.950	-1.212	-2.540	0.809
2.061	-1.887	-2.696	1.392	-0.718	-2.057	-0.159	0.977
-1.921	-0.191	-2.358	0.351	-1.196	-3.031	1.210	-0.805
-2.376	-3.146	-3.266	-1.346	-2.398	-1.572	-1.123	-2.574
-1.939	-3.388	-1.143	-2.374	-1.433	-1.089	-1.638	-1.064
-2.064	-2.996	0.053	-0.584	-2.208	-1.042	-2.797	-1.502
-0.216	1.007	-1.735	1.944	-1.496	-1.195	-0.453	0.529
0.647	-1.169	0.000	-4.326	0.000	0.000	0.000	-0.373
-0.481	-0.364	-1.392	-1.510	-3.789	-2.893	0.000	-0.202
-3.237	-2.462	-1.167	-2.890	-1.870	-3.414	-0.554	-0.021
-2.939	-2.978	0.296	-2.917	1.048	1.184	0.281	-2.091
-0.205	-2.804	-3.606	-1.553	-2.136	-0.156	-1.846	-2.407
-0.788	-2.914	0.208	-1.423	-2.069	0.536	1.445	2.212
1.963	-0.718	0.056	-2.754	0.653	-0.149	-0.605	1.510
-3.143	0.757	-1.143	2.883	0.473	-0.256	-3.988	-1.464
-1.761	-3.900	-1.082	-1.261	-1.715	-1.235	-0.089	-2.525
-1.832	-0.362	-3.058	-2.521	-0.300	-1.528	0.048	-1.217
-3.237	-3.670	-2.208	-1.546	-1.826	-3.254	-1.966	-0.715
0.450	-1.840	-1.639	-2.158	-1.213	-2.696	-0.305	-0.622
-2.977	-3.313	-0.166	-2.972	-1.223	1.390	-1.031	-0.086
-3.364	0.309	-0.011	-0.274	-2.464	-2.191	-1.721	-0.468
-0.536	-1.234	-0.510	-1.910	-1.193	-3.558	-0.375	0.224
-0.634	-2.341	-0.423	-3.356	0.234	0.239	-2.714	-2.772
-2.605	-1.468	-0.146	-2.431	-2.260	-2.470	-0.610	-2.462
0.137	-2.706	-0.440	-3.651	-1.782	-0.367	0.333	-0.056
0.000	0.338	0.000	-0.144	0.000	0.000	0.204	0.633
0.000	0.309	-0.273	0.000	-0.883	0.137	0.460	0.137
-0.931	-1.542	-2.794	-3.491	0.804	-2.143	-1.233	-2.533

Table35.txt

-1.970	-1.960	-1.989	-3.362	-1.206	-1.142	-2.365	-2.810
-1.694	-3.081	-1.489	-0.858	-2.007	-1.599	-1.336	-1.186
-1.915	-3.149	-0.395	-2.385	-2.026	2.445	1.867	1.948
0.295	3.511	0.154	-0.851	-0.121	-0.635	0.529	1.127
-1.668	-0.913	-2.116	-3.574	-1.000	-1.134	-1.570	-2.044
-2.650	-2.822	-0.469	-0.469	0.053	-0.850	4.905	8.814
-0.819	1.909	0.257	2.132	-1.205	-4.565	-2.231	-0.189
-0.742	-2.325	-1.887	-2.139	-0.117	-1.496	-1.759	-0.234
-0.827	-2.331	-0.524	-2.799	-2.189	-1.337	-2.075	-4.223
-2.447	-2.222	-1.667	-3.005	-1.214	-0.382	-1.621	-0.717
-1.698	-2.688	0.436	-1.984	-0.245	-3.682	-3.142	-0.609
-0.700	-0.611	-1.233	-2.364	0.238	-0.217	-0.835	-0.578
-0.749	-1.690	0.524	-4.010	0.137	0.000	0.100	-0.468
-0.850	-1.225	-0.812	-2.559	0.373	-0.763	-2.440	-1.093
-2.700	-3.314	0.960	-0.553	0.227	-1.676	1.419	1.907
-1.050	0.439	-0.888	-4.116	-1.512	-1.030	-0.288	-1.401
-0.466	-0.387	0.577	-0.777	0.702	-0.094	0.174	0.405
-1.777	-1.673	-0.836	-2.872	-1.232	-0.944	-1.058	-1.287
-1.783	-1.837	0.762	-2.509	0.349	-1.595	-0.447	0.783
-0.378	-0.972	-0.442	-1.254	0.966	0.769	-1.249	0.016
1.984	3.510	-0.323	0.664	0.640	-0.139	-1.690	3.657
-0.854	-0.232	-0.356	-0.614	2.028	1.595	0.224	-1.193
1.036	-1.378	-0.381	-0.331	-2.801	-2.331	-2.208	-1.452
-2.110	-2.790	-1.673	-3.288	-1.017	-2.467	-1.248	0.568
0.924	-1.551	-0.882	-0.981	-0.921	-0.077	0.218	-1.672
-0.602	-1.312	0.013	-0.775	-0.143	-2.752	-2.361	0.168
-1.110	-3.642	-0.719	-4.294	-1.263	-1.679	-2.318	-5.740
-1.430	-2.219	-3.184	-1.424	-0.397	-0.947	-2.039	-2.163
-3.386	-1.480	-1.955	-1.383	-3.209	-0.712	-2.294	-1.770
11.193	11.559	9.838	17.397	6.168	6.565	11.605	7.907
-0.698	4.694	7.169	3.408	4.368	5.089	4.710	9.258
8.708	15.205	2.686	9.788	17.568	8.700	3.875	5.587
-2.154	0.693	-2.116	-2.271	-0.282	-2.748	-3.036	-2.920
-1.177	-0.625	-0.227	0.558	-0.735	-0.287	-0.905	-1.270
-2.841	0.073	2.048	-3.114	-3.003	-2.169	-0.223	-0.568
-1.416	-2.658	0.291	-0.285	-2.905	-2.660	-3.034	-1.528
-1.137	-2.725	-0.405	-1.454	0.351	-1.294	-0.922	-1.724
-1.976	-1.769	-0.869	-2.070	-0.533	-1.553	-0.498	0.749
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-1.256	-0.507	0.000	-0.933	0.000	0.000	0.000	0.000
-0.790	-0.378	0.000	0.000	0.000	-2.706	0.000	0.050
-0.144	0.772	0.000	0.000	0.333	-0.790	-1.256	0.000
0.000	0.030	0.000	0.000	0.000	-0.736	-2.190	0.000
0.000	-0.831	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	-0.116	0.000	0.000
0.000	0.000	0.000	0.000	0.000	-0.736	0.000	0.000

Table35.txt

0.000	-0.144	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.137	0.000	0.137	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	-1.169
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.137	0.000	0.000	-2.884	0.000	-0.027	0.000	0.000
0.000	-1.169	0.000	0.000	0.000	0.000	0.000	0.137
0.000	0.000	0.000	-1.214	0.000	0.000	0.000	0.000
-1.705	-0.920	-1.169	-0.660	-0.137	0.186	0.762	0.093
-1.482	-0.021	0.000	0.581	0.000	0.000	0.000	-0.144
0.000	-0.641	0.000	0.000	-0.099	0.000	0.000	0.000
-2.851	-2.492	-1.338	-3.313	-2.498	-2.672	-2.215	-2.349
-1.242	-1.262	-1.252	-2.179	-2.323	-0.798	-1.692	-1.848
-2.470	-3.516	-1.241	-2.002	-0.951	-3.729	-3.153	-0.332
-2.054	-2.133	-1.004	-2.624	-2.050	-3.018	-1.722	-2.486
-0.963	-2.471	-0.351	-0.423	0.131	-0.927	-0.690	-1.432
-2.785	-2.575	-0.460	-3.194	-1.287	-0.491	0.174	0.586
0.874	-1.921	3.770	1.752	-1.078	-1.069	-0.351	4.479
-0.297	-0.434	0.182	1.347	0.670	0.890	-0.628	-1.597
-1.092	-1.534	-0.723	-2.718	-1.609	2.103	-1.356	0.831
-1.314	-2.659	-0.441	-3.501	-1.831	-2.509	-0.130	0.484
-1.527	4.403	-0.349	-2.587	0.451	-2.601	-0.691	-0.060
-1.817	-2.121	-0.708	0.009	-2.108	-1.323	-1.740	-2.718
-3.070	-1.989	-0.243	-5.214	-2.064	-2.382	-2.582	-0.723
-1.890	-1.089	-0.900	-3.954	0.465	-1.847	-0.937	-0.796
0.207	-0.473	-2.326	-1.869	-1.444	-0.417	-2.151	0.000
0.870	-1.214	0.268	1.365	0.922	0.482	0.966	2.723
2.492	2.650	-1.023	0.006	0.000	0.433	0.000	-0.547
-1.832	-2.696	1.991	3.892	-1.893	1.444	-1.615	-0.177
-4.187	-2.273	-3.686	-3.116	-3.457	-3.699	-2.297	-2.687
-1.104	-3.251	-0.614	-2.293	0.067	-2.102	-0.052	-2.152
-0.573	-3.204	-1.180	-1.240	-2.664	-1.305	-1.063	-2.877
-1.991	-4.076	-2.212	-1.628	-2.577	-5.583	-0.496	-4.186
-1.176	-2.783	-1.765	-1.771	0.966	-0.919	-1.290	-0.784
-1.638	-3.167	-1.827	-0.060	-2.694	-3.139	-1.009	-1.451
-1.172	-4.393	-1.032	-0.275	-2.900	-3.206	-0.668	-2.603
-0.828	-2.303	-2.262	-1.631	-0.700	-1.914	-1.363	-0.765
-2.478	-1.504	0.134	-2.576	-1.193	-2.244	-1.567	-0.310
0.049	0.731	-2.427	-2.708	3.090	1.467	0.182	-1.165
0.514	2.288	1.229	8.565	0.000	0.000	-1.054	-2.039
0.986	5.967	4.375	-2.193	5.597	1.236	-0.244	-0.673
-1.598	-4.675	-1.536	-3.027	-2.365	-2.543	-1.600	-1.460
-1.387	-3.601	0.451	-2.772	1.375	-2.836	-1.313	-0.723
-1.802	-1.553	-0.956	-2.498	-4.079	-0.421	-1.829	1.203
-1.802	0.250	-3.506	-1.253	-1.921	-3.121	2.150	7.254

Table35.txt

-1.555	3.745	-0.219	1.150	2.655	2.249	0.056	-1.374
0.089	1.527	-0.210	1.025	-2.849	4.516	3.570	-0.329
0.575	-3.929	-0.600	-3.212	-1.507	-3.154	-1.739	-3.124
-1.125	-1.936	1.434	1.305	-0.872	-0.160	-1.059	0.278
-0.481	-1.479	1.062	-1.824	-3.330	-1.725	-0.320	-2.387
-2.219	-2.687	-1.992	-3.345	-3.535	-3.815	-0.027	-1.422
-2.005	-0.890	-0.328	0.464	0.608	0.089	-1.350	-0.690
-1.365	-0.667	-0.662	-1.362	-1.238	-1.733	-1.436	-1.000
-3.402	-2.911	-1.905	-0.118	-1.241	-1.788	0.174	-2.437
-1.478	-0.325	-0.433	-1.997	-0.531	-0.402	-2.476	-1.958
-0.736	-0.008	-0.898	-2.362	0.111	-2.593	-1.725	-0.995
-0.507	1.227	-0.497	-0.963	-0.677	-1.344	5.812	7.590
0.123	5.025	-2.179	1.682	4.830	5.846	-0.157	0.450
1.437	-0.762	-1.431	-1.969	1.066	6.237	1.429	-0.742
-0.596	-1.626	-0.531	-3.281	-1.401	-1.642	-1.958	-1.063
-0.664	-2.206	0.144	-1.282	1.015	-0.637	-1.002	-0.974
-1.150	-1.965	-0.197	1.493	-3.207	-2.185	-1.116	-0.050
-1.427	-1.767	1.229	-0.288	0.264	1.374	-0.449	-0.577
-0.920	-2.727	-1.212	-1.174	-0.786	-0.928	0.187	0.006
-2.161	-0.326	-0.500	2.285	-3.347	-1.199	-0.596	-0.819
-1.896	1.371	0.553	2.508	4.359	6.886	4.726	7.945
-0.792	0.435	-0.736	-0.045	6.485	2.868	4.735	7.813
-1.643	-0.363	0.778	-2.321	0.482	6.641	0.437	-0.625
-1.158	-2.234	-0.083	-2.898	-0.902	-2.533	-4.621	-3.709
-1.898	-1.210	-0.482	-2.521	0.084	-1.244	0.133	-1.843
-0.856	-0.807	-2.151	-0.814	-2.002	-2.420	-0.387	-0.670
-1.409	-4.592	-0.116	-0.288	-1.108	-0.549	-1.882	-1.344
-1.061	-2.708	0.079	-3.254	-2.467	-2.046	-1.461	-1.652
-0.986	-1.327	0.062	0.285	0.659	0.587	-0.888	-1.381
0.000	-1.650	0.762	-0.737	-0.378	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	-0.378	-0.823	0.000
0.651	-3.090	0.000	0.000	-1.086	0.000	-2.202	0.000
0.285	-0.660	-3.465	-1.513	-0.377	-2.114	-2.312	-3.090
-0.970	-0.119	-0.424	0.000	-0.445	0.193	-1.237	0.000
0.000	0.153	0.184	0.433	-2.943	-0.876	-1.133	-1.547
-1.827	-0.086	0.090	-0.498	0.244	-1.214	0.000	0.000
-3.205	-1.169	-0.736	-0.541	0.000	-2.433	-1.821	-0.144
0.000	-0.912	0.176	0.165	0.022	0.433	-2.260	-2.248
0.000	1.064	-1.157	0.000	-0.064	0.000	0.000	0.000
0.000	0.441	0.000	0.000	0.000	0.000	0.629	0.000
0.000	0.309	0.000	0.000	0.000	0.000	0.366	-3.090
-0.369	-1.952	-2.068	-1.878	-0.165	-1.117	-1.528	-1.214
-0.499	-0.592	0.062	0.000	-2.085	-4.345	-3.207	-0.728
0.000	0.242	0.051	-0.237	-0.796	-0.433	-2.279	-0.760
-1.621	-1.152	-3.108	-1.780	-0.454	1.385	-0.699	-0.375
0.564	-0.505	0.000	0.000	-0.320	-0.573	1.570	-3.090
0.050	-2.121	-0.583	-2.387	1.428	-1.745	-3.263	-4.339
0.329	-2.014	-0.383	-1.158	-0.905	0.546	-0.364	0.000

Table35.txt

3.085	0.487	0.000	0.595	-2.363	-2.210	-1.014	-1.256
-1.074	-0.694	0.441	-0.708	-0.177	-1.319	-1.122	-1.287
-1.828	-1.854	-1.049	-0.526	-0.559	-1.256	-0.460	0.000
-0.659	-0.215	0.969	0.000	0.000	-1.204	-0.883	0.000
0.725	0.504	0.000	-0.545	-1.236	-1.327	-3.382	-0.182
-1.214	0.053	-0.306	0.217	-0.389	0.000	0.000	0.000
-2.202	0.000	0.000	0.651	0.000	-1.479	0.382	0.000
0.000	0.000	0.050	-2.059	-1.672	0.000	-0.916	0.460
-1.330	-1.672	-0.650	-1.790	-0.723	0.178	0.556	0.000
-0.711	-0.375	1.329	0.993	0.460	-0.169	-3.387	-1.093
0.000	-2.140	0.000	-1.522	-1.670	-0.845	-2.006	-0.285
-0.098	-2.861	-1.137	0.537	-2.382	0.000	-0.665	0.000
0.000	-0.261	0.000	0.000	0.000	-0.540	-1.146	-1.148
0.000	0.050	-1.214	-0.861	-0.935	-0.382	-0.500	-2.557
-1.214	0.000	-0.217	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.969	0.000	-0.059	0.000
-1.191	-1.210	-0.567	-0.517	-0.318	0.309	-0.341	0.000
-0.534	-0.378	-0.992	0.000	0.000	-1.385	-1.515	0.000
0.000	-0.623	0.000	-0.516	-1.692	0.000	-1.827	-0.829
0.000	-0.789	0.173	-0.253	-1.273	0.137	-0.145	0.000
-3.090	-0.736	-2.058	0.000	0.000	-1.680	-1.943	0.000
0.000	-1.100	-0.777	-1.497	-1.675	-1.548	0.016	-1.921
0.000	-1.674	-1.904	-0.736	-0.736	0.000	0.022	0.000
-0.823	0.000	0.000	0.000	0.000	-0.144	-0.225	0.000
-0.395	0.000	-1.214	-0.217	-0.686	0.000	0.816	0.000
-0.976	-0.785	-0.719	-1.294	-2.639	0.000	0.000	0.000
-0.911	0.357	1.195	0.000	0.000	-0.401	-2.574	0.000
0.000	0.651	-0.572	-2.011	-3.826	-1.547	-0.505	-1.003
0.000	-0.505	-0.002	-0.277	-0.920	0.000	-0.790	0.000
0.460	0.460	-0.736	0.460	0.000	-0.366	-1.081	0.000
0.000	0.000	0.000	0.233	-2.495	0.000	0.137	-0.906
-1.005	0.521	-1.713	-3.677	0.338	0.000	-2.629	0.000
-2.489	-2.332	-0.439	0.000	-0.342	-0.043	-0.690	0.000
0.529	-0.790	-0.054	-0.404	-1.008	-1.755	-1.427	-0.027
-0.654	-0.736	-0.313	-2.270	-3.113	0.000	-1.214	0.000
-1.811	0.000	0.000	-0.445	1.416	0.529	-2.931	0.000
0.000	-0.610	0.366	-0.050	-2.561	-0.578	0.127	-3.084
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	-1.169	0.000	0.000
0.000	0.000	0.000	-0.823	0.561	0.000	0.000	0.000
-2.197	-1.671	-4.538	-2.822	4.313	0.559	-2.677	-3.090
0.185	-1.011	2.138	-0.584	2.308	5.293	11.463	0.107
-0.661	5.627	0.768	0.471	-0.159	-1.493	-1.076	0.616
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.765	0.210	-0.583	-0.215	-0.011	0.000	0.000	0.000

Table35.txt

0.309	0.000	0.000	0.000	0.000	-0.687	0.575	0.000
0.000	-0.910	0.000	0.621	-0.746	0.000	-1.244	0.000
0.000	-2.127	2.534	-1.418	0.529	-0.378	0.000	0.000
0.000	0.000	0.000	0.000	0.000	-0.445	-2.024	0.000
0.000	0.000	-0.267	-0.801	-0.314	0.000	0.703	-0.790
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.676	-2.617	-2.238	-2.027	0.274	-1.301	0.397	-0.378
-1.081	-0.096	-1.168	-1.144	0.003	-0.191	-1.493	0.527
0.075	-0.273	-0.074	-1.336	-1.581	-0.261	-1.175	-0.897
-0.144	0.218	-0.302	-0.922	-0.831	-0.445	-2.054	0.000
0.309	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-0.378	0.000	-0.413	-1.856	0.137	1.043	-0.923
-0.906	-2.450	0.486	7.559	-0.201	-0.445	-1.271	3.412
-0.047	4.430	-1.974	-1.834	-1.421	3.077	-0.516	-0.198
-1.730	-0.275	2.864	-1.832	-1.299	-1.735	1.961	-0.405
-0.442	-0.598	-0.573	-0.163	-2.260	0.000	0.000	-0.445
-0.161	0.000	-0.144	0.137	0.969	-0.740	-1.371	0.000
0.000	0.000	-0.498	-2.839	-1.760	-1.163	-2.211	-0.460
-1.029	-2.441	-2.662	-2.097	0.573	-1.371	-0.222	-0.378
-0.036	-0.563	1.928	-1.405	-0.953	-0.795	-0.657	-1.068
-1.486	-0.089	0.316	-0.713	-0.073	-1.667	-3.553	-1.403
-1.097	-1.948	0.000	-1.201	-1.671	-0.375	-1.093	0.000
0.000	-0.541	-0.445	0.000	-0.823	-0.691	-0.221	-0.378
0.309	-0.105	0.000	-2.340	-1.864	-3.214	0.276	-1.854
-1.660	-0.656	0.497	-0.036	-0.787	-0.867	0.405	-0.489
-0.621	4.687	2.979	-0.768	0.246	-3.244	1.264	0.498
-0.750	-1.544	0.538	-1.990	-1.020	7.536	-0.724	0.409
-1.273	-1.314	0.260	0.380	1.200	-0.170	-1.447	-0.445
-1.653	0.721	-1.918	0.000	0.000	-0.337	-1.507	0.000
0.000	-0.078	0.000	0.389	-2.240	0.213	-3.624	-0.796
0.218	-1.400	0.088	-1.246	0.595	-0.541	-0.823	0.000
-1.714	0.000	0.000	0.000	0.000	-1.365	-1.816	0.000
0.000	0.000	0.050	0.223	0.092	-1.098	0.281	0.274
0.000	-0.249	-1.145	0.430	-0.206	0.000	0.000	0.000
0.115	-0.074	-1.214	0.000	0.000	-1.905	0.000	0.000
0.000	0.896	0.000	-0.472	-1.230	-0.339	-0.540	-0.619
2.440	6.776	-1.159	1.828	-1.485	1.618	1.724	0.163
-0.868	0.347	3.103	-1.487	0.293	-0.285	2.553	-0.507
-0.944	-0.882	0.725	-0.153	1.697	-1.420	-2.845	-1.679
0.529	-1.240	-0.436	-0.027	0.000	0.000	-0.089	0.000

Table35.txt

-0.378	0.000	-1.169	0.000	0.000	0.501	-2.409	0.000
0.000	0.000	-0.445	-0.445	-0.394	-1.169	0.000	-3.090
-0.099	-1.618	-2.074	-0.590	-0.955	0.218	-1.835	-0.215
1.120	-1.326	0.648	0.637	-0.868	-1.129	-1.679	0.000
-0.252	-3.450	-0.564	1.029	-3.197	-0.805	-2.942	-1.414
-1.780	2.230	4.576	0.329	0.303	0.067	-1.911	-0.004
-0.166	-0.155	-1.997	0.524	-0.899	-1.697	-1.951	-2.333
1.284	-1.243	0.431	-0.019	-0.403	-0.755	0.057	-0.793
0.895	-1.473	-0.852	2.224	-1.022	1.558	-0.335	-0.736
0.720	-2.384	-0.080	-2.059	-2.985	0.146	-2.531	-0.005
0.181	-0.040	0.835	-1.608	-2.070	0.299	-1.826	1.802
-2.323	-4.061	-3.375	0.265	-3.365	-0.650	-2.293	0.000
-1.575	-0.783	-2.475	0.664	-0.378	-1.140	-3.210	0.228
-0.219	-2.476	-0.084	-2.318	-2.623	-1.975	-0.323	-0.510
-0.079	-1.085	0.045	-1.185	0.300	0.232	-3.399	0.460
-0.778	0.139	-1.844	0.000	0.285	-1.914	-0.508	-1.191
-3.260	-0.595	-0.089	-0.283	-0.094	-1.452	-2.378	-1.237
-2.094	-0.193	4.185	0.974	-2.001	-1.516	-2.400	1.011
-0.553	0.180	-0.549	-0.022	0.527	0.303	0.077	-1.530
-0.851	-0.192	-3.003	-1.106	-0.959	-3.226	-3.571	-0.168
3.675	3.241	-3.934	-0.487	-1.742	-0.090	-1.002	0.383
0.355	-0.915	0.585	-1.532	0.252	0.116	-0.067	-1.245
0.290	-1.523	-0.944	-1.164	-4.771	0.440	-4.375	-2.840
-0.256	-0.874	0.644	-0.673	-0.162	0.972	-2.210	-0.147
-0.959	0.572	-0.923	0.838	-2.010	-1.298	-0.302	0.554
0.723	-0.055	-1.908	-1.641	-1.815	0.079	-2.960	-2.068
3.916	-0.717	-1.735	3.904	-0.074	-0.786	-1.156	0.233
-0.797	0.000	0.514	0.566	-0.513	-2.866	-2.188	-0.828
-2.666	0.254	-1.268	-0.914	-0.841	0.655	0.797	-0.211
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.561	-3.090	-0.445	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	-3.090	0.000	0.050	0.000
-0.541	-2.364	0.210	0.018	0.000	0.000	-0.321	0.000
-2.268	0.000	-0.925	0.000	0.000	0.309	-0.573	-0.378
0.000	-0.550	0.137	-1.819	-2.224	-1.301	-1.547	0.097
-0.745	3.085	-2.603	-1.038	-0.833	-0.978	0.709	0.000
0.059	-0.267	-0.948	-0.625	-1.619	0.885	-2.225	-1.300
-0.321	-1.119	-1.295	-1.084	-1.189	-0.099	-0.634	-1.873
-0.579	0.504	-0.490	-1.575	-4.091	-0.516	0.384	0.000
-0.840	0.595	-0.950	0.000	-0.378	-1.115	-0.673	-0.144
0.000	-1.610	0.139	-1.546	-1.793	-3.003	-1.018	-0.982
-1.348	-1.288	-0.304	-3.339	-1.188	-2.885	-1.283	-1.934
-0.220	-1.867	-1.051	-3.043	-1.890	-2.269	-0.264	-0.449
-2.179	-3.166	-0.221	-2.356	-3.196	-2.179	-1.355	0.375
-0.487	0.911	0.774	-0.856	-0.582	-2.298	0.480	2.719

Table35.txt

-1.198	-0.790	-1.072	3.595	2.486	-1.060	-2.183	-0.172
-1.525	-3.840	1.454	0.162	1.111	-2.685	-0.503	-1.974
-1.885	-2.652	-0.044	-3.539	-1.432	-2.360	-0.639	-0.367
-1.855	-2.373	0.028	-0.766	-0.467	0.719	-1.868	-2.142
-3.425	-1.109	-2.524	-2.453	-2.688	-3.360	-2.194	-1.042
0.286	-4.372	-2.379	-2.960	-0.024	-2.416	-2.518	1.391
-0.034	-1.830	2.129	0.331	1.277	5.141	-1.150	-0.916
-2.046	-1.581	-0.210	-1.470	5.920	-2.646	-0.337	-0.595
-1.939	-1.222	2.231	-3.486	-0.948	-3.599	0.044	-2.395
-1.753	-3.617	2.207	5.328	1.166	-1.736	-2.251	-1.652
-3.474	-2.282	1.456	-2.210	14.095	-3.146	-2.356	-3.221
-1.445	-2.267	-1.434	-2.039	-0.508	-2.966	-0.225	-1.673
-2.734	-2.142	-0.139	2.889	-0.396	-0.070	-1.630	-1.083
0.335	0.316	-0.176	2.597	-1.034	-1.802	-0.520	0.240
-4.011	-3.159	-1.322	-1.439	-0.698	-2.081	-0.328	-1.869
-2.721	-0.224	0.394	-2.152	-0.190	-0.997	-1.115	-1.266
-1.731	-1.758	-0.716	0.827	-2.176	-1.979	-0.829	-1.747
3.274	-0.933	-0.823	-1.608	-0.884	-0.721	0.583	2.726
-3.025	-2.615	-1.328	0.082	0.861	-0.332	-0.113	-1.255
-1.018	-2.391	0.799	-2.089	-2.634	-0.925	-1.130	-0.262
-0.216	-1.673	-0.989	-0.610	1.520	-2.852	0.559	-0.306
-1.593	-2.252	-1.985	-1.553	-0.416	-0.984	1.585	1.532
-1.202	-2.006	-1.329	1.831	-0.844	-1.042	-2.364	-1.759
-3.153	-2.613	-4.219	-3.288	-1.650	-3.553	0.391	1.122
-1.498	-1.598	2.409	-2.776	1.051	0.131	0.358	-0.846
-1.414	-0.732	-0.141	-1.520	1.543	-2.467	0.149	-1.505
0.267	0.060	-1.615	0.257	-0.804	-2.333	-1.604	-1.091
-1.838	-2.274	0.420	-1.719	-0.073	-0.966	-3.888	-1.461
0.094	-1.643	-0.908	-0.504	-2.564	-1.013	-2.492	-3.648
0.000	-0.214	0.108	-0.044	-0.445	-1.679	-0.459	0.137
-0.474	0.000	0.000	1.123	-0.437	0.163	0.000	1.179
-1.108	-2.554	0.000	-1.852	-1.313	2.016	-1.153	-1.214
-1.885	-0.985	-1.235	-2.463	-1.600	0.021	-2.306	-1.807
-0.722	-2.695	-0.893	-2.239	2.638	1.619	0.636	1.842
-0.536	-1.397	-1.383	-1.794	-2.996	-0.947	-2.065	-1.280
-1.171	-3.838	-1.330	-1.751	-3.431	-0.952	-2.228	-1.162
-0.482	0.761	-1.046	0.150	-0.123	-1.404	-0.358	-1.710
-2.177	-1.889	-0.774	-0.190	-1.337	1.069	-1.961	-1.767
-1.904	-0.743	-0.488	-0.424	-0.924	1.633	0.251	-0.035
5.990	-0.846	-0.745	-1.661	2.396	-1.424	-1.007	-2.842
1.853	3.590	2.892	6.986	-1.387	-1.228	-0.809	0.097
-0.692	-3.274	-0.387	-0.891	-2.678	-2.371	-0.764	0.027
-1.462	-2.764	-2.270	-3.433	1.152	-1.151	-0.111	0.403
0.971	-2.088	2.819	-3.070	-0.502	-0.295	0.282	-0.410
-0.179	3.566	2.899	1.310	2.169	1.856	8.010	16.112
4.620	16.846	7.774	2.330	9.036	7.698	-1.545	-0.859
-1.747	-2.530	-0.290	-1.517	2.773	14.569	1.520	-1.024

Table35.txt

2.519	-2.458	-2.251	-2.824	0.861	-3.918	-2.661	-2.642
-1.042	-0.210	-1.538	-1.924	-0.175	0.769	-1.162	-1.620
-2.775	-2.200	-1.930	-1.511	-0.638	-2.022	-0.789	-0.359
-2.619	-4.288	-2.333	-1.797	-2.616	-3.624	-3.057	-1.077
-1.165	-2.440	0.326	-2.455	-0.837	-1.890	-1.650	-2.114
-2.675	-2.959	0.084	0.189	-0.223	-1.111	-2.436	1.062
-2.505	-0.532	-2.122	-1.970	-1.661	-1.285	-0.220	-2.888
-1.433	-4.107	-2.464	-3.049	-0.212	0.235	-0.658	-1.285
-1.930	0.648	-2.161	-2.805	-3.354	-2.410	-1.496	-0.033
-3.067	-1.510	0.444	-3.121	-2.388	-3.600	-4.229	-1.857
-0.665	-1.679	-0.065	-4.032	-2.776	-2.315	0.326	-2.520
-1.193	-2.509	-2.546	-1.037	-1.312	-0.928	-1.727	-1.109
-2.135	-3.175	-0.524	-2.471	-2.140	-1.932	-1.501	-3.287
-1.036	-1.696	-0.765	-2.436	-2.474	-1.461	-1.125	-1.116
-1.601	-4.563	-1.645	-1.347	-1.443	-2.888	-0.434	-0.695
-0.684	-0.560	-0.821	-1.998	-0.220	-0.583	-2.189	-0.830
-1.103	-0.191	2.921	4.248	0.764	-2.118	-0.748	-1.399
-1.713	-1.524	-0.606	-2.979	-1.633	-1.209	-0.785	0.637
-0.532	-0.835	-2.240	-2.000	-2.603	-2.156	-1.349	-1.152
-0.695	-2.231	-0.283	-3.404	-1.746	-1.399	-1.153	-2.094
-1.429	-0.903	0.619	-1.882	-2.601	-0.890	-0.780	-0.876
-2.145	-1.290	0.790	11.034	-1.148	-1.883	-0.966	-0.721
-1.033	-1.641	-0.211	-0.067	-1.912	-0.874	-0.226	0.984
-2.209	7.199	-1.557	0.523	15.603	-1.326	2.270	0.147
-1.216	-3.821	-2.164	-1.478	0.798	-3.532	-1.611	-1.656
-1.773	-2.499	-1.142	-1.667	-0.586	-0.957	-2.244	-0.678
-3.508	-0.557	0.255	0.740	0.575	-1.074	-2.202	0.522
-1.722	-3.208	-0.033	-2.555	-2.055	-1.412	2.164	4.618
-2.096	-1.149	-0.099	-2.466	0.717	-2.734	-1.645	1.756
-1.603	-4.001	-1.446	3.510	-3.190	0.695	-1.243	-1.459
-2.406	-3.286	-2.229	-2.685	0.113	-3.866	0.806	1.299
-1.924	-1.185	-1.914	-3.576	-1.951	0.590	-2.180	-2.606
-0.152	-0.586	-0.303	-2.312	0.015	-1.043	-2.277	-0.882
4.025	-1.583	-0.007	7.317	-2.450	-0.371	5.696	7.223
-1.115	-0.113	2.655	-3.932	3.911	5.353	-2.210	-1.757
-1.417	-1.791	3.618	1.915	-1.377	-2.836	5.296	0.258
-1.968	-1.333	-1.223	-2.566	1.722	-2.913	-1.458	-1.278
-0.952	1.149	-0.964	-0.964	-0.687	-0.664	-1.400	1.755
-0.761	-1.612	-1.040	2.449	-0.720	0.223	-0.937	-0.197
-2.666	-2.556	-0.313	-2.870	0.542	-1.572	-1.466	-2.289
-1.000	-0.927	0.715	-0.986	-1.306	-1.625	-1.632	-2.556
-2.181	-0.377	0.021	-3.288	-2.543	-1.934	-0.567	1.642
-1.553	-2.648	-0.653	-2.004	-1.038	-2.657	-2.882	0.100
0.208	-1.180	-0.700	-1.148	-0.555	-0.983	-0.739	-2.683
-2.064	-1.674	-1.573	-1.900	-1.559	-1.464	-0.965	-0.019
12.030	2.804	-1.902	-2.447	0.457	1.803	0.868	8.432
1.156	5.026	4.662	1.227	3.867	0.110	-1.010	3.727
-0.216	2.646	-0.379	2.772	1.472	2.739	-0.826	-2.016

Table35.txt

-2.710	-2.244	-3.180	-3.939	-1.625	-3.168	-1.147	-3.378
0.604	-1.950	-3.296	-2.946	-2.597	-0.669	-0.571	-0.562
-0.425	-0.556	0.340	-1.861	-2.060	-2.466	0.604	-0.395
-2.283	-2.300	-2.714	-2.557	-0.532	-3.001	-0.717	-2.392
-0.279	-1.373	-1.641	-2.559	-2.404	-2.663	-0.771	-0.052
-0.597	-1.239	-1.360	-0.888	-1.380	-1.337	-1.203	-1.331
-3.001	-1.314	0.356	-2.046	1.253	1.026	-1.188	-4.100
-0.649	0.418	2.649	3.694	-0.798	-1.978	-0.360	2.134
-0.083	-2.526	-1.182	-0.186	1.946	-1.564	-2.955	-0.961
6.751	-2.105	0.636	-2.952	0.820	-3.320	5.920	5.844
-1.361	-2.435	1.288	-1.593	3.315	-2.128	3.874	0.751
0.139	11.768	-1.188	6.193	-0.648	-0.114	-1.702	-0.378
0.861	0.359	4.008	11.310	7.636	14.724	-0.464	-1.056
2.108	-0.803	-0.283	0.223	5.902	4.545	5.420	7.769
4.337	5.848	-2.167	14.005	-1.662	8.348	3.452	-1.072
-2.014	-0.160	-0.505	1.552	1.887	10.339	-1.783	-1.134
0.279	-1.713	-1.342	-0.306	6.248	4.510	0.545	-0.745
-2.925	-2.141	0.364	9.482	-2.849	0.249	0.990	-0.995
-0.327	-2.684	-0.980	-2.673	-0.499	-1.815	3.797	2.668
-0.078	-1.935	2.521	-1.112	0.960	-0.788	-1.816	1.278
-1.767	4.683	0.132	3.645	3.702	-1.032	-0.090	-0.456
-1.025	-2.647	-1.976	-1.499	-1.445	-3.911	0.026	4.217
-2.191	-2.312	-1.361	-1.364	2.874	-1.778	-1.535	-1.789
-2.723	-1.006	4.197	3.979	-1.100	-0.912	-1.487	-2.169
3.573	-3.225	-2.721	-2.346	-1.875	-3.001	-0.797	-1.814
0.188	-0.119	-0.151	-2.096	3.206	1.806	-3.015	3.625
0.072	1.167	-1.129	-1.699	-1.423	3.054	-2.263	-0.495
-0.268	-2.428	-0.514	-3.857	-1.059	-0.932	-2.308	-0.477
-2.430	-0.333	-1.727	-1.090	-0.152	-2.050	-0.265	-0.811
-0.259	-0.750	-1.889	-1.617	-1.227	-1.372	-0.053	-0.835
-2.113	-1.357	-1.093	-1.991	-0.886	-3.825	2.316	0.392
-0.950	-1.938	0.539	-2.399	2.642	-2.748	0.748	-2.934
0.294	-2.190	0.212	4.703	-2.599	-0.772	-2.101	-0.025
-0.860	-1.627	-2.602	-3.060	-1.411	-3.051	-1.723	-2.485
-2.002	-0.636	-0.302	-1.783	-2.450	-0.104	-1.425	-2.872
-2.201	-1.075	-0.653	-1.455	-2.137	-0.152	-2.480	-1.280
-1.506	-2.208	0.145	-1.056	-1.102	-2.238	-1.295	-2.765
0.193	-0.333	-0.687	-1.784	-0.723	-2.668	-1.049	-0.910
-0.920	-2.269	-1.271	-3.285	-1.422	-1.343	-1.174	-0.637
-3.873	-3.693	2.320	2.093	-0.351	-3.569	-2.898	-3.241
-4.454	-2.230	1.845	-3.073	2.711	-1.312	-1.477	-2.007
-2.130	-1.627	-0.495	-1.863	5.484	-4.203	-0.370	-1.625
-1.261	-3.470	1.019	1.703	-0.675	-2.900	-2.631	-2.348
-0.808	-2.610	-1.649	-3.213	1.196	-0.987	-2.405	-0.493
-1.734	-1.130	-1.606	-0.773	1.569	-2.267	3.555	-1.488
-1.169	0.000	0.000	-0.144	-0.144	0.000	0.000	-0.420
0.000	-0.541	0.000	-2.464	0.000	0.000	0.000	0.000
0.529	0.000	0.000	-0.823	0.000	0.000	0.000	0.000

Table35.txt

-1.569	-0.920	-1.937	-0.747	-0.981	-0.051	-1.101	-0.569
0.741	-0.544	0.558	-2.677	0.129	-0.862	-1.964	1.411
-1.256	-0.204	0.447	3.892	-2.602	-1.929	-0.745	-1.412
2.263	-3.614	1.234	-3.770	-0.855	-1.228	-2.347	-2.990
3.818	1.631	0.350	-0.519	1.850	-0.475	-0.885	2.801
-2.662	-1.945	-1.155	-0.295	3.665	-1.523	0.958	-0.531
3.814	-3.468	-0.837	-1.510	1.988	-0.467	-0.515	4.857
-0.706	2.076	2.282	-0.103	1.587	-1.023	2.279	3.845
-1.343	-2.858	-0.772	6.894	-0.792	-1.171	-1.076	-2.011
-3.653	-1.501	-0.694	2.279	-1.770	-1.917	-2.566	-2.856
1.355	4.539	2.825	-0.109	1.150	-1.192	-0.234	-2.753
0.631	2.056	1.699	5.295	1.223	-0.562	-0.672	-1.303
6.004	12.233	1.304	2.630	-0.984	6.950	4.024	11.103
-1.533	-1.988	0.289	8.955	-0.195	-3.249	-0.038	-0.673
-2.217	-2.354	2.012	4.255	-2.287	5.052	1.487	-1.743
-1.004	-3.455	-0.494	-2.930	-1.795	-3.623	-1.530	-2.467
-1.132	-3.484	-1.045	-2.315	0.568	-2.008	-0.529	-2.509
-0.674	-1.563	-2.001	-2.814	1.827	-1.392	-2.827	0.220
8.285	7.942	6.943	11.635	5.453	10.356	4.629	12.657
6.739	6.806	2.904	11.498	3.459	3.924	6.756	8.544
7.368	7.021	5.865	8.662	12.671	8.568	5.351	5.333
0.126	-1.350	5.458	7.506	-1.350	-3.238	3.266	-3.054
-3.157	-1.855	2.255	3.536	3.534	-0.945	1.633	-0.376
0.040	-2.269	-0.436	-0.412	10.274	7.157	1.345	-2.617
-1.054	-3.062	0.090	-2.478	-1.439	-3.756	-1.050	7.771
7.745	-2.620	-0.251	-2.784	-0.833	-2.442	-2.392	-1.121
-1.282	9.278	-0.645	-2.403	-1.405	0.187	-1.549	0.120
-2.247	-3.392	0.059	-1.088	-2.521	-2.520	-1.595	-1.491
-2.312	-0.988	-1.264	-1.239	0.729	-0.070	-1.702	-0.524
-0.971	-3.012	-0.728	-2.719	-1.868	-1.423	0.765	-2.142
-0.376	-3.974	-0.541	-0.668	0.000	-2.793	-0.074	-1.016
-0.635	0.583	-0.378	0.527	0.000	-0.027	0.000	-0.144
0.366	-0.521	-0.059	-0.754	-1.464	-1.874	0.309	-0.445
-1.021	-3.265	-0.941	-1.424	-0.311	-3.331	-0.941	-3.826
-0.653	-0.835	0.137	-0.519	-1.843	-0.881	-0.686	-2.062
-1.716	-1.437	0.342	-0.767	-2.124	-1.525	-0.023	-0.691
0.000	-2.223	-2.804	-2.207	0.000	-0.256	0.717	-0.334
-0.170	-0.583	0.000	-2.654	0.000	0.000	-0.790	0.529
0.740	-0.840	0.050	-0.479	0.366	0.137	-0.311	0.000
-2.772	-0.122	-1.009	-1.174	-2.069	-1.031	0.000	0.064
-1.064	-1.441	0.137	-2.588	1.236	0.362	-0.925	-2.334
-0.434	-2.630	-0.256	-0.664	-2.067	0.210	-2.640	0.865
0.000	0.763	0.137	0.000	-1.169	-2.334	0.000	-0.459
0.728	-0.288	-1.234	-0.184	0.000	-0.002	-1.256	-0.337
-1.256	-0.824	0.000	-1.093	-0.623	0.000	0.000	0.000
-2.083	-2.846	0.204	-1.250	1.038	-0.887	0.676	-0.150
-0.988	0.168	-1.418	0.769	1.091	-0.376	-1.023	-0.644
-0.130	-3.458	1.218	3.374	-1.603	-0.118	-1.638	1.089

Table35.txt

-3.322	-1.933	-1.435	-0.857	-2.858	-3.265	-0.969	-1.234
-1.785	-1.601	0.750	-1.946	-2.166	-0.867	-0.882	-1.259
-2.941	-2.432	-2.268	-4.470	-2.632	-1.971	0.257	-0.444
-1.000	-1.734	-1.949	-5.567	-2.641	-1.399	-1.331	-2.131
0.102	-0.367	-1.299	-0.208	-0.243	0.830	1.427	-0.776
0.199	-2.017	-0.804	-1.952	-0.933	-2.749	-0.757	-0.240
-1.479	-1.115	-2.652	-1.989	-1.641	-2.057	-0.089	-0.521
1.086	-1.942	-1.176	-2.515	0.399	-0.493	-1.959	-1.638
-2.026	-1.577	-0.332	-0.341	-2.443	-1.189	-0.177	-1.126
-0.736	-0.549	0.000	-1.169	-0.027	-1.214	0.000	0.000
0.676	0.000	0.000	0.284	0.000	0.000	0.000	0.460
0.000	-1.256	0.000	0.394	0.000	0.000	0.000	0.000
-0.419	-0.773	-0.369	-0.620	-2.241	-0.831	-3.273	-2.271
-0.787	-0.773	-0.196	-1.010	-1.577	-0.954	-0.839	-0.212
-2.929	0.205	-2.460	-0.494	-1.430	-1.408	-1.985	-0.654
-0.768	-2.566	-0.624	-2.805	0.015	-3.570	3.682	1.125
0.582	-0.964	-3.719	-3.067	-0.553	-4.680	1.154	-1.542
0.217	-1.766	-0.615	-1.566	-1.102	-2.933	-1.348	0.440
-1.734	-1.918	-1.874	-0.716	-1.439	-1.173	-1.660	0.276
0.911	-0.490	-1.215	-0.580	-0.689	-1.023	-0.001	-2.153
-1.636	0.018	-1.218	-0.829	0.307	-0.604	0.137	0.008
3.522	-0.491	-0.361	-1.031	-1.078	-0.681	2.866	-0.939
-1.493	-3.010	-2.079	0.567	-0.836	-1.459	-1.766	1.016
-1.135	-1.500	-1.861	3.325	-2.884	0.109	-1.309	-0.519
-0.797	-0.910	-0.460	-1.314	0.114	-1.375	-1.832	-2.022
-2.292	-0.123	0.793	-3.089	-0.864	-0.307	-0.217	-0.955
-1.095	-1.548	-1.169	-0.289	-1.989	-1.348	-1.383	0.460
2.195	-0.302	-1.274	-2.567	-0.815	0.813	-0.912	-0.669
-0.317	-0.175	-0.115	-1.561	-1.070	-1.150	-0.974	-0.795
-2.322	-2.620	-0.195	-0.808	-1.966	0.066	-1.906	0.000
0.453	-0.410	-1.005	-3.371	-0.927	-2.033	-0.850	-1.560
-0.687	-1.923	-1.404	-1.532	-1.596	1.181	-2.143	-2.090
-1.773	-2.141	0.693	-1.721	-1.864	0.190	-1.036	-0.375
-0.240	-1.736	-1.269	-0.571	0.133	-2.804	-0.652	-3.225
0.047	-1.454	-1.198	-2.962	0.470	-2.146	-2.107	-0.550
-1.479	-0.736	-0.551	-2.739	-1.821	-1.191	-1.373	-1.224
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-5.068	-1.141	0.378	-1.454	-0.463	-2.677	-0.628	-1.335
0.237	-2.341	0.350	-1.644	-0.782	-3.797	-3.760	-1.017
-0.301	-0.016	-0.036	1.163	-0.731	-1.677	-0.532	1.199
-1.379	-1.852	-3.007	-1.512	-1.079	-0.653	0.545	-0.046
-0.973	0.095	-1.530	-1.865	-0.498	-0.792	-0.994	-1.714
-1.039	-1.786	-0.779	-0.936	-1.216	-1.426	0.628	0.799
-1.792	1.709	-1.125	-2.343	-2.396	-3.952	0.000	-1.688
-0.879	-4.063	0.000	-4.785	0.000	-0.660	-0.351	-2.353
-0.294	-1.073	-2.265	-2.083	0.114	-1.356	-0.152	-0.145

Table35.txt

0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-3.294	-1.425	-0.549	-1.978	-2.731	-2.368	-0.735	-0.787
-0.841	-1.135	-0.511	-0.878	0.833	-0.235	-1.913	-1.980
-1.023	-1.808	0.478	-1.503	-1.364	-2.851	-0.026	0.233
-5.895	0.818	-0.285	-2.938	-1.203	-1.982	-0.944	-1.247
-1.217	-0.194	-1.031	-3.117	-1.181	-1.111	-0.510	-1.035
-1.093	-0.772	-1.153	-0.623	1.553	-0.466	-0.377	0.179
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2.355	5.082	2.961	3.157	4.593	3.755	-0.544	-0.885
-1.834	-1.219	1.680	-0.255	2.275	2.018	2.610	1.426
1.438	-2.375	-0.425	4.106	-0.681	-3.623	-0.843	2.380
-1.194	-2.032	-0.932	-0.968	-0.563	4.042	-2.284	-2.124
0.289	-1.162	-2.864	-2.172	-1.777	-0.538	-0.446	-2.267
1.533	-0.603	3.913	9.793	-2.141	-1.292	-1.770	1.129
-1.588	-2.072	2.113	4.511	-1.971	-0.863	0.415	-0.530
7.061	10.017	0.319	-3.225	-1.917	0.995	-0.353	-2.088
0.061	-0.064	2.338	3.091	5.335	-1.143	-1.476	1.428
0.369	-0.826	-1.320	-2.261	-2.228	-0.321	-0.007	-0.155
-0.270	-0.289	-0.790	-1.343	-0.686	0.941	0.293	-2.217
0.585	0.566	-0.886	-1.436	-1.002	-4.233	-1.816	-0.712
1.301	-2.526	-1.588	-3.236	-1.690	-2.158	2.429	1.373
-0.923	-1.132	0.028	-1.520	1.820	0.753	-2.272	1.493
-0.413	-1.080	-0.741	0.038	-0.161	-0.043	-1.641	-1.662
0.000	0.164	-2.381	-1.185	-0.528	-1.536	-0.292	-0.544
0.595	-1.585	0.000	-0.645	0.000	-0.961	0.000	0.000
-1.340	-1.698	0.000	-0.071	-1.678	0.366	-1.031	0.000
-2.181	-1.350	-0.277	3.692	-0.926	0.612	0.041	-0.673
0.858	0.219	1.950	-2.338	3.589	3.497	-1.327	1.327
-1.402	0.432	1.706	6.117	-0.825	0.291	0.999	1.123
-0.354	-0.490	1.030	0.516	-2.244	-1.370	-1.253	4.407
-0.251	-0.046	-0.653	1.974	3.121	-2.424	-1.385	-2.220
-0.714	-3.143	-0.840	0.481	-2.908	7.261	1.863	-0.439
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-2.413	-3.149	-1.356	-0.396	-2.973	-1.931	-0.302	-2.124
-2.036	-2.463	-2.477	-1.660	-1.562	-2.234	-0.463	-3.779
0.679	-3.505	-0.976	-1.955	-1.604	-3.067	-2.106	0.264

Table35.txt

-2.287	-2.501	-1.227	-1.631	0.338	-1.477	-0.216	-3.302
-0.727	0.615	0.543	-1.334	-0.534	-3.096	-2.419	-2.882
-0.864	-2.670	0.737	0.122	-3.701	-1.490	-2.178	-2.136
-1.112	-0.772	-3.837	-1.351	-2.160	-0.836	-0.897	-0.179
0.890	-1.803	-0.445	-1.911	-1.647	0.130	0.743	-0.303
-1.138	-2.532	-0.782	-1.446	1.315	-2.461	-1.635	-1.227
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.344	0.024	-1.635	-2.565	1.869	-1.831	-1.329	0.895
-0.732	-1.271	0.696	-0.086	-1.410	-4.890	-1.594	-0.129
0.178	-0.248	-1.978	-2.583	-3.430	-0.399	-0.272	-1.540
0.570	-0.416	0.912	0.243	-0.767	-1.555	-3.182	0.000
0.717	0.754	-1.097	-0.592	0.000	-1.332	0.274	-1.329
-1.792	-1.316	-2.159	-1.441	-2.893	-1.070	-0.047	-2.904
-0.388	-1.361	-0.268	-2.874	-0.581	0.050	-1.341	0.000
0.014	-0.027	0.000	0.000	-0.445	-0.754	-2.897	0.000
0.000	-0.485	0.561	-0.711	-2.386	-1.545	-1.076	-2.315
-0.712	-0.627	-1.463	-1.874	0.000	0.000	-1.214	0.000
-0.730	0.459	0.050	0.000	0.000	0.206	-2.686	0.000
0.000	-0.217	0.000	-0.926	-1.452	-0.754	-3.325	-0.267
0.000	0.000	0.000	-3.090	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.637	0.000	0.969	0.000
-2.158	-5.514	-1.909	-0.114	-1.462	-1.117	-0.184	1.620
0.645	-0.643	0.698	0.153	0.233	-2.024	1.538	0.805
3.362	-1.297	0.770	-1.818	-0.205	0.772	-1.327	-1.728
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-0.144	-0.736	0.000	0.000	0.000	0.000	0.000
-1.389	-3.090	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.022	0.000	0.000	0.000
0.603	-2.928	-1.016	-0.221	0.789	1.336	-1.309	-0.723
-0.405	2.095	3.467	0.717	-0.161	3.114	2.748	-0.057
0.139	-0.719	-1.440	-1.596	-1.891	-2.559	-1.471	-1.156
0.043	4.836	4.447	5.024	0.601	-1.558	-0.612	4.131
1.694	2.445	-0.039	1.267	4.574	4.326	-1.841	0.208
-0.026	1.726	-0.735	0.470	-1.547	-1.356	-2.043	0.992
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.366	0.000	0.000	0.000
-0.353	0.814	1.366	2.041	-0.266	0.759	-0.729	-2.761
-1.173	-0.600	1.867	1.283	1.821	-1.915	-2.592	0.000
0.131	2.235	-0.516	-1.228	-2.776	3.281	4.433	1.056

Table35.txt

-0.557	-0.553	-2.121	-0.027	-0.338	-3.086	-1.937	0.922
-0.796	0.115	0.304	2.359	4.221	-2.196	-1.022	0.073
0.577	-0.868	0.000	-1.580	0.003	1.133	-3.473	-1.435
-1.080	-0.488	-0.560	6.886	-1.696	0.184	-0.540	-0.298
4.037	-1.472	4.107	-0.043	1.733	0.595	-1.216	-1.137
-1.685	3.888	2.542	0.067	-0.184	7.514	6.155	-2.362
-2.457	-1.413	-2.770	-2.285	-1.657	0.560	-0.217	0.000
-0.994	0.573	1.789	-0.027	-2.131	-1.863	-1.299	0.097
-1.714	0.137	-2.786	-0.613	-2.776	-1.548	-1.208	-0.899
-0.864	0.192	-2.418	0.646	-2.726	-1.938	-1.367	2.194
1.493	1.512	3.208	-0.445	-1.560	4.251	1.056	-1.964
-2.245	0.926	-1.245	-1.205	-2.008	-1.066	-1.898	3.429
-0.775	-1.726	-1.108	-0.894	-2.251	0.270	-1.247	-2.727
0.457	-0.834	-0.284	-0.352	-1.748	-0.937	-2.353	-0.326
-0.697	-0.798	-0.204	-1.448	-2.197	-4.171	-1.990	0.332
-1.113	-1.823	-2.524	0.059	-0.580	-0.003	-2.175	-1.004
-1.334	-0.265	-0.605	-0.416	0.436	-2.664	-2.081	-0.611
0.173	-2.047	-1.389	-1.074	-1.573	-0.080	-2.599	0.714
-1.116	1.828	-0.096	-2.725	-1.180	-0.814	-2.391	0.690
-0.939	0.969	-2.373	-1.508	2.036	-2.174	2.440	-1.776
-0.315	-1.003	-0.345	-2.062	-2.702	-2.100	-0.560	-2.593
-0.909	-2.474	-1.251	-0.954	-0.713	-0.400	-0.278	1.667
1.059	0.125	-0.836	0.030	0.821	0.256	-0.427	1.107
-0.786	0.996	-1.421	-0.672	-0.368	-1.366	1.154	1.013
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.378	-1.169	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	-2.199	0.000	0.000	-3.090
-0.205	-3.354	-1.006	-2.764	-0.508	-1.287	-1.562	-0.182
-0.864	-0.719	1.054	-0.363	-0.679	-1.592	-1.330	-0.826
-1.711	-0.627	-0.884	-0.565	-0.376	-1.115	-2.300	-2.269
2.677	-1.741	-1.780	-1.699	-1.511	-1.461	0.447	2.393
0.455	4.237	3.718	-0.592	0.850	1.179	-2.395	0.372
-0.763	0.035	-1.340	-0.510	-2.613	0.227	-1.071	-0.442
0.000	0.000	0.000	0.000	0.309	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-3.117	1.793	-2.791	-1.480	-3.154	1.172	0.035	0.277
0.601	-1.403	-0.902	0.000	-0.305	-2.530	-0.591	-0.576
-4.983	-0.488	-0.307	0.436	-2.616	-0.831	-2.617	0.549
0.623	-2.726	-1.150	-0.207	-2.633	0.801	-1.533	0.000
-0.034	0.121	-2.373	-0.520	-0.445	-0.604	1.351	0.855
-1.153	-0.658	-0.249	1.501	-2.578	-1.547	-2.501	-2.266
-2.396	-1.777	-1.477	-1.143	-0.589	-0.173	-1.014	-1.833
-0.247	-0.489	-1.713	1.271	-2.304	-0.026	12.426	-0.172
-1.462	0.075	-0.840	-0.492	-1.731	-0.572	7.503	-0.923
0.443	0.490	-3.588	-0.732	0.685	-0.033	-0.977	-1.563
-0.473	1.469	-0.574	-1.407	-0.294	-1.218	-2.190	1.722
-0.874	-1.849	-0.414	-2.046	-2.557	-0.815	-2.300	-0.117

Table35.txt

0.297	-2.205	-2.200	-0.396	0.600	-0.972	0.574	-0.805
0.222	0.458	-1.473	-0.664	-1.328	-1.652	-1.185	-2.090
-0.902	-0.856	0.000	-2.120	0.019	-1.156	-3.862	-0.323
-0.664	-0.094	-0.432	-0.322	8.830	0.819	-1.797	0.552
-1.495	-1.840	-0.223	2.622	-1.200	0.210	0.576	-0.906
-0.672	-1.044	-1.334	-1.610	-1.943	-1.420	-1.104	-1.093
0.009	0.463	-1.944	-0.324	-3.514	-0.384	-1.333	-0.661
0.753	0.204	-1.949	0.418	-0.303	-3.455	5.983	-0.058
0.143	-1.163	-0.555	-2.705	-2.618	-1.264	-1.561	-0.315
-1.290	-1.828	-2.087	-0.490	-1.912	-1.029	0.838	-0.653
-1.334	-2.503	0.244	0.924	-2.096	-0.184	-1.775	-1.340
-2.253	-1.301	-0.090	-0.086	-3.696	-1.668	-2.648	-1.569
-1.752	-1.174	-1.344	4.086	-1.139	-1.173	-1.427	-0.802
0.442	-0.103	-2.993	-0.073	-0.987	-0.632	11.577	0.893
-1.645	-0.524	0.973	3.866	-0.635	-2.739	-3.287	-3.785
0.235	-1.261	-0.243	-1.088	-2.850	-1.336	-0.337	-0.084
-0.933	0.373	-0.861	-0.297	-0.225	-1.302	7.429	-1.970
-0.604	-1.631	-1.206	-2.235	-0.845	-3.757	-0.462	-0.404
0.020	-0.540	-0.696	0.010	-0.107	-0.733	0.986	-1.910
-0.138	-0.206	-1.768	-1.576	-0.366	9.932	-0.994	-1.103
-2.176	-0.441	-1.567	-1.789	0.353	-0.487	11.806	-1.463
-1.502	-2.845	-1.985	-1.680	-0.895	-0.414	-2.016	-0.532
-0.682	-0.264	-0.958	-0.062	-0.663	-1.624	-3.099	-0.221
-1.595	-1.791	0.732	-1.057	-2.170	-1.606	-2.253	-1.380
0.293	-2.840	-2.767	-1.329	-0.606	-1.754	-0.132	0.091
-1.016	-1.452	-1.667	-1.168	-1.410	-2.342	-1.239	-1.168
0.235	-0.583	0.551	0.185	-3.145	-1.583	-1.916	-0.717
-0.514	-2.150	-2.626	-1.474	-1.548	-0.300	-1.007	-1.203
-1.343	-0.379	-2.002	1.491	-0.067	-4.005	-2.370	0.216
0.008	-1.799	-2.102	-0.709	-2.547	-2.315	-2.010	-0.159
-2.629	-2.397	-1.338	-0.067	0.281	-1.186	-0.516	-0.162
-0.810	-2.762	-0.476	-0.503	0.787	-0.344	-0.038	-0.384
0.306	-1.524	-0.038	-2.743	-1.921	-1.070	-0.629	-1.430
-2.125	-1.124	-1.118	-0.889	-1.535	-1.838	-0.372	0.000
0.000	0.000	0.000	-0.910	0.749	2.744	-1.439	-0.999
2.604	0.014	-1.422	-2.252	-1.410	-0.622	7.195	-0.344
-0.693	-1.791	-0.751	-1.410	-1.195	-2.730	-1.404	4.295
0.392	-0.912	-1.806	-2.227	-0.835	-0.219	-2.484	6.365
-1.065	-0.715	-0.198	-1.779	-1.891	-2.327	-1.264	-0.581
-0.472	-1.102	-0.903	1.138	7.481	2.480	1.954	2.808
1.474	1.467	1.293	1.284	0.998	-0.396	10.413	0.820
2.602	7.323	2.487	-0.840	-1.656	4.943	5.921	3.854
-2.143	-0.843	0.230	-2.552	2.208	3.444	3.166	0.000
3.090	1.110	0.893	-0.824	0.357	-0.480	-2.079	0.809
-0.952	3.634	1.994	0.203	-2.317	0.171	1.859	2.957
-0.119	-0.207	5.538	-0.230	-1.850	-1.159	-0.301	0.731
0.199	-0.369	-1.702	-2.296	-2.719	-3.936	-0.676	3.815
-0.114	-0.817	-1.256	-2.906	-4.133	1.701	-2.223	-0.124

Table35.txt

0.432	-0.656	-0.860	-1.627	-0.045	-1.824	-0.811	-0.753
-0.769	-0.471	-0.489	0.868	1.064	-0.373	-0.091	1.659
-0.837	-0.601	1.366	-0.032	-0.984	0.218	-0.307	-0.799
-1.021	-1.634	-1.399	-1.775	-1.552	-0.540	-2.600	-1.547
-1.330	0.160	-0.661	-0.745	-3.261	-2.368	0.843	-2.467
-0.505	-3.332	0.181	-2.026	-2.201	-0.469	-0.800	-1.209
0.873	-2.202	-2.800	-2.312	0.186	1.708	0.093	-0.178
0.495	-0.969	-1.809	0.800	-0.664	-0.271	-0.848	0.357
-1.720	-0.061	-0.216	-2.224	-1.476	0.557	2.909	-2.571
0.226	-2.574	0.966	-1.934	-1.097	-0.408	-0.424	1.204
-0.009	-1.659	-0.266	-0.921	-0.201	-1.431	0.193	1.253
-1.848	-1.192	0.202	-2.357	0.137	-0.219	12.414	-2.515
-2.028	-1.393	0.350	-0.566	-1.920	-0.572	-0.347	-0.319
1.058	-1.496	-0.615	0.075	-1.547	0.015	-0.803	-0.236
0.071	-1.120	-0.416	0.175	-2.514	-1.434	0.314	-0.459
6.303	8.116	-2.297	11.838	10.098	4.703	5.193	5.476
5.943	5.397	10.072	1.615	2.991	-1.389	0.171	-0.232
-1.707	4.064	4.630	1.244	2.164	0.025	5.734	8.833
0.714	-0.479	-0.475	-1.896	-0.106	-1.089	-1.123	-1.334
-1.352	0.263	-2.500	-0.408	-2.445	-0.156	-1.442	1.034
-1.370	0.051	-0.261	-2.830	-1.497	0.193	-2.200	-0.210
2.775	8.984	-0.709	0.000	7.245	3.444	7.782	-0.910
4.137	-1.196	0.978	0.000	1.823	6.555	5.274	0.742
-2.318	-0.071	2.823	5.858	-3.201	0.002	12.878	6.917
3.373	6.180	8.205	4.273	-1.148	0.834	0.035	0.000
3.136	-2.182	4.240	-0.027	1.704	-0.219	-0.784	3.282
2.092	-0.643	3.736	0.006	1.454	-1.468	-0.386	-0.372
7.533	0.295	13.642	4.551	1.951	6.751	6.104	4.361
6.541	-0.729	0.833	0.026	-0.676	4.682	4.379	2.258
0.235	3.289	3.090	6.196	10.348	9.783	10.710	7.881
0.000	0.000	0.000	-0.413	-0.736	0.000	-1.169	0.000
-1.169	0.000	0.476	0.137	-3.090	0.144	1.413	0.000
0.000	0.000	0.000	-0.069	-0.384	-1.708	-1.459	-1.564
0.307	-0.204	0.746	14.074	3.907	5.144	3.693	5.927
6.847	6.808	11.981	0.030	8.478	2.414	6.024	0.895
0.261	-3.483	3.000	8.432	14.912	6.992	10.311	-1.247
-0.841	6.324	15.578	-2.527	-0.696	-0.225	-0.643	4.362
3.090	-1.103	6.650	1.165	-1.630	7.117	4.885	-2.508
1.723	-1.725	0.627	8.972	-1.220	-1.431	6.283	9.927
1.034	-1.167	-1.159	0.000	-0.695	-0.104	0.361	0.000
1.677	-1.065	-1.632	1.527	-2.904	-1.129	-1.147	-2.417
-1.817	0.863	0.000	-1.375	-1.923	-0.274	-2.161	-2.387
-1.390	11.659	13.216	6.539	2.659	1.920	0.404	1.540
0.416	0.750	-0.055	2.411	0.774	0.097	8.374	0.051
5.349	3.154	-1.361	9.391	3.284	7.629	6.323	12.326
-1.400	-2.568	-0.090	-2.424	-1.622	0.369	-2.504	-2.116
-0.934	0.123	-1.112	1.890	-0.923	-0.368	-0.920	1.100
-1.205	0.043	1.869	-1.638	-0.015	-1.265	-2.275	-1.550

Table35.txt

-2.517	2.777	-0.625	-2.615	2.571	1.475	2.749	2.752
5.387	-0.226	5.344	-0.650	2.846	-0.241	-0.865	-2.169
3.792	2.951	0.487	6.966	-1.628	0.933	5.814	3.475
8.408	0.082	-0.505	-2.053	0.499	0.000	0.000	0.000
0.000	-1.404	-0.754	3.145	-0.190	1.600	-0.601	0.000
0.000	0.075	0.000	-1.153	1.405	-0.529	7.730	0.339
-1.507	0.416	0.960	0.669	1.735	-0.947	1.594	0.000
0.000	1.256	-0.451	1.148	0.034	-0.459	1.718	1.437
0.223	0.652	0.000	-0.359	0.407	-0.830	2.985	1.893
5.954	9.738	10.738	6.091	7.703	-0.117	-0.677	4.370
5.015	0.493	7.574	3.532	4.165	11.041	12.573	4.770
2.534	7.318	2.615	11.757	16.209	2.393	16.061	5.917
0.926	2.987	4.792	-0.706	4.631	-0.887	0.637	2.343
5.268	3.090	3.668	3.131	0.355	-0.643	1.970	5.792
1.642	2.631	1.087	4.102	2.305	1.269	12.582	2.846
-0.265	0.186	2.659	-0.813	0.662	-0.927	-0.455	6.698
6.219	1.329	14.684	0.518	3.174	-0.301	11.334	0.033
2.307	0.201	2.249	9.236	4.521	0.729	16.495	11.735
3.679	-2.434	6.212	-1.892	2.455	-0.455	5.139	0.000
6.553	-1.127	3.597	-0.892	0.472	0.294	-2.613	-0.902
-1.054	0.114	0.000	5.093	2.743	-1.310	-0.642	-0.085
-0.295	-0.171	-0.863	-1.654	-1.959	-0.425	-2.209	-0.426
-1.842	-2.898	-2.206	-0.653	-2.530	-1.458	1.139	0.141
1.012	-0.596	-1.225	0.902	-2.282	-3.184	-2.229	-1.242
1.549	-2.975	0.369	-0.904	-1.149	-1.523	-0.850	-0.430
-0.289	0.350	-2.819	0.468	0.418	-0.653	-3.471	-0.957
-0.584	-1.365	-1.252	-0.656	-1.526	-2.378	-2.550	-2.139
0.909	0.904	1.871	-1.173	-1.065	-2.516	0.303	-0.147
0.657	0.292	-0.818	-0.697	-2.306	-0.932	-0.188	-0.640
1.711	1.431	0.251	-2.004	-0.086	-0.212	12.167	0.437
-1.783	-0.295	0.343	0.243	-0.584	-1.132	-0.086	0.507
-2.393	-0.906	-2.173	0.456	-0.339	-0.667	14.078	-1.794
-1.664	-2.427	0.231	-1.654	-2.351	-1.074	-1.451	-1.438
1.255	0.350	-0.662	-1.149	-1.508	0.747	-1.292	0.098
1.961	0.194	1.190	0.973	1.818	-1.798	0.582	-0.846
2.250	0.506	-0.020	-0.611	0.559	7.221	11.408	-0.884
1.078	-0.946	-2.340	-1.592	0.059	-0.931	1.674	1.412
-0.338	-1.126	-0.086	-0.963	-0.090	0.444	0.567	-1.190
0.057	0.561	-1.110	-0.447	-2.588	-2.191	-2.820	-2.251
-1.874	-1.487	-2.118	-0.724	-1.427	-0.681	8.952	-2.322
-0.678	-0.758	-0.292	-0.462	-2.040	0.785	-0.112	4.758
5.214	-1.467	-0.256	-0.540	-0.985	-0.627	-0.233	-1.522
-2.860	-2.933	0.028	-2.036	0.546	0.065	-0.674	0.265
0.053	0.762	0.946	-0.618	-2.485	-1.238	-1.408	-0.548
0.733	-0.760	0.442	-1.439	-2.712	-1.082	-0.344	-2.712
-0.507	-0.013	-1.213	-1.324	-0.417	-1.640	-0.959	-0.985
-0.130	-0.922	0.035	-0.812	1.234	-0.944	-1.584	-2.158
-1.431	-0.728	0.117	-2.356	-2.506	-0.419	-1.309	-2.731

Table35.txt

-0.970	-0.475	10.532	-0.625	-2.277	0.781	-1.203	-1.465
-0.530	-0.545	-3.212	1.402	0.201	-0.841	-0.666	-0.431
-0.905	-2.518	-0.771	-0.744	-0.758	-1.897	-2.225	-0.289
-0.791	-2.018	-3.212	-0.128	-3.119	-1.879	-2.421	0.258
-0.104	-0.852	-1.435	-1.445	-1.060	-2.036	-1.437	-0.253
-1.056	-0.545	-0.718	-3.121	-1.926	-1.337	0.468	-2.939
-1.315	-2.064	-1.030	-1.743	-1.095	-1.974	-1.780	-1.303
-0.168	-0.587	-1.498	-0.254	-1.991	-1.444	-0.476	-1.917
0.038	-1.354	-2.016	-1.276	-1.339	-2.771	-2.000	-0.379
10.472	14.730	16.390	14.993	10.123	5.497	11.406	6.098
5.244	6.644	13.332	3.530	4.737	12.603	15.935	6.916
4.665	9.840	1.686	12.735	16.172	12.495	15.497	13.528
8.744	11.305	21.435	15.450	10.778	9.276	10.964	7.914
9.213	-1.421	8.300	0.478	8.495	15.706	10.582	10.032
2.548	11.046	4.440	10.713	9.315	9.452	8.957	14.276
-1.735	-3.011	-1.271	-0.815	-3.798	-0.456	-0.881	-1.111
-1.070	-1.353	-0.131	-1.330	0.358	0.235	-1.127	0.406
-0.498	-1.090	-0.409	-1.931	-0.960	-1.734	-0.353	-0.469
-3.090	-1.112	-2.584	-3.115	0.544	-0.345	-1.040	-1.202
-2.192	-0.199	-1.484	-0.240	-2.883	8.307	-1.432	-0.713
-0.255	-1.517	-0.831	0.469	-1.591	-2.819	-0.660	-3.769
1.664	7.397	-0.360	0.442	1.221	-0.391	3.892	3.090
2.776	2.102	4.539	2.643	3.701	1.213	5.430	1.016
4.041	0.847	4.324	-0.480	-2.082	-0.294	0.965	0.039
1.510	0.015	-1.087	0.109	-0.266	-0.834	-0.325	-0.195
2.568	-1.634	-0.421	0.532	-0.514	-0.608	-2.379	0.860
0.771	2.087	1.769	-0.039	-1.106	-0.037	-1.104	-2.924
-2.483	-2.233	-2.149	-3.852	-2.491	-0.115	-0.510	-0.676
-0.927	-0.960	-1.831	0.416	-0.593	-1.893	-1.696	-2.564
-0.046	0.492	0.997	-1.105	-1.151	-0.740	-0.536	-1.285
-0.586	-0.411	-1.316	-1.749	-2.552	-1.015	-0.722	-0.307
-0.841	-2.117	-1.411	0.897	1.134	-0.945	-0.269	-1.221
-0.436	-1.900	-1.985	-0.448	-2.236	-1.540	-1.183	-0.122
-1.247	-1.771	-1.279	-1.757	-1.485	-2.012	-1.010	-0.082
-0.273	-0.140	-3.410	0.361	-0.088	-1.304	-0.430	-0.837
0.400	-1.567	0.287	0.404	-3.505	-3.731	-1.317	-2.013
0.000	-2.496	-1.081	-0.876	-2.106	0.000	-1.281	0.000
0.000	-3.090	0.000	-0.217	0.000	-0.966	-0.933	0.137
0.000	0.000	0.000	-2.575	-1.150	0.000	-1.754	-1.256
-2.535	-2.869	-1.516	-1.280	-0.826	-1.282	-0.890	-0.130
-1.529	-1.528	-0.439	-0.898	-0.730	-0.591	-2.079	-1.361
-2.448	0.341	0.376	-0.369	-1.113	-3.318	-2.137	-1.077
-1.102	-0.578	-1.114	-1.901	-3.966	-0.510	-1.557	-0.513
-2.008	0.578	-2.610	-0.809	-1.997	-0.426	10.483	0.187
-0.429	-1.804	-0.912	-0.870	-3.217	-0.937	-3.421	-2.558
-0.927	-2.855	-0.328	-1.143	-2.534	-1.160	-1.799	0.358
-0.112	0.149	-2.304	-0.236	-1.768	-1.327	13.287	0.256
-1.700	0.708	0.466	-2.002	-3.104	-1.980	-0.538	-2.020

Table35.txt

-1.648	-2.672	-1.903	-2.339	-2.548	-0.296	-0.660	-0.491
-2.400	-3.090	-3.077	-1.421	-1.543	-1.085	-2.489	-1.291
-1.878	-0.499	-1.305	-1.300	-3.622	-1.220	-3.288	-0.495
-2.010	-1.037	-1.006	-2.907	-0.367	-1.048	-1.309	0.358
-1.947	0.017	-4.321	-0.707	-1.447	0.238	-2.722	-0.452
-0.745	-1.092	-0.997	-0.055	-1.968	-1.079	-2.315	-1.184
2.771	8.471	-1.160	2.494	1.925	1.760	6.499	5.324
2.099	3.756	2.378	2.658	0.175	2.116	2.514	-0.072
1.453	-2.208	-0.076	-0.452	0.622	1.461	6.660	1.439
-1.533	-1.603	-4.004	-1.675	-0.812	0.386	-0.396	-1.636
-0.221	1.079	-3.227	-1.931	0.000	-2.746	8.968	-1.173
-1.822	0.000	-1.511	-1.935	-1.393	-1.743	-1.761	-1.279
-2.339	-1.877	-1.684	-2.408	0.101	-0.493	-1.096	-0.817
-0.110	-1.824	-1.036	-0.122	0.640	0.031	-1.508	-0.410
-0.068	-0.992	-0.445	-1.937	-1.005	-1.214	-1.636	-3.116
-0.831	-1.651	-1.958	-3.007	-0.207	-2.006	-1.392	0.373
0.047	-0.592	-4.413	-0.757	-0.276	-1.093	-1.113	-0.532
0.101	0.505	-1.547	-2.017	-3.414	-3.742	-1.375	-0.185
6.139	11.413	-1.370	-1.481	-0.549	-1.039	0.110	0.860
1.799	0.000	0.000	-0.864	0.597	-1.150	2.930	0.000
0.000	0.039	0.324	-0.912	-3.478	0.000	19.066	-0.305
1.025	-3.655	-3.848	-1.238	0.094	-2.579	0.420	-0.220
-0.146	-1.165	-0.137	-0.864	-0.360	-1.696	-0.176	-2.806
-0.724	-1.423	-1.087	-2.246	0.325	-1.400	-3.036	-2.224
-1.165	-1.154	-1.453	-0.675	-1.601	-0.373	-1.937	-0.901
0.614	0.166	-0.297	0.616	-1.375	-0.445	5.544	-1.666
0.022	2.021	-0.031	7.127	-1.189	-1.207	-1.261	-0.328
-2.490	-1.409	-1.978	-0.376	-0.577	-0.897	0.279	-2.492
-1.165	-2.575	-2.035	-0.048	-1.049	0.155	-1.243	-0.537
-0.220	-0.698	-0.358	-0.039	-2.930	-1.499	-1.636	-0.231
0.242	5.000	0.065	9.178	3.163	1.385	1.866	1.653
3.090	0.485	0.952	-1.259	-0.758	3.321	-0.298	3.809
3.874	-1.383	3.132	6.308	-0.922	-1.733	0.232	-1.939
8.842	8.272	10.270	0.191	5.454	0.577	3.738	0.617
-2.059	-1.885	-0.308	4.685	8.039	0.214	-2.370	-1.892
0.582	3.225	4.353	-0.356	-0.012	-0.927	-0.038	2.495
4.277	-2.334	11.909	5.350	11.822	-0.535	5.319	0.739
8.015	-1.591	-0.682	-0.747	-0.409	2.802	11.828	2.871
0.536	8.983	4.258	6.749	-0.673	1.893	5.023	8.054
-0.118	-0.775	-2.591	-1.199	-1.590	-2.930	1.097	-0.265
-1.712	-0.283	-2.334	0.155	-0.422	-3.310	-1.122	0.100
-0.605	-1.561	0.878	0.677	-0.181	-0.589	-3.737	-1.155
-1.790	-2.369	-1.055	-1.337	-0.674	-1.847	-0.055	-1.072
-0.187	1.044	-0.324	-0.362	-2.352	0.264	11.641	-0.077
-1.153	-0.016	0.289	-0.490	-1.545	-1.553	-2.137	-1.168
0.006	-1.061	3.546	-0.707	-0.497	0.692	-0.373	-1.154
-0.043	-1.330	-0.620	0.947	-0.327	-1.675	2.034	4.822
3.417	0.388	3.512	2.923	5.934	0.107	-1.267	1.443

Table35.txt

-0.721	-0.399	-2.608	-0.513	-1.114	0.013	-0.253	-0.037
1.056	0.210	-1.941	-0.247	0.081	-1.031	12.154	-2.035
-1.987	-0.104	-1.674	5.457	-1.690	-0.157	-0.353	-1.432
-2.557	-1.339	-2.789	-1.403	-1.323	0.149	-1.535	-2.478
0.001	-0.156	-2.588	-1.525	-1.313	-3.625	-3.114	0.281
-2.003	-0.660	0.688	-2.630	-0.956	-1.398	-4.730	-0.311
-0.278	-0.676	-0.463	-2.791	-1.532	-0.925	-3.135	-0.940
-1.136	2.817	12.049	-0.472	-2.224	-3.526	-1.156	0.582
-0.061	-1.422	0.691	-2.362	-1.361	-1.012	-0.857	-1.812
1.619	4.520	10.819	8.961	3.339	1.528	8.711	4.333
5.683	4.319	8.647	-0.565	4.492	0.068	-0.200	2.351
2.301	0.903	0.328	-0.885	-0.185	1.974	0.515	0.284
0.298	1.327	-0.882	4.328	-1.158	-1.497	2.556	0.811
1.660	-1.159	2.876	-0.418	0.632	-0.268	-0.377	-0.484
-1.154	-0.101	2.186	-0.268	0.161	-0.264	-0.530	1.163
4.295	12.112	15.574	10.809	9.814	7.429	6.741	0.725
-1.884	0.045	10.364	5.198	3.690	-2.670	5.428	2.322
3.499	-0.429	-0.330	4.124	8.130	13.416	9.686	6.489
-0.551	-2.356	-2.719	-1.192	-1.142	-0.537	-1.615	-0.497
0.400	0.561	-0.527	-0.810	-2.356	-1.896	0.698	-0.582
0.299	0.314	-1.285	-0.249	-1.804	-2.408	-0.329	-2.569
3.721	14.607	7.951	-0.787	2.899	-0.816	1.251	3.907
5.348	1.880	4.910	2.546	0.972	-1.886	6.912	2.719
1.465	-0.057	3.019	0.757	10.113	5.163	11.441	-1.093
-0.938	-2.180	-3.124	0.087	-0.317	-0.532	-0.950	-0.747
-1.487	-0.818	-1.421	0.435	1.975	-0.863	-3.015	0.639
1.479	-0.439	-0.421	-0.058	-3.410	-2.257	-1.803	0.191
9.603	2.015	7.565	2.362	3.533	5.018	5.593	3.090
6.075	4.346	4.888	0.019	-0.332	3.875	10.440	3.517
5.124	5.641	3.367	7.342	11.475	0.307	9.002	7.832
8.506	16.979	1.952	4.280	8.100	3.441	-0.119	6.128
3.411	0.334	-0.706	3.090	3.835	7.663	0.602	1.267
1.887	1.067	2.254	3.345	7.084	9.680	7.251	6.042
-2.086	0.033	0.302	-0.850	-2.472	1.230	-2.080	-0.570
0.162	-0.581	-0.594	-0.288	0.286	-2.317	-1.623	-1.092
0.523	-1.884	-0.145	-0.354	-0.749	-1.077	0.302	-1.603
-3.480	-2.126	-2.817	0.571	-0.009	-2.078	-0.591	0.527
0.650	-0.839	-1.684	-0.247	-0.102	-1.805	-1.923	-0.049
-0.471	-0.230	-2.268	-0.838	-1.926	-3.098	-3.155	-0.558
-1.428	0.628	-1.052	-1.298	-0.336	0.505	0.985	0.554
1.424	0.542	0.478	0.402	-1.937	-1.245	-2.550	-0.022
-0.893	-0.959	-0.508	0.433	-1.083	-0.678	-0.102	0.255
0.863	-2.704	0.754	-2.439	5.423	-0.043	-1.469	5.065
-0.354	5.743	10.251	-0.714	4.950	8.129	10.644	3.394
1.685	-2.016	2.007	7.707	6.577	12.763	10.727	9.176
6.675	4.710	12.562	0.496	-0.885	-0.705	1.771	3.479
4.173	0.234	11.257	-0.484	0.456	0.969	3.408	-0.051
-1.365	-0.987	4.479	0.454	9.339	-0.964	2.220	5.747

Table35.txt

0.171	2.172	2.773	-0.895	0.581	2.544	-1.228	3.516
2.998	5.200	9.100	1.338	-1.462	8.590	11.638	5.051
4.327	0.364	-0.698	-0.177	0.662	-1.655	-1.113	-1.787
0.802	3.106	13.262	13.933	5.420	2.711	6.071	3.892
5.241	0.807	7.417	-0.339	0.072	0.496	3.780	1.865
-0.254	4.198	-0.362	-1.879	4.684	-1.159	3.078	9.117
-1.029	-0.390	-1.348	-1.740	2.017	-1.327	0.148	-0.899
-1.852	-1.084	-0.576	-0.861	-0.046	-3.867	-1.240	-0.724
-1.008	-1.339	-2.314	-0.370	-1.059	-1.211	-0.285	-2.624
-1.844	-1.715	-2.223	-0.990	-1.482	-0.832	-3.406	-0.857
-0.668	-0.468	0.057	1.391	-0.784	0.497	-1.402	0.164
-0.098	0.283	1.098	-0.842	-2.166	-0.970	-0.802	-2.317
0.080	-2.223	-1.744	0.067	-0.329	-1.245	-0.196	0.410
-0.072	-0.363	-0.222	-0.147	0.868	0.133	-0.195	0.149
-0.227	-0.830	0.000	-4.584	0.047	-2.024	-0.560	-0.779
-0.337	3.536	10.724	5.439	4.286	1.247	0.864	3.090
3.783	0.206	7.337	-0.812	5.107	0.048	4.354	1.900
1.245	1.446	2.979	13.136	14.923	9.999	0.982	7.832
0.042	-1.522	-1.760	-0.711	-1.944	-1.308	-1.203	0.662
-1.063	-1.854	-3.056	0.158	-1.735	-2.000	0.783	-1.087
0.432	0.242	0.930	-2.138	-0.842	-2.249	-1.853	-1.514
6.117	8.937	10.486	-0.323	0.399	4.023	5.037	0.000
0.000	5.536	5.835	-1.336	1.494	-1.358	1.870	3.101
0.995	2.117	-0.327	7.768	10.536	6.123	11.097	7.995
-0.684	0.681	-0.068	-0.874	-1.006	-1.031	-0.806	-1.802
-0.742	0.588	-1.374	-0.346	-0.537	-1.928	-2.388	-1.001
0.715	-0.431	-0.350	-0.489	-2.725	-1.201	-1.767	-0.823
-1.568	-1.390	-0.509	1.223	-1.396	-0.934	3.732	0.531
-0.388	0.490	-1.072	-0.137	0.984	-0.134	8.117	-2.563
-1.147	-0.522	-0.254	-0.229	-1.512	-1.117	0.476	-0.691
-0.886	-2.312	0.124	-1.720	-1.543	-0.159	-0.929	-3.534
-0.818	-1.192	-0.415	-1.069	-0.375	-0.455	1.124	-0.509
-0.264	-1.569	-0.524	-2.191	-1.942	0.365	-2.337	-0.594
-0.735	-2.374	-0.628	-0.886	-0.298	-0.031	0.072	-0.766
-1.158	-1.339	-0.946	-0.540	0.159	-2.039	-0.551	-2.057
-0.674	-2.619	-0.852	-1.476	-1.954	-1.441	-1.401	0.257
0.082	-0.092	-0.557	-1.814	-1.180	1.043	-0.861	-2.444
-0.293	-2.281	-0.101	-0.308	-1.255	-1.290	-0.767	-0.901
-0.526	-1.501	-0.414	-0.598	-0.579	-0.999	0.278	0.034
6.500	2.232	8.827	5.052	-1.358	-0.083	2.968	3.112
6.698	-0.101	5.810	-1.481	1.869	6.706	-2.716	0.447
2.533	-0.172	6.238	10.480	4.854	-0.917	-0.951	-5.678
3.415	10.664	12.168	8.832	2.622	5.194	5.883	3.090
0.000	8.399	4.642	4.359	6.094	0.000	7.477	0.702
0.446	3.785	4.056	5.141	9.728	5.758	5.557	-0.909
0.322	-0.627	8.821	-0.716	1.683	-2.140	0.235	1.160
0.477	0.342	0.497	0.851	0.157	2.622	-3.133	-0.703
0.521	-1.545	-0.925	1.527	1.351	-1.198	-2.372	0.761

Table35.txt

-0.807	-0.464	5.407	0.000	-0.969	0.000	4.365	0.000
0.000	0.771	-1.678	3.176	4.003	0.262	-3.023	1.081
0.215	0.000	0.000	2.843	-0.682	1.780	0.674	0.000
11.114	5.934	0.303	5.539	4.669	9.381	-2.280	4.136
6.758	6.798	6.069	4.127	3.474	3.356	9.368	-0.948
1.296	5.101	6.143	7.261	14.841	-0.516	7.352	-2.054
2.798	10.452	11.215	-0.367	-0.054	-0.463	-0.034	4.473
4.593	4.343	10.256	0.000	2.857	-0.850	5.283	0.891
-0.126	-0.765	-1.048	0.087	-2.481	3.212	-1.654	-0.828
-2.197	-2.431	3.221	-1.451	-0.255	0.651	3.312	0.019
3.613	-2.253	2.250	-2.768	-0.353	0.818	0.745	-1.908
-0.612	0.636	-0.900	-1.410	-1.875	0.555	1.210	-1.863
4.044	7.253	0.000	3.287	3.772	0.690	0.000	0.000
0.000	2.031	4.345	1.724	2.022	2.546	3.090	1.263
4.211	3.504	0.000	0.366	3.989	7.380	5.939	2.889
1.224	10.684	12.357	0.222	2.575	0.119	-1.388	5.506
4.795	-1.206	6.053	1.191	1.280	-1.527	-1.060	-0.488
1.238	-1.638	0.916	-3.505	0.082	-1.467	2.692	0.610
4.926	6.454	5.163	0.177	3.168	0.311	1.430	0.000
4.369	4.794	2.136	1.677	4.287	-0.061	5.616	5.113
2.407	1.265	2.349	4.702	11.565	7.120	11.791	6.987
-1.897	-1.319	-0.896	4.597	0.000	-1.509	-0.374	0.000
0.000	0.000	0.000	3.282	-0.555	-1.490	-0.993	-0.436
-0.043	2.019	0.000	-1.526	-3.372	-1.577	11.478	0.000
4.026	8.165	0.513	1.551	0.971	-0.319	-0.839	3.464
6.619	-0.179	-0.519	-1.809	2.682	1.579	7.941	-0.519
1.137	1.052	-1.817	1.004	9.946	8.511	14.389	-1.632
3.090	1.572	4.813	-0.480	3.499	3.658	4.967	2.166
4.369	3.921	1.226	2.318	-0.309	3.400	8.883	3.133
1.149	2.774	3.750	6.627	5.881	4.706	2.754	0.021
4.066	13.795	-0.232	5.908	2.897	1.119	4.079	4.357
4.363	1.978	-1.466	3.090	2.977	7.292	5.976	0.000
4.309	-0.993	0.000	-1.040	1.676	6.659	-1.731	6.819
4.072	11.339	0.664	9.063	0.044	3.745	6.842	2.406
6.630	2.036	2.276	3.003	4.573	2.005	-0.130	1.071
-1.307	7.977	2.400	6.399	5.476	8.752	6.651	-0.330
5.308	8.379	-2.094	0.263	0.982	-1.726	2.309	3.279
5.931	-0.930	5.086	-0.142	0.068	-1.643	-1.473	-1.127
5.335	-2.118	0.452	2.958	9.128	-1.478	1.123	4.877
0.937	0.808	6.175	-2.306	4.711	0.754	1.877	4.836
5.496	-1.355	-2.154	-1.177	-0.380	-0.139	-0.900	-1.238
1.557	0.173	2.441	-0.396	-0.541	-0.369	-0.487	3.021
-0.922	0.015	-1.749	-1.256	0.425	-1.102	0.118	-0.367
-0.305	-0.349	-0.656	-0.328	1.416	-1.939	-2.122	-0.870
-0.272	-0.024	-0.702	0.002	-0.371	-2.612	-1.545	-2.238
0.402	-1.974	-2.900	-1.105	-3.500	-2.266	-0.343	0.001
-2.779	-0.266	-2.314	1.446	4.562	-2.583	-0.327	-0.332
-3.195	-2.398	-1.747	-2.458	-1.773	-1.877	-1.223	-3.090

Table35.txt

-3.552	0.120	-3.016	7.140	-1.966	0.332	-0.349	-0.192
-2.015	-0.225	-1.155	-0.268	-0.389	-2.128	8.323	-0.171
-1.967	0.361	-0.534	8.810	8.693	-0.766	-1.804	-0.773
2.799	11.456	14.588	6.044	7.385	0.537	4.663	3.817
9.306	6.162	7.061	2.067	-3.700	6.285	6.498	3.053
3.093	5.341	0.916	5.458	5.144	5.976	4.791	7.060
3.591	7.725	12.984	-1.591	9.955	3.901	-1.674	3.049
6.867	0.864	4.829	4.226	0.414	3.583	0.711	0.835
6.077	8.085	2.420	4.428	3.704	0.838	2.177	4.999
-2.284	-0.874	-1.572	-1.394	-0.859	-0.118	0.153	-0.603
-0.685	-0.905	-2.156	-0.557	-3.903	-0.938	-2.601	-1.447
0.694	-0.877	-0.758	-0.144	-3.714	-1.518	-2.391	-0.101
0.000	0.000	0.000	-0.131	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.092	-1.477	-0.420	-0.610	0.000
0.000	0.000	1.607	0.312	-1.161	-2.077	-0.704	0.000
5.731	10.093	-1.404	1.336	-2.480	-0.514	-2.159	-1.250
-0.841	0.756	-1.389	-0.583	-0.185	-1.244	-1.453	-0.284
0.343	-1.030	0.094	-3.090	-0.746	-1.451	-3.352	0.537
3.884	7.687	8.767	-0.087	1.600	7.966	5.274	6.038
2.436	-2.297	2.255	3.141	1.408	6.262	12.843	7.893
1.497	4.508	5.636	5.510	12.659	9.286	13.585	6.049
1.728	2.212	-0.134	-0.797	4.101	3.940	0.997	4.960
7.225	0.667	5.609	1.378	0.280	-0.752	3.423	-0.880
-1.294	5.330	5.695	1.451	4.446	3.093	1.931	2.604
-1.605	-1.485	-2.701	-1.209	-2.764	-1.462	-1.970	-1.330
-2.020	-1.704	-0.743	-0.270	0.007	-1.248	-1.338	0.077
-0.015	-0.213	-0.872	-1.136	-1.798	-0.342	-0.572	-1.969
6.240	10.354	-0.338	7.269	9.552	7.972	7.256	-1.328
-0.403	0.447	-1.936	4.941	3.625	11.692	11.488	0.273
-0.195	7.166	0.093	-0.771	-0.462	7.708	11.629	9.132
3.126	6.572	-1.266	-1.372	8.963	-0.781	0.309	-1.606
1.039	1.156	-0.199	-0.982	-1.718	2.627	3.897	-1.287
-0.486	0.751	-1.372	-1.998	-0.288	-0.499	-2.405	-2.653
-0.347	-1.564	-1.077	-1.961	-2.195	0.097	-1.758	-1.966
-0.087	0.361	-1.372	-0.126	0.633	-3.067	2.524	-1.846
-2.434	-0.516	-2.672	-1.328	-2.234	-1.471	-2.714	-1.224
1.094	2.210	-0.748	-2.198	-1.791	1.755	1.137	2.437
-0.689	0.062	-1.966	-0.874	4.086	0.386	-0.448	0.000
-0.231	-1.621	0.524	0.685	-0.164	0.231	-0.217	-3.031
-1.225	-1.452	-1.389	-1.743	-2.473	-0.661	-0.455	-1.091
1.880	-0.925	-1.177	2.641	1.981	-0.777	-2.350	-1.732
-0.894	-0.388	-2.120	0.683	-2.224	-0.959	-1.792	-2.652
-3.619	0.875	0.512	-1.316	0.079	1.747	-2.074	3.281
6.065	1.990	1.939	3.503	1.996	0.347	-2.138	2.019
-0.264	2.392	4.118	1.441	7.066	-0.756	-1.398	3.973
-1.068	-0.473	-2.054	-1.914	5.563	0.642	5.081	0.000
3.090	-0.117	3.880	-2.183	-2.090	1.571	1.612	-0.468
0.457	-1.342	0.794	10.654	-1.998	-2.515	12.285	1.496

Table35.txt

-1.006	6.036	1.442	0.822	5.566	-0.215	-0.902	3.023
3.090	1.214	-0.322	5.638	-1.790	2.165	5.514	-3.161
-2.446	-2.320	4.117	-0.682	-1.983	4.794	6.712	3.090
4.556	8.279	8.315	2.359	6.638	-0.786	1.986	3.340
7.265	0.164	4.427	-1.641	1.234	8.291	2.419	1.863
-0.045	0.634	-0.922	6.913	-0.641	9.060	3.880	8.074
0.033	6.337	0.000	6.226	0.000	-0.733	3.449	0.000
0.000	0.000	0.000	-1.642	4.020	9.060	6.439	1.076
0.641	0.497	3.285	6.048	16.348	5.597	0.532	0.000
3.082	3.174	0.000	-2.753	0.000	0.000	-2.103	0.000
-0.075	-1.195	-2.167	0.000	3.268	-1.772	0.107	-0.006
-0.420	1.207	0.000	4.797	5.283	-0.503	-2.513	0.000
0.486	1.559	-0.708	-0.796	3.626	-0.584	1.855	1.101
4.564	1.794	1.065	1.479	2.961	3.372	-0.764	3.505
1.374	-2.612	0.106	-0.689	-1.243	4.440	1.717	-0.374
-3.261	-3.274	-2.157	-0.977	-0.073	0.402	-2.000	0.581
-1.165	0.618	-0.301	0.451	-1.800	-2.501	-1.505	-0.430
-1.189	-0.864	-1.277	-0.978	-0.716	-1.756	-1.541	-2.906
-1.151	2.184	-1.353	-0.694	-0.491	-0.111	-0.385	0.000
0.154	0.309	0.988	1.262	0.218	-1.622	-1.768	-0.467
-1.879	-0.261	0.000	-1.751	-1.297	-1.214	-0.229	-1.157
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.554	3.521	3.943	0.162	-0.948	-1.266	5.399	4.354
4.166	4.396	3.916	0.226	1.488	-2.237	1.539	3.221
-0.007	1.218	-1.944	2.262	7.149	1.940	0.877	5.077
-1.524	0.651	1.113	3.078	0.282	-0.126	1.304	-1.396
-1.152	1.246	-1.628	0.644	1.988	-1.927	-1.967	1.160
2.992	-0.527	1.030	-1.939	-2.110	-0.516	-0.910	0.144
0.251	1.699	-1.225	-1.665	-0.885	-1.578	-0.799	-1.093
-1.315	-0.110	-1.164	0.204	-0.538	-2.447	-2.183	-0.768
-0.453	-1.618	-1.305	-0.697	-3.687	-3.152	-1.394	-0.990
-1.028	-2.555	-1.863	-1.338	-1.185	-1.547	-1.303	-0.946
0.551	-2.128	-0.325	-1.438	0.980	-1.386	-1.425	-0.109
-1.413	-0.154	-0.969	-2.214	-3.272	-2.803	-0.359	-1.839
-1.235	-2.870	-2.581	-0.585	-2.195	-2.501	-0.694	2.068
0.144	-0.250	-0.417	1.008	0.487	-1.567	-0.592	-1.181
1.516	0.360	0.588	-2.731	-2.483	-1.139	-1.574	-1.572
-1.774	-1.403	-2.107	-2.231	-0.304	-2.097	6.694	-1.170
-1.469	-0.829	-2.213	-0.683	0.036	-1.555	-1.213	-0.333
-1.859	0.026	-0.660	0.611	-2.447	-2.800	-1.738	-1.233
-1.124	-3.077	-2.540	-1.676	-0.948	-0.443	-0.280	0.718
-0.054	-0.916	-0.584	-0.171	-0.299	-0.887	-0.823	-1.192
-1.665	-1.514	-2.354	-2.629	-2.799	-0.454	-3.487	-0.447
-1.177	-0.126	-1.140	-2.974	-2.164	0.468	-1.341	0.014
-0.086	-0.257	-0.284	0.778	0.285	-0.650	9.148	0.507
0.265	-1.434	0.824	-0.843	-1.661	-1.502	-0.993	8.462

Table35.txt

-1.236	-1.198	-1.902	-2.240	-2.683	-0.295	-2.408	-1.375
-0.251	-2.101	-0.171	-1.614	-1.235	-0.881	0.357	-0.446
-2.215	0.562	-0.663	-1.607	-2.041	-1.206	0.523	-2.485
-2.192	-1.964	-1.006	-2.958	-0.158	-0.708	-0.086	-3.188
-0.039	-0.312	-0.769	0.571	-1.231	-2.419	-1.502	1.823
0.389	1.212	1.584	-1.403	-2.918	-0.824	0.002	-3.129
-0.658	-0.150	-0.592	0.198	-1.457	-0.387	-0.080	0.180
1.087	-1.084	-1.799	-3.169	-1.340	-1.284	-1.846	-1.465
0.240	-0.631	-0.158	-2.751	-4.465	-1.869	-3.207	-1.430
-1.170	-2.645	-3.240	-1.250	-0.523	0.448	-1.924	-1.634
0.001	-0.870	-3.235	-0.206	-1.878	-0.589	6.486	-2.167
-2.407	0.022	-0.379	-2.196	-0.877	-1.897	-2.119	-1.116
-2.334	-1.657	-0.576	-0.366	-1.901	0.224	-1.962	-1.379
0.921	-0.448	-1.483	-0.181	-1.445	-1.379	-2.301	-0.641
-1.299	-1.172	0.197	-2.938	0.428	-1.466	6.378	-1.026
0.150	-1.761	-1.770	-2.297	-2.778	-2.084	-0.984	0.239
-1.446	-1.561	-2.721	-0.622	-0.646	0.900	-2.192	-1.137
-2.224	-1.269	0.393	-2.833	-0.997	-1.410	-2.479	-1.002
-0.082	-2.179	-1.154	4.823	-3.947	-0.681	6.553	-0.300
0.136	-0.903	-2.127	0.368	-0.895	-2.381	7.430	-1.114
-1.417	-0.820	-0.585	-1.155	0.382	-3.097	-2.407	-0.607
0.676	-3.032	-1.870	-2.206	4.416	3.067	4.865	-0.602
-1.180	0.010	0.304	0.732	-0.476	-2.685	-0.860	-2.270
1.066	0.211	1.374	7.496	10.689	-4.624	4.430	0.702
-0.366	-0.171	-1.332	-2.063	-0.328	0.000	-0.650	-0.144
0.000	0.000	-0.176	0.000	0.000	0.178	-1.996	-0.378
0.000	-0.314	0.000	-2.443	-1.094	-0.572	-2.612	0.474
2.512	7.957	8.167	1.875	-0.336	1.036	-1.725	0.000
2.166	0.287	-0.029	-0.388	1.103	1.004	-1.421	0.572
0.597	3.561	0.000	-1.889	0.471	1.713	11.956	3.790
0.744	-0.784	-1.836	-0.445	-0.208	-0.442	-2.305	0.000
0.000	-1.118	0.120	-1.256	-1.087	-0.654	-0.805	-0.245
0.000	-0.497	-0.877	-3.003	-1.886	-1.436	-2.678	-1.942
-1.603	-2.203	15.611	-0.496	7.595	4.719	6.999	3.584
0.079	1.203	-2.435	0.686	1.818	-2.809	2.659	-0.460
5.759	1.815	-3.604	-0.825	-2.185	-0.721	-0.052	1.698
-0.790	0.238	0.440	2.379	0.362	-2.389	0.651	0.000
-0.217	0.000	0.853	0.000	0.000	-1.869	0.000	-1.700
0.163	0.137	-0.445	-0.284	-1.559	-0.256	1.176	-0.404
-0.946	-0.414	-2.934	-0.606	-1.013	-2.748	-0.664	-0.214
0.041	-1.565	-1.519	-2.236	-2.088	-2.679	-0.003	1.348
2.466	-0.947	-2.313	-2.769	-2.752	-1.054	-2.928	-1.213
0.321	-0.415	0.969	0.975	0.000	-0.054	1.208	0.000
0.000	-3.090	-0.178	0.123	0.000	-0.139	-2.401	-0.226
-1.318	-1.010	0.000	1.087	1.550	-1.489	-2.746	-0.174
-1.302	-1.513	-3.974	-2.223	-0.549	-1.243	-2.997	-1.224
0.301	-1.475	0.203	-0.628	0.517	0.156	-1.377	-0.457
-0.948	-2.171	-1.099	-1.277	-1.835	-2.745	-3.282	-2.301

Table35.txt

-0.571	1.293	0.000	0.490	0.453	1.064	0.460	0.000
0.000	-0.592	-0.936	0.000	0.000	-1.187	-0.485	-0.910
0.231	-0.378	0.000	-0.076	0.586	-0.361	1.254	1.406
0.959	1.239	0.206	0.000	1.835	0.000	0.000	0.000
0.000	-0.442	2.952	0.000	0.000	0.372	1.298	0.000
2.647	3.175	0.000	0.912	0.827	1.066	1.486	-0.705
1.225	8.406	10.348	3.090	0.956	3.090	6.838	0.000
4.062	0.121	-0.638	0.106	1.289	5.137	5.285	6.810
5.431	1.700	4.805	1.481	2.386	3.847	7.797	3.073
-1.021	-1.089	-4.623	-1.746	-0.718	-2.668	-1.126	-0.257
-2.182	-1.135	-0.486	-1.342	-1.417	-0.463	-2.146	-2.192
-2.646	-0.937	-1.456	-1.674	-0.422	-0.947	-1.025	-0.164
0.000	-0.592	0.000	0.000	0.218	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	-0.823	0.000	-0.736	0.000	0.000
-1.407	-0.308	0.001	-1.373	-1.141	-1.802	2.713	1.360
1.159	0.386	-1.200	1.354	-0.389	4.812	3.841	0.111
-0.345	0.676	-0.155	-1.325	1.429	-1.320	2.988	-2.147
0.642	-1.148	-2.761	-0.519	-0.676	0.896	-1.834	-0.942
-0.577	0.212	-1.637	-0.969	-1.577	-0.581	0.610	0.875
-0.430	-0.510	-1.529	-1.654	-3.981	-3.034	-3.383	-0.525
-0.124	-1.461	-2.079	-1.170	-1.546	-1.955	-0.748	-0.557
-1.260	-0.359	-1.253	-0.187	-0.452	11.139	-1.905	-2.497
0.044	-3.480	-0.931	4.998	3.062	-1.394	-0.735	-1.221
-0.988	-2.627	-0.418	-0.608	-2.260	-1.263	-1.135	-1.663
-0.276	0.712	0.118	-0.641	-1.040	-2.124	-1.384	-0.729
-2.592	0.288	-0.530	-2.450	-1.918	-0.637	-0.098	-1.772
-0.352	-1.009	-1.074	-0.625	-0.330	-0.694	-3.325	1.593
0.025	0.013	-1.594	-0.398	-1.319	0.602	-1.737	-0.818
0.247	-0.357	-1.365	-0.347	-2.064	-2.301	-2.596	-0.418
-2.110	-2.796	-2.976	-4.729	-2.252	-0.296	-2.159	-0.540
-2.702	-1.689	-2.426	0.833	-1.710	-0.607	-2.783	0.825
-0.694	-1.174	1.394	-0.973	-1.923	-2.515	-0.595	-0.997
0.000	-0.536	-0.117	-1.093	-0.144	0.000	0.000	0.000
0.000	-3.090	0.245	0.000	0.000	0.050	-0.718	0.000
0.000	0.000	0.000	-0.790	1.364	-1.667	-0.334	0.000
-1.255	-1.713	0.000	0.478	-0.480	1.898	0.000	0.000
0.000	-0.553	0.487	0.000	1.876	-0.683	-2.145	-0.445
-0.027	-1.793	-0.628	0.325	-3.340	0.324	-2.038	-1.439
5.697	-1.876	-1.335	-1.013	-1.376	-0.055	-1.003	-1.500
0.814	-0.104	-0.690	-1.231	-1.556	1.117	-2.070	-1.128
-1.418	-0.502	-0.615	-3.221	-2.502	-0.778	-0.692	-1.394
2.972	7.503	11.212	4.338	3.424	3.083	0.000	0.000
5.000	5.921	8.833	0.694	6.499	11.400	10.680	-0.296
-0.455	-2.154	0.000	-1.703	-1.584	-1.244	6.575	1.208
-0.874	-0.516	-1.588	-0.274	-1.757	0.000	-0.269	-0.004
0.013	-2.687	-0.456	0.145	0.527	-2.686	-1.052	-0.525
-1.256	-0.219	-0.455	0.583	-1.480	-2.292	0.320	-0.241

Table35.txt

0.112	-0.546	-2.115	-0.852	-0.907	1.105	-0.241	-0.854
-1.529	-0.238	-2.209	0.364	-0.567	5.833	-0.992	-3.090
-0.977	-0.530	-0.745	-1.288	-2.259	-2.305	-0.172	-2.485
8.646	6.847	5.690	3.012	5.167	2.652	-1.770	3.090
3.090	3.497	5.343	3.036	3.262	4.871	7.586	5.195
6.117	0.000	1.733	5.311	12.364	-1.231	6.974	7.253
0.000	0.000	0.051	-1.234	-3.090	0.137	0.000	0.000
0.000	-0.378	0.000	-1.316	0.000	-0.532	0.000	0.000
0.204	-0.823	0.000	0.137	-0.744	0.420	-1.060	-1.214
3.218	5.167	5.492	0.088	0.348	7.551	6.607	0.000
4.362	1.790	7.387	-0.562	2.827	2.559	0.884	6.482
5.732	-0.807	4.316	2.457	3.797	2.396	-1.150	8.081
2.403	6.465	2.976	2.190	0.292	-0.608	6.230	3.888
1.666	0.137	-0.821	1.483	5.042	-0.675	0.263	0.721
3.207	4.429	3.485	-0.501	2.257	3.781	-0.395	-0.048
1.648	4.046	0.958	-4.996	-0.171	-0.179	0.000	0.561
1.032	-2.939	-1.423	2.461	-1.242	1.845	8.462	-0.988
4.306	5.224	0.000	2.037	4.505	2.016	0.331	-1.363
-0.613	-3.334	-2.670	-4.084	0.119	-1.515	0.076	-2.667
0.291	-0.423	-2.132	-1.212	-2.532	-2.191	0.462	0.095
-0.036	-2.350	-1.013	-1.202	-3.751	-0.403	4.750	-1.294
2.142	5.207	8.878	2.994	1.129	-0.535	-0.117	0.745
-0.189	0.142	0.931	0.382	2.902	0.770	-0.916	0.843
2.918	1.808	1.036	6.174	9.469	1.039	-1.932	-3.130
0.398	3.655	0.001	0.817	5.007	-0.026	-1.429	2.085
1.591	1.721	3.298	2.184	-1.012	1.776	1.193	0.927
-0.031	-0.290	2.102	-1.361	0.144	0.287	1.195	3.053
5.955	0.168	-1.617	3.934	0.221	-1.744	-1.611	-0.405
0.106	-0.428	-0.961	-0.725	-0.668	11.220	7.798	0.467
0.220	-0.873	0.485	-0.417	-2.358	-1.926	-0.801	-1.125
-0.500	-0.855	-3.163	-2.176	-0.133	0.027	-1.781	1.205
-0.003	-0.344	-0.465	0.582	-1.640	-1.231	-0.297	-0.693
2.513	-0.479	0.625	-2.884	-0.903	-0.143	-1.023	-0.910
-0.416	-0.588	-2.555	-2.654	-1.363	-0.700	-0.289	-3.033
-1.281	-0.175	-1.154	-0.372	0.220	-0.291	-1.258	-1.909
-0.495	-1.706	0.820	0.268	-1.326	-0.093	-0.152	-2.257
-0.482	13.006	0.000	12.908	-0.432	0.000	0.000	3.090
4.339	4.382	3.090	2.475	0.872	-0.812	11.842	0.294
2.129	0.000	-2.706	8.969	-0.851	11.942	12.077	-1.228
-0.641	-2.557	-1.846	-2.270	-2.729	-1.227	0.000	-0.894
-0.627	0.041	-1.067	-0.321	0.228	-1.017	1.324	-2.946
0.373	-0.342	-4.608	-1.038	-2.817	-1.577	-2.257	-0.959
-0.947	-1.800	-1.680	-1.916	-1.452	-2.133	-2.181	0.460
-2.487	-1.349	-1.976	-0.036	-3.090	0.027	-1.691	0.528
-1.028	-1.022	0.000	-0.685	-2.176	-1.677	-3.429	-1.923
2.996	9.853	-1.752	3.596	-1.423	0.276	-1.237	3.314
-0.449	-0.660	-1.494	0.184	0.410	-2.272	-4.431	1.401
0.784	0.385	0.114	-0.118	-1.929	0.153	-0.724	6.127

Table35.txt

-0.713	-3.639	-1.800	-0.535	-0.710	-0.934	-1.529	-0.215
-1.279	0.002	-1.577	0.816	-1.962	-2.286	9.675	-1.992
-2.170	-0.407	0.020	-1.957	-1.070	-1.135	-2.165	-1.837
1.028	0.543	-1.232	-1.416	-0.559	-0.559	-0.701	0.233
0.730	-0.014	-2.223	-0.294	-0.654	-0.115	-0.900	-2.837
-0.427	-0.593	-1.562	5.940	-3.478	-1.324	-3.723	-2.696
-0.914	-1.973	-4.568	-2.782	-1.718	-2.768	-1.453	-2.878
-0.370	0.419	0.065	-0.058	-1.456	-1.889	4.930	0.158
0.262	0.697	0.209	-1.840	-4.055	-2.700	-1.457	-1.467
1.633	-3.166	-2.315	0.193	-0.650	0.100	-0.219	-0.874
-0.494	-0.921	-1.752	1.596	0.550	-0.141	-2.608	0.266
-0.472	-0.618	-0.594	-3.435	-2.116	-1.567	-2.352	-1.140
0.348	1.893	-3.130	-1.452	-1.775	0.000	-0.507	0.000
0.706	-0.910	-3.239	0.050	0.000	-0.204	1.954	-0.736
0.000	-0.975	0.165	-0.915	-1.230	-1.946	-3.620	-1.853
0.000	-0.261	-1.280	-0.144	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	-0.606	0.000
0.000	0.000	0.000	0.000	1.468	0.000	0.000	0.000
-1.399	-1.912	-1.191	0.870	-0.770	3.503	3.337	2.306
-0.204	-0.861	-0.856	0.543	0.608	4.705	0.568	0.154
-1.361	-0.796	2.490	-3.298	-0.552	2.470	-0.844	5.073
0.816	-1.253	-2.286	-1.338	-1.387	-1.011	0.075	-0.616
-1.904	-0.191	-2.005	0.062	-2.133	-2.339	-2.460	-1.742
-1.019	-1.419	0.378	-0.930	-0.690	-1.527	-2.259	-3.333
2.168	3.952	-1.314	1.968	3.375	-0.481	1.504	-0.910
4.569	-2.181	-0.562	1.061	2.669	1.059	-1.086	-0.769
1.359	1.938	3.118	0.374	4.755	2.780	11.581	6.781
-1.959	-1.568	-1.482	-2.010	-2.321	-2.461	-0.664	-0.118
-1.073	-1.726	-2.988	-2.375	-0.997	-1.385	-1.165	-0.370
-1.870	0.355	-1.075	0.590	-1.014	-0.980	-2.160	-0.884
-0.678	-1.529	-0.294	-0.758	-1.896	0.844	-0.127	-0.338
0.220	0.903	-0.692	1.631	-1.812	-0.113	0.806	-0.759
-1.600	-2.325	0.735	-1.169	-0.408	-2.841	-0.268	1.331
-0.564	0.735	0.796	1.655	0.669	0.342	-0.102	0.000
0.000	0.959	-0.749	0.551	0.217	-0.562	-3.168	0.000
-0.961	-0.576	0.969	3.857	1.046	-1.991	-1.752	-1.337
-0.615	-2.052	-2.475	-1.539	-1.699	-0.342	-1.439	0.652
1.085	-0.210	-2.714	-3.111	-0.996	-0.704	-2.444	2.439
1.986	-1.450	-0.868	5.689	7.658	0.470	-0.652	-0.706
7.226	3.325	4.119	-0.887	2.547	3.415	-1.889	0.362
0.000	2.327	0.364	1.581	2.132	5.245	7.626	-1.298
-2.456	-2.534	0.717	6.299	11.235	5.124	6.163	0.006
2.973	1.328	14.931	0.005	2.425	0.770	-0.307	5.136
3.540	0.179	3.576	6.042	4.207	9.572	0.092	-1.372
0.448	-1.159	5.735	-3.749	-0.440	4.490	2.479	9.607
0.848	-2.509	-2.275	-1.978	-2.597	0.164	-0.713	0.251
-1.528	-0.032	-0.208	1.676	-1.463	0.158	-2.156	0.287
0.029	1.144	-0.225	-2.005	-0.726	-1.726	-0.600	-0.144

Table35.txt

-0.144	-1.654	0.104	-0.250	-0.783	0.428	-2.529	-0.683
-0.771	0.455	-1.067	-0.633	-0.345	-2.222	-1.039	0.419
-0.896	0.588	0.149	-0.515	-0.924	-3.136	-1.186	-1.851
-2.027	-2.278	-2.782	-0.771	-2.451	-0.378	-2.195	0.050
-1.173	-2.939	-0.771	-0.942	0.512	-2.085	-1.953	-0.784
-3.090	-0.674	-0.855	-0.832	-3.442	-1.051	-2.005	-1.592
-2.430	-0.775	-1.692	-2.572	0.045	-0.717	2.673	0.745
0.296	-1.591	-1.324	-1.575	-1.031	-1.468	-1.595	-0.154
-0.702	-3.011	-1.073	-0.706	-2.025	-1.985	-2.114	-0.881
0.804	-2.147	-2.969	-0.863	-0.181	-2.450	-0.551	-1.284
-0.809	-0.924	-1.577	-1.214	-2.618	-1.038	-1.105	-0.355
-0.479	-1.055	-0.228	-2.393	-1.667	-1.786	-2.575	-0.285
-0.839	-2.040	-1.443	-1.166	-3.526	-0.168	-0.234	-1.967
-2.126	-0.575	-0.008	-3.090	-2.966	-1.738	-1.652	-1.423
-0.202	0.406	0.627	0.276	-1.916	-1.070	-1.550	-1.122
-2.158	-1.943	1.268	-0.049	-0.591	-1.188	3.054	0.000
0.000	-1.167	-1.158	0.000	3.090	-1.946	-2.246	-0.705
0.000	-0.276	-0.375	-1.674	-1.815	-2.180	4.592	0.000
1.302	0.713	-1.038	-1.415	-0.400	-1.358	-0.751	-0.475
-0.763	-4.484	-2.605	-0.226	0.625	-2.076	-2.666	0.341
-0.537	-0.118	-0.501	0.670	-1.436	-2.325	-3.049	0.448
0.000	0.309	-1.759	-2.555	0.000	0.000	0.161	0.000
0.651	0.000	0.865	-0.217	0.000	0.748	-0.293	0.000
-1.169	0.000	0.000	-1.761	-0.727	-1.975	-0.998	0.000
-0.125	-1.711	-0.321	-1.916	-0.395	-0.202	0.290	-1.304
-0.781	-1.461	-0.032	-2.824	-0.808	-0.357	7.200	8.041
0.413	-1.359	0.824	0.103	0.368	-1.071	-0.501	0.232
-1.629	0.086	-2.534	-0.712	-1.509	-0.689	-1.881	-1.132
13.795	17.790	1.401	-2.489	1.711	0.801	9.862	13.954
-2.094	-0.738	-0.217	-0.421	-0.206	-1.865	-1.920	0.775
-1.448	-0.437	-0.174	-1.395	0.391	-1.885	-1.245	1.408
-1.208	-0.611	-2.467	-3.040	-0.337	12.993	-1.597	7.374
-0.949	-2.111	1.704	-0.297	-1.466	-0.029	-0.660	-0.049
-1.865	18.591	-0.153	-0.411	0.041	-2.337	-0.342	-1.178
-1.704	-0.155	-1.470	0.738	-1.078	0.585	-1.630	-0.708
0.269	-0.912	-0.775	-0.779	0.093	-0.783	-1.401	-0.265
-0.748	-0.233	-0.762	-0.975	-0.863	-1.619	0.540	-0.913
0.075	-0.818	-1.525	-1.655	0.170	0.415	-1.053	1.299
4.458	-1.131	-0.866	0.285	0.488	0.009	-0.839	-0.804
0.349	-0.270	-1.360	-1.003	8.812	13.157	-1.867	0.410
-1.227	0.798	1.321	-2.209	12.004	0.275	-0.480	-0.752
11.930	12.992	11.230	17.932	0.640	3.223	0.883	-0.333
7.873	18.472	7.345	15.384	-0.300	5.793	1.517	8.013
7.221	7.185	7.210	13.217	-2.965	1.976	-0.176	-0.133
-2.194	8.304	-1.157	2.684	18.240	0.678	-1.122	-0.022
13.182	4.881	12.336	16.216	12.624	21.641	0.622	17.708
-0.593	4.666	9.806	18.328	13.089	13.683	9.927	12.406
12.702	14.936	6.641	18.976	16.959	13.470	13.997	-1.401

Table35.txt

12.656	20.110	11.970	23.355	8.464	19.084	8.360	9.802
11.425	18.366	7.121	19.206	12.242	12.327	11.553	5.419
12.767	14.578	5.384	9.573	17.528	11.855	1.159	7.528
-2.454	-2.278	-0.137	-2.902	-1.413	-0.209	1.159	-0.562
-0.045	-1.603	1.760	-1.111	-1.393	-0.789	0.692	-1.584
-3.055	0.861	-0.415	-1.906	-0.676	-1.863	-2.639	-0.470
-0.770	19.101	3.257	1.482	2.921	2.466	4.275	15.919
4.455	13.015	8.608	8.534	3.476	3.015	0.213	0.146
-0.652	3.047	1.587	3.093	-2.326	1.751	1.060	-0.145
13.085	21.380	12.691	26.234	3.409	-2.343	0.028	-0.117
11.988	15.517	8.334	0.640	12.514	13.964	-0.222	-1.618
-0.872	-0.445	-0.546	2.494	14.430	4.390	15.193	8.570
2.433	3.716	1.752	5.611	0.277	5.887	3.223	-1.582
0.453	-0.940	3.377	1.182	-1.105	3.420	2.175	-2.132
3.084	-0.109	0.383	0.475	8.416	0.724	1.078	1.418
4.739	8.440	4.110	16.999	-0.104	16.223	6.715	3.060
10.909	17.135	8.929	18.551	1.674	13.068	7.606	11.894
7.361	5.085	5.244	2.798	20.251	11.535	14.587	6.187
0.177	16.192	0.142	-4.289	-2.102	-1.995	-0.702	-0.910
0.087	-1.286	-1.210	-0.228	-0.636	-1.806	-2.104	-2.324
1.361	11.732	-1.372	-0.051	-1.515	-1.803	-1.704	-0.580
-0.024	0.326	-0.653	3.809	-0.348	-1.848	7.211	5.722
-1.272	-1.353	-0.251	11.211	-1.122	-1.531	0.155	0.978
1.176	-0.121	-0.789	4.895	1.836	4.540	8.281	-0.833
-1.427	-2.500	0.183	-1.805	-1.764	-1.987	-1.587	-0.201
-0.343	-1.471	-0.988	0.175	-2.424	-0.042	-1.169	5.538
-0.069	-1.555	-0.892	0.379	-1.817	-1.719	-0.394	0.425
-2.389	-0.693	0.411	-0.836	-1.370	0.833	-1.913	-1.706
-0.469	-0.508	0.268	-1.327	-2.495	-2.345	0.373	6.014
-0.541	0.114	1.741	-1.784	-2.310	-2.005	-1.718	-0.561
-2.226	-2.587	-0.519	-1.759	0.082	-1.878	-1.392	-2.549
0.174	-1.682	0.555	-1.506	-1.632	-1.467	4.952	8.868
-0.933	-1.389	-2.659	-1.086	-0.934	0.635	-0.385	-1.096
-1.161	-2.983	-2.176	-2.890	-0.474	-0.876	2.815	-1.419
-0.877	-1.697	-2.461	-3.020	-1.204	-2.042	-1.944	-1.128
-2.842	-1.398	-0.500	-4.339	-2.099	-0.652	-2.157	-0.582
3.207	14.185	13.160	4.711	1.653	11.314	2.899	1.427
10.038	16.196	0.226	12.931	10.116	8.558	3.008	10.602
7.664	7.385	7.555	7.134	11.596	6.161	11.317	0.325
-1.252	-3.265	-1.730	-1.857	-3.241	-0.595	-0.455	-1.477
-0.810	0.319	0.296	-0.376	-2.303	0.453	-1.401	-1.106
6.874	10.511	0.616	-1.487	-1.150	0.202	-0.306	0.438
4.909	19.508	9.867	13.072	4.124	6.825	11.351	19.292
1.765	2.419	7.027	18.784	9.894	0.370	2.033	5.566
16.064	16.965	1.639	1.055	0.916	2.078	1.755	-0.309
-2.162	11.638	0.083	3.366	-1.896	1.573	8.738	1.651
7.089	1.801	5.158	2.791	3.222	-0.280	-0.307	1.239
-1.390	0.246	4.211	1.215	2.359	-0.816	5.941	6.285

Table35.txt

-1.759	-0.261	-1.144	-1.091	0.604	-1.474	0.063	-1.474
0.523	6.735	0.411	-4.412	-0.966	-1.878	-1.283	3.366
-0.678	-1.478	-0.269	-1.028	-1.127	-0.907	-1.031	-0.802
0.263	-0.832	-0.407	-2.272	-0.675	0.845	0.027	0.432
-0.092	-1.634	-0.027	-0.279	0.084	0.352	-0.178	-1.453
0.049	1.155	1.137	-0.288	-0.392	-1.504	-0.694	1.974
0.043	0.753	13.958	26.232	10.428	20.274	-1.710	0.833
1.549	22.369	2.236	14.763	-1.467	-0.370	-1.544	14.859
15.966	16.871	-0.922	16.882	-0.703	16.609	2.349	9.683
-1.152	1.038	13.483	26.074	-2.372	8.649	-0.968	7.421
0.411	21.946	12.072	5.320	15.520	13.803	12.674	14.681
15.220	17.538	5.377	14.943	1.326	9.447	13.575	3.458
-1.882	-1.261	-0.373	3.177	-1.167	-2.159	-2.202	8.806
-1.912	-2.280	1.845	4.205	-0.438	-1.748	2.624	-2.143
-2.942	5.335	-0.560	-1.941	9.332	8.682	3.796	-1.225
1.600	0.242	-0.248	-1.343	-1.601	-0.569	5.834	-0.098
2.594	-0.609	0.721	-0.193	2.969	-0.631	0.016	0.879
2.959	0.157	2.710	-1.736	-1.746	-2.027	3.595	-0.605
-0.067	-1.966	-1.396	0.092	-0.542	-0.988	-1.133	-1.172
-1.757	-0.335	-0.419	-0.884	-2.167	-1.169	11.523	12.065
-0.088	-1.279	1.380	-1.082	-0.660	-0.238	0.290	-0.940
-1.808	-1.486	-1.651	-1.588	-2.292	-1.727	-0.829	-1.764
-0.408	-0.166	-1.589	0.461	-1.499	-0.198	-2.050	-0.068
-1.142	-0.661	-0.473	0.290	-0.264	-2.093	-3.172	-0.147
3.080	20.983	5.047	2.362	5.314	6.554	3.829	12.527
5.851	10.827	3.633	19.435	0.825	7.296	12.854	10.469
8.787	10.493	1.617	8.654	19.786	14.703	13.435	5.352
2.074	17.021	3.612	1.201	2.714	-0.067	2.810	6.220
4.212	5.285	-0.032	14.538	-0.179	4.398	8.093	6.373
4.618	5.783	1.893	6.700	13.628	9.713	9.546	2.559
-1.756	-1.292	-0.596	-1.462	0.703	-1.589	0.103	-0.876
0.556	-0.819	0.241	-0.995	-1.809	-0.502	-1.126	6.554
-0.892	-1.796	0.406	-2.223	-0.925	-1.739	-1.228	0.413
-1.804	-1.181	-0.781	-0.466	-2.688	-0.843	-1.600	-0.098
1.663	-0.146	1.638	-1.057	-2.036	-0.843	-0.505	-2.669
-1.944	-0.026	1.067	-0.331	-0.262	-0.887	-0.295	-0.484
-0.582	-0.749	-0.815	-3.181	-1.540	-2.801	-0.325	-2.924
-0.703	0.544	0.842	-5.250	-0.978	-0.194	-1.223	-2.082
-1.983	-2.831	-2.929	-1.944	-1.403	-0.559	-1.770	-0.947
0.711	-1.799	-1.574	-1.533	-1.223	-2.258	0.491	-0.842
2.891	3.496	0.358	-0.948	-2.120	0.798	1.370	0.700
-1.287	-0.068	1.090	-0.589	-1.043	-0.959	-0.055	2.140
-0.750	0.797	-0.795	-0.545	-1.084	-1.304	6.645	-1.671
-0.200	-0.243	0.393	-2.276	-0.054	-1.265	-0.072	-2.228
-0.730	-1.167	-1.815	-0.211	-0.218	-1.959	-2.161	-0.848
-0.492	1.384	1.872	-3.649	-0.922	-0.880	6.759	0.730
-1.884	-1.447	-2.029	0.632	-0.553	-1.140	-0.573	0.260
-0.863	0.110	1.653	-0.397	0.669	-3.251	-0.523	-1.350

Table35.txt

-1.294	0.197	-2.047	-2.675	-2.372	-0.183	0.812	0.259
0.717	0.715	-1.953	-1.167	-1.136	-0.565	-1.159	0.402
-0.571	-2.037	-0.946	-1.851	0.587	-0.621	0.221	0.638
1.626	-0.164	-1.243	7.416	2.902	6.910	4.437	5.122
8.502	4.411	3.538	0.000	4.361	-1.050	-0.851	4.650
4.534	10.141	3.090	-1.811	-1.692	6.687	1.054	11.066
6.932	-0.520	-2.232	-1.265	-0.304	-0.403	-1.667	-2.656
1.993	5.121	5.319	-0.462	-0.453	0.408	7.502	-0.282
2.010	-2.270	2.628	6.040	-1.486	-1.426	-1.054	7.150
0.501	-1.347	-1.243	-3.007	2.530	-0.897	-1.603	-2.250
-1.121	0.024	0.762	-0.853	-0.754	-3.791	-2.003	-0.022
-1.906	0.083	-1.086	0.239	-3.546	-0.977	-0.687	-1.289
0.220	-0.984	-1.874	-1.082	2.478	-0.030	-0.853	-1.193
0.750	-1.376	-0.723	1.852	-1.172	-2.159	-0.501	-1.233
-0.798	-1.932	1.844	-2.576	-1.409	-1.024	-1.376	-0.916
-2.101	0.844	-1.440	-0.582	0.075	-0.374	-1.371	0.129
2.112	-0.753	-0.785	-0.103	0.069	-0.350	-0.490	1.538
-1.944	0.565	-0.437	-0.716	-1.823	0.413	-1.621	-1.436
-2.241	-1.801	0.821	1.076	-1.141	-1.705	-1.188	-2.807
-1.358	-0.406	-2.950	0.394	-1.597	0.690	15.272	2.018
-0.957	0.762	-0.874	-1.599	-1.685	-0.806	-0.961	-0.561
-0.801	-1.218	-1.388	0.315	-2.304	-3.561	-1.175	-0.409
-1.621	-0.006	0.181	-0.990	1.050	2.138	1.938	0.093
-0.905	-0.272	0.953	-0.449	-2.247	-0.091	-2.349	-3.872
-1.571	-2.113	-0.770	-1.790	-1.179	-1.772	-2.656	-1.534
-0.799	0.116	-1.543	1.713	-1.681	-0.870	5.065	-4.178
-2.669	0.513	3.090	-1.266	-3.533	-1.410	1.247	-1.364
0.211	-0.542	-0.472	-2.344	0.410	-0.215	-0.857	-1.472
-1.284	-1.055	-0.831	-0.359	-0.926	-2.228	-1.221	-2.550
-0.631	-0.871	-0.808	-0.757	-2.316	-3.147	-2.159	-1.184
0.412	-1.324	-1.923	-4.582	-2.200	-1.202	-2.817	-1.238
0.094	-1.010	-0.021	-0.843	-0.524	-1.021	-2.198	-1.207
0.827	-1.943	-0.348	-2.818	-0.703	-2.407	-3.482	-1.290
11.436	13.260	2.210	7.503	1.312	11.083	6.107	17.054
2.325	5.445	9.231	19.320	8.545	9.246	9.596	13.387
10.303	5.454	1.905	16.721	4.148	12.016	10.943	1.098
4.828	-1.959	0.916	-1.153	-0.321	-0.536	1.374	-2.693
-1.130	-0.092	1.146	1.959	-3.058	-1.411	3.724	7.466
0.191	1.559	-1.291	-0.932	3.807	-2.050	-1.099	-0.816
6.931	10.671	-0.440	-1.211	-0.257	0.399	0.606	-0.764
13.281	0.665	7.250	-1.091	14.239	1.337	0.503	15.117
0.102	17.562	-0.439	0.011	4.144	-0.903	-0.326	-0.583
0.927	-0.757	-1.025	-2.029	0.066	0.105	-0.562	-2.062
-1.712	0.904	-0.430	-1.784	-0.370	-0.024	-4.463	-0.834
-1.468	0.000	-1.704	2.130	0.104	-1.261	-2.115	-2.514
-0.820	-1.909	-1.220	-3.318	-1.561	-0.707	0.640	-0.408
-0.585	-0.364	-1.252	-0.618	0.396	-1.080	-1.859	8.875
-0.226	-0.331	-0.812	-2.227	-0.281	-2.067	1.125	-0.614

Table35.txt

-2.324	-1.979	-0.879	-0.733	-2.522	0.091	-2.410	0.130
-0.396	-2.967	-0.448	-0.259	-1.387	-2.166	-1.630	0.053
2.473	0.104	-0.576	-1.012	-0.273	-1.412	-1.195	-1.315
0.370	-0.279	-0.917	0.365	-0.761	-1.221	-0.073	0.552
-1.167	-0.114	2.130	6.161	-0.262	0.430	3.574	4.025
-0.905	-0.668	0.975	-0.628	0.094	-1.001	1.924	-0.448
-0.577	-0.940	-0.427	-0.974	0.241	-0.555	0.070	-2.465
-0.751	-0.356	0.376	-1.311	-1.971	0.669	-0.779	12.997
-0.748	-1.860	-0.510	0.626	-2.545	-4.035	0.329	-2.256
1.327	-1.079	5.941	3.981	8.020	4.659	4.203	0.335
0.897	-1.868	-1.168	-0.575	-0.917	0.083	1.208	-0.016
-0.481	0.946	1.850	-0.452	-1.781	4.899	10.957	0.843
0.210	-0.910	-1.832	0.120	-2.026	-1.620	-3.246	-1.072
-0.563	0.032	-1.223	2.388	0.042	-2.161	13.057	-1.616
0.511	0.470	-1.311	-2.127	-2.787	-1.592	-2.412	-1.695
-1.041	-1.232	-1.871	-1.803	-0.387	-2.263	-0.665	-2.678
-0.729	-1.731	1.460	-2.529	-0.852	-1.454	-2.734	0.549
-3.155	-1.479	-2.334	-1.957	-1.638	-0.027	-0.599	0.127
-0.108	5.300	0.544	7.635	-0.735	1.257	4.013	0.000
4.365	7.124	8.753	1.598	4.476	3.726	1.428	3.476
5.349	2.249	2.446	6.736	10.569	11.574	4.662	5.303
-1.996	-2.156	-1.409	0.254	-0.633	-1.647	-0.621	-2.495
0.476	-0.557	-0.313	-1.319	-1.117	-1.389	-0.191	2.074
-2.403	-0.975	-0.783	-1.704	-0.471	-2.048	-2.258	-2.852
-2.259	-0.965	-1.440	-0.687	-1.652	-1.876	-0.393	-2.501
-0.756	-1.414	-1.570	-1.244	-0.813	-1.306	-1.882	-1.301
-0.366	-2.401	0.421	-1.295	-2.407	-1.532	0.277	-1.829
-2.055	-2.307	-1.342	-1.896	-0.194	-2.423	-1.356	-2.977
-1.458	-0.642	-0.989	-2.280	-1.149	-1.114	4.478	5.038
-0.370	-3.942	-0.332	-0.927	-1.922	-1.319	0.169	-0.356
-1.246	-3.977	-0.051	-1.247	-0.257	-2.687	-1.014	-2.100
4.302	3.421	-0.595	-1.104	0.143	-1.030	0.865	3.703
-0.949	-0.166	-0.468	-2.282	-1.179	-2.489	-0.941	-0.801
-2.751	-3.186	-2.416	-2.275	0.001	-2.086	5.267	9.224
-0.070	-2.306	-0.029	-1.165	-0.707	-1.982	-0.941	-2.376
4.435	6.126	0.220	-1.481	-3.991	-2.282	-3.174	4.200
-2.752	-1.079	-1.515	-0.199	-2.200	-2.778	-2.107	-2.139
-0.818	-1.381	0.152	-0.763	0.095	-1.834	-2.038	4.246
-2.964	-2.800	-2.211	-1.565	-0.372	-0.771	-2.032	-2.799
-1.162	-1.835	0.581	-2.010	-1.470	-0.566	-1.953	-2.347
-1.432	-1.102	-0.398	-0.353	-2.852	-1.071	-2.297	-0.699
-2.608	-1.039	-0.870	-0.664	-1.714	-4.059	-0.852	0.707
-3.129	-1.565	0.033	-2.102	-1.462	-1.712	-0.094	-0.751
-0.321	-2.345	-1.350	19.414	0.156	-0.887	0.605	-1.059
0.107	-1.713	-0.645	-0.890	-2.047	-1.528	-0.663	-1.508
7.520	17.298	-1.574	12.085	-1.405	27.515	3.495	20.571
9.812	9.127	11.986	3.546	0.447	14.606	-1.889	15.870
10.851	15.577	0.797	17.207	10.287	-1.923	11.363	8.205

Table35.txt

-1.266	-0.599	-1.560	-2.263	-1.425	20.475	-1.548	-1.174
1.112	-1.165	-0.564	-1.882	-1.192	-1.459	8.006	13.059
-0.704	-0.589	-2.428	-0.413	-1.740	-1.199	-0.090	-0.233
-2.181	-1.222	-3.795	-0.088	0.108	-0.320	0.637	-0.019
-1.092	-0.066	-0.418	0.694	1.201	0.541	0.013	7.203
-0.191	0.678	-1.346	-1.895	-1.315	-1.608	-1.004	-0.200
16.152	-1.254	16.420	25.702	-1.471	11.378	-0.286	18.637
12.518	16.739	10.626	18.129	15.300	13.378	0.594	-0.207
13.360	-0.764	-1.488	-1.532	19.328	3.776	12.835	7.262
20.482	21.898	14.703	26.114	12.369	23.979	12.423	20.060
15.890	18.342	10.358	16.705	11.186	9.380	13.264	19.861
10.461	16.001	12.664	16.615	17.877	15.297	11.618	9.641
-1.425	-0.080	-1.959	-1.664	-0.774	0.056	5.633	9.480
-0.608	-0.081	-1.620	-0.104	-0.594	-0.001	10.620	11.967
0.403	-1.213	-2.439	-0.595	-1.923	-0.979	1.925	-0.722
-0.661	0.762	4.265	22.279	0.220	-2.594	-0.821	3.253
0.113	3.150	8.413	14.976	-1.797	-0.068	0.144	4.572
13.125	16.791	-0.137	-0.704	-1.614	-0.987	2.007	-0.777
-1.769	-0.945	1.122	-2.904	-1.031	-1.175	-1.503	-0.499
-1.604	1.290	7.481	-0.585	-0.575	-1.246	-1.182	7.986
-0.094	2.263	-0.958	-0.790	-0.204	-0.661	1.839	-0.637
-1.829	-1.473	-0.409	-1.580	0.126	-0.176	-1.880	-1.475
-0.115	-1.272	-1.894	-0.715	0.184	-1.922	-0.499	-0.064
-0.104	0.826	-0.872	-0.790	-1.349	0.099	-0.320	-1.998
-0.149	-3.090	-1.132	-1.996	-2.865	-0.242	-1.672	0.000
0.000	-2.733	-0.032	-3.090	-0.215	-1.129	-1.921	-1.691
0.000	-0.882	1.109	-2.918	2.965	-0.898	-0.542	0.000
-2.960	-1.569	-1.182	-0.961	-2.053	0.248	-2.347	0.366
-0.650	0.164	-1.220	-1.306	0.225	-1.184	-1.049	-0.168
-0.430	0.492	-1.166	-0.675	-1.337	-1.182	-2.673	-0.607
0.000	0.137	0.000	0.000	0.000	0.000	0.000	0.000
0.000	-1.214	-3.090	0.000	0.000	0.000	1.854	0.000
0.000	0.000	0.000	0.650	0.000	0.309	-0.762	-0.949
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.137	0.254	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2.288	3.657	9.514	5.340	3.929	0.000	4.969	-0.074
-0.728	4.130	3.419	1.109	6.721	2.600	-1.647	-0.611
-0.944	0.095	1.645	0.590	-1.003	-1.854	3.942	-2.451
-0.020	-0.741	-1.700	-0.815	-2.823	-1.110	-1.161	0.671
-1.379	-1.200	-0.539	0.000	-0.603	-0.910	7.757	0.925
1.164	-1.127	-0.158	0.748	-3.455	-1.568	-2.324	-0.130
-0.041	-1.667	-2.691	-1.294	-0.918	0.646	-1.200	2.150
-0.173	0.281	-0.223	-1.104	-0.302	-2.045	0.802	-1.159

Table35.txt

0.194	1.696	-0.751	0.463	-2.391	-2.385	-2.785	0.837
8.305	5.042	2.081	-0.968	-1.503	-2.000	-0.373	5.966
4.343	4.797	7.279	2.484	2.854	-0.604	8.735	4.463
4.087	5.534	4.944	3.970	-0.131	2.788	12.581	-1.810
-0.065	-1.164	-2.660	0.034	-2.162	-1.230	0.063	-0.176
0.828	0.285	-1.460	-0.823	-0.428	-1.738	-2.035	-0.513
-0.859	-0.119	0.792	-1.013	-1.775	-1.224	-0.849	-1.680
0.128	-1.934	0.977	1.633	0.526	-0.893	1.027	2.031
3.215	0.896	-1.036	-0.126	1.925	2.888	-1.504	0.299
2.368	1.543	1.271	-1.260	1.400	-1.446	-0.636	-0.286
-1.310	-1.400	-1.929	13.531	-0.037	-2.006	-0.486	1.048
1.019	-1.065	-2.075	0.161	0.158	-0.080	-1.757	1.044
0.653	-0.919	0.258	0.610	-1.809	-1.242	-0.289	-0.738
0.000	3.090	-1.473	3.900	-0.962	0.146	2.700	0.000
2.272	-0.870	0.680	-0.727	-0.040	-1.014	-1.173	-1.934
0.168	-0.456	0.000	3.932	6.158	4.285	5.044	3.979
5.636	-0.528	2.588	-2.388	7.945	-0.554	-2.641	3.858
5.989	1.233	1.254	-1.431	0.653	1.342	4.482	2.859
2.187	-1.759	3.076	0.066	19.950	9.325	10.920	2.327
-1.475	-1.739	-1.543	-0.725	0.270	-0.463	-1.029	-3.442
1.368	-1.055	-1.228	0.337	-1.497	-0.514	-2.017	-2.581
-2.360	-0.055	-0.585	0.275	0.612	-2.034	-0.156	-0.965
0.282	-3.283	-2.182	-1.631	-1.396	-0.646	-0.416	-2.237
0.634	-0.781	-0.682	1.287	-3.080	-1.029	-1.850	1.247
-0.005	-0.933	-1.085	-1.609	-1.695	0.140	-0.559	0.458
0.356	-0.886	-1.317	1.674	0.244	-2.410	-1.220	-0.508
1.200	0.251	-1.580	-0.485	-0.735	-0.476	13.277	-1.498
-1.031	-0.030	-2.667	-0.430	-1.277	-1.270	-3.039	-0.888
2.474	2.337	-0.125	11.461	-2.027	0.217	0.212	4.779
2.811	4.395	5.941	4.367	4.897	3.025	8.468	-0.191
-2.040	0.838	4.022	0.115	2.452	8.324	11.394	1.695
0.455	-1.617	-0.999	-2.172	-2.231	-0.970	-1.258	-0.590
0.726	-1.098	-1.373	-1.119	-1.330	1.235	-0.683	-1.428
0.380	-0.166	0.415	-0.174	-1.992	-1.132	-1.713	-1.591
-1.019	-1.013	-1.237	-1.461	-1.355	-0.894	-1.972	0.292
0.166	-1.414	-0.481	-1.606	0.085	-1.874	15.209	-0.859
-0.426	-1.142	-0.738	-1.565	-2.053	-1.268	-1.837	-1.252
1.463	15.474	0.638	-1.579	-1.020	0.180	7.553	6.482
5.254	0.327	2.174	-0.843	0.219	7.500	2.657	0.089
-0.382	5.197	1.163	2.994	-1.492	7.038	4.029	8.275
-3.422	-0.415	-3.039	-1.212	-0.277	-1.826	-0.043	1.273
-1.065	-0.831	-1.776	-0.162	-0.667	-4.030	-0.806	-1.012
-0.712	-0.887	-0.656	-1.740	-0.486	-1.950	-1.631	-2.161
-0.825	-0.827	-0.839	-1.355	-0.764	-2.155	-1.630	-3.090
0.201	-2.652	-1.145	0.000	-1.076	-0.700	-0.562	1.341
0.922	0.655	-0.702	-0.087	-3.438	-0.108	-0.920	-1.551
-0.945	0.041	-1.714	3.110	2.564	3.093	5.410	3.992
3.558	1.344	9.176	1.887	6.546	2.752	0.300	0.222

Table35.txt

-0.921	4.312	2.107	10.836	12.275	8.503	2.806	1.668
2.184	8.678	7.226	7.610	-1.764	1.323	1.290	3.090
7.702	0.191	0.381	-0.309	7.068	11.205	8.846	1.998
2.659	1.818	-0.450	11.687	0.927	-0.544	8.456	7.539
0.611	3.657	5.353	-0.407	-0.427	1.517	1.493	-2.215
5.635	-2.217	1.196	0.104	1.544	-0.983	1.582	-0.807
0.035	-1.174	0.951	-0.572	-2.470	3.195	-0.005	-2.324
0.927	0.409	0.963	-2.638	0.568	7.880	5.608	0.000
3.581	1.402	-1.522	3.533	1.676	-0.353	0.164	1.660
2.131	-1.506	0.000	1.345	9.128	2.397	1.539	-1.230
-0.298	-2.010	-0.639	0.268	0.694	-2.409	-1.427	-1.419
-0.451	0.421	-0.903	0.230	0.384	0.795	9.211	-1.643
5.099	-0.683	0.295	-0.807	-0.150	-0.784	10.759	-0.882
-1.192	0.130	-1.673	-1.241	-1.430	0.239	0.687	-0.546
0.353	0.710	-0.393	-0.073	-1.112	-1.686	-0.049	-0.928
-0.494	0.065	0.366	-3.674	-3.081	-1.523	0.054	-0.471
-0.140	0.259	1.563	-0.715	2.351	-0.911	-0.743	4.273
5.167	1.349	0.094	2.023	3.486	7.258	0.796	-0.127
-2.200	-0.516	2.015	-1.869	-2.023	-2.041	0.005	7.375
1.028	-0.415	-1.825	-1.450	0.171	0.723	-1.358	-0.562
-0.229	-1.672	-2.757	0.152	0.120	-1.245	-1.623	-2.014
0.754	2.959	0.000	-0.681	-2.212	-1.707	-2.645	-3.287
-0.130	-0.285	-0.889	-1.185	-0.033	-1.603	-1.434	-1.186
1.336	4.756	6.492	1.275	-2.719	6.500	7.179	0.267
-0.124	-0.192	4.345	-2.181	-0.032	-1.809	-1.329	0.314
0.718	11.443	15.443	10.371	3.788	1.834	4.091	5.295
4.897	7.212	9.728	-1.973	-0.461	1.857	0.867	0.474
-0.353	6.334	4.603	3.287	16.660	10.165	11.714	9.346
0.010	-0.669	-2.456	-0.190	-0.068	-1.132	-0.242	-1.330
0.385	-0.019	-2.409	-2.000	-0.174	-1.000	-0.229	-0.422
-0.713	-0.067	0.302	0.197	0.289	-1.103	-1.577	-1.026
-0.174	-2.470	1.022	-0.584	0.083	0.830	0.480	-2.363
0.420	0.588	-0.867	0.064	-0.330	-1.935	-1.047	-0.189
-0.810	-0.194	0.965	-0.097	0.223	1.040	-2.189	-0.041
-0.663	-2.674	-1.200	11.360	-1.897	-0.031	8.140	4.374
8.992	5.073	1.043	3.737	0.978	-0.574	-2.030	-0.417
4.835	-0.700	5.138	-0.551	2.697	-0.788	-1.006	1.370
-0.254	1.574	-1.281	0.154	-2.413	-1.879	-0.474	-0.797
2.480	-2.476	-2.233	-0.249	-1.405	1.413	3.579	-1.529
-0.639	-0.571	-0.720	-1.713	-1.427	-0.102	-3.583	-2.052
6.397	16.952	15.856	6.941	10.073	7.937	9.702	4.866
8.022	6.734	10.842	3.681	-1.575	12.417	3.215	5.506
4.932	0.038	5.337	5.405	12.246	10.157	10.563	11.355
-0.207	-0.582	-3.838	-0.650	1.019	-0.359	-2.109	0.434
0.648	-0.934	-0.555	-1.316	-1.965	-1.806	-0.578	0.413
0.000	-0.991	-1.886	0.183	-2.178	-1.717	-2.517	-2.533
0.261	-0.735	-0.692	-1.331	-1.962	-0.222	-1.678	-0.888
1.097	0.042	-1.266	0.165	-0.110	-1.396	-3.406	-3.214

Table35.txt

-0.042	-2.373	-0.695	-0.908	-2.709	-0.783	-2.554	-1.841
-0.987	-1.073	-1.309	7.429	-1.674	1.730	10.191	-0.584
-0.732	0.243	1.139	-0.713	-1.097	-1.342	15.079	0.282
-1.107	1.614	-0.410	-1.634	0.093	-0.668	0.161	-0.438
-0.911	0.394	-1.216	-3.145	1.735	-2.028	-1.019	-0.055
-1.020	1.023	0.474	-0.657	-0.107	-1.358	-1.573	-0.037
-0.569	1.851	-0.924	-2.168	-0.995	-0.326	-0.836	-0.491
6.110	1.916	4.367	6.597	4.307	5.293	4.364	0.000
4.160	-0.327	5.843	0.059	-1.954	7.952	0.989	0.874
-0.541	0.386	0.052	-0.691	6.529	-1.052	8.672	8.953
3.857	12.231	10.015	6.559	2.978	0.484	5.050	2.215
5.515	0.911	5.039	1.083	0.042	2.984	5.114	1.887
0.185	-0.315	3.604	-2.214	5.510	4.468	1.911	6.994
0.189	-0.312	-1.017	-0.909	-0.846	-1.403	-1.660	0.000
3.427	-1.353	-2.556	-3.090	-0.771	-1.768	-0.693	-1.381
0.000	-0.059	-3.090	-0.194	-2.697	-2.659	-2.115	-0.918
-0.582	-2.167	0.000	-0.643	-1.447	0.000	0.000	0.000
0.000	-1.079	0.310	0.614	-1.256	0.187	-2.729	-0.161
0.529	1.283	0.000	-2.024	-1.202	-1.607	-0.838	0.000
-0.074	-1.353	0.000	-1.591	6.304	-0.752	0.610	-0.526
0.213	0.454	-1.752	-1.221	-1.598	0.000	6.991	-0.650
-1.508	-1.850	-0.272	-1.105	-2.729	-2.386	-3.957	3.065
4.218	4.186	3.881	0.519	0.570	1.748	1.225	0.000
0.000	0.174	1.755	-1.214	0.798	2.561	3.387	-1.511
-0.823	-1.722	-0.002	3.068	1.112	2.332	4.318	0.222
-1.278	-2.156	-0.128	-0.649	1.497	0.544	-3.281	-1.380
0.292	0.722	-1.078	0.304	2.448	-0.274	-2.465	0.831
2.691	-0.609	-0.676	-1.734	-1.960	-0.864	4.285	-0.527
0.177	0.000	3.043	4.029	-0.889	4.980	-1.586	0.000
0.000	0.000	0.000	0.176	1.477	3.860	1.395	3.074
0.000	-0.815	3.850	1.742	1.004	5.519	2.389	1.882
1.258	4.999	0.330	1.174	0.000	0.000	0.732	0.000
2.059	0.703	2.154	0.000	0.050	1.241	3.776	0.000
2.260	2.509	0.000	2.479	2.374	1.460	5.582	0.612
4.043	0.344	2.022	0.490	0.846	0.267	0.735	0.919
3.040	-0.155	-2.060	0.011	0.209	-0.816	-1.851	0.080
-0.996	-1.181	-1.960	-2.745	-1.712	-1.739	6.151	-0.308
0.344	0.103	-1.660	5.222	-1.436	-0.342	-1.019	-2.262
-1.105	-0.240	-1.351	-3.155	-0.533	-2.730	-2.068	-0.465
-3.938	-0.638	-0.833	0.230	-0.318	-2.487	-1.430	-1.158
-0.080	-1.700	0.358	-2.591	-0.769	-0.989	-0.392	0.590
3.080	-0.811	-0.355	0.184	-0.823	-0.459	-1.915	3.442
3.090	-0.378	0.097	-1.646	-1.997	-1.195	-4.093	-0.334
-0.744	-2.908	-0.662	-1.833	1.632	-0.576	-0.910	0.649
-0.069	0.605	0.947	0.750	-0.733	-0.884	-0.235	-0.573
-0.031	0.674	0.000	-1.784	-2.813	-1.587	-1.881	-0.843
-2.372	-0.824	-2.048	0.343	-2.106	0.047	-0.421	1.475
-0.949	-0.845	-0.757	-0.178	-1.435	0.077	-0.650	-1.076

Table35.txt

-4.181	-0.615	-2.218	-2.351	-1.575	-1.260	-3.539	-1.764
-0.199	-0.842	-0.728	-3.875	-0.938	-0.683	-0.276	-2.080
-0.107	0.807	-2.163	-0.150	-1.321	0.099	-0.323	-0.457
-1.793	-1.216	0.609	-0.937	-0.789	0.356	0.497	-1.761
-0.230	-1.400	-2.546	-0.335	-1.988	0.657	0.797	-1.744
-1.274	-0.471	-0.794	-0.808	-0.036	-2.721	0.238	-0.640
-0.822	-0.484	-0.866	-0.572	-3.441	-0.273	-1.794	-0.139
-1.242	-0.939	-2.724	-1.001	-0.799	-1.013	0.501	0.017
-0.719	0.719	-1.792	-2.146	-0.378	-1.049	-0.424	-0.977
0.329	0.767	0.072	-1.885	-0.645	-0.935	-1.183	-1.050
-2.085	-0.892	-0.575	-0.066	-1.420	-0.156	0.736	-2.054
0.057	-1.098	-0.676	-0.817	-1.105	-3.908	-1.822	-0.623
0.302	-0.745	-0.844	9.176	12.148	-1.373	-1.581	0.238
-0.808	-0.913	-0.652	-1.517	0.986	-2.752	-2.509	-1.945
-0.529	-0.023	-1.451	0.473	-0.821	2.389	-3.933	-1.382
0.040	0.028	1.001	-1.282	-0.093	-2.761	-0.565	-1.179
0.149	-0.923	-2.468	-1.883	-0.076	-1.806	-2.078	-0.062
-1.689	0.186	-1.147	-0.156	-2.285	-0.836	-1.703	1.306
-1.886	-1.131	-0.635	-0.466	-1.741	-0.485	-1.920	-1.025
-2.039	-0.737	-1.015	-1.946	-1.608	-1.104	-0.935	1.319
0.899	-0.658	-0.807	-0.995	-0.899	-1.321	15.942	0.681
0.073	0.213	-0.376	-0.830	-3.209	-1.164	-2.610	-3.393
-0.470	-1.762	11.353	-0.747	-0.279	-0.840	2.169	0.045
4.007	0.580	12.020	1.371	4.617	-2.260	-0.947	0.087
0.679	2.359	-0.352	-1.140	0.844	6.735	-1.158	10.113
4.075	1.849	6.105	6.617	1.895	0.989	5.134	3.090
5.320	4.731	-0.863	1.202	-2.695	-2.202	-0.495	3.033
-0.688	1.310	-1.245	11.907	0.444	7.774	7.969	6.430
-1.335	-1.685	0.855	-1.547	-0.645	-0.598	-1.255	-1.845
-1.475	-2.126	0.080	-1.128	-0.333	-2.144	-2.173	-0.337
-0.462	0.176	1.333	-2.740	-1.978	-2.004	-1.633	0.180
0.375	-1.747	-0.881	-2.585	-0.750	-0.402	-0.834	0.895
4.344	-2.890	-1.385	-0.817	1.118	-1.341	-2.034	3.755
5.220	0.796	-1.095	1.219	-2.273	5.903	9.643	-1.023
3.879	0.309	12.806	0.510	2.204	2.824	2.150	1.821
1.287	6.601	3.982	2.756	4.823	3.720	-1.607	2.416
2.780	-0.692	-0.332	-0.994	5.610	8.119	-0.935	4.146
-0.213	-1.516	-4.020	-2.401	0.021	0.000	-1.562	-0.961
-1.182	-1.064	-0.997	-0.074	0.000	0.395	-1.214	-1.426
0.095	-0.566	0.561	-1.022	-3.588	-1.703	-1.142	-1.880
-0.189	11.847	-1.529	-3.138	7.274	1.167	-0.145	3.767
4.491	5.106	5.458	3.090	-0.707	8.778	-2.373	0.165
0.002	3.572	2.679	2.053	-1.824	6.196	-1.413	2.062
0.585	0.328	0.789	3.175	2.155	-0.317	3.420	0.334
-0.200	0.053	-0.883	0.574	-0.494	-3.220	12.728	-1.062
0.006	0.353	-1.098	12.115	3.770	5.039	11.685	-1.945
-1.492	-0.773	-2.721	-1.309	-2.831	-1.414	-1.279	-2.138
-2.093	-1.456	-1.809	-0.035	0.166	-1.760	-1.247	1.254

Table35.txt

0.176	0.386	1.150	-1.375	-1.383	-0.574	-1.982	-2.420
0.816	-0.456	-1.620	-0.812	-0.631	0.287	0.032	-0.409
0.684	0.298	-0.956	0.384	-0.347	-1.310	-0.565	-0.774
0.267	-1.236	-1.283	-3.395	-2.617	-1.387	-1.286	-0.110
-0.773	-1.482	-1.460	-2.105	0.000	-0.902	-1.511	0.000
-2.049	-0.832	-1.918	0.000	-1.289	-2.265	-1.294	-1.855
-0.836	2.071	-0.687	-1.178	-3.125	-0.674	-3.325	-1.272
-2.566	-0.412	-2.486	2.711	-2.875	-1.586	-0.119	-0.678
-0.144	0.379	-1.194	-0.139	-1.139	-1.247	7.652	1.281
-1.046	-1.853	-0.424	-2.550	-2.112	-2.021	-0.343	-0.168
-3.090	-2.194	-2.163	-0.947	-2.389	0.000	-1.507	0.137
0.000	-0.445	-2.380	-0.074	-1.642	-0.459	-1.686	-0.549
0.089	-0.237	0.922	-1.190	-1.100	-1.586	-0.287	-1.955
-1.366	-1.035	-1.963	-1.014	-0.617	-0.906	0.337	0.000
0.158	-1.706	-0.523	-3.090	-2.306	-0.166	-0.542	-0.979
-0.353	-1.399	-0.217	-2.096	-0.774	-1.091	-0.675	-1.613
3.090	-0.137	-0.099	3.960	2.690	-0.372	0.000	0.000
0.000	-1.922	0.264	-1.706	-0.591	0.850	-1.379	0.339
-2.045	-0.279	0.000	3.247	5.941	-0.185	-1.781	1.785
-0.240	-1.565	-2.542	-0.895	-1.833	-0.942	-0.485	0.385
-0.622	0.063	-0.766	0.118	-0.944	-0.354	-0.859	-0.912
-0.863	-0.689	-1.237	0.209	-0.106	-2.267	4.825	0.095
0.000	3.090	0.257	-2.229	-0.812	0.061	1.841	0.000
0.000	-0.042	-0.740	-1.518	-0.729	-1.168	6.039	-0.357
-1.607	-1.128	0.000	0.254	1.077	-1.611	1.952	0.000
-3.096	-2.018	-1.832	-0.817	-0.047	0.690	-1.489	-2.520
-0.988	0.302	-0.421	1.839	-0.505	-1.236	-1.818	0.994
0.415	-1.514	0.003	0.054	-4.118	-0.739	9.824	-2.483
-1.566	-0.042	-1.541	-3.395	-0.029	-0.274	-2.062	-1.659
-1.603	-0.205	-0.839	0.289	-0.992	-3.324	4.294	-0.070
-0.973	-1.743	0.717	-1.182	-2.935	-0.763	-2.025	-2.606
-1.789	-0.616	-1.193	-1.400	-0.369	-0.594	0.151	1.296
4.719	-0.899	-1.565	0.888	-0.695	-1.564	-1.377	-0.597
0.000	-0.939	-0.731	-1.439	-0.030	-0.566	-1.442	0.615
-0.373	-2.723	-0.568	-2.810	-2.631	-1.640	-1.044	-0.346
-0.181	-1.441	-0.855	-2.821	0.413	-1.116	-1.211	-1.984
-0.453	0.129	0.517	-2.332	-2.780	-0.047	-2.581	-1.552
-1.358	-3.085	-2.250	-0.615	-1.064	-0.459	-1.353	-0.215
-2.408	-0.662	-0.960	0.187	-1.347	-1.500	18.710	-2.759
-0.466	-0.326	0.172	-0.638	-3.452	-0.725	-0.043	0.982
-1.267	2.590	3.836	-0.901	0.000	3.078	0.000	0.000
3.090	4.720	3.742	1.175	1.689	4.077	7.229	-0.320
3.586	0.623	0.000	0.306	-0.282	0.036	-0.702	-0.443
-1.755	-0.412	7.259	-2.465	-1.530	-3.338	1.965	1.976
4.816	-3.474	0.466	0.266	3.633	-2.021	-0.805	-1.096
-1.036	2.501	0.000	-0.155	0.496	-0.229	5.646	4.936
-0.053	-1.487	-2.140	-0.177	-2.093	-0.756	-1.167	-0.542

Table35.txt

-1.993	-0.754	-0.306	-1.553	-0.392	-2.012	-3.514	-0.868
0.203	-1.046	-1.098	0.108	-2.342	-0.298	-4.265	-1.901
-0.026	2.271	11.473	6.440	0.375	-0.839	1.205	3.535
5.035	2.888	4.609	-0.406	-0.813	-0.573	-0.792	1.381
-0.100	-0.097	0.908	4.005	-0.443	1.764	3.029	-3.700
-0.313	-0.203	-2.057	0.982	3.134	-0.221	-0.423	0.755
0.412	-2.370	1.491	-0.300	-0.163	-0.151	-2.418	0.663
0.009	2.204	-1.603	-2.246	-0.891	-2.248	-0.992	-1.529
-1.659	-2.221	-1.467	-0.711	-0.467	-0.495	-3.209	-0.745
0.760	-1.097	-1.823	1.177	0.250	-0.108	15.850	-1.026
-0.652	-1.869	-0.325	-2.107	-1.074	2.491	5.711	-2.840
0.003	-2.285	-1.990	-0.444	-1.182	-0.042	-0.861	-0.349
-0.048	2.529	-0.993	-1.627	-0.636	-1.725	2.592	-0.355
-0.593	-2.803	-1.306	0.275	-1.532	-0.520	-2.379	-0.535
-1.200	-1.758	-2.705	-1.918	-0.678	0.147	-0.899	0.617
-0.854	-0.811	-0.892	-0.220	-1.323	-1.531	-2.188	-1.810
-1.655	-0.907	-0.760	-0.234	-2.808	-0.648	-2.828	-2.866
-1.057	-0.449	-0.679	0.243	4.328	1.291	-1.813	0.000
0.000	1.096	-2.430	-1.360	-1.534	-0.918	-1.789	1.258
-0.439	0.730	-0.661	5.169	6.710	-1.858	0.099	-0.955
-0.017	-0.056	-2.004	-1.553	-1.146	-1.446	-2.035	-0.482
0.577	-0.019	-2.862	-0.503	-2.214	-2.201	-1.345	-0.456
0.205	-3.048	0.082	-1.461	-1.710	-2.731	-1.539	-2.402
4.137	3.778	11.706	0.898	7.343	0.080	4.354	4.676
7.025	5.374	1.377	-1.497	3.311	10.514	6.786	1.258
-0.681	1.921	0.882	-1.491	4.901	7.368	0.061	7.372
0.000	0.561	-0.366	-0.736	0.000	0.000	-0.143	0.000
0.000	0.000	0.349	0.000	-0.378	0.309	-0.726	0.000
0.000	0.000	0.000	-1.645	2.909	-1.906	-0.736	0.000
0.643	-1.497	8.257	5.020	0.381	-0.983	1.343	1.088
1.755	-1.182	-1.999	0.172	-0.121	-1.424	0.413	-0.789
1.826	0.592	3.400	-2.261	-2.490	-2.653	-3.728	-0.252
-1.976	-1.675	0.000	-2.480	0.000	-0.463	0.000	0.000
0.000	0.000	0.000	0.372	-0.517	0.000	9.979	-0.982
2.926	3.989	0.000	3.759	3.055	-0.382	-2.119	-1.454
-1.346	0.157	-0.366	-2.218	-0.663	-1.712	-1.733	-1.148
-1.562	-2.075	-1.963	-0.425	-0.756	-0.707	-2.407	-0.931
-1.170	-0.887	-1.148	-0.972	-1.551	-2.870	-1.169	-0.747
0.248	-1.872	7.146	5.435	-2.033	-1.601	-1.635	0.000
0.000	-0.263	-0.073	1.674	0.978	-1.402	0.103	8.806
5.551	0.000	-1.620	12.021	9.738	-1.286	-2.134	0.000
0.284	-1.668	-0.805	-0.197	-2.300	-2.945	0.398	-0.874
-0.380	0.278	-2.638	1.142	0.463	1.448	-2.317	0.806
0.059	-1.920	-0.601	-0.629	-1.469	-0.531	-1.378	-1.017
1.201	0.000	0.000	-1.958	0.000	0.000	0.137	0.000
0.000	-0.650	-1.162	0.000	-3.090	2.204	-1.750	3.715
-1.256	-1.169	-0.736	-1.353	6.652	-1.256	5.137	0.410
3.774	5.261	0.594	2.200	3.129	1.192	3.478	0.000

Table35.txt

0.000	-1.030	-0.734	0.676	0.039	3.207	5.216	-1.400
0.657	-0.546	0.000	4.933	3.387	2.856	14.707	3.788
3.313	8.639	-2.997	-0.527	-0.513	-0.692	-2.489	0.214
-1.345	-0.209	-1.598	-0.228	-3.241	-2.503	-0.287	-0.673
-1.061	-2.334	-0.165	-0.449	-2.448	-0.774	-3.891	-0.716
-0.380	0.074	0.000	4.157	5.274	-0.197	2.653	0.000
0.000	-0.103	0.863	1.495	4.306	10.136	9.834	1.123
4.059	-1.273	0.000	6.084	8.227	0.146	6.724	-2.110
0.067	-2.436	0.872	-1.725	-0.204	0.000	0.252	0.000
2.426	-0.436	0.045	0.000	2.269	-0.078	-2.184	-2.439
0.163	0.000	-0.027	0.312	2.973	0.522	2.706	0.218
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.994	-2.043	-2.194	-1.625	-0.348	-1.136	-1.977	-1.533
-3.370	-0.122	-1.665	0.120	-0.407	-0.318	-3.814	-1.516
-0.429	-1.053	-0.188	-2.616	-1.975	-3.299	-2.262	-0.994
-0.904	-0.760	-1.274	-2.123	-2.655	-1.549	-1.247	-1.199
-0.322	-1.028	-2.719	-0.975	0.215	-2.518	-1.326	-1.012
-0.513	-0.052	-2.722	-1.516	-1.537	-1.535	-4.751	-0.662
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-2.416	-3.087	-3.662	-3.363	-0.990	-0.408	0.756	-0.376
0.146	2.122	-1.423	-0.660	0.561	-1.827	-1.188	-2.659
-1.021	-0.025	0.882	-0.360	-3.224	-0.593	-1.312	-2.449
-0.952	-2.165	-1.516	-1.807	-0.451	-1.978	-0.244	-0.308
-3.055	0.357	-1.879	0.937	0.153	-2.013	7.904	-1.222
-0.507	0.268	-1.240	-3.324	-2.331	-2.136	-1.841	-1.111
0.358	0.746	-1.018	-3.040	-2.352	-1.293	-0.769	0.019
-0.032	0.000	-0.154	0.111	-1.238	-0.674	-1.544	-0.183
0.508	-0.814	-1.764	-1.493	-1.051	-1.227	-0.307	-0.002
-1.118	-3.123	-1.247	-2.432	-0.438	-0.759	0.093	-0.907
0.647	0.219	-0.139	-0.762	-0.826	0.513	-2.130	-0.533
-0.662	-2.144	-0.287	-1.280	-1.639	0.276	-2.671	-1.047
0.833	-1.396	-1.650	-1.078	5.560	0.657	-1.117	0.000
2.356	0.899	-2.614	1.638	0.686	-0.527	-0.277	-0.061
0.285	4.142	0.000	1.534	0.353	2.486	5.303	0.916
2.550	1.143	2.422	-0.835	0.402	0.000	0.000	0.000
1.526	-0.395	-0.544	0.333	0.969	1.578	-0.493	0.001
-0.188	0.434	0.000	0.272	4.029	3.483	4.929	-1.376
-0.790	-0.212	-3.555	-0.865	0.791	0.366	0.000	0.000
-1.185	0.000	-1.030	-0.445	-0.074	-1.501	-0.532	0.266
0.000	0.000	0.000	-1.926	1.401	-1.396	0.137	1.142
9.673	11.525	-1.353	-1.740	-0.065	-0.183	-1.659	1.882
1.999	-1.108	-1.000	-0.577	0.848	-2.402	5.580	-1.775
-0.069	-0.161	-2.570	-0.119	-0.511	-2.451	-2.109	-2.767
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table35.txt

0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
-0.025	-0.338	4.199	9.559	-1.067	-2.364	4.938	1.273
8.194	-1.394	-0.121	-3.006	-0.686	-1.981	8.320	1.539
2.763	4.603	0.000	-1.629	-1.858	7.809	-0.107	4.836
-0.880	-0.034	-3.183	1.109	-3.234	-3.090	-0.013	0.000
0.000	1.049	0.000	0.000	1.554	-1.720	4.952	-2.450
-0.413	0.395	0.000	2.069	-2.892	0.744	-2.325	-0.944
-0.477	-1.092	-2.098	-0.291	-1.683	-0.925	-2.853	0.010
-1.778	-1.627	-1.693	-0.420	0.012	-2.127	-1.424	2.419
3.205	-0.782	1.189	0.245	-2.056	-1.699	-2.603	-1.545
-1.754	4.427	5.753	-0.719	-1.395	0.067	0.469	2.858
0.284	0.213	-1.153	-1.609	0.825	-0.558	2.676	-1.099
0.126	0.092	1.657	2.838	-1.559	-1.936	16.461	2.913
0.328	-1.764	-0.007	0.011	-1.138	-1.313	-0.896	-0.611
-1.319	-0.321	-2.015	0.329	-0.805	-1.569	6.430	-1.530
-0.044	-1.140	-1.402	-1.291	-2.008	-1.383	-1.734	-1.666
2.132	3.629	-0.203	1.482	3.059	-2.262	0.155	0.000
0.000	0.000	0.000	0.695	0.022	6.012	5.884	3.766
3.090	5.228	0.932	1.728	0.268	4.368	9.077	-0.686
4.305	5.878	5.800	2.248	5.988	2.585	4.051	-1.049
-0.026	3.462	4.844	1.550	-2.961	0.215	-0.212	-1.286
3.645	0.142	0.000	4.648	1.083	0.152	0.091	3.101
-0.147	-2.846	0.763	-1.921	-1.877	0.201	-0.556	0.237
-1.960	-0.327	-0.553	0.000	-0.535	-0.940	-1.535	-0.121
0.542	-0.068	-0.009	-0.542	-2.466	-0.978	-1.199	-2.341
-0.694	-1.998	-1.513	-4.027	-1.833	0.888	-0.680	0.099
0.314	-0.658	0.772	-1.150	0.309	-3.858	-1.140	-1.481
-0.445	0.651	-0.206	-2.531	-0.566	-1.159	0.696	-1.499
-0.631	-2.227	-3.509	-1.139	-0.653	-0.411	-0.013	-0.752
-2.345	-1.914	-0.821	-2.842	-1.195	-2.537	-0.643	-0.597
-0.841	-0.475	-0.832	-0.557	-2.516	-1.403	-1.787	-1.585
-0.586	-1.756	-1.458	0.493	-2.183	-1.003	-3.207	-0.220
-0.101	0.124	-2.228	0.000	-0.375	-2.544	13.698	-2.167
-2.551	-0.651	0.139	-1.095	-1.449	-2.752	-2.145	-0.663
-0.217	-0.855	-0.049	-1.245	-0.696	0.050	-0.514	-0.144
-3.084	-1.256	-2.192	0.000	0.071	-0.176	-0.042	0.561
0.000	-0.736	0.000	-0.384	-1.270	-0.350	-1.417	-1.112
5.366	1.539	8.892	2.019	1.513	-1.480	-1.126	3.928
6.328	0.093	5.061	0.398	-0.933	0.142	2.683	0.351
2.182	-1.365	4.314	6.276	1.542	3.440	0.997	0.528
0.986	2.104	1.643	-0.856	-0.319	-2.595	-2.021	0.000
0.000	0.000	0.000	1.002	1.504	1.887	6.725	1.996
0.315	-0.264	-2.232	9.286	1.265	5.101	-1.405	0.000
1.514	6.906	-1.129	-0.428	5.507	1.017	4.186	0.000
0.248	0.106	-0.131	-0.183	-0.048	-2.484	0.401	-2.314
1.685	-0.215	0.000	-1.948	-1.888	6.665	4.163	-1.855

Table35.txt

-0.511	-0.564	-2.374	-2.369	0.224	-2.070	1.192	-1.441
-1.050	-0.986	-1.549	-0.381	-0.259	-1.101	-2.072	-2.178
-1.392	-1.416	1.354	-0.449	-2.488	-1.565	-0.961	-3.459
2.539	4.727	3.055	-0.946	-3.004	0.122	-0.081	0.389
-1.483	1.232	-0.629	-0.421	0.363	-1.608	-3.071	1.722
2.150	0.485	-1.290	4.245	4.027	-0.716	-0.415	0.076
1.285	-0.431	-1.603	-1.698	-2.694	-1.264	-2.149	0.999
0.785	-1.775	-0.649	-2.033	0.492	-0.202	0.672	-1.148
0.668	-0.079	-0.583	-2.609	0.118	-0.752	-1.297	0.000
-0.874	-0.701	0.114	-2.719	-0.401	-2.601	-0.575	0.168
-0.332	-0.736	0.185	-0.768	-1.102	-0.131	0.192	3.411
1.060	1.607	-0.986	-1.371	-1.717	2.028	-1.906	0.410
7.126	7.136	-0.188	-1.814	6.799	11.596	4.023	8.598
-1.982	-2.283	4.882	8.432	4.422	5.194	-0.696	-1.762
-2.938	-0.853	1.651	6.422	5.770	3.514	2.290	1.054
11.243	12.025	0.057	-0.720	8.574	12.734	6.059	8.647
-3.309	-1.076	6.412	13.307	5.300	6.721	-0.075	-1.495
-2.431	-0.966	4.588	7.460	10.306	5.757	7.094	-1.864
-2.329	1.712	-0.693	-1.071	0.279	-0.363	0.301	-1.483
0.640	-1.773	-0.443	0.175	-0.389	0.181	-0.632	0.071
-2.128	0.412	-0.240	-1.820	0.162	-0.089	-1.249	-0.002
2.085	-0.818	-1.162	-2.209	0.228	-0.596	-1.801	0.235
4.302	5.442	-1.503	0.232	-0.264	-0.306	0.345	0.573
-1.266	0.398	-1.308	-0.483	0.235	0.648	0.131	-0.876
-1.538	-0.888	-2.249	-1.697	-2.259	-1.381	-2.043	-0.102
6.425	10.743	4.474	8.765	5.152	5.891	-0.300	-0.827
-1.092	-0.274	3.422	8.794	10.895	-0.925	-1.192	-0.324
-1.720	-1.585	1.471	-3.548	-0.142	-1.287	-1.496	-0.125
0.720	-1.008	-1.051	2.018	-0.515	0.382	1.458	-3.249
0.902	-3.493	-1.094	2.164	-2.332	-3.029	0.205	0.891
-0.359	-0.664	3.325	8.219	4.844	8.827	-2.356	-0.094
-2.480	8.037	-1.227	-0.027	4.153	2.226	2.239	7.689
6.061	6.866	-1.493	-1.394	-1.066	-1.733	4.891	-0.556
-1.144	-2.588	-0.868	-1.859	-0.150	0.200	-1.687	0.092
-1.680	-0.328	-0.367	0.567	0.214	0.596	1.030	-0.574
0.957	-0.664	-0.486	-0.546	-2.501	0.069	-1.026	-0.310
-2.146	0.107	-0.785	-0.770	-1.241	0.578	-0.077	-2.017
5.650	7.324	3.321	7.864	-1.945	-0.564	0.733	-1.157
0.958	0.105	-1.362	-1.031	11.285	2.981	-3.640	1.259
-0.392	1.198	-0.327	-2.709	-0.167	6.044	-2.293	-0.727
-0.225	0.068	0.020	0.514	-0.526	-2.118	-2.790	0.618
-1.453	-1.213	0.199	1.961	-1.180	-2.562	-0.906	0.030
-0.008	-1.183	-0.689	-0.385	-1.910	-2.366	-1.106	-0.402
0.219	-1.346	-0.944	-1.016	-2.015	0.520	-0.926	-0.437
-1.247	-1.598	-0.343	-3.944	-0.704	0.981	-1.906	0.051
7.510	-0.767	-1.025	-0.965	-1.924	1.060	-0.685	-1.036
0.505	-1.491	-1.820	-0.195	-0.566	1.452	-0.077	0.539
-0.475	-1.116	-1.214	-1.358	-0.275	0.027	-1.210	-0.270

Table35.txt

3.817	-0.330	-1.271	0.394	-0.687	0.014	-1.475	-2.617
4.732	4.800	-0.335	-0.058	-1.721	-2.463	0.214	0.307
-0.462	-0.990	-2.958	-0.763	-2.243	-2.013	-0.072	-1.342
-0.111	-2.238	4.319	2.085	-0.916	9.142	-1.619	1.502
0.220	0.308	-3.002	-1.195	-1.292	0.461	-0.658	-0.164
0.502	-1.440	-0.177	0.473	11.221	-0.561	7.650	0.295
-0.029	-2.237	0.658	-1.471	-3.022	-1.576	-0.814	-2.471
7.656	5.703	-0.104	1.256	-0.562	-1.742	-0.634	0.173
-1.126	-0.652	-0.674	1.324	0.183	0.280	4.030	2.633
6.417	-0.436	0.011	-1.227	-1.383	-0.315	-0.772	-1.313
-0.906	-1.245	-0.340	-1.982	-1.984	-0.046	-1.215	-1.624
-2.254	-1.740	-0.111	-1.762	-0.258	0.930	0.640	-2.930
-2.409	-1.900	-2.648	-0.129	-0.393	7.873	-1.311	-2.309
0.325	-1.405	0.152	-1.359	-0.133	1.510	1.092	0.004
-1.698	-1.880	-1.521	-1.565	-1.730	-2.264	0.241	0.280
-0.939	-1.821	-0.422	-2.217	-1.453	6.076	-0.308	-1.311
-1.670	-0.474	-1.396	2.476	-0.939	0.165	-0.787	1.066
-1.330	-0.508	-0.812	0.771	0.345	-2.144	-0.686	-0.541
-0.069	-2.469	-0.402	-1.333	-0.828	-0.018	0.176	0.564
-1.213	-0.817	0.375	-0.549	-0.138	-1.893	0.774	-3.169
-2.267	-0.599	-0.213	-0.436	-1.155	-0.525	-0.015	0.637
-0.827	-0.661	8.180	18.366	-0.289	2.213	-2.663	-1.858
1.532	-0.378	8.958	9.525	-0.838	-0.174	-0.919	1.617
-0.193	2.697	0.223	4.948	-1.583	2.610	3.013	0.849
-1.911	-1.606	-1.624	-1.080	-1.193	-1.371	-0.357	-0.085
6.991	8.829	-2.209	-0.645	0.191	-0.462	0.938	-1.474
-0.089	-1.191	-1.389	9.930	-2.318	-1.164	-0.822	-1.636
-1.303	0.028	0.640	-0.918	-2.106	-1.175	0.165	-2.997
-0.315	-1.245	-1.305	-2.323	-2.450	-0.039	-0.258	0.567
-1.020	-1.451	-1.755	-3.426	12.450	-2.290	2.169	-3.135
0.215	-2.135	4.764	11.401	-0.507	-1.509	-0.271	-2.231
-1.850	-0.458	5.763	0.760	0.897	-0.937	-0.753	-1.716
-0.864	-1.396	-1.016	-0.425	0.033	-0.672	-2.002	2.830
-3.253	-2.646	-3.018	-1.574	-3.587	-1.472	-0.328	0.331
-1.633	-2.827	-1.582	-0.007	-0.408	1.563	-0.323	-1.082
-0.862	-2.094	1.603	-3.010	-1.859	-0.266	-0.194	-0.746
-0.118	-0.209	-2.311	0.092	-0.411	-0.708	-1.315	-1.124
-1.350	0.464	-2.320	-1.854	-2.105	-0.696	-0.560	-2.245
-2.650	0.921	-1.052	-1.281	-1.967	-2.509	0.100	0.487
-0.397	-2.422	-0.824	-1.769	-0.759	-3.090	-2.012	-0.064
0.075	3.709	0.000	-1.404	-1.396	0.022	-0.427	-1.240
-0.023	-1.343	-1.272	-0.703	-0.889	-0.077	-1.021	-0.402
-1.359	-2.738	-1.204	-0.970	-1.063	-2.599	0.094	-2.450
0.837	-0.763	-2.751	-2.195	-0.423	-0.625	-1.392	-2.187
-2.654	-1.117	1.328	-0.630	-2.387	-1.484	-0.333	-0.936
-2.138	-1.449	-0.220	-2.583	-1.128	-1.375	-0.341	-0.017
-0.953	-1.512	6.940	7.460	0.230	-2.102	0.613	-1.821
-0.445	10.889	-1.227	0.922	-1.105	0.765	0.113	-1.723

Table35.txt

-2.332	-0.418	-0.078	-2.264	-1.517	4.116	-0.780	-1.006
1.536	-0.738	-0.599	0.565	-0.275	-0.332	-2.687	0.516
-1.620	0.083	0.173	-0.905	-0.464	0.267	-1.184	0.269
-1.491	-0.297	-0.545	-2.769	0.010	0.702	-0.709	-0.439
10.690	14.327	-2.288	-0.399	-1.640	-0.021	-0.940	-0.623
0.002	-1.138	-0.690	0.734	-0.468	0.019	-0.038	-1.353

			Cancer				
chr16q_AI	chr17p_AI	chr17q_AI	chr18p_AI	chr18q_AI	chr19p_AI	chr19q_AI	chr20p_AI
chr20q_AI	chr21q_AI	chr22q_AI	Type		Subtype		
		Stage					
9.384	8.159	4.070	9.828	15.576	7.780	8.667	6.152
6.339	0.344	-0.778	Colorectal		NA		
		NA					
-0.883	0.166	8.212	-0.039	-3.055	0.130	-0.683	-0.953
2.060	0.310	-0.506	Colorectal		NA		
		NA					
5.122	0.424	0.332	-0.543	-0.781	1.368	1.421	6.865
6.141	-0.041	-1.956	Colorectal		NA		
		NA					
-1.574	8.900	9.457	-0.832	13.758	3.142	6.785	10.474
5.508	0.744	0.287	Colorectal		NA		
		NA					
11.933	7.048	1.011	-0.205	14.189	2.465	3.310	0.401
2.597	4.324	8.728	Colorectal		NA		
		NA					
-1.707	-0.306	-0.458	-0.394	-0.487	0.159	-2.019	-0.129
-0.837	0.187	-0.309	Colorectal		NA		
		NA					
8.862	-1.321	1.069	-2.694	13.414	-1.796	-0.598	4.541
7.569	1.613	-0.552	Colorectal		NA		
		NA					
14.178	0.111	2.029	5.501	14.033	-0.013	0.974	8.570
0.083	-1.182	0.631	Colorectal		NA		
		NA					
9.741	7.441	0.446	6.767	9.920	0.304	-1.501	5.937
7.940	-1.265	-1.225	Colorectal		NA		
		NA					
-1.604	0.676	0.982	2.177	0.357	0.211	-0.132	0.169
0.506	0.178	-0.113	Colorectal		NA		
		NA					
-1.225	-1.961	-0.228	-2.008	-0.193	1.114	-0.655	-1.857
-0.928	-2.303	-0.776	Colorectal		NA		
		NA					
-1.099	7.840	8.774	8.493	16.516	-0.252	-0.410	-0.478

Table35.txt

-1.411 11.110 6.668 Colorectal NA
NA
10.598 8.148 4.011 6.730 13.886 -1.435 0.223 0.260
-1.897 -0.685 4.927 Colorectal NA
NA
-1.714 3.828 0.934 3.847 10.504 -0.539 -0.003 3.958
2.385 -0.784 -1.026 Colorectal NA
NA
0.138 7.028 9.389 9.503 13.966 7.998 8.993 7.009
7.902 -1.187 -0.236 Colorectal NA
NA
-2.522 -0.779 13.682 -0.390 3.683 6.714 8.065 3.573
8.119 0.274 -0.391 Colorectal NA
NA
0.900 0.033 0.198 6.181 13.355 -0.583 -0.801 8.192
9.159 0.119 2.405 Colorectal NA
NA
5.272 6.220 11.241 4.893 9.840 2.785 3.697 5.608
5.896 2.452 3.742 Colorectal NA
NA
-0.644 7.724 6.415 7.335 13.403 2.984 6.176 7.864
6.626 6.899 5.286 Colorectal NA
NA
13.130 7.508 4.254 8.703 17.636 2.957 5.068 7.863
7.208 9.124 -0.433 Colorectal NA
NA
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8.825 12.474 2.684 Colorectal NA
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Table35.txt

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-0.378 -0.174 -3.205 Colorectal NA
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Table35.txt

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Table35.txt

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-1.410 -1.385 -1.439 Colorectal NA
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NA
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Table35.txt

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-1.221 -0.290 -1.897 Colorectal NA
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Table35.txt

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2.877 2.591 1.553 Colorectal NA
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Table35.txt

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-0.671 1.457 0.646 Colorectal NA
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7.508 7.036 6.188 Colorectal NA
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11.030 6.357 7.290 5.716 12.022 4.677 2.037 4.830
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Table35.txt

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2.184     -1.148    -1.222    Colorectal          NA
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-1.138    0.491     -1.415    Colorectal          NA
                    NA
8.922     6.245     0.926     3.548     7.944     -1.521    -1.777    6.771
4.237     1.038     -0.345    Colorectal          NA
                    NA
-1.976    7.561     6.371     7.458     13.537    -0.221    0.546     7.956
6.765     8.655     -1.022    Colorectal          NA
                    NA
1.745     6.491     9.129     6.387     15.986    2.519     2.669     3.451
4.120     1.394     5.028     Colorectal          NA
                    NA
-2.180    8.140     1.871     7.588     14.781    3.478     5.987     8.880
8.724     6.935     6.200     Colorectal          NA
                    NA
9.077     7.237     4.953     10.068    -1.673    6.514     8.860     0.519
-0.125    4.281     7.120     Colorectal          NA
                    NA
-0.258    2.462     1.431     0.583     -1.476    0.706     -2.242    1.020
1.727     -1.396    0.764     Colorectal          NA
                    NA
7.684     7.735     6.792     7.347     12.660    2.461     4.664     1.422
1.079     6.626     0.177     Colorectal          NA
                    NA
-1.644    4.974     0.265     5.953     13.286    1.373     1.077     -0.333
7.647     11.474    -0.561    Colorectal          NA
                    NA
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1.221     10.782    -1.700    Colorectal          NA
                    NA
-0.980    5.999     7.533     4.963     0.201     -1.332    2.568     4.171
3.603     6.447     7.143     Colorectal          NA
                    NA
2.197     1.008     1.139     4.838     13.741    -0.365    -0.255    0.383
6.491     10.716    7.000     Colorectal          NA
                    NA
0.055     -2.474    5.376     1.769     0.418     0.624     0.421     -1.203
-0.599    -1.445    -1.563    Colorectal          NA
                    NA
-1.321    6.177     5.952     8.191     15.125    5.600     8.002     -1.203
0.014     7.396     6.539     Colorectal          NA
                    NA
-0.084    6.211     3.914     6.256     11.855    6.198     9.371     6.803
5.337     0.315     -1.451    Colorectal          NA
                    NA
-0.358    -0.898    -0.699    -1.325    -0.559    0.047     -0.618    1.739
```

Table35.txt

0.587	-0.565	-2.490	Colorectal		NA			
			NA					
-0.065	0.005	-1.642	0.334	-2.489	0.039	-1.154	-1.061	
-0.644	-3.423	-3.518	Colorectal		NA			
			NA					
3.491	4.286	0.980	5.259	2.176	5.342	3.090	3.277	
2.131	-1.761	4.370	Colorectal		NA			
			NA					
0.360	-0.495	1.689	7.768	14.410	0.602	-1.230	7.193	
6.841	0.159	0.395	Colorectal		NA			
			NA					
1.326	3.403	6.084	7.000	9.951	1.844	6.370	6.317	
4.224	2.923	3.594	Colorectal		NA			
			NA					
-0.323	-0.676	2.721	-0.127	1.488	-0.449	-0.007	2.982	
0.963	0.772	-1.536	Colorectal		NA			
			NA					
3.958	8.513	11.365	6.615	14.697	5.059	7.868	8.566	
7.808	9.645	5.731	Colorectal		NA			
			NA					
-1.465	-1.256	-1.368	0.000	-1.001	0.000	-2.104	0.000	
0.595	0.000	0.000	Colorectal		adenocarcinoma			
			I					
-1.424	0.092	-1.720	0.000	-2.311	-1.634	-0.675	0.000	
-2.340	-1.792	-1.145	Colorectal		adenocarcinoma			
			IIA					
0.225	-1.365	-0.137	0.705	-1.117	1.022	2.191	0.000	
2.985	-0.491	-0.856	Colorectal		adenocarcinoma			
			IIA					
-1.977	-1.646	-1.761	-0.737	-1.702	1.463	2.122	-0.929	
-2.415	0.896	-1.819	Colorectal		adenocarcinoma			
			IIA					
-1.757	-0.943	-2.357	-1.858	-1.662	-1.214	-0.178	-3.018	
-1.342	-1.022	-0.215	Colorectal		adenocarcinoma			
			IIA					
1.322	-0.823	0.350	-1.571	-1.333	0.203	-1.112	0.000	
2.364	0.000	0.615	Colorectal		adenocarcinoma			
			I					
-2.845	-1.403	-1.921	-1.140	-0.043	-0.455	-2.319	0.740	
-3.722	0.226	-2.097	Colorectal		adenocarcinoma			
			I					
6.958	-1.076	-2.951	6.495	-1.028	5.013	6.218	5.858	
15.895	-1.113	1.305	Colorectal		adenocarcinoma			
			I					
0.411	1.479	1.944	-1.472	-0.591	1.478	1.355	-0.541	
-0.937	3.670	3.554	Colorectal		adenocarcinoma			
			IIIC					
0.000	0.000	1.582	0.000	0.000	-1.378	1.098	-1.338	

Table35.txt

0.854 2.266 1.514 Colorectal adenocarcinoma
IIIB
-0.236 -0.246 -0.399 -1.536 0.763 -0.756 0.303 0.000
2.357 1.044 -0.803 Colorectal adenocarcinoma
IIIB
-1.145 0.605 0.000 -1.415 -2.106 0.450 -1.945 0.000
9.086 -1.451 0.128 Colorectal adenocarcinoma
IIIA
0.000 0.841 0.000 -0.825 -1.358 -0.813 -2.214 0.000
2.341 0.000 -0.943 Colorectal adenocarcinoma
IIIB
-1.875 0.391 -4.011 -1.299 -1.149 -0.329 -1.428 0.978
13.064 0.051 -1.434 Colorectal adenocarcinoma
IIA
-1.510 0.955 0.893 0.634 -0.608 8.142 -0.951 1.100
5.203 -1.710 -0.227 Colorectal adenocarcinoma
IIA
2.416 0.917 3.052 1.549 -3.494 -1.256 -0.794 1.763
6.104 1.772 -0.687 Colorectal adenocarcinoma
IIIB
-1.433 -0.883 -2.189 -0.500 -3.109 -2.366 -2.750 -0.790
-0.971 -1.073 -1.256 Colorectal adenocarcinoma
IIA
0.636 0.689 -0.275 -2.098 -1.178 2.852 3.970 -0.699
-1.010 3.678 1.598 Colorectal adenocarcinoma
IIC
0.950 -1.906 -1.201 -2.089 -0.201 -2.553 -0.750 -1.113
-0.301 -0.161 1.433 Colorectal adenocarcinoma
IIIB
-1.995 -1.409 -3.710 2.328 -3.187 0.262 -2.721 0.671
-2.216 -1.644 -2.146 Colorectal adenocarcinoma
I
0.000 0.000 0.000 -0.217 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal adenocarcinoma
IIA
2.095 0.000 -0.220 0.000 1.418 0.865 0.955 0.000
-1.648 0.269 -0.790 Colorectal adenocarcinoma
IIB
1.353 -1.364 2.017 -0.587 -0.475 -0.104 -0.008 -0.610
-1.387 -0.180 0.166 Colorectal adenocarcinoma
IIIB
-3.362 -1.237 -3.035 -2.303 3.484 0.145 -0.144 4.190
10.691 -2.015 -0.418 Colorectal adenocarcinoma
IIA
-2.391 -1.361 -0.135 -3.334 -2.059 0.783 -1.012 -0.524
-4.514 0.789 1.469 Colorectal adenocarcinoma
IIIB
-1.320 -1.072 -3.017 3.814 -3.323 -0.210 -0.245 -0.881

Table35.txt

-2.305 3.816 1.968 Colorectal adenocarcinoma
IIA
1.381 3.090 0.535 -1.036 -1.891 -0.758 0.807 -1.057
-1.746 1.501 2.927 Colorectal adenocarcinoma
IIIB
-1.805 -1.389 -1.779 -0.445 0.355 -0.263 -1.773 -0.407
-4.945 0.799 -0.991 Colorectal adenocarcinoma
I
-1.292 -3.084 -0.091 -0.107 -0.488 -1.753 2.512 -0.171
2.553 -0.378 -1.467 Colorectal adenocarcinoma
I
-2.223 -2.722 -2.871 0.769 -2.598 -1.528 -2.289 -0.103
3.725 -0.817 -1.243 Colorectal adenocarcinoma
I
-2.518 -1.677 -3.750 -0.054 -2.275 -1.010 0.985 -2.020
-0.620 1.606 0.857 Colorectal adenocarcinoma
I
-0.834 -0.204 -0.054 0.288 1.962 -0.513 0.717 0.000
-2.660 -0.848 -1.845 Colorectal adenocarcinoma
IIA
6.005 -3.033 -1.384 -1.141 0.345 -1.680 -0.554 1.075
8.179 1.878 1.852 Colorectal adenocarcinoma
IIIB
0.180 -1.227 -0.898 -1.429 1.332 -2.212 -2.371 1.552
6.863 -1.821 -0.206 Colorectal adenocarcinoma
IIIC
0.499 3.636 2.820 1.934 2.540 -1.356 -3.296 -1.535
-1.911 -2.258 -1.632 Colorectal adenocarcinoma
IIIB
-2.013 -0.426 -4.476 -1.352 -1.342 4.562 6.520 -0.412
-2.305 -2.087 0.193 Colorectal adenocarcinoma
IIA
-0.812 -1.188 -0.954 0.000 4.922 7.217 -0.737 0.000
6.091 -0.587 -0.392 Colorectal adenocarcinoma
IIA
-0.853 -0.165 16.659 7.289 -0.614 7.877 14.251 1.692
3.673 -0.146 0.388 Colorectal adenocarcinoma
I
-1.412 -1.200 -1.692 -0.282 -1.677 1.523 -0.183 1.215
-2.366 -2.161 -2.860 Colorectal adenocarcinoma
IIIB
-1.150 -1.013 -1.749 -0.758 -1.666 -0.642 -1.601 -0.347
-1.960 -1.321 1.239 Colorectal adenocarcinoma
IIIB
-0.990 -1.285 -1.949 -0.746 -0.884 -1.475 -0.139 -1.660
-1.538 -0.792 -1.009 Colorectal adenocarcinoma
I
2.842 -2.082 -0.934 -1.831 -2.281 -0.427 -0.957 2.102

Table35.txt

5.671	2.049	1.560	Colorectal		adenocarcinoma			
			I					
-1.669	-2.135	0.388	-1.784	-1.184	5.386	5.727	-1.027	
-1.276	3.090	2.943	Colorectal		adenocarcinoma			
			I					
3.214	4.663	5.947	6.129	-2.035	0.082	0.957	3.270	
7.820	3.093	3.691	Colorectal		adenocarcinoma			
			IIIC					
1.895	0.000	0.000	-0.321	-3.153	4.775	1.448	0.000	
-0.247	3.444	-2.770	Colorectal		adenocarcinoma			
			IIIB					
0.000	0.138	0.000	1.302	1.286	-0.320	-0.533	0.000	
8.257	0.665	1.729	Colorectal		adenocarcinoma			
			IIIB					
-0.911	-2.903	-3.153	0.564	-1.989	1.447	-1.850	-0.159	
-1.614	-1.739	-2.604	Colorectal		adenocarcinoma			
			I					
-1.078	-1.711	-2.382	-0.506	-3.159	-1.006	-0.828	-1.424	
-1.300	1.497	-0.471	Colorectal		adenocarcinoma			
			I					
-3.097	0.271	-2.167	1.019	2.704	-1.870	-1.322	0.423	
1.581	-4.640	-0.302	Colorectal		adenocarcinoma			
			IIA					
18.135	9.953	15.506	-0.355	-1.569	5.636	2.022	7.740	
14.694	5.281	6.083	Colorectal		adenocarcinoma			
			IIA					
5.374	-1.527	7.651	-0.526	1.149	0.579	-0.172	3.090	
4.218	3.647	3.733	Colorectal		adenocarcinoma			
			IIA					
-3.419	-3.083	-2.663	0.441	-2.087	-1.979	-3.323	-0.824	
-2.111	-2.452	-1.746	Colorectal		adenocarcinoma			
			IIB					
10.851	8.587	16.232	-3.198	1.089	6.420	9.078	7.247	
14.430	5.788	1.943	Colorectal		adenocarcinoma			
			IIA					
4.260	0.183	1.962	2.833	5.635	1.245	4.416	-0.529	
-1.373	1.606	-0.679	Colorectal		adenocarcinoma			
			IIA					
-0.201	-0.219	5.709	-1.553	6.138	-0.668	0.059	-0.020	
11.719	0.644	1.066	Colorectal		adenocarcinoma			
			IIIC					
1.177	0.225	2.930	1.063	-0.014	0.500	-0.245	-3.090	
-1.805	0.000	0.000	Colorectal		adenocarcinoma			
			IIIB					
0.660	-1.953	-4.112	3.806	-0.249	2.214	5.712	0.181	
-2.314	-2.414	-0.183	Colorectal		adenocarcinoma			
			IIIB					
-1.303	-0.665	-1.490	0.823	-1.601	-0.483	-3.483	-0.694	

Table35.txt

-1.127 -0.215 -1.810 Colorectal adenocarcinoma
IIA
-2.704 1.250 1.604 0.660 0.669 -1.689 -2.608 1.526
4.309 -2.089 0.276 Colorectal adenocarcinoma
IIIB
-1.609 -2.686 -2.351 -1.317 -1.893 -0.616 -1.803 -1.900
-2.358 0.312 1.130 Colorectal adenocarcinoma
IIA
0.361 0.060 0.050 0.569 -0.155 -0.572 0.789 -0.539
-3.581 -0.265 -1.264 Colorectal adenocarcinoma
IIIB
-0.812 -1.774 0.923 -0.798 -1.490 -0.829 -2.160 -1.169
-0.339 -0.597 -0.775 Colorectal adenocarcinoma
IIIC
0.053 0.710 -0.539 -0.315 -2.452 9.429 11.167 4.785
-1.544 -1.169 -2.096 Colorectal adenocarcinoma
IIIB
-1.715 -1.161 4.677 -3.001 -2.086 -1.955 -0.783 -1.071
-2.892 0.477 -1.187 Colorectal adenocarcinoma
IIA
-1.544 0.000 0.109 -1.934 0.280 0.146 -1.704 -1.214
-1.268 -1.017 -0.275 Colorectal adenocarcinoma
IIA
2.083 0.000 3.090 2.947 3.789 1.969 5.081 0.000
4.539 4.582 3.670 Colorectal adenocarcinoma
IIA
7.221 -0.477 3.201 3.991 3.732 -3.321 3.505 5.343
3.918 12.773 -0.330 Colorectal adenocarcinoma
IIIC
-1.240 3.621 1.413 -0.646 8.631 2.038 2.821 2.271
1.379 -0.723 8.388 Stomach NA
NA
-1.546 2.857 3.186 -0.175 6.180 3.173 1.962 1.449
2.272 -0.505 6.963 Stomach NA
NA
11.070 5.946 -0.540 -0.550 11.844 1.268 6.558 0.165
-0.363 11.067 7.844 Stomach NA
NA
5.607 3.642 6.129 2.144 9.526 4.069 8.080 4.589
5.333 8.226 0.203 Stomach NA
NA
-1.224 1.384 0.085 1.845 -0.733 -3.844 5.558 1.331
-0.654 -0.361 -2.375 Stomach NA
NA
-1.181 5.181 1.912 5.445 12.963 0.763 0.282 3.005
-0.320 -0.567 0.221 Stomach NA
NA
-0.725 3.049 -0.056 5.753 6.057 3.205 0.435 -1.316

Table35.txt

-0.043	-0.261	-1.593	Stomach		NA		
		NA					
-0.325	4.355	0.139	6.914	6.570	4.002	1.280	-0.562
0.296	-0.564	0.478	Stomach		NA		
		NA					
4.908	3.506	0.835	6.914	9.632	2.541	2.984	3.319
2.021	1.568	-0.711	Stomach		NA		
		NA					
2.664	4.082	0.578	6.020	7.696	0.222	1.935	0.911
2.973	3.449	-2.069	Stomach		NA		
		NA					
6.355	6.316	0.434	6.319	6.313	6.022	-0.191	7.424
3.794	9.133	7.099	Stomach		NA		
		NA					
10.084	9.056	9.005	8.288	12.891	5.926	5.603	4.172
7.095	9.895	8.343	Stomach		NA		
		NA					
7.526	8.101	8.260	6.838	10.487	5.153	3.852	3.362
5.491	9.040	7.494	Stomach		NA		
		NA					
4.314	5.474	9.464	-1.437	-0.385	2.206	2.343	0.538
3.466	3.366	-0.354	Stomach		NA		
		NA					
7.754	7.702	-1.006	0.169	5.977	2.879	5.053	-1.459
6.467	4.842	4.769	Stomach		NA		
		NA					
7.760	3.297	3.735	0.151	3.804	5.523	1.905	-1.006
2.142	2.297	-1.196	Stomach		NA		
		NA					
14.158	7.344	1.056	7.285	4.698	2.874	2.143	0.407
0.349	-0.716	0.209	Stomach		NA		
		NA					
7.216	4.712	1.595	-0.399	7.076	3.791	4.687	8.250
5.238	-1.128	4.203	Stomach		NA		
		NA					
-3.041	0.458	0.528	0.566	0.119	-0.049	-0.199	2.061
-0.218	0.946	0.806	Stomach		NA		
		NA					
-1.892	3.436	7.000	-1.450	-1.269	-1.347	-0.406	-1.083
0.519	-0.981	0.745	Stomach		NA		
		NA					
-0.753	5.684	0.557	5.776	10.339	-0.901	-1.485	-0.312
0.089	-1.908	6.668	Stomach		NA		
		NA					
10.958	6.945	8.620	4.779	14.913	6.052	8.611	8.785
6.854	9.113	7.677	Stomach		NA		
		NA					
0.048	-0.347	-0.345	0.151	0.080	-0.964	-0.575	-0.934

Table35.txt

-0.624 -0.757 -1.144 Liver hepatocellular carcinoma
NA
-1.040 6.470 7.932 0.432 -0.899 -0.182 -0.480 -0.351
0.854 1.261 0.491 Liver hepatocellular carcinoma
NA
1.146 -0.802 0.909 0.433 -0.885 4.532 3.460 -0.368
0.200 0.351 -0.563 Liver hepatocellular carcinoma
NA
-1.663 6.064 8.281 -0.455 -2.695 -1.094 -0.795 -0.057
1.087 -0.400 1.445 Liver hepatocellular carcinoma
NA
-0.601 6.440 -1.356 -0.523 -0.705 -1.244 -0.789 -0.385
-1.919 8.341 -1.251 Liver hepatocellular carcinoma
NA
-2.665 6.219 1.074 6.066 0.160 1.770 0.288 2.255
2.194 2.655 -0.848 Head and neck NA
NA
2.659 0.921 1.619 -2.295 -1.100 -0.551 1.032 8.048
6.814 -1.197 -0.769 Head and neck NA
NA
6.872 7.510 2.131 6.336 11.773 5.604 8.081 5.945
0.429 12.098 1.937 Head and neck NA
NA
1.370 8.911 2.449 4.516 8.701 4.298 7.923 10.938
7.057 1.301 4.371 Head and neck NA
NA
10.363 10.545 2.316 0.388 -0.904 0.664 8.590 -1.717
0.775 -0.273 8.959 Head and neck NA
NA
12.454 9.268 5.824 9.706 13.513 0.170 10.168 -0.034
-2.044 -0.157 7.427 Head and neck NA
NA
9.037 6.578 6.707 6.169 9.974 3.090 6.367 -1.273
2.386 1.595 4.260 Head and neck NA
NA
-1.739 -1.211 0.580 -1.742 -0.527 1.808 -0.583 -0.249
-1.217 -0.586 -1.050 Head and neck NA
NA
-1.548 4.783 2.780 2.461 1.833 0.299 4.652 0.841
5.144 9.934 5.523 Head and neck NA
NA
1.550 1.031 -0.970 -1.458 0.538 -1.295 1.470 -0.338
-0.811 0.297 0.287 Head and neck NA
NA
1.685 -1.578 5.787 7.382 15.614 6.009 7.553 10.001
7.538 9.612 0.014 Head and neck NA
NA
-0.301 -1.107 0.601 -0.277 9.084 0.968 6.576 -1.652

Table35.txt

3.588	-0.946	1.053	Head and neck	NA			
NA							
-2.385	-0.526	-0.639	0.094	8.596	0.517	0.685	-0.037
-0.668	-0.023	-1.753	Head and neck	NA			
NA							
0.573	2.913	4.886	2.854	2.165	0.834	0.519	2.021
1.238	3.027	-0.080	Head and neck	NA			
NA							
-1.532	-0.495	2.706	0.581	1.889	0.577	-0.535	0.220
-1.783	0.632	-1.088	Head and neck	NA			
NA							
10.628	-0.190	0.099	2.843	5.262	-1.892	-2.780	3.945
3.002	-0.234	0.964	Head and neck	NA			
NA							
-1.632	1.158	0.242	-0.069	1.516	0.405	0.286	2.455
-2.095	-0.930	-0.052	Head and neck	NA			
NA							
5.256	6.590	7.964	7.323	15.969	3.993	2.663	2.319
0.971	10.599	1.909	Head and neck	NA			
NA							
-1.005	4.638	-1.865	-1.768	-0.071	-0.130	0.367	-0.293
-0.118	-0.088	0.424	Head and neck	NA			
NA							
1.620	6.536	7.290	1.121	13.201	5.718	4.861	-1.320
-1.636	8.520	1.973	Head and neck	NA			
NA							
-1.560	-2.200	0.226	1.792	0.317	-0.428	-0.792	0.308
-0.249	0.159	-0.319	Head and neck	NA			
NA							
-1.146	0.732	3.026	0.265	-0.171	-0.945	0.248	1.121
4.940	0.119	5.694	Head and neck	NA			
NA							
1.091	7.035	7.137	1.436	0.134	2.771	2.334	4.014
3.111	1.829	5.093	Head and neck	NA			
NA							
0.443	-0.124	-0.100	-0.076	-0.588	1.889	0.715	4.161
4.281	-0.793	3.089	Head and neck	NA			
NA							
7.025	0.084	-0.683	-1.207	-0.820	2.178	3.797	2.633
-1.267	6.177	-2.013	Head and neck	NA			
NA							
0.301	1.015	1.884	1.460	10.033	0.178	-0.473	-0.073
0.792	-0.720	-2.917	Head and neck	NA			
NA							
1.697	0.387	-1.067	6.475	9.891	-1.057	-0.598	-0.981
1.117	10.526	0.969	Head and neck	NA			
NA							
-0.766	7.879	1.479	2.939	1.753	3.090	-0.270	0.655

Table35.txt

1.230 0.596 4.520 Head and neck NA
NA
10.328 6.616 9.877 8.356 16.603 4.915 6.911 8.610
6.036 10.441 5.850 Head and neck NA
NA
-0.880 -1.296 0.010 -1.070 -0.746 2.211 -1.040 0.203
0.154 9.847 0.493 Head and neck NA
NA
1.280 0.403 -0.720 -1.732 -2.907 1.956 0.456 9.219
4.612 10.832 0.419 Head and neck NA
NA
-0.500 2.101 -1.833 -0.863 -0.433 2.238 -0.199 -0.750
-0.669 1.203 -0.109 Head and neck NA
NA
-0.181 4.601 0.884 -2.265 12.857 0.512 -0.505 -0.282
1.827 -0.541 1.692 Head and neck NA
NA
8.285 8.566 9.829 -2.557 7.515 4.392 9.904 7.704
9.052 10.186 5.570 Head and neck NA
NA
-3.434 -2.218 -1.568 -1.759 0.094 -0.901 -1.625 -0.473
-1.474 -0.509 -2.619 Head and neck Adenoid Cystic Carcinoma
NA
-2.356 -0.827 -2.414 5.312 10.748 1.611 2.274 2.619
7.395 -0.225 -1.861 Head and neck Adenoid Cystic Carcinoma
NA
-2.455 -0.431 -1.086 -0.449 -0.565 1.030 -2.094 0.000
-0.492 -3.090 -0.281 Head and neck Mucoepidermoid Carcinoma
NA
-2.096 -1.434 -0.315 -0.477 -0.871 -0.319 -0.438 -2.107
-1.595 -0.645 1.137 Head and neck Mucoepidermoid Carcinoma
NA
-1.063 -0.635 -0.833 -1.435 -2.558 -1.765 -1.175 -1.477
-1.573 -0.402 -1.587 Head and neck Adenoid Cystic Carcinoma
NA
-1.133 -3.594 -2.456 -0.011 -0.947 -2.264 -1.164 6.374
13.090 6.108 0.000 Head and neck parotid/adenoid cystic
NA
-2.207 5.141 -1.228 -0.637 -1.303 -1.038 9.341 0.168
-3.349 -0.145 -1.078 Head and neck submandibular/adenoid cystic
NA
-1.104 -2.431 -0.896 -1.018 -1.746 -1.335 0.500 -0.222
-1.419 -0.016 0.374 Head and neck parotid/adenoid cystic/adenoid
cystic NA
-0.670 -1.087 -2.390 -0.875 -2.003 0.011 -0.725 -2.649
7.133 -2.278 -1.965 Head and neck submandibular/adenoid
cystic/adenoid cystic NA
-3.028 -1.573 -2.833 0.839 -2.639 -1.381 -3.324 -1.800

Table35.txt

0.028 -0.466 -3.287 Head and neck adenoid cystic carcinoma/adenoid cystic NA
-2.388 -0.527 -2.071 -3.077 -0.269 -2.172 -0.701 -1.165 -1.908 -1.193 -2.001 Head and neck adenoid cystic carcinoma NA
-2.503 -0.418 -2.300 -0.737 1.777 -0.389 -1.412 -0.918 -0.617 5.415 -0.509 Head and neck lip/adenoid cystic NA
-1.276 -0.982 -2.854 -1.064 -1.096 -1.231 2.221 0.292 -1.056 6.939 0.065 Head and neck maxilla/adenoid cystic NA
-3.098 -0.002 -3.462 -0.368 -0.155 -0.712 -0.346 -1.283 -1.550 -0.400 0.486 Head and neck maxilla/adenoid cystic NA
3.063 -1.499 -3.022 -0.408 -0.236 -1.355 -1.801 -0.505 -1.949 0.503 -1.268 Head and neck tongue, NOS/adenoid cystic NA
-0.852 0.520 -1.970 -0.851 -0.705 9.467 12.151 -1.118 -0.699 -2.300 -1.268 Head and neck nasal septum/adenoid cystic NA
-3.198 -1.060 -0.477 -0.956 -0.496 -0.179 -2.531 -1.051 -1.292 -0.373 -1.203 Head and neck maxilla/adenoid cystic NA
-2.052 -0.345 -3.672 -2.154 -3.593 -1.811 -0.476 -0.467 -1.693 -1.690 0.141 Head and neck mailla/adenoid cystic NA
-2.703 -0.697 -3.653 -3.349 -0.027 -2.482 -1.946 0.054 -1.052 6.795 -0.350 Head and neck orbital/adenoid cystic NA
-0.646 0.058 -1.830 -1.684 -2.004 -2.288 -2.579 -0.363 -2.179 -0.772 0.241 Head and neck parotid/adenoid cystic NA
-0.888 -0.357 -2.619 -1.667 -2.806 -1.233 -0.402 -0.535 -2.095 0.681 -0.900 Head and neck submandibular/adenoid cystic NA
-1.918 -0.488 -2.654 -0.906 -3.156 -2.206 -1.148 -2.254 -1.423 0.128 -1.540 Head and neck maxilla/adenoid cystic NA
-1.224 -3.520 -0.882 -0.641 -0.540 -0.881 -2.049 0.893 -0.919 -2.837 -1.421 Head and neck maxilla/adenoid cystic NA
19.969 -2.054 14.493 -1.886 0.586 8.664 9.794 4.896 3.103 -1.159 3.254 Head and neck keratinizing SCC IVA
8.878 5.170 -0.821 0.238 3.818 3.956 1.986 -0.615 -0.253 9.818 -0.606 Head and neck SCC IV
14.149 0.107 -0.490 -0.534 0.259 4.067 4.192 4.663

Table35.txt

-1.244 8.335 3.222 Head and neck SCC
IV
-2.607 -0.591 -2.221 0.761 3.138 -0.979 -2.645 -1.385
-2.667 -1.807 -0.633 Head and neck recurrent SCC
IV
1.930 3.993 -2.745 0.831 2.536 0.744 5.899 4.433
-1.163 5.978 -0.542 Head and neck SCC
IVA
-1.105 -1.165 2.041 0.155 -0.908 0.939 -0.249 0.853
1.877 -0.185 2.707 Head and neck SCC
I
16.872 5.561 13.990 -2.507 -1.075 7.847 6.226 4.962
14.216 8.778 -2.864 Head and neck SCC
III
5.601 9.375 -2.505 1.487 0.074 5.589 11.990 3.286
10.071 2.696 6.770 Head and neck SCC
IVA
-2.139 -0.555 -2.706 3.108 -1.364 -0.781 0.210 -2.954
-0.711 -2.332 -0.197 Head and neck NA
NA
-0.050 7.041 15.682 1.689 5.761 0.288 12.546 4.881
12.154 10.040 13.959 Head and neck NA
NA
17.969 11.098 19.089 -0.865 3.947 11.725 -2.255 9.297
18.062 10.640 12.125 Head and neck NA
NA
2.911 0.139 -2.115 3.312 3.411 12.743 6.497 5.228
1.699 6.678 8.018 Head and neck NA
NA
0.644 -0.805 19.363 0.781 7.011 0.632 1.334 7.979
9.370 9.082 -0.202 Head and neck NA
NA
1.298 1.100 6.778 0.707 -0.296 0.615 0.500 4.910
6.476 5.437 5.021 Head and neck NA
NA
-1.510 6.539 2.496 -1.815 -1.139 -0.971 2.267 0.296
1.255 5.735 5.127 Head and neck NA
NA
-0.738 -0.940 -1.968 -1.815 0.564 -1.527 -1.121 6.704
18.489 12.018 14.353 Head and neck NA
NA
-1.232 -0.363 0.162 -0.126 -0.605 -1.345 0.242 0.505
-0.569 -1.024 0.455 Head and neck NA
NA
9.320 -2.260 -0.064 4.277 9.644 3.090 -1.241 4.113
-1.034 0.427 2.932 Head and neck NA
NA
-0.747 0.774 -2.123 0.945 11.550 10.363 -0.754 1.759

Table35.txt

16.438 -0.136 11.032 Head and neck NA
NA
2.218 12.856 23.787 7.280 15.065 14.053 8.635 14.726
23.703 12.778 14.327 Head and neck NA
NA
0.299 -0.285 -1.672 2.397 -1.327 -1.491 -0.805 2.235
3.069 2.195 1.629 Head and neck NA
NA
12.428 -4.023 1.600 8.783 -2.073 -1.560 -0.682 7.555
15.885 13.307 5.772 Head and neck NA
NA
-1.975 -0.153 19.069 7.918 19.554 11.059 17.842 4.615
7.983 14.502 12.732 Head and neck NA
NA
2.661 -1.123 -0.512 10.657 18.218 -0.711 -0.344 5.073
6.572 12.065 11.840 Head and neck NA
NA
19.394 -1.449 22.709 4.119 10.675 -1.100 1.684 2.326
-0.068 12.320 -0.060 Head and neck NA
NA
-0.203 -1.379 -1.411 0.693 -2.825 -0.446 -0.326 -2.211
-0.535 -0.592 0.098 Head and neck NA
NA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Head and neck SCC
IV
4.033 1.753 7.747 -0.438 -0.350 1.559 0.117 2.494
3.238 3.958 1.675 Head and neck SCC
I
-2.388 -1.322 -1.228 -2.486 -2.897 -1.282 -1.440 -1.957
-3.815 -2.690 0.615 Head and neck SCC
I
0.000 0.000 0.000 0.000 0.000 -3.090 0.000 0.309
0.000 0.000 0.000 Head and neck SCC
IVA
-0.335 0.137 -1.369 0.000 0.126 0.000 -2.305 -0.445
-2.097 0.000 0.000 Head and neck SCC
I
-1.935 -0.848 -0.431 0.595 -3.109 -1.221 -1.682 2.567
3.805 -1.015 -1.554 Head and neck SCC
IVA
-0.903 -0.731 -2.649 -1.198 -3.274 -2.767 -0.975 0.670
-2.505 3.023 2.208 Head and neck SCC
I
-1.123 -2.522 0.027 2.740 -2.281 -2.889 -1.195 -3.690
-1.195 0.000 0.000 Head and neck SCC
III
3.708 -2.233 -2.381 4.795 3.410 1.957 3.373 1.607

Table35.txt

3.006 8.731 9.475 Head and neck SCC
II
-2.428 0.346 -3.058 2.741 2.343 -2.317 -1.721 1.225
2.632 -1.492 0.002 Head and neck SCC
II
-1.647 -1.625 -0.927 3.112 -1.068 3.889 -0.663 7.111
11.407 -0.353 -0.978 Head and neck SCC
IVA
2.397 -0.689 -3.254 0.295 -1.647 -1.234 -1.095 2.395
10.433 -0.415 -2.367 Head and neck SCC
I
0.400 0.182 -0.703 0.949 -1.744 0.770 -2.286 -1.837
0.995 -0.096 -1.444 Head and neck SCC
I
10.560 0.000 3.930 -0.332 0.000 0.000 0.825 3.129
4.466 3.090 0.000 Colorectal Adenocarcinoma
IIA
2.014 3.090 4.357 -0.398 -1.249 0.759 0.835 3.068
4.236 3.674 -0.171 Colorectal Adenocarcinoma
IIA
-1.237 0.228 2.774 4.215 7.735 0.856 0.485 -1.236
3.891 -1.956 -0.412 Colorectal Adenocarcinoma
IIA
5.352 5.032 -2.256 0.413 -2.233 3.090 3.090 -2.937
5.301 2.642 0.550 Colorectal Adenocarcinoma
IIA
2.451 4.325 -0.124 6.376 8.051 -0.329 -0.115 4.959
6.548 5.269 0.472 Colorectal Adenocarcinoma
IIA
0.520 0.561 -0.385 2.345 3.083 1.004 -1.786 4.707
4.684 0.034 -0.387 Colorectal Adenocarcinoma
IIIB
8.777 2.641 0.250 -0.009 7.611 0.640 -1.867 -0.715
5.450 6.472 0.000 Colorectal Adenocarcinoma
IVA
-1.166 -0.242 -0.732 1.103 3.457 1.126 3.366 7.653
6.362 8.293 0.000 Colorectal Adenocarcinoma
IIIB
-0.886 1.368 -0.230 1.412 5.522 -0.779 -0.861 5.390
5.310 4.897 1.612 Colorectal Adenocarcinoma
IIA
-1.148 -0.445 -0.116 0.130 -1.539 -0.656 0.366 0.000
0.000 0.050 0.000 Colorectal Adenocarcinoma
I
-0.735 -0.340 -0.112 0.356 -1.468 0.000 -0.361 -0.920
-0.232 -1.635 1.653 Colorectal Adenocarcinoma
I
-2.252 -1.712 -0.789 -0.873 -0.902 -0.784 -0.164 -1.328

Table35.txt

0.888 -0.833 -0.123 Colorectal Adenocarcinoma
IIA
0.000 0.000 -0.677 -0.971 0.564 0.163 0.529 -0.169
-0.285 -1.228 0.000 Colorectal Adenocarcinoma
IIIC
-3.090 0.000 0.000 -2.557 -0.736 0.000 0.000 2.406
0.000 0.000 0.000 Colorectal Adenocarcinoma
I
0.000 0.000 2.697 0.000 0.000 0.000 0.000 -0.617
-1.171 0.677 -0.027 Colorectal Adenocarcinoma
IVA
2.493 0.000 0.776 0.000 0.046 0.000 0.000 -1.199
-1.324 1.338 -0.144 Colorectal Adenocarcinoma
I
-0.532 0.000 0.959 5.157 6.211 -0.277 -1.433 0.005
4.563 -0.761 1.029 Colorectal Adenocarcinoma
IIA
-2.085 -0.613 -1.181 -0.217 0.175 -0.421 -0.919 -0.443
0.028 -0.612 -1.677 Colorectal Adenocarcinoma
IIA
0.000 0.000 1.330 -0.514 0.194 0.000 0.000 0.163
0.000 0.019 0.000 Colorectal Adenocarcinoma
IIIB
2.530 0.000 3.238 4.725 2.506 2.220 -0.447 -0.732
1.399 1.373 0.000 Colorectal Mucinous Adenocarcinoma
IIA
2.054 0.022 1.475 2.866 2.037 0.000 -0.439 -0.416
2.700 1.242 0.229 Colorectal Mucinous Signet Ring Cell
Adenocarcinoma IIA
0.000 0.000 0.000 0.000 0.610 0.050 0.000 0.218
-0.234 0.000 0.000 Esophagus Squamous Cell Carcinoma
IIA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Liver Hepatocellular Carcinoma,
Acinar Type II
-0.858 0.000 0.497 -0.624 -2.788 1.472 0.026 2.534
0.176 2.338 -0.005 Liver Hepatocellular Carcinoma,
Solid Type II
2.668 4.000 -0.605 0.314 -1.056 1.785 -0.114 1.384
3.523 5.158 -0.967 Liver Hepatocellular Carcinoma,
Pleomorphic Type II
0.000 0.000 -2.814 -0.645 -0.002 -1.214 0.000 0.460
0.000 -1.544 0.000 Liver Hepatocellular Carcinoma
n/a
0.090 1.756 0.017 1.919 -0.662 -0.713 0.122 1.517
-0.267 -1.108 0.621 Liver Adenocarcinoma
IIB
0.459 0.000 -0.123 -0.989 0.000 0.000 1.653 0.000

Table35.txt

1.961	-2.021	1.001	Colorectal			Adenocarcinoma, NOS		
			I					
0.997	0.000	-0.177	-0.593	0.000	-0.505	0.000	-0.322	
1.222	-0.808	0.000	Colorectal			Tubular adenocarcinoma		
			IIA					
1.080	0.000	-1.754	0.000	0.791	-0.715	-0.618	2.318	
0.883	0.995	0.451	Colorectal			Adenocarcinoma, NOS		
			IIA					
-0.208	0.000	2.109	0.000	1.308	0.000	0.000	0.000	
3.928	0.248	-0.790	Colorectal			Adenocarcinoma, NOS		
			I					
5.786	1.612	-1.304	0.749	2.316	-0.710	0.430	5.908	
5.236	-0.446	-2.686	Colorectal			Adenocarcinoma, NOS		
			I					
-1.325	-0.215	0.605	-0.271	-0.557	-0.381	-0.822	-2.526	
-1.191	-0.026	0.656	Colorectal			Mucinous adenocarcinoma		
			I					
-1.040	1.078	-0.305	-2.745	-1.015	-1.316	-0.506	-3.204	
-0.979	-0.699	1.043	Colorectal			Adenocarcinoma, NOS		
			IIIB					
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	Colorectal			Adenocarcinoma, NOS		
			IIB					
-1.865	-0.274	-2.030	-1.267	-1.538	-3.735	-0.299	-0.040	
1.254	-0.868	-0.061	Colorectal			Adenocarcinoma, NOS		
			IIIB					
0.593	0.639	0.285	1.432	0.050	0.429	-1.019	1.327	
1.271	-1.090	0.731	Colorectal			Adenocarcinoma, NOS		
			IIIA					
0.000	2.018	0.646	0.137	0.000	-0.437	0.366	2.700	
1.717	-1.442	0.000	Colorectal			Adenocarcinoma, NOS		
			IIIB					
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.163	0.000	Colorectal			Adenocarcinoma, NOS		
			IIB					
-0.505	0.000	0.000	-0.823	0.000	-0.505	0.000	-0.783	
0.000	-1.794	0.050	Colorectal			Adenocarcinoma, NOS		
			IIA					
1.165	-0.030	-0.003	0.167	-1.015	0.012	-0.252	-1.281	
-0.707	-0.589	1.382	Colorectal			Adenocarcinoma, NOS		
			IIA					
-1.026	0.000	0.722	0.000	4.353	0.499	-0.815	2.088	
2.801	0.730	0.000	Colorectal			Adenocarcinoma, NOS		
			IIIB					
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	Esophagus			Squamous cell carcinoma, NOS		
			IIA					
3.237	0.629	-2.534	1.489	3.695	-0.296	-2.008	-1.926	

Table35.txt

-1.853 -2.219 2.439 Colorectal Mucinous adenocarcinoma
IIA
3.981 -0.336 -0.496 0.000 0.000 2.935 4.908 0.137
-2.543 -0.902 0.000 Colorectal Gastrointestinal stromal
tumor, NOS IIIA
0.175 0.000 -1.533 0.000 -1.165 0.000 0.000 0.000
1.676 0.762 0.000 Esophagus Adenocarcinoma, NOS
IB
-1.214 0.000 -0.265 -0.877 -0.682 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma, NOS
IIB
-0.945 0.000 -0.137 0.000 -0.261 0.905 -1.120 -1.543
-0.019 -0.586 -0.868 Colorectal Papillary adenocarcinoma, NOS
IIB
-1.053 0.924 -1.144 -0.934 -1.629 0.182 -0.654 -0.630
-2.627 0.404 -0.614 Colorectal Mucinous adenocarcinoma
IIA
0.190 0.000 1.347 0.000 0.309 -0.025 0.050 -3.090
0.000 1.294 0.493 Esophagus Squamous cell carcinoma, NOS
II
-2.037 -1.584 -0.175 -0.587 -2.079 3.642 -2.254 -1.217
-2.343 1.370 -0.855 Colorectal Mixed cell adenocarcinoma
IIA
0.000 0.000 -0.541 0.441 0.703 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Mucinous adenocarcinoma
IIIB
0.000 0.000 0.287 0.516 0.329 0.998 1.521 0.424
1.244 -2.384 0.035 Liver Hepatocellular carcinoma,
Trabecular II
0.017 -0.051 0.940 5.145 5.314 1.926 0.678 -1.858
-1.822 3.815 0.043 Esophagus Squamous cell carcinoma, NOS
(8070/3) III
-1.901 -2.146 -1.385 -1.709 0.085 0.260 -1.836 -0.944
-0.470 0.726 -1.140 Colorectal Mucinous adenocarcinoma
IIA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Liver Hepatocellular carcinoma,
Solid Type IIIC
-1.790 -0.431 0.668 -2.095 -0.712 1.538 -0.721 0.567
-0.111 -0.615 -1.696 Colorectal Mucinous adenocarcinoma
IIA
1.420 0.000 0.484 1.351 3.585 0.137 -0.002 -0.969
-1.118 1.170 2.323 Colorectal Mucinous Adenocarcinoma
IIA
-0.909 2.432 6.446 5.999 10.990 -0.496 -0.067 3.987
2.446 0.582 0.007 Colorectal Adenocarcinoma
IIA
13.434 0.285 9.350 0.513 -1.510 -2.145 -0.224 5.573

Table35.txt

```
10.736    0.620    -0.099    Colorectal          Adenocarcinoma
                      IIA
9.737     1.319    0.671     0.681     2.838     1.892     2.871     0.611
0.113     -0.966   -1.907    Colorectal          Tubulo-papillary
Adenocarcinoma                        IIA
-1.553    0.000    -1.472    -1.169    4.265     0.029     0.865     2.550
1.635     -1.281   -0.074    Colorectal          Adenocarcinoma
                      IIA
-1.795    0.689    3.605     3.090     3.647     -1.112    -0.156    2.406
3.116     4.326    -0.823    Colorectal          Papillary Adenocarcinoma
                      I
-1.182    -0.834   0.239     -2.291    -0.447    -0.167    0.291     0.728
-0.010    -1.367   -0.729    Colorectal          Mucinous Adenocarcinoma
                      IIA
-0.687    0.335    2.011     -0.307    5.205     1.830     -0.527    1.255
1.955     -0.864   -0.656    Colorectal          Adenocarcinoma
                      IIIB
0.000     1.529    0.000     0.000     0.000     0.000     0.000     -0.230
-0.415    -0.378   0.000     Colorectal          Adenocarcinoma
                      IVA
-3.617    4.726    11.029    6.637     17.038    7.698     -1.251    2.591
-0.081    -0.344   -0.466    Colorectal          Adenocarcinoma
                      I
-2.031    -1.049   -2.370    -1.433    -2.162    0.000     -0.798    0.000
0.595     0.000    0.000     Colorectal          Adenocarcinoma, Villoglandular
type                  IIB
-3.909    -0.431   -2.430    -2.565    -3.690    -0.620    -0.603    -0.557
-1.364    -0.605   -0.897    Colorectal          Villoglandular Adenocarcinoma
                      IIA
-3.090    -0.626   12.607    -1.922    -1.870    2.624     2.311     -1.338
4.320     -0.186   -1.369    Colorectal          Mucinous Adenocarcinoma
                      IIIA
-0.220    1.903    1.567     -2.423    0.400     0.362     -2.156    0.561
-0.813    0.000    0.000     Colorectal          Adenocarcinoma
                      I
2.757     -1.433   3.537     -2.441    -2.451    -0.959    -3.810    0.085
13.381    -2.011   -0.156    Colorectal          Adenocarcinoma
                      I
-1.470    -2.028   0.287     -1.475    -2.126    3.429     2.308     2.671
16.646    1.603    5.344     Liver               Cholangiocarcinoma
                      IV
-1.480    0.661    -2.474    -0.294    -0.298    1.420     3.070     0.488
-1.080    -0.427   -1.929    Colorectal          Adenocarcinoma, NOS
                      IIIA
-1.619    -0.286   -1.248    -1.120    -1.645    -1.004    -1.537    0.638
-0.279    0.652    -0.219    Colorectal          Adenocarcinoma, diffuse type
                      IB
11.415    6.771    9.502     3.568     10.320    6.647     10.380    3.607
```

Table35.txt

10.938 5.170 7.472 Colorectal Adenocarcinoma, NOS
IIA
0.904 1.171 -0.491 0.196 1.817 -1.256 -1.556 2.056
4.332 3.478 0.757 Colorectal Adenocarcinoma, NOS
IIIA
-1.345 0.344 -1.355 -1.158 -1.434 -1.979 1.167 -0.685
0.852 0.079 0.344 Colorectal Adenocarcinoma, NOS
IIIA
5.894 -0.467 4.769 4.265 5.126 -0.144 -2.280 2.311
0.726 2.610 2.828 Liver Hepatocellular carcinoma,
clear cell type IIIA
-2.753 -0.407 -1.096 -1.556 -1.416 -1.887 1.500 -0.566
-1.293 -1.132 -2.527 Colorectal Adenocarcinoma, NOS
IIIA
-1.915 0.116 -0.940 -0.105 -1.375 1.065 0.442 3.761
9.073 1.220 0.347 Colorectal Adenocarcinoma, NOS
IIIB
-2.278 0.080 -1.524 -1.007 -1.839 -0.640 -1.913 -1.614
-0.336 0.603 -0.662 Colorectal Mucinous adenocarcinoma
IIIB
10.180 -2.202 12.815 9.865 15.487 3.867 1.443 0.861
-0.987 11.527 9.039 Esophagus Squamous cell carcinoma
IIB
11.062 4.512 9.696 -0.240 -1.022 -2.590 -0.960 0.000
11.432 4.306 -2.976 Liver Hepatocellular carcinoma,
Trabecular IIIA
15.110 8.479 3.946 -0.626 -2.802 7.372 13.255 5.029
5.064 6.312 7.794 Esophagus Squamous cell carcinoma, NOS
IIA
6.607 2.195 5.291 6.886 4.755 1.034 6.197 3.540
2.207 3.193 -0.992 Esophagus Squamous cell carcinoma, NOS
IIA
19.931 6.638 13.735 -0.682 0.142 7.599 7.273 9.638
4.740 7.164 9.754 Liver Hepatocellular carcinoma,
pleomorphic type IIIA
5.442 1.200 1.837 5.702 -1.539 -0.687 0.444 -1.104
-0.668 -0.590 -0.637 Colorectal Adenocarcinoma, NOS)
I
9.980 1.567 2.360 3.827 10.531 -0.117 1.688 -1.907
1.047 9.604 8.307 Colorectal Villoglandular adenoma
IIA
1.404 0.811 -0.119 5.494 5.764 0.209 0.676 3.010
7.090 1.440 0.212 Esophagus Adenosquamous carcinoma
IV
-2.265 -1.756 -0.919 -1.409 -0.677 -0.133 -0.999 -0.332
-1.703 -3.679 0.030 Colorectal Adenocarcinoma, NOS
IIA
-0.693 -1.351 -1.663 -2.154 0.314 -2.587 -0.743 -0.437

Table35.txt

-0.936 -1.398 -0.903 Colorectal Tubular Adenocarcinoma
IIIB
-3.527 -0.511 -0.705 -0.588 -0.906 1.396 0.253 -1.634
7.946 -0.925 0.004 Colorectal Adenocarcinoma
IIIA
-2.792 0.027 -0.166 2.293 4.630 10.796 12.411 -0.460
6.412 -1.812 -0.760 Colorectal Papillary Adenocarcinoma
IIA
-2.965 -0.448 -0.859 -0.547 -0.441 -1.321 -1.520 0.000
-0.918 -0.266 -0.604 Colorectal Papillary Mucinous
Adenocarcinoma IIA
-1.990 -0.539 -2.350 0.088 -0.594 -1.976 -0.744 0.538
-1.357 -1.655 -1.774 Colorectal Papillary Mucinous
Adenocarcinoma IV
-1.436 -0.730 -2.925 -0.935 0.431 -0.454 -1.690 -0.465
-0.414 -2.736 0.560 Colorectal Adenocarcinoma
IIA
-2.095 1.464 -0.677 -2.297 -0.576 0.159 -3.765 2.992
12.463 0.081 -0.213 Liver Hepatocellular Carcinoma,
Trabecular Type II
-2.176 0.547 5.941 -0.765 -2.737 -0.871 -3.066 1.600
5.222 0.491 -0.161 Colorectal Papillary Adenocarcinoma
IIA
10.666 0.843 4.585 2.975 6.108 8.260 10.107 3.004
4.898 -1.515 -1.051 Colorectal Tubular Adenocarcinoma
IIA
7.626 0.223 0.692 -2.573 0.376 -0.076 1.712 1.325
4.291 3.893 3.178 Colorectal Adenocarcinoma
IIIC
-4.095 8.650 0.504 3.120 3.467 2.808 6.290 0.660
10.738 1.082 3.782 Colorectal Adenocarcinoma
IIIB
-1.595 -0.912 -0.910 3.319 4.654 -2.230 -1.613 1.534
10.148 5.629 4.357 Liver Hepatocellular Carcinoma
II
-0.531 1.153 -1.104 0.102 -1.508 0.081 -0.946 0.000
-1.216 -0.774 -0.053 Colorectal Adenocarcinoma
IIIA
0.129 0.137 0.309 0.000 0.000 0.928 1.308 0.000
-1.062 -0.144 -0.143 Colorectal Adenocarcinoma
IVA
0.000 0.566 -1.622 -0.409 -0.877 -0.505 -0.966 0.000
-1.089 -0.914 -1.080 Liver Hepatocellular Carcinoma,
Solid Type IIIA
-1.979 -1.295 -3.059 -1.391 -1.371 0.459 2.124 1.726
2.113 -0.565 -1.189 Colorectal Adenocarcinoma
IIIB
-1.181 -1.044 1.334 -0.757 0.620 -0.249 -1.829 -0.480

Table35.txt

-0.771	-0.666	-1.642	Colorectal		Adenocarcinoma			
			IIA					
-0.977	2.199	-0.384	1.027	-0.472	-0.678	0.392	0.914	
4.150	-1.419	-1.966	Colorectal		Adenocarcinoma			
			I					
-1.475	-1.791	-0.913	-1.639	5.746	-0.591	4.166	-0.213	
0.030	-2.091	-0.675	Colorectal		Adenocarcinoma			
			I					
-2.227	1.760	-0.921	4.554	8.260	1.446	0.968	9.905	
6.684	-3.518	-1.545	Colorectal		Adenocarcinoma			
			IIA					
0.037	0.634	-0.917	1.218	3.023	-0.389	-1.525	-0.811	
-0.788	0.407	0.197	Colorectal		Adenocarcinoma			
			NA					
-0.704	-3.090	-1.972	-0.015	-0.279	0.000	-0.378	0.223	
-0.335	-0.797	-0.350	Colorectal		mucinous adenocarcinoma			
			NA					
3.321	-0.420	-0.621	6.052	3.914	-2.338	1.853	-1.285	
1.109	-2.627	-2.451	Colorectal		Adenocarcinoma			
			NA					
0.922	0.000	4.503	-1.345	-0.823	0.068	0.083	0.563	
-0.187	3.589	0.000	Colorectal		Adenocarcinoma			
			I					
-0.600	1.070	7.096	3.624	7.755	0.779	-0.400	0.871	
0.651	-1.177	-0.431	Colorectal		Adenocarcinoma			
			IVA					
-0.910	1.629	-1.754	-0.119	2.351	1.039	0.194	-1.407	
1.990	-0.695	0.428	Colorectal		Adenocarcinoma			
			I					
1.603	3.878	2.575	-2.004	2.886	-0.442	1.127	0.724	
-0.121	-3.108	4.088	Colorectal		Adenocarcinoma			
			IIIC					
-1.664	-0.423	-1.086	0.268	-0.970	-0.427	-0.247	-1.899	
2.590	-0.235	-0.432	Colorectal		Adenocarcinoma			
			IIIB					
-0.282	0.000	-1.940	2.126	4.071	-0.217	0.531	2.401	
1.337	1.802	0.350	Colorectal		Adenocarcinoma			
			IIA					
-3.346	-1.759	-2.875	-0.031	-1.847	0.000	-0.144	-0.007	
-0.661	-3.002	-0.291	Liver		hepatocellular carcinoma			
			n/a					
-0.920	0.000	-1.600	-0.739	0.539	-1.914	-1.214	1.432	
-1.385	-2.552	0.000	Colorectal		Adenocarcinoma			
			IIA					
-0.896	0.000	0.091	0.224	2.780	-1.316	-0.736	-0.338	
-1.699	0.066	-1.891	Colorectal		Adenocarcinoma			
			IIIB					
-1.879	0.834	0.056	-0.927	-2.953	0.092	-0.216	0.237	

Table35.txt

-2.095	0.247	-2.879	Colorectal		Adenocarcinoma			
			I					
-2.052	1.078	-0.253	3.900	4.009	-2.792	0.046	-0.432	
1.953	3.618	2.540	Colorectal		Adenocarcinoma			
			IIA					
4.474	4.488	1.197	1.917	1.944	0.628	0.778	4.774	
4.978	5.380	3.278	Colorectal		Adenocarcinoma			
			IVB					
-1.238	4.481	3.059	5.492	5.298	-0.965	1.344	5.746	
7.224	-1.519	1.739	Colorectal		Adenocarcinoma			
			IIIC					
-0.782	-0.597	-2.035	0.084	0.811	-1.737	-3.967	0.596	
-0.649	-1.051	0.788	Colorectal		Adenocarcinoma			
			IIIA					
-0.770	-1.214	-0.471	0.741	-1.328	-1.396	-1.825	-1.114	
-0.386	-0.669	-1.453	Colorectal		mucinous adenocarcinoma			
			IIA					
-1.232	-0.737	0.683	-0.144	0.596	0.005	-0.372	-0.742	
1.558	-1.239	0.511	Colorectal		Adenocarcinoma			
			I					
2.021	0.865	1.687	1.979	0.288	1.293	-1.070	-0.382	
-0.542	0.203	-0.321	Colorectal		signet-ring cells carcinoma			
			IVB					
2.368	2.976	-0.082	4.302	5.644	1.003	0.926	0.703	
3.175	-1.502	6.006	Colorectal		Adenocarcinoma			
			IIA					
1.474	5.159	1.925	4.160	-1.229	2.844	3.526	6.185	
4.474	2.192	7.193	Colorectal		Adenocarcinoma			
			I					
2.046	1.577	5.660	4.160	5.671	-0.004	0.902	6.179	
5.452	-0.673	-0.924	Colorectal		Adenocarcinoma			
			IVA					
11.727	2.585	3.685	-1.249	1.552	1.688	0.220	4.521	
-1.884	2.414	1.906	Colorectal		Adenocarcinoma, NOS			
			II					
0.589	4.352	-1.065	-1.073	-4.024	-0.513	-0.164	2.257	
-2.242	-0.739	-1.491	Colorectal		Adenocarcinoma, NOS			
			IIB					
6.496	0.414	-1.618	-3.163	-1.934	-1.585	4.017	-0.063	
-1.257	4.332	1.140	Colorectal		Adenocarcinoma, NOS			
			I					
5.537	4.460	5.800	5.903	5.080	-2.392	-1.067	3.023	
-1.177	3.829	2.066	Colorectal		Adenocarcinoma, NOS			
			I					
-1.501	-0.332	-1.742	0.926	2.085	0.090	-0.133	0.904	
0.017	0.827	0.890	Colorectal		Adenocarcinoma, NOS			
			I					
-0.256	-0.174	7.619	-1.113	-4.713	-0.780	-0.558	-0.669	

Table35.txt

-1.766 -0.699 0.407 Colorectal Mucinous adenocarcinoma
I
11.474 -1.213 -2.718 -2.628 -2.821 10.760 1.579 2.169
3.886 6.264 4.172 Colorectal Adenocarcinoma, NOS
I
-3.484 0.338 6.001 0.587 -0.528 -0.902 -1.339 -0.572
-1.189 -0.666 -0.941 Colorectal Adenocarcinoma, NOS
IIB
17.542 6.273 -0.997 10.921 17.718 8.308 9.427 0.355
18.625 13.162 8.882 Colorectal Adenocarcinoma, NOS
IIIB
0.000 -1.281 0.000 0.000 0.014 0.000 -1.169 0.000
1.736 0.000 0.000 Colorectal Adenocarcinoma, NOS
IIIB
11.232 -2.253 0.145 3.158 7.302 -2.088 -0.517 3.017
7.908 -1.505 -0.636 Liver Hepatocellular carcinoma,
Trabecular II
13.806 1.705 11.009 4.193 -1.116 1.598 2.372 3.323
2.504 0.491 2.736 Colorectal Mucinous adenocarcinoma
(8480/3) IIA
-1.388 -0.157 -2.420 -1.079 0.167 -0.867 -0.949 -0.720
-0.515 -0.711 -0.059 Colorectal Adenocarcinoma, NOS
IIA
15.269 -2.394 2.381 -0.863 3.402 -2.557 -0.015 3.595
5.844 0.285 -1.592 Colorectal Adenocarcinoma, NOS
III
11.606 1.967 4.694 5.075 10.986 4.654 3.094 6.721
7.837 10.258 6.792 Esophagus Squamous cell carcinoma, NOS
IIA
-4.142 -2.065 -2.327 -2.785 -2.696 -0.340 -2.409 -1.028
-1.312 -1.009 -1.780 Colorectal adenocarcinoma
IIA
-1.163 -2.009 -2.232 -0.796 -1.011 -0.772 -1.424 -0.843
-2.273 0.734 -0.900 Colorectal adenocarcinoma
IIIC
9.883 -0.299 1.366 7.282 10.933 7.818 13.217 1.700
8.539 -1.358 -1.530 Colorectal carcinoma
IIIA
-3.350 -1.914 -3.813 -0.858 0.037 4.300 3.745 1.679
4.324 2.095 -1.646 Colorectal adenocarcinoma
IIIB
-2.830 -1.175 8.691 9.698 16.472 10.681 2.042 0.018
0.078 0.370 -1.815 Colorectal adenocarcinoma
IIA
1.346 0.125 1.231 0.767 1.027 4.220 2.183 0.000
8.443 1.212 -0.518 Colorectal adenocarcinoma
I
-3.388 -1.215 -0.736 -0.080 -1.572 -0.771 0.134 -1.647

Table35.txt

-3.019	-1.240	-1.198	Colorectal		adenocarcinoma			
			IIIB					
6.086	4.522	4.401	0.805	1.367	1.798	9.226	-1.048	
2.507	-0.265	-0.058	Esophagus		adenocarcinoma			
			IIIC					
-2.258	-2.357	-2.734	-0.529	-1.215	-1.772	-2.364	1.021	
-1.890	-2.582	0.220	Colorectal		adenocarcinoma			
			IIB					
11.171	0.707	3.064	4.507	4.192	-0.298	-1.355	0.163	
-1.438	8.599	5.750	Colorectal		adenocarcinoma			
			IIIB					
-2.337	0.150	-2.624	-1.992	-3.056	-1.559	-0.500	-1.617	
0.505	-2.399	-1.134	Liver		cholangiocarcinoma			
			II					
-1.781	0.989	0.468	0.377	-1.136	-0.994	-1.527	0.766	
-0.239	-0.591	-1.476	Colorectal		mucinous adenocarcinoma			
			IIIC					
14.233	9.479	16.048	5.256	-1.764	-3.104	-3.712	2.281	
7.552	0.634	-0.149	Colorectal		adenocarcinoma			
			IIA					
4.758	0.866	9.126	-2.152	-2.151	-0.247	-1.938	-0.912	
0.008	0.382	0.330	Colorectal		adenocarcinoma			
			IVA					
2.733	0.673	-1.935	0.683	-1.658	-2.105	-0.065	-1.494	
1.167	-0.179	0.305	Esophagus		squamous cell carcinoma			
			IA					
-0.176	0.087	0.452	0.985	-2.289	0.368	-0.374	0.877	
1.687	-0.826	-0.002	Colorectal		mucinous adenocarcinoma			
			IVB					
-1.582	-1.363	-1.488	-0.389	-2.520	4.308	4.196	1.003	
3.575	3.584	3.233	Colorectal		adenocarcinoma			
			IVA					
0.167	8.972	-1.561	-1.463	-1.719	4.714	9.352	-1.523	
-0.996	2.582	-1.627	Colorectal		adenocarcinoma			
			I					
-0.975	2.934	10.373	5.162	-3.120	4.375	2.033	1.270	
2.256	4.312	-1.409	Colorectal		adenocarcinoma			
			IIA					
-2.064	-1.613	-1.304	0.537	-2.818	1.199	-0.689	-2.842	
15.906	5.306	0.196	Liver		hepatocellular carcinoma			
			n/a					
-1.930	-1.096	-2.422	0.491	-2.956	-0.103	-3.682	0.845	
-0.815	-0.994	-0.849	Colorectal		adenocarcinoma			
			IVB					
-3.542	0.965	-1.456	7.240	11.925	-0.046	1.822	7.720	
14.007	9.546	6.355	Colorectal		adenocarcinoma			
			IIIC					
-1.645	-0.896	-2.313	-2.263	-1.275	-1.860	-2.847	0.023	

Table35.txt

2.662	-1.420	-0.157	Liver			hepatocellular carcinoma								
			I											
-3.259	-1.933	11.129	-0.377	-2.583	0.803	-2.616	4.411							
13.816	0.426	-1.459	Colorectal			adenocarcinoma								
			I											
9.027	0.849	12.851	5.053	7.089	1.784	7.768	4.406							
10.138	3.283	1.415	Colorectal			adenocarcinoma								
			IIA											
-1.135	-0.116	15.584	5.541	0.175	-2.563	-0.103	2.730							
-2.909	5.262	4.667	Colorectal			adenocarcinoma								
			I											
-1.871	-1.907	-2.897	7.035	11.805	5.532	6.878	5.132							
8.058	5.711	5.538	Colorectal			adenocarcinoma								
			IIIB											
-1.397	-0.659	0.513	1.072	-1.829	5.196	0.533	5.235							
11.001	-1.908	-0.928	Colorectal			adenocarcinoma								
			IIA											
-1.479	6.546	11.474	-1.504	2.645	2.915	5.922	3.079							
4.234	0.177	1.030	Colorectal			adenocarcinoma								
			I											
-1.988	0.437	-0.366	-2.228	-1.877	4.162	4.001	-0.954							
-0.412	-1.661	-0.416	Colorectal			adenocarcinoma								
			IIIB											
13.936	-0.625	-2.654	-0.140	-2.559	-0.301	-0.832	6.583							
4.483	8.438	5.504	Liver			hepatocellular carcinoma								
			n/a											
14.680	3.004	5.732	1.145	13.413	-0.717	-1.240	0.950							
5.911	12.716	10.140	Liver			cholangiocarcinoma								
			II											
0.976	-1.166	6.285	-0.841	0.681	0.712	2.011	3.195							
4.261	2.423	5.648	Liver			hepatocellular carcinoma								
			n/a											
7.092	6.522	4.516	-2.184	7.837	0.765	-1.958	1.316							
8.810	-1.503	0.461	Colorectal			adenocarcinoma								
			I											
-1.153	-1.131	-1.869	-1.344	-0.220	-2.271	-1.738	1.289							
-1.644	-0.323	-1.132	Colorectal			mucinous adenocarcinoma								
			IIIB											
7.080	-0.880	-1.864	0.071	3.439	-0.281	-1.249	-1.552							
2.967	0.020	-0.337	Colorectal			adenocarcinoma								
			IIA											
3.429	2.020	1.744	3.531	1.563	-2.141	-1.753	0.659							
5.966	-0.108	0.608	Colorectal			adenocarcinoma								
			IIA											
-1.946	-3.234	-0.098	1.614	-1.882	-1.409	-2.305	-0.349							
-0.671	-0.196	-3.043	Colorectal			Adenocarcinoma								
			I											
6.568	-1.270	-1.455	-1.622	-2.318	-2.034	-2.385	3.428							

Table35.txt

0.721	-2.100	-1.666	Colorectal		Papillary adenocarcinoma			
			I					
12.831	2.414	0.650	6.634	-0.610	-0.951	-0.499	2.153	
3.852	0.951	-1.259	Colorectal		Adenocarcinoma, NOS			
			IIB					
11.871	-3.512	13.668	-0.416	0.141	7.449	9.741	5.857	
-1.594	-0.648	0.047	Colorectal		Tubular adenocarcinoma			
			IIB					
-3.388	-0.989	2.360	11.506	14.624	8.000	8.170	-0.849	
3.985	2.585	2.494	Colorectal		Adenocarcinoma			
			IIB					
2.351	-3.139	4.544	-0.988	-0.197	10.770	10.121	6.403	
16.562	10.012	8.136	Colorectal		Adenocarcinoma			
			IIB					
7.466	-0.259	-1.805	-0.482	-0.395	11.903	-0.510	2.437	
4.103	-1.389	-1.544	Colorectal		Adenocarcinoma			
			IIB					
-1.204	2.906	6.426	0.488	-2.091	-0.838	-1.659	-0.068	
7.239	0.168	-0.954	Colorectal		Adenocarcinoma			
			IIIB					
16.337	-0.558	9.517	1.324	-0.633	9.066	10.531	5.697	
11.613	-2.133	-1.531	Colorectal		Adenocarcinoma			
			IVA					
-1.256	-1.296	-2.242	-0.812	-6.093	2.625	0.340	-1.260	
1.598	-1.375	-2.211	Colorectal		Tubular adenocarcinoma			
			IIA					
3.454	-1.121	3.484	0.156	2.536	9.596	12.232	1.775	
8.536	0.923	-0.236	Colorectal		Adenocarcinoma			
			IVA					
-1.314	-1.267	-1.794	-2.862	-2.668	3.555	6.962	2.117	
5.537	-3.239	-1.771	Colorectal		Papillary adenocarcinoma			
			IIB					
0.994	0.000	4.419	-2.252	-0.372	5.276	6.713	3.090	
10.103	-0.498	-0.097	Colorectal		Adenocarcinoma			
			IIB					
7.378	-0.100	-3.102	-2.587	-2.002	2.535	5.978	6.195	
-1.754	0.551	-1.442	Colorectal		Adenocarcinoma			
			IVA					
-0.940	0.251	0.229	-0.669	2.282	-0.433	1.735	0.068	
-0.057	-0.510	-0.848	Colorectal		Mucinous carcinoma			
			IIIB					
7.227	2.357	3.951	3.630	4.401	1.743	-0.886	4.485	
15.250	-2.246	-0.436	Colorectal		Adenocarcinoma			
			I					
4.896	-3.264	5.605	0.999	2.916	0.628	1.584	-3.841	
1.744	3.963	3.453	Colorectal		Adenocarcinoma			
			IIA					
9.108	-0.466	-1.154	1.703	-1.234	-0.845	-1.913	3.189	

Table35.txt

9.449	4.798	-0.722	Colorectal		Mucinous carcinoma			
			IIIA					
2.014	-2.133	3.663	3.046	4.257	4.398	-0.535	1.303	
0.839	7.082	4.352	Esophagus		Adenosquamous carcinoma			
			IIA					
-2.590	9.789	1.219	0.943	0.297	0.443	0.009	4.302	
2.080	8.956	7.947	Esophagus		Keratinizing Squamous Cell Carcinoma			
			II					
-3.055	3.265	4.243	3.820	6.973	2.457	3.371	2.061	
4.692	-0.497	3.960	Colorectal		Adenocarcinoma			
			II					
-1.817	1.304	2.190	0.361	0.521	-2.838	-0.879	-2.209	
-0.989	-1.019	-0.341	Colorectal		Adenocarcinoma			
			IIA					
1.112	-0.203	0.299	-1.276	-1.122	1.023	-1.172	1.179	
10.402	0.138	-0.874	Colorectal		Adenocarcinoma			
			III A					
-3.211	5.649	4.083	1.498	3.590	1.541	0.273	2.836	
4.851	1.483	0.368	Colorectal		Adenocarcinoma			
			II A					
4.749	5.413	-3.350	-1.725	-0.559	9.084	6.601	2.117	
10.336	2.520	1.699	Liver		Hepato-Cholangiocarcinoma			
			III A					
1.084	1.852	-2.063	8.913	12.184	8.025	0.883	-1.464	
1.856	7.745	8.265	Esophagus		Keratinizing Squamous Cell Carcinoma			
			II A					
6.899	-0.806	-1.034	-2.211	-2.434	-0.523	-1.106	-0.823	
1.315	-1.614	1.317	Colorectal		Papillary Adenocarcinoma			
			II A					
11.154	0.239	10.981	-0.757	1.082	-1.424	-1.247	4.815	
9.234	-1.739	0.667	Colorectal		Adenocarcinoma			
			II A					
3.483	0.000	-1.707	3.648	2.173	2.861	3.903	0.000	
2.878	-0.868	-0.920	Colorectal		Adenocarcinoma			
			II A					
6.316	9.679	10.393	-1.087	0.196	-0.364	-0.941	4.993	
15.969	0.989	2.037	Colorectal		Adenocarcinoma			
			III A					
-2.677	-3.648	-0.927	-0.163	-2.299	-0.254	-0.385	0.000	
2.579	-0.951	-0.579	Colorectal		Papillary Adenocarcinoma			
			II A					
-1.410	-0.531	-3.118	-2.585	-1.589	-2.243	-0.769	1.318	
9.287	-0.428	-1.626	Liver		Hepatocellular Carcinoma, Solid Type			
			III A					
11.304	2.199	-4.355	8.340	-1.856	2.846	8.880	4.204	
3.376	9.909	7.346	Esophagus		Keratinizing Squamous Cell Carcinoma			
			II B					
7.042	-0.266	-2.440	-1.060	-1.144	1.440	-0.374	-1.506	

Table35.txt

0.319	4.056	-1.045	Colorectal		Adenocarcinoma			
			III A					
7.966	3.497	2.071	9.087	-2.084	9.168	12.086	4.847	
6.574	7.551	7.391	Liver		Cholangiocarcinoma			
			IV					
13.536	-1.077	-1.856	-0.861	-1.206	0.137	3.167	6.964	
9.869	-0.172	-0.776	Liver		Hepatocellular Carcinoma			
			II					
5.777	4.878	7.747	-1.528	-1.613	-1.498	-2.072	-1.226	
-0.562	2.726	3.422	Colorectal		Adenocarcinoma			
			II A					
14.819	8.432	13.061	2.041	8.195	-0.365	-1.922	3.605	
-0.870	5.288	4.857	Colorectal		adenocarcinoma			
			IIA					
-2.583	-2.080	-1.117	1.859	-3.019	-0.973	-0.863	1.708	
-3.657	2.689	8.467	Esophagus		adenosquamous carcinoma			
			IIIA					
0.079	4.025	7.514	3.784	9.139	-1.851	2.496	0.000	
9.819	-0.425	-1.786	Colorectal		adenocarcinoma			
			IIA					
-1.594	-0.698	-2.998	5.132	3.052	-0.382	2.970	1.119	
0.470	-0.377	-1.112	Colorectal		adenocarcinoma			
			IVA					
10.133	2.754	5.210	2.070	5.056	2.496	1.899	-1.338	
-3.081	8.998	8.220	Colorectal		adenocarcinoma			
			IIIA					
-2.569	0.869	-3.002	-0.496	-1.868	6.542	10.218	3.078	
17.072	3.090	0.000	Colorectal		adenocarcinoma			
			IIIB					
-2.477	1.009	-1.375	-1.514	-2.078	0.635	-1.067	4.426	
7.903	5.617	2.009	Colorectal		mucinous adenocarcinoma			
			IA					
-2.030	2.662	1.305	-1.648	-1.173	1.053	4.996	1.847	
3.573	7.600	1.852	Colorectal		adenocarcinoma			
			IIIC					
18.933	0.529	6.264	-0.447	0.351	-1.958	0.540	6.315	
10.429	4.733	4.602	Colorectal		adenocarcinoma			
			IIIB					
0.955	12.426	19.748	3.887	4.185	9.274	12.522	7.885	
17.884	11.937	7.954	Colorectal		adenocarcinoma			
			IIIC					
1.765	4.319	2.079	0.773	-3.311	3.919	3.288	0.000	
5.307	-0.318	-0.430	Colorectal		adenocarcinoma			
			IIIB					
-2.161	-1.317	-2.666	-0.894	-1.812	9.178	-1.316	2.566	
14.091	-0.956	0.502	Colorectal		adenocarcinoma			
			IVA					
4.030	5.617	0.337	7.078	-2.753	2.847	4.261	3.696	

Table35.txt

6.064	0.702	0.281	Colorectal		adenocarcinoma			
			IIA					
5.900	2.247	5.126	-0.520	-3.344	0.856	5.411	0.505	
5.425	3.126	3.321	Colorectal		adenocarcinoma			
			I					
-1.882	-0.463	-1.340	1.116	-1.733	6.347	1.342	-1.235	
-2.357	-0.126	-1.343	Colorectal		adenocarcinoma			
			I					
5.701	4.679	7.181	2.249	0.740	4.152	4.283	-0.444	
1.620	4.833	5.389	Esophagus		tubular adenocarcinoma			
			IIIA					
-1.330	0.684	5.988	9.162	-0.626	9.457	13.351	-0.281	
0.038	1.383	-1.562	Colorectal		adenocarcinoma			
			IIIB					
-0.107	6.193	6.932	8.821	14.388	5.245	9.039	1.271	
13.154	-2.075	-1.627	Colorectal		adenocarcinoma			
			IA					
0.000	0.419	-1.214	0.292	-1.859	-2.064	-1.975	-2.829	
-1.428	0.000	-1.846	Colorectal		adenocarcinoma			
			IIA					
21.141	8.596	16.961	7.807	17.748	11.210	15.137	1.170	
8.718	6.503	9.999	Colorectal		adenocarcinoma			
			IVA					
9.701	4.941	19.189	0.100	-1.438	3.726	6.807	-0.872	
-0.253	7.274	2.450	Colorectal		adenocarcinoma			
			IIIB					
-1.457	-1.558	-1.686	-0.321	-1.280	7.724	9.496	1.828	
-3.009	0.949	1.082	Colorectal		adenocarcinoma			
			IIA					
4.926	4.709	15.634	7.360	10.503	-0.451	0.561	-0.786	
1.449	5.563	3.488	Colorectal		adenocarcinoma			
			IIA					
1.256	-0.468	-0.607	-1.031	-0.312	0.366	-1.286	0.309	
-0.958	0.843	0.772	Colorectal		Adenocarcinoma			
			I					
10.935	0.711	-1.201	1.811	15.493	9.406	15.913	0.815	
1.809	5.156	7.508	Colorectal		Adenocarcinoma			
			I					
5.652	6.134	12.265	0.277	-2.121	0.812	-1.976	3.989	
16.986	4.387	1.470	Colorectal		Adenocarcinoma			
			I					
4.700	0.606	4.273	7.996	9.353	4.812	7.391	2.363	
8.119	7.019	7.131	Colorectal		Adenocarcinoma			
			I					
13.007	-0.149	9.732	3.026	10.688	7.997	12.053	0.608	
3.865	3.664	3.014	Colorectal		Adenocarcinoma			
			I					
8.738	1.291	3.163	-1.503	-1.900	7.513	8.061	-0.924	

Table35.txt

-1.961 2.636 1.760 Colorectal Adenocarcinoma
II B
-3.928 1.095 -2.729 -1.575 -4.391 0.125 -2.282 5.375
-3.026 -1.864 -1.729 Breast Infiltrating Lobular
Carcinoma, Classic Type III B
-1.164 -1.203 -1.312 -0.583 -2.822 -1.706 4.024 -1.695
-2.124 -0.959 2.308 Colorectal Adenocarcinoma
II B
2.400 -1.497 -0.967 1.256 3.335 4.762 5.254 1.014
9.863 -1.008 -0.858 Breast Infiltrating Ductal Carcinoma,
NOS III A
-2.080 -0.196 -0.961 -0.821 -0.578 -2.605 -1.258 -1.114
-1.529 -2.384 0.114 Colorectal Papillary Adenocarcinoma
II B
1.754 7.211 -2.752 5.011 10.080 -2.729 -1.957 2.207
-0.885 5.161 5.468 Colorectal Papillary Adenocarcinoma
I
-2.247 -1.986 -2.213 5.449 -2.397 0.172 2.061 -1.499
-1.751 -1.474 -2.360 Colorectal Adenocarcinoma
III B
-3.440 -0.011 -0.113 2.880 3.126 -0.131 -1.091 -1.295
10.369 3.069 -0.256 Breast Infiltrating Lobular Carcinoma
with Pagetoid Expansion intII A
3.227 9.827 -2.132 1.146 2.406 -2.320 0.923 3.425
0.286 -1.167 6.530 Breast Infiltrating Ductal Carcinoma,
NOS I
-3.672 4.142 -1.364 -0.375 0.050 -0.453 -1.224 1.095
9.022 1.245 -1.204 Breast Infiltrating Ductal Carcinoma,
NOS I
-3.378 0.362 -2.349 -0.091 -0.319 -1.890 -0.825 1.066
1.191 2.670 -0.736 Breast Infiltrating Ductal Carcinoma,
NOS I
-0.962 0.588 -0.260 4.929 -0.436 0.908 5.114 -0.405
3.372 -2.106 -1.355 Colorectal Adenocarcinoma
IV
-4.221 -0.793 -2.039 1.150 -2.236 1.129 0.306 0.297
0.047 -0.209 -2.862 Colorectal Mucinous Adenocarcinoma
II A
-2.678 -0.593 -0.949 4.034 -1.707 1.436 2.820 0.159
-1.974 -0.091 1.377 Colorectal Mucinous Adenocarcinoma
II A
0.596 -0.378 0.121 0.208 -1.185 0.000 0.561 -0.592
1.283 0.137 1.020 Esophagus Keratinizing Squamous Cell
Carcinoma III
0.000 -0.215 0.266 -0.269 -1.709 -0.052 -3.090 -0.628
0.000 -0.628 0.000 Liver Clear Cell Hepatocellular
Carcinoma III A
0.449 0.000 -2.241 1.451 0.255 0.266 0.366 1.705

Table35.txt

0.956 1.351 0.169 Colorectal Adenocarcinoma
II A
3.322 2.083 2.529 -2.030 -0.710 0.000 0.439 2.994
3.722 -1.139 0.000 Breast Infiltrating Ductal Carcinoma,
NOS III A
1.888 0.000 -2.234 0.000 -0.567 0.382 1.075 3.291
1.619 0.352 2.306 Breast Infiltrating Ductal Carcinoma,
NOS with Mucinous DifferentII A
-0.893 0.415 3.452 2.138 4.919 0.611 -0.628 2.813
0.000 -0.822 3.070 Colorectal Adenocarcinoma
IV
0.000 0.000 -1.281 0.000 -0.143 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma with Signet
Ring Cell II A
0.000 0.000 0.000 -1.169 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma,
NOS II A
-0.694 0.000 0.051 0.000 1.070 0.000 0.000 0.231
0.000 0.000 0.000 Breast Mucinous Carcinoma
II A
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
III A
0.218 0.000 1.153 0.137 0.000 0.000 0.000 -0.054
0.000 -1.316 0.000 Esophagus Keratinizing Squamous Cell
Carcinoma II A
-1.329 0.000 1.825 0.000 -0.022 0.529 0.000 0.717
0.000 -0.736 0.000 Breast Infiltrating Ductal Carcinoma,
NOS III A
3.636 0.000 0.885 0.438 2.334 2.501 0.000 -2.762
0.882 0.914 -0.041 Breast Infiltrating Ductal Carcinoma,
NOS II B
0.833 -1.214 0.089 -0.275 -0.296 -0.187 -0.429 1.414
1.550 -0.480 1.044 Colorectal Adnocarcinoma with Mucinous
Production II A
-3.090 0.000 0.558 0.000 0.000 0.000 0.000 0.000
0.000 -0.395 -0.736 Colorectal Infiltrating Ductal Carcinoma,
NOS II A
-0.826 0.922 -2.038 1.392 2.820 2.392 -1.708 4.771
0.521 0.975 -0.274 Colorectal Adenocarcinoma
II A
5.115 0.000 4.361 2.516 5.314 2.228 1.153 0.881
0.829 4.129 2.981 Breast Infiltrating Ductal Carcinoma,
NOS III A
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Poorly Differentiated
Adenocarcinoma with Signet Ring CellII A
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

Table35.txt

0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma, NOS III A
0.000 0.000 0.000 0.000 0.527 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma, NOS II B
0.000 0.000 0.369 -1.364 0.000 -1.281 0.000 0.000
0.000 -3.090 0.000 Colorectal Adenocarcinoma with Mucin Production II A
0.451 2.938 1.733 3.026 8.633 -0.497 -0.182 4.580
3.911 2.106 3.421 Breast Infiltrating Ductal Carcinoma, NOS II A
1.241 0.202 -0.022 2.032 1.654 -1.265 -0.234 -2.133
1.330 1.601 0.639 Breast Infiltrating Ductal Carcinoma, NOS 0
-0.462 9.180 10.218 0.054 -1.249 -0.148 -1.344 4.710
-1.233 -1.408 -0.282 Colorectal Adenocarcinoma II B
3.008 -0.792 -2.157 6.870 11.128 4.449 -0.394 3.254
10.846 -0.428 0.943 Colorectal Adenocarcinoma II B
-2.481 -2.217 0.904 -0.913 -0.433 0.466 0.876 -0.236
9.146 0.096 -1.426 Colorectal Adenocarcinoma II B
-1.000 -2.707 -1.156 0.479 -2.233 -0.395 -0.940 -0.283
-0.043 -1.722 -0.823 Colorectal Adenocarcinoma II B
1.350 0.000 5.015 2.588 -2.742 -0.138 0.723 3.277
0.564 4.710 0.832 Colorectal Adenocarcinoma II B
9.776 4.156 4.649 0.372 9.730 2.968 0.975 0.699
2.806 0.360 5.151 Breast Infiltrating Lobular Carcinoma Alveolar Type, with PagetoiII A
-0.847 0.000 0.000 0.000 -0.505 0.000 0.000 0.000
0.075 0.000 0.000 Colorectal Adenocarcinoma II A
-3.660 0.000 0.000 0.000 0.000 0.366 -0.618 0.260
2.941 0.460 0.000 Colorectal Adenocarcinoma II A
-0.907 -0.578 -0.563 -0.880 -0.954 0.089 -0.709 1.082
1.058 -0.011 0.528 Breast Adenoma of nipple 0
0.000 0.000 -0.121 0.000 0.000 0.000 0.441 0.460
0.000 -0.505 0.000 Colorectal Signet ring cell adenocarcinoma NA
-0.429 0.694 0.630 4.416 1.595 1.639 -0.929 2.209
0.308 -1.417 0.000 Colorectal mucinous adenocarcinoma NA
1.473 -1.107 -0.831 0.902 -3.452 -2.592 -0.948 -0.091

Table35.txt

-0.656 -1.001 1.435 Breast Infiltrating ductal carcinoma
0
1.596 0.000 0.050 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
NA
-1.196 0.000 0.947 0.000 4.429 1.029 -1.807 7.259
5.509 -1.314 -0.789 Liver Hepatocellular carcinoma,
pleomorphic type 0
0.000 0.000 0.000 -0.058 0.595 -0.505 0.000 -0.259
-0.868 -1.256 -0.445 Breast Infiltrating ductal carcinoma
0
-0.052 0.000 -0.512 0.000 0.000 0.000 -1.169 0.000
1.505 -0.378 0.000 Colorectal Adenocarcinoma
II A
0.036 0.000 -0.762 0.595 0.000 0.000 0.366 -0.351
-0.137 1.011 -0.137 Colorectal Adenocarcinoma
NA
0.000 0.000 0.000 0.000 0.137 0.000 0.595 -0.290
0.000 0.804 0.006 Colorectal Adenocarcinoma
NA
0.000 0.000 0.000 0.000 -0.541 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma,
NOS II A
0.000 0.000 0.000 1.763 -0.426 0.000 0.000 -1.319
0.000 -3.090 0.000 Colorectal Adenocarcinoma with Mucinous
Differentiation NA
0.000 0.000 1.092 0.000 0.530 0.000 0.000 -1.169
2.364 -0.017 -1.054 Breast Mixed Ductal Carcinoma and
Myoepithelial Carcinoma I
0.000 0.000 -0.823 0.637 -1.037 0.233 0.000 0.000
0.000 -2.600 0.000 Breast Infiltrating Ductal Carcinoma,
NOS I
-0.840 0.000 0.196 0.000 1.878 1.027 0.745 1.973
5.365 -1.038 -1.756 Colorectal Adenocarcinoma
NA
0.000 0.000 -0.375 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Liver Cholangiocarcinoma
I
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
II A
-0.539 0.000 -0.081 0.000 0.000 0.000 0.000 -0.547
0.540 0.831 0.000 Breast Infiltrating Ductal Carcinoma
with Mucinous DifferentiatiIII C
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma
with Spindle Cell MetaplasiaI A
-3.090 0.865 1.236 -1.746 -0.391 0.000 0.791 -1.783

Table35.txt

0.427 0.000 -2.439 Liver Hepatocellular Carcinoma, Adenoid Type II
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Lobular Carcinoma, Classical Type III C
0.163 0.000 0.959 0.000 0.000 0.000 -0.505 0.000
0.303 0.367 0.000 Colorectal Adenocarcinoma II B
-1.639 1.245 -1.190 -1.169 -1.103 -1.266 -1.596 2.577
0.771 0.458 -1.043 Colorectal Papillary Adenocarcinoma I A
3.587 0.814 0.407 -0.299 2.970 0.515 -0.777 -0.753
0.525 -0.348 -2.257 Breast Infiltrating Lobular Carcinoma, Classical Variant II A
0.000 0.000 3.090 0.000 0.000 -1.256 0.000 0.000
0.000 0.000 0.000 Colorectal Mucin-producing adenocarcinoma IIIA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Mucinous adenocarcinoma IIIB
-1.110 -0.853 0.926 -1.248 -2.621 1.693 -0.687 -0.625
-0.367 -0.491 0.138 Colorectal Adenocarcinoma IIIA
-0.386 -3.498 -0.471 -0.272 -0.082 -2.841 -0.296 -1.089
-0.100 2.008 -1.213 Colorectal Adenocarcinoma with Mucinous Differentiation II A
-2.724 -0.602 0.303 0.198 -1.330 0.000 -1.243 -1.339
-0.323 -3.002 -1.380 Colorectal Mucinous Adenocarcinoma II A
0.000 -1.096 -1.792 -0.448 -0.562 -2.630 -1.256 -0.564
0.050 1.142 -0.059 Breast Infiltrating Ductal Carcinoma with DCIS Component III A
0.000 0.000 -3.090 0.000 0.000 0.000 0.000 0.865
0.000 0.000 0.000 Colorectal Adenocarcinoma II
0.356 0.361 0.772 -0.907 3.713 0.000 0.827 0.000
-1.060 0.107 -0.947 Colorectal Papillary Adenocarcinoma I
-0.503 -0.736 0.922 0.426 -1.306 0.000 1.236 0.381
-1.169 1.273 0.000 Breast Infiltrating Ductal Carcinma, NOS II B
-1.087 0.000 -0.107 0.000 0.000 0.022 4.829 -0.202
-0.673 -0.815 0.000 Colorectal Papillary Adenocarcinoma II A
-1.287 -0.015 -1.169 -2.097 -0.914 -1.724 -1.754 -0.516
-2.902 -1.527 0.211 Liver Cholangiocarcinoma III A
-0.366 0.969 0.000 0.137 -0.471 0.000 -0.445 -0.736

Table35.txt

-0.233 -0.510 0.000 Breast Infiltrating Ductal carcinoma, NOS I
0.000 0.000 -0.217 0.050 0.615 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating Ductal Carcinoma, NOS I
-2.185 0.000 0.000 -0.022 -1.533 0.309 -0.686 -0.728
-1.419 0.000 1.112 Esophagus Mucinous-Signet Ring Cell Carcinoma III
-0.029 -0.321 3.724 1.133 2.981 4.048 0.230 2.807
-0.733 2.764 1.876 Breast Infiltrating Ductal Carcinoma, NOS II A
0.570 1.776 1.265 2.031 6.269 -0.790 -1.435 -1.607
-4.699 -1.660 2.550 Breast Mucinous Carcinoma with Pagetoid Infiltration into Breast II A
5.221 0.000 -1.071 1.921 0.612 0.754 0.247 -0.977
-1.084 -0.361 -0.505 Breast Infiltrating Lobular Carcinoma, Solid Variant III B
2.799 0.000 1.705 0.694 -1.598 0.102 -1.194 1.382
0.290 6.634 1.419 Liver Hepatocellular Carcinoma III A
1.804 5.850 1.788 8.066 13.447 0.935 -3.299 6.613
6.269 0.175 6.127 Colorectal adenocarcinoma III C
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Breast lobular carcinoma IIA
0.000 0.000 -0.444 0.000 1.723 -0.378 -1.044 -0.282
-0.382 0.134 0.826 Breast lobular carcinoma NA
1.081 0.323 -0.702 -1.324 -1.758 1.526 0.000 3.816
5.583 1.591 0.000 Colorectal adenocarcinoma III A
0.518 0.000 0.089 0.000 -1.901 0.051 -0.215 -4.029
2.897 -2.003 -0.652 Colorectal adenocarcinoma IIA
4.631 1.095 5.261 2.406 4.362 0.410 -0.983 3.646
2.519 0.197 2.809 Colorectal adenocarcinoma III B
-1.099 -0.341 -0.513 -2.485 0.083 -1.321 -0.957 -0.894
-2.128 -0.425 0.545 Colorectal adenocarcinoma IIA
-0.478 2.056 0.597 4.293 4.667 -2.092 -0.161 3.266
7.290 -0.878 3.084 Colorectal adenocarcinoma IVA
0.204 2.162 -0.226 -0.230 0.079 1.582 -0.404 -1.868
-0.296 0.967 -2.344 Colorectal adenocarcinoma IIA
0.605 0.000 1.935 1.406 0.637 0.880 -1.484 0.861

Table35.txt

4.001	1.725	0.744	Colorectal		adenocarcinoma		
			III B				
6.808	4.370	6.147	5.308	6.146	1.642	-2.293	5.152
4.317	0.504	4.353	Colorectal		adenocarcinoma		
			IIA				
2.779	-0.439	0.399	0.000	1.966	-1.255	2.145	-0.169
2.921	-0.960	2.215	Colorectal		adenocarcinoma		
			IVA				
-1.042	0.000	-2.409	1.164	-1.556	0.595	0.366	-0.650
-0.990	-2.380	0.233	Colorectal		adenocarcinoma		
			III B				
2.952	0.548	-0.545	0.694	-0.149	-0.324	-0.512	-3.399
-1.062	0.410	2.376	Breast		ductal carcinoma		
			NA				
-3.582	-1.923	-1.564	-1.098	-2.657	-1.780	-2.686	-0.724
-0.810	-0.533	0.095	Colorectal		adenocarcinoma		
			IIA				
-1.218	-1.256	-0.381	-1.287	-2.119	-0.116	-0.941	-0.090
0.433	-0.248	-0.823	Breast		ductal carcinoma		
			NA				
1.004	2.996	4.723	3.275	4.968	1.106	0.310	-0.019
1.029	-1.078	1.236	Colorectal		adenocarcinoma		
			III B				
-0.379	-0.612	-1.004	-1.483	-1.970	-0.376	-0.788	-0.417
-1.013	-2.211	-0.736	Colorectal		adenocarcinoma		
			IIA				
3.613	0.000	1.699	1.382	1.321	-0.497	0.424	2.698
0.405	-0.390	0.169	Colorectal		adenocarcinoma		
			III B				
-0.325	0.000	4.216	-1.473	-1.111	-1.508	-0.340	0.674
-0.699	2.043	1.047	Breast		ductal carcinoma		
			NA				
0.045	0.053	0.085	0.224	-1.810	-0.551	-1.106	-1.174
-1.141	-2.239	-4.183	Breast		ductal carcinoma		
			NA				
0.594	-0.811	0.357	-0.273	-1.016	0.646	-0.742	-0.584
0.048	-1.934	-0.416	Breast		ductal carcinoma		
			NA				
1.834	0.529	1.506	-0.135	-3.189	0.146	-1.414	-0.512
-2.485	-1.453	1.117	Breast		lobular carcinoma		
			NA				
-2.871	2.082	-0.298	-0.652	-3.284	-2.413	-1.398	1.294
4.827	-1.081	0.506	Breast		ductal carcinoma		
			NA				
-1.539	-1.179	0.426	0.779	0.769	-0.482	-1.388	-0.120
-2.399	-0.091	2.579	Colorectal		adenocarcinoma		
			III B				
-0.640	1.371	-0.157	-0.592	1.102	0.136	5.252	-1.397

Table35.txt

5.267 0.505 2.953 Breast lobular carcinoma
NA
3.443 -0.971 0.823 -0.922 3.253 0.496 -1.217 -0.295
-1.514 -0.664 -0.792 Breast ductal carcinoma
NA
-1.312 -3.165 0.211 0.174 -1.915 -0.478 -0.472 -0.238
0.954 -1.017 -0.701 Colorectal mucinous adenocarcinoma
III B
3.492 0.000 -0.330 0.456 -0.545 3.298 -1.461 -0.167
-1.183 2.311 0.000 Breast ductal carcinoma
IIA
0.000 -0.838 1.693 -1.553 -2.320 0.362 1.178 -2.673
-1.077 2.269 0.502 Breast ductal carcinoma
IA
-2.759 0.000 2.558 0.000 0.835 0.137 -1.316 -0.505
3.106 -0.741 -1.316 Colorectal adenocarcinoma
IIA
0.921 0.000 1.728 0.000 0.000 -0.541 -1.182 1.195
3.146 -0.128 0.639 Colorectal adenocarcinoma
IIA
-1.538 0.000 0.000 -1.396 -0.526 -0.577 0.733 2.960
6.526 0.000 -0.792 Colorectal adenocarcinoma
I
-1.945 -1.368 -0.602 -0.664 -0.843 0.871 -0.736 -0.202
-1.199 -2.603 -0.883 Liver hepatocellular carcinoma
NA
0.458 -1.339 -0.073 0.211 -3.299 -0.002 -0.680 -1.189
-0.685 -2.083 -0.044 Colorectal adenocarcinoma
IIA
-0.675 0.051 -0.504 0.864 -1.679 -2.722 -1.663 0.136
-0.807 -2.385 -2.445 Colorectal Adenocarcinoma
IIIA
0.000 0.000 0.000 0.000 -1.281 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
IIIA
-0.261 0.000 -0.121 0.000 0.000 0.000 0.000 3.090
0.959 0.522 0.000 Colorectal Adenocarcinoma
IV
-0.217 0.000 -1.420 0.000 0.000 0.139 -0.790 1.700
0.000 0.000 0.000 Colorectal Adenocarcinoma
IIIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
IIIB
0.442 0.000 0.197 6.078 8.517 0.483 0.000 8.600
3.755 -1.483 0.527 Colorectal Adenocarcinoma
IIIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

Table35.txt

0.000 0.000 0.000 Esophagus Squamous cell carcinoma, keratinizing III
-0.383 2.915 2.813 1.790 -1.749 -1.602 2.217 2.178
-0.929 2.444 3.676 Breast Infiltrating ductal carcinoma IIIA
1.236 -0.144 1.565 -0.445 1.005 0.527 0.000 -1.360
0.000 0.000 0.000 Esophagus Squamous cell carcinoma, keratinizing III
3.038 1.903 3.251 -1.524 -0.191 0.689 3.104 -0.405
-2.184 3.090 0.924 Breast Infiltrating ductal carcinoma IIB
0.554 1.010 0.065 0.634 1.578 -0.137 0.122 -0.471
-3.271 -0.417 0.651 Breast Infiltrating ductal carcinoma IIA
0.254 0.000 -0.417 0.291 5.636 -0.938 -1.638 0.167
-1.025 0.202 -1.017 Colorectal Mucinous adenocarcinoma IIA
0.000 0.000 0.369 -0.251 -0.878 0.089 -0.637 0.000
-0.805 1.236 0.932 Breast Infiltrating ductal carcinoma IIIA
-1.940 -0.638 1.915 2.953 -1.511 2.719 -0.298 0.709
-2.227 2.708 -1.455 Liver Hepatocellular carcinoma, Trabecular IIIA
0.456 0.000 0.000 0.000 3.949 -0.158 -0.450 -0.207
-0.466 1.653 -0.521 Colorectal Adenocarcinoma IIA
10.802 6.431 4.364 5.640 7.821 0.000 -1.457 2.512
0.488 6.172 -0.955 Esophagus Adenosquamous carcinoma II
2.400 2.119 -0.583 2.344 -0.533 2.118 0.885 6.826
3.837 -0.185 4.368 Colorectal Adenocarcinoma I
3.219 5.804 6.821 -1.530 -2.055 2.557 1.463 2.943
1.560 -0.204 1.154 Colorectal Adenocarcinoma IIA
0.069 2.525 0.000 -1.342 0.000 0.382 -0.370 -0.717
-0.613 0.475 1.955 Colorectal Papillary adenocarcinoma IB
1.471 -0.104 2.744 -0.725 0.865 -1.467 -0.638 -0.566
-0.181 1.259 2.272 Breast Infiltrating ductal carcinoma IIA
0.608 0.000 0.000 -3.090 0.000 0.000 -0.541 -0.935
-0.113 0.000 -1.214 Colorectal Adenocarcinoma IIA
0.000 0.000 0.000 0.000 0.137 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma IIB
0.142 0.000 0.000 -0.736 0.000 0.000 0.000 -0.378

Table35.txt

0.000 0.000 0.000 Colorectal Adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.309 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Adenocarcinoma
IIA
0.000 0.000 -3.090 0.000 -0.240 0.000 0.000 0.000
0.000 0.000 0.000 Liver Hepatocellular carcinoma,
Solid Type II
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Colorectal Papillary adenocarcinoma
IIA
0.000 0.000 1.563 -0.316 -1.340 0.000 0.443 0.212
0.000 0.460 0.000 Colorectal Adenocarcinoma
IIB
-4.216 1.310 0.346 -1.154 -2.111 -1.009 0.769 1.994
-0.002 1.340 0.468 Colorectal Adenocarcinoma
I
0.277 -0.649 -0.912 0.100 0.348 -0.647 -2.024 0.000
0.043 0.083 0.000 Liver Hepatocellular carcinoma,
Solid Type II
0.923 4.687 1.083 3.093 2.692 -0.437 4.114 0.919
-0.390 5.293 0.000 Esophagus Squamous cell carcinoma,
keratinizing IIA
10.745 4.081 8.966 -0.399 -1.480 7.660 9.964 4.639
10.281 3.674 3.968 Colorectal Adenocarcinoma
IIA
-1.411 1.692 5.380 -0.873 -2.328 2.556 3.764 -1.179
4.412 -1.217 -0.648 Liver Hepatocellular carcinoma,
Trabecular II
-0.362 -1.521 -0.960 1.444 0.219 -0.855 -1.908 0.000
1.496 -1.686 0.560 Colorectal Adenocarcinoma
IIB
3.111 -0.686 -2.736 -0.965 -3.533 -0.330 -1.780 -0.888
-0.155 -1.406 -0.043 Colorectal Mucinous adenocarcinoma
II
-1.954 0.023 -1.466 -2.203 -0.002 -0.129 -2.873 1.024
5.247 -1.865 0.352 Colorectal Adenocarcinoma
IIA
-0.494 1.382 0.865 -0.540 -1.516 -0.069 -0.364 -0.503
1.393 4.325 -0.342 Colorectal adenocarcinoma
III C
7.764 1.964 0.874 2.429 3.030 1.056 -3.169 -0.066
4.973 -1.526 -1.460 Colorectal adenocarcinoma
III B
-1.595 0.296 0.535 0.541 -1.792 -0.983 0.472 -1.930
-2.986 -1.573 -1.560 Colorectal adenocarcinoma
I
-0.618 -4.314 -1.268 -0.662 -0.811 -0.445 -0.191 -1.652

Table35.txt

-0.445	-1.240	-3.090	Liver		hepatocellular carcinoma			
			NA					
0.000	0.000	-0.448	0.000	-3.498	0.670	-0.027	0.000	
0.000	0.000	0.000	Breast		ductal carcinoma			
			IIA					
-1.158	0.297	-1.092	-1.889	-0.769	-1.121	0.305	0.174	
0.270	-2.904	-0.685	Colorectal		signet-ring cells carcinoma			
			IIA					
-2.108	0.000	5.202	0.030	4.939	0.506	-0.397	-3.346	
-1.176	6.158	0.000	Breast		ductal carcinoma			
			IIA					
0.281	-0.344	0.054	-0.472	-0.153	-0.004	-1.477	-0.338	
-0.935	-0.075	0.869	Breast		lobular carcinoma			
			IIB					
0.000	-1.697	-0.893	-1.208	-0.127	0.675	-3.018	-2.400	
0.913	-2.382	0.001	Breast		ductal carcinoma			
			III A					
-0.285	0.030	0.344	-0.126	-0.568	2.415	0.906	2.015	
3.288	-0.491	1.042	Liver		hepatocellular carcinoma			
			NA					
-1.320	-0.521	-0.549	4.922	1.254	0.159	5.195	-0.325	
1.433	-0.165	0.000	Liver		hepatocellular carcinoma			
			NA					
-1.949	2.010	1.359	1.053	0.397	0.000	-1.508	0.445	
0.463	-0.798	-0.493	Esophagus		adenocarcinoma			
			IIA					
0.672	0.000	-1.291	2.126	1.512	0.204	-1.209	0.000	
0.027	-0.015	0.703	Colorectal		adenocarcinoma			
			IVA					
0.620	0.000	2.594	3.306	-0.114	-1.316	0.379	-0.253	
0.781	0.287	1.483	Colorectal		adenocarcinoma			
			IIA					
4.019	-0.461	-1.802	5.292	5.209	-1.277	-0.693	-0.499	
1.682	-1.364	3.684	Colorectal		adenocarcinoma			
			IIA					
-0.935	1.338	4.368	2.715	4.354	-0.179	0.427	3.073	
6.383	3.118	-0.109	Colorectal		adenocarcinoma			
			III A					
-1.024	1.213	0.412	2.777	4.195	-0.629	0.548	3.826	
-1.547	-1.535	-1.005	Colorectal		adenocarcinoma			
			III A					
-1.707	0.869	-1.248	-0.965	-0.304	-0.350	-1.657	0.076	
-0.472	-0.674	-0.102	Colorectal		signet-ring cells carcinoma			
			IVA					
0.000	0.000	-1.214	0.000	0.000	0.000	0.000	0.000	
0.000	-3.090	0.000	Colorectal		adenocarcinoma			
			III B					
-1.575	-0.505	-1.563	0.449	-0.536	-1.426	0.236	-2.354	

Table35.txt

-0.967	0.867	0.000	Liver		hepatocellular carcinoma			
			NA					
-1.683	-0.464	-0.431	-1.191	0.154	-0.910	-0.432	-0.609	
-0.454	-3.608	-1.099	Colorectal		mucinous adenocarcinoma			
			IIA					
-0.700	0.000	-0.505	0.000	0.000	0.000	-0.144	0.000	
0.969	0.000	0.000	Colorectal		adenocarcinoma			
			IIA					
-2.373	-0.872	-0.135	-0.523	0.235	-1.988	-1.368	-1.074	
-0.503	-0.968	0.315	Liver		hepatocellular carcinoma			
			NA					
0.116	-1.259	-2.114	0.535	1.594	-0.303	1.777	-0.082	
-0.423	-1.080	0.134	Breast		lobular carcinoma			
			III C					
-4.029	1.642	1.518	1.451	-0.061	-1.529	1.305	0.801	
2.942	2.312	0.635	Colorectal		Adenocarcinoma			
			NA					
-1.868	0.000	0.574	6.072	6.160	-1.181	-1.811	-1.879	
-0.842	-1.702	0.000	Colorectal		adenocarcinoma			
			III A					
0.000	0.000	-0.430	-0.943	-3.090	-0.736	0.030	-1.169	
-0.505	3.212	-0.670	Breast		ductal carcinoma			
			IIA					
-1.753	0.000	0.000	1.364	2.761	-0.324	-0.457	0.000	
3.318	0.000	0.000	Colorectal		adenocarcinoma			
			III B					
-1.952	0.000	-0.832	0.309	1.382	3.869	2.201	0.000	
6.875	-1.945	-2.010	Colorectal		adenocarcinoma			
			IIA					
0.956	3.085	2.510	3.375	3.599	0.701	0.070	0.850	
5.232	-0.270	-0.183	Colorectal		adenocarcinoma			
			III B					
-0.371	2.915	-0.534	2.561	2.191	-0.836	-0.287	-1.807	
-0.691	-1.300	0.432	Colorectal		adenocarcinoma			
			III B					
0.843	-0.229	-1.357	0.991	2.316	-2.712	1.377	2.018	
-0.224	-2.056	0.660	Breast		ductal carcinoma			
			NA					
-1.048	-1.878	0.854	-1.229	-0.637	-0.203	-0.874	0.713	
-1.213	-0.329	-0.174	Breast		ductal carcinoma			
			IA					
2.099	-1.159	0.553	0.891	0.134	0.309	-1.458	-2.371	
-1.080	-0.414	-0.378	Breast		lobular carcinoma			
			IIA					
0.225	1.724	4.497	-1.466	-0.513	0.773	-0.821	-1.569	
-0.067	0.306	3.224	Breast		ductal carcinoma			
			IA					
-0.823	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

Table35.txt

0.000 0.000 0.000 Colorectal adenocarcinoma
III B
-0.294 -3.237 0.028 -0.363 -1.273 -1.387 0.959 -1.179
-0.821 0.211 -1.141 Colorectal adenocarcinoma
IIA
-1.108 2.321 1.154 4.251 6.902 1.060 0.430 4.157
2.765 0.961 0.000 Colorectal adenocarcinoma
III B
4.464 2.590 0.118 2.848 2.885 -0.688 0.149 -0.340
2.555 0.575 1.607 Colorectal adenocarcinoma
III C
-0.945 -0.522 -0.432 -1.572 3.038 -1.621 -0.807 -3.502
0.290 3.454 0.294 Esophagus keratinizing squamous cell carcinoma
IB
0.074 1.588 0.466 0.000 0.000 0.000 -0.538 0.159
-0.798 -0.638 0.000 Colorectal adenocarcinoma
IVA
1.631 -0.600 -1.622 -0.431 14.659 9.243 4.611 5.856
9.795 9.043 -1.350 Colorectal Papillary adenocarcinoma
IIA
3.887 5.519 1.643 7.460 3.090 0.066 -1.739 0.000
-1.121 -1.580 -0.267 Liver Hepatocellular carcinoma
IIIA
-2.404 0.152 -0.449 -1.173 -0.572 -3.893 -0.942 0.779
-1.320 -1.736 -0.888 Colorectal Tubular adenocarcinoma
IIA
10.336 -3.144 -2.540 3.388 5.407 0.252 -2.381 2.596
14.615 0.237 2.143 Colorectal Adenocarcinoma
IIA
-1.479 2.617 3.090 4.932 -1.033 0.000 3.503 0.000
4.507 3.090 2.425 Esophagus Squamous cell carcinoma
IIB
-1.405 -0.054 0.366 -0.392 -0.249 0.254 1.467 -0.396
0.095 -0.048 -0.859 Colorectal Adenocarcinoma
IIA
6.634 -1.740 15.006 -1.017 -0.834 -0.595 -1.147 0.823
10.431 10.237 2.605 Esophagus Squamous cell carcinoma, keratinizing
IIB
1.589 -1.053 -0.987 -1.034 -1.301 -0.735 -2.108 -1.124
-0.449 1.047 -0.562 Colorectal Mucinous adenocarcinoma
IIA
1.688 6.853 12.836 -0.179 0.704 -1.385 -0.970 4.724
-2.207 8.101 5.417 Colorectal Adenocarcinoma
IIA
0.718 2.840 -0.432 -2.599 4.415 4.707 7.710 3.838
12.133 1.574 -2.254 Breast Infiltrating ductal carcinoma
IIIA
6.242 -0.856 3.160 2.578 0.152 3.900 0.079 0.016

Table35.txt

6.515 3.228 -0.427 Breast Infiltrating ductal carcinoma
IIIA
-3.379 -0.356 -3.811 5.815 8.987 -0.374 0.106 6.238
-1.506 0.247 0.339 Breast Infiltrating ductal carcinoma
I
-1.487 0.746 1.018 4.637 5.505 2.416 0.654 -0.252
2.237 3.104 3.120 Esophagus Squamous cell carcinoma
IIA
0.083 1.724 1.411 -1.679 0.629 0.695 0.148 1.190
12.072 1.842 -0.401 Breast Infiltrating ductal carcinoma
I
-1.117 -0.593 -2.083 4.295 0.000 7.224 10.730 0.000
-2.016 -2.351 -1.128 Liver Hepatocellular carcinoma,
Acinar Type II
1.146 -1.032 -2.209 1.343 -2.071 -1.731 0.898 0.000
3.471 0.902 -0.662 Liver Hepatocellular carcinoma
IIIA
4.339 0.620 -2.016 -0.995 5.846 -1.742 -2.274 3.144
7.297 -1.897 -0.512 Breast Infiltrating ductal carcinoma
IIIA
-0.993 1.486 1.247 3.237 6.600 0.458 -0.153 1.382
10.981 0.986 0.146 Breast Infiltrating lobular carcinoma
IIB
-2.215 4.281 8.946 3.178 8.732 -0.319 5.940 4.358
0.744 7.703 5.521 Esophagus Squamous cell carcinoma,
keratinizing IIA
10.355 -0.397 -1.230 2.733 5.072 0.419 7.880 1.867
14.635 4.300 6.295 Liver Hepatocellular carcinoma,
Trabecular IIIA
0.797 -0.895 0.808 9.591 9.803 5.588 7.868 -0.820
-0.664 12.590 9.652 Breast Intraductal carcinoma
I
-2.019 0.000 -3.359 -2.602 1.570 2.537 0.163 -0.910
0.000 -0.224 -2.653 Breast Infiltrating ductal carcinoma
IIB
0.000 0.000 0.000 0.000 -0.378 0.000 0.000 0.000
0.000 0.000 0.000 Breast Infiltrating lobular carcinoma
IIIB
-1.402 5.093 4.404 4.107 7.818 -0.146 0.130 -0.448
6.156 -2.222 4.244 Breast Infiltrating ductal carcinoma
IIIC
6.313 -1.348 0.435 -0.443 9.334 -1.103 -0.459 -0.023
-1.292 -2.103 -1.509 Breast Infiltrating ductal carcinoma
IIIB
11.238 3.684 7.971 -3.752 10.179 5.473 6.914 2.459
5.443 10.130 8.157 Breast Infiltrating lobular carcinoma
IIB
-1.000 -2.712 -2.496 4.329 10.897 -2.061 6.871 2.541

Table35.txt

```
0.832     4.562     0.000     Breast                Infiltrating ductal carcinoma
                          IIB
-0.665    -2.575    -0.583    3.716     5.623     1.662     -0.572    -0.911
-1.167    2.116     0.884     Breast                Infiltrating ductal carcinoma
                          IA
-1.697    6.137     0.330     0.123     0.189     -1.499    -2.450    0.000
0.348     0.000     0.000     Breast                Infiltrating ductal carcinoma
                          IIIB
0.638     5.044     10.380    3.180     5.815     7.453     3.727     -0.286
2.849     2.216     -0.294    Breast                Infiltrating ductal carcinoma
                          IIB
-2.658    -0.359    -0.007    -0.111    -1.926    -0.070    -1.244    0.000
0.040     0.713     -0.694    Breast                Infiltrating ductal carcinoma
                          IIB
-1.899    0.639     -1.036    -1.689    0.776     1.091     1.102     -1.220
-5.121    1.854     -1.303    Breast                Infiltrating ductal carcinoma
                          IIB
8.999     -0.514    9.108     5.177     7.284     12.459    13.540    3.406
17.030    8.936     8.894     Breast                Infiltrating ductal carcinoma
                          IIB
-4.481    0.174     3.958     -2.010    -2.508    0.112     -2.101    1.472
-3.531    -0.830    0.856     Breast                Infiltrating lobular carcinoma
                          IIA
-0.141    3.090     2.066     0.985     2.234     2.353     5.692     3.012
3.458     0.000     -0.749    Breast                Infiltrating ductal carcinoma
                          IIB
-2.852    2.065     -0.630    -0.366    -0.757    -1.820    -0.253    0.000
-0.849    0.000     0.810     Breast                Infiltrating ductal carcinoma
                          IIB
-0.568    3.029     3.170     -1.163    -2.549    -1.148    0.262     1.766
8.178     -0.930    -1.421    Breast                Infiltrating ductal carcinoma
                          IIB
1.610     -1.383    0.000     -0.568    0.249     0.173     -1.211    -0.321
1.369     2.383     0.007     Breast                Metaplastic carcinoma
                          IIIB
0.471     3.090     3.090     5.052     -0.544    6.307     9.297     0.000
7.013     0.000     0.000     Esophagus             Neuroendocrine carcinoma
                          IIA
1.153     -2.385    0.000     0.000     0.000     -0.306    0.326     -0.450
-0.618    0.000     -0.403    Esophagus             Squamous cell carcinoma,
keratinizing                    IIA
-0.634    -0.718    -2.094    -0.756    -1.659    1.407     0.845     0.704
0.905     0.795     -0.582    Pancreas              Intraductal papillary
carcinoma                            III
16.052    -0.880    0.337     -0.840    -1.213    1.144     7.310     0.411
2.680     4.645     7.134     Esophagus             Squamous cell carcinoma
                          IIA
8.066     3.569     5.285     3.220     4.943     2.854     3.265     1.327
```

Table35.txt

2.047 4.313 1.669 Esophagus Squamous cell carcinoma, keratinizing IIA
6.659 -0.391 -1.198 0.256 -2.447 0.151 0.777 4.088
7.869 6.489 3.696 Esophagus Squamous cell carcinoma IIB
9.620 2.870 11.318 6.966 -1.597 3.861 6.545 4.085
1.060 4.418 -1.946 Esophagus Squamous cell carcinoma, keratinizing III
4.942 0.324 2.896 0.771 -0.819 -3.379 0.939 -1.937
0.054 8.065 3.209 Esophagus Squamous cell carcinoma, keratinizing IIA
-1.289 0.927 -1.389 0.724 5.011 10.256 6.830 7.697
3.657 12.470 11.075 Esophagus Squamous cell carcinoma, keratinizing IIB
3.090 2.629 0.000 0.883 -1.025 -0.638 0.092 2.778
6.688 0.880 1.037 Esophagus Squamous cell carcinoma, nonkeratinizing, III
3.734 -0.168 0.000 0.000 0.000 5.139 3.090 1.101
0.202 3.090 5.167 Esophagus Squamous cell carcinoma, nonkeratinizing, III
-2.776 -0.290 -0.285 1.379 -3.154 -1.477 -0.574 0.644
1.525 -0.335 1.398 Breast ductal carcinoma IIA
-3.510 3.470 9.143 -0.391 1.601 -0.475 -3.593 -0.096
1.482 -1.457 -1.128 Liver hepatocellular carcinoma II
-3.440 7.855 16.451 8.457 13.807 9.376 10.335 0.352
1.623 -1.231 -1.258 Breast ductal carcinoma IIA
-1.356 0.975 -1.625 -1.000 -0.319 3.673 5.052 -1.017
2.232 3.762 2.720 Stomach adenocarcinoma, partially of signet ring cell-type - diffuIV
4.370 0.000 0.000 2.322 4.584 9.134 12.998 0.000
16.497 3.090 3.090 Stomach adenocarcinoma - intestinal type IIB
15.479 5.690 11.623 1.912 11.582 12.391 7.587 0.690
10.382 3.090 0.000 Stomach adenocarcinoma IIB
-1.722 -0.201 0.125 -0.690 -5.193 0.150 -2.135 1.856
7.577 -1.402 -4.486 Stomach adenocarcinoma IIB
7.104 -2.204 5.677 1.116 2.964 6.800 11.028 1.747
11.840 6.389 -0.511 Ovarian carcinoma - serous papillary type III C
1.407 3.955 -2.847 1.543 1.309 0.228 1.862 -1.290
-1.026 -2.112 -1.464 Esophagus adenocarcinoma - intestinal type III B
14.617 3.002 7.257 8.723 17.795 0.088 -2.153 3.583

Table35.txt

11.578	0.528	-2.094	Ovarian		carcinoma - serous type			
			IV					
3.788	8.878	12.672	9.212	6.610	7.507	13.383	4.228	
12.649	9.306	6.481	Esophagus		adenocarcinoma			
			III C					
0.147	0.024	1.226	-0.822	-1.615	-1.776	-1.142	0.614	
5.797	-0.837	-1.507	Pancreas		adenocarcinoma			
			IB					
-2.448	0.344	-0.588	0.079	-2.352	-2.142	4.254	0.000	
0.441	0.000	-2.969	Pancreas		adenocarcinoma			
			IIB					
-0.056	-0.378	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	Pancreas		adenocarcinoma			
			IIB					
-0.087	0.000	-1.472	0.000	-2.192	-0.279	-1.024	0.000	
-0.369	-3.090	0.460	Pancreas		adenocarcinoma			
			IIB					
-0.418	-1.073	2.329	-1.063	-1.818	2.095	-0.697	-0.221	
3.558	8.137	1.842	Liver		NA			
			NA					
11.548	-1.308	-0.761	3.851	7.876	1.417	-0.071	-2.205	
0.101	2.020	0.776	Liver		NA			
			NA					
14.663	-0.863	-1.260	-3.188	0.022	-0.374	-1.908	-0.442	
3.181	-0.079	-1.652	Liver		NA			
			NA					
6.554	7.784	7.652	-0.101	-0.382	0.066	-0.227	5.150	
1.264	6.176	2.655	Liver		NA			
			NA					
-0.578	-2.217	-2.146	-0.654	-3.000	-3.090	-0.185	-1.349	
-1.229	-0.783	-0.185	pancreas		adenocarcinoma			
			IIB					
-3.132	0.000	-0.208	-0.916	1.165	0.000	-1.215	-1.892	
-0.056	-1.396	0.762	pancreas		adenocarcinoma			
			IIB					
-1.565	1.493	-1.426	-1.862	2.929	0.071	-2.541	-0.497	
-0.447	-0.845	-0.742	pancreas		adenocarcinoma			
			IIB					
-0.707	-0.027	-1.360	-1.281	0.218	0.000	0.000	0.000	
1.153	-3.342	-1.316	pancreas		adenocarcinoma			
			IIB					
-2.966	-0.114	-3.023	-0.105	1.070	-0.889	0.613	0.329	
-0.437	-1.719	-0.832	pancreas		adenocarcinoma			
			IIB					
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	pancreas		adenocarcinoma			
			IV					
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

Table35.txt

0.000	0.000	0.000	pancreas		adenocarcinoma						
			IIA								
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000				
0.000	0.000	0.000	pancreas		adenocarcinoma						
			IIB								
-1.531	0.266	-0.851	-1.707	0.138	-0.925	0.518	-1.402				
0.000	0.000	2.827	pancreas		adenocarcinoma						
			IIB								
0.000	0.000	0.137	0.000	0.000	0.000	0.000	0.000				
0.000	0.000	0.000	Pancreas (Bile Duct)		adenocarcinoma						
			IIB								
-0.074	0.000	0.037	0.595	-0.378	0.000	-2.766	0.000				
-0.505	-0.375	-4.337	pancreas		adenocarcinoma						
			IIA								
-0.502	0.000	-1.476	1.460	-2.438	-0.027	-0.961	-0.457				
0.595	-2.600	0.309	pancreas		adenocarcinoma						
			IIA								
-1.419	-0.596	-1.286	-1.245	1.475	-0.325	-0.740	-0.892				
-2.294	1.768	-1.030	pancreas		adenocarcinoma						
			IB								
-1.953	0.602	0.035	1.698	1.539	0.053	0.651	-0.348				
-0.374	0.588	-0.774	pancreas		adenocarcinoma						
			IB								
-2.649	-1.032	0.196	-1.698	-0.790	-0.695	-1.115	-0.582				
-1.374	-1.580	-0.172	pancreas		adenocarcinoma						
			IV								
-1.744	1.442	-0.388	-1.134	-1.082	-0.064	-0.819	-1.160				
0.320	-2.045	-0.322	pancreas		adenocarcinoma						
			IIB								
-0.682	-1.107	-2.155	5.131	-0.028	1.325	-0.039	-0.359				
-1.125	0.265	-0.011	Pancreas (Ampulla)		adenocarcinoma						
			IIB								
0.000	0.000	-0.995	-0.144	0.250	0.000	0.000	0.000				
0.000	0.865	-0.378	pancreas		adenocarcinoma						
			IIB								
-2.972	-2.779	0.651	0.879	-2.882	-0.446	-2.047	-2.868				
-0.227	-2.790	-1.536	Pancreas (Ampulla)		adenocarcinoma						
			III								
-0.831	-0.265	-0.430	-0.247	-1.959	0.000	-2.169	-0.755				
-0.124	-1.609	-0.131	pancreas		adenocarcinoma						
			IIB								
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000				
0.000	0.000	0.000	pancreas		adenocarcinoma						
			IIB								
-0.174	0.865	0.500	-0.290	0.756	-0.505	0.284	1.185				
-0.276	-2.881	-0.654	pancreas		adenocarcinoma						
			IIB								
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000				

Table35.txt

0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
-2.757	-1.118	0.150	-1.238	-2.365	-1.029	0.111	-1.373
0.754	-2.309	-2.563	pancreas		adenocarcinoma		
			IIB				
-2.516	0.366	-1.065	1.866	0.621	0.000	0.272	0.381
0.344	-0.650	0.000	pancreas		adenocarcinoma		
			IIB				
0.000	3.090	0.000	3.090	0.000	4.119	0.952	-1.963
0.370	0.372	0.000	pancreas		adenocarcinoma		
			IA				
5.237	3.090	-1.840	-0.105	4.044	-1.414	1.275	1.631
-1.021	0.398	2.891	pancreas		adenocarcinoma		
			IA				
-2.110	0.000	0.782	-1.108	0.000	0.000	-0.938	-0.544
0.000	0.098	0.000	pancreas		adenocarcinoma		
			IV				
-1.129	0.000	-1.215	0.502	2.428	-0.392	-1.071	-1.178
-1.613	4.212	2.552	pancreas		adenocarcinoma		
			IV				
-1.258	-0.190	1.477	-0.555	1.751	3.649	1.274	1.203
0.435	4.416	0.000	pancreas		adenocarcinoma		
			IV				
-0.101	-2.335	-0.099	-1.776	-2.548	0.340	-0.903	-0.197
-0.580	-0.152	-1.130	Pancreas (Ampulla)		adenocarcinoma		
			IIB				
-2.693	7.187	2.772	5.658	10.134	0.763	1.861	0.340
-1.068	3.017	2.046	pancreas		adenocarcinoma		
			IIB				
1.838	1.901	2.234	0.895	1.602	0.288	-1.206	-1.978
-2.351	1.077	-0.914	pancreas		adenocarcinoma		
			IIB				
0.608	-1.697	1.858	-0.909	2.941	1.637	-2.427	-1.034
-3.097	-0.603	-1.630	pancreas		adenocarcinoma		
			IB				
-1.945	3.073	-1.158	-1.085	4.008	-0.088	-2.118	0.301
0.246	1.111	0.075	pancreas		adenocarcinoma		
			IIA				
2.993	2.255	4.324	1.869	2.498	-0.578	-1.147	0.033
-0.396	-1.105	1.532	pancreas		adenocarcinoma		
			IV				
-0.839	3.808	0.326	6.132	3.373	0.697	-0.102	-0.768
-0.406	1.222	-0.364	pancreas		adenocarcinoma		
			IIB				
-2.739	6.003	2.623	2.602	0.371	-1.010	-0.435	-1.417
2.072	1.874	3.320	pancreas		adenocarcinoma		
			IIB				
-2.110	-2.843	0.711	-0.514	0.814	1.195	0.185	1.188

Table35.txt

0.535	-0.860	-1.307	pancreas		adenocarcinoma		
			IIB				
-0.850	3.601	0.870	2.017	5.096	1.420	-0.473	-0.382
1.050	0.324	0.443	pancreas		adenocarcinoma		
			IIB				
-2.302	0.690	-0.679	0.714	3.368	0.653	0.579	-0.109
-0.480	0.999	1.855	pancreas		adenocarcinoma		
			IIB				
1.537	7.177	0.880	7.382	5.587	0.520	0.568	3.881
2.702	1.024	0.599	pancreas		adenocarcinoma		
			IIB				
6.390	6.848	4.007	7.608	9.703	2.377	7.849	7.856
4.788	3.853	0.412	pancreas		adenocarcinoma		
			IIB				
-1.180	-1.480	-0.107	-0.391	-2.001	0.149	-0.731	-0.146
-0.997	0.135	-1.214	pancreas		adenocarcinoma		
			IIB				
-0.131	0.472	-0.129	-0.095	0.003	-1.476	0.676	0.679
0.470	-0.768	0.630	pancreas		adenocarcinoma		
			IIB				
-0.027	0.000	0.000	0.000	0.460	0.000	0.000	0.000
0.000	0.137	0.000	pancreas		adenocarcinoma		
			IIB				
2.587	2.905	-0.273	0.398	3.462	-0.935	0.312	-0.557
-1.408	-0.694	1.602	pancreas		adenocarcinoma		
			IIB				
-0.334	-1.557	-1.061	4.562	-1.112	0.376	0.444	0.693
4.034	-0.350	-1.106	pancreas		adenocarcinoma		
			IIB				
-0.790	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
-0.793	0.000	-1.329	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
-0.761	2.030	2.461	1.768	2.692	0.716	-1.527	-1.241
2.034	0.110	1.110	pancreas		adenocarcinoma		
			IIB				
-2.373	0.628	-2.531	2.257	-1.206	0.235	-1.214	-0.994
0.699	-0.129	0.662	pancreas		adenocarcinoma		
			IIA				
-1.650	2.427	0.728	-1.369	2.562	2.408	1.275	2.369
0.653	1.558	-0.050	pancreas		adenocarcinoma		
			IIB				
-1.832	2.132	2.048	0.734	1.093	3.320	0.606	-0.616
0.064	-0.067	1.355	pancreas		adenocarcinoma		
			IIB				
-2.018	-0.823	-0.267	-1.218	-1.316	0.000	0.740	0.024

Table35.txt

-0.216 -2.527 -1.706 pancreas adenocarcinoma
IIB
0.904 0.351 -1.139 -0.989 -1.127 -0.285 0.527 -2.591
-0.415 -0.352 -0.467 pancreas adenocarcinoma
IIA
-0.196 0.067 -0.214 1.629 2.396 0.321 0.153 -0.139
0.007 -2.752 -1.102 pancreas adenocarcinoma
IIA
-1.796 0.000 0.064 0.000 0.310 -0.022 -2.557 -0.445
-1.498 -1.203 -0.925 pancreas adenocarcinoma
IIA
-1.932 0.163 -1.417 -3.107 -0.505 -1.389 -1.214 -0.414
-0.616 -0.084 -1.273 pancreas adenocarcinoma
IIB
-0.228 1.933 1.127 0.309 2.880 -0.584 -1.230 -1.880
-1.342 2.092 -1.999 pancreas adenocarcinoma
IIB
0.346 -1.842 -0.667 -1.050 -1.863 -1.479 0.130 0.059
-2.173 0.588 -1.324 pancreas adenocarcinoma
IIB
-1.825 2.017 2.532 -0.402 3.149 -0.480 -2.014 2.501
-0.020 1.325 4.219 pancreas adenocarcinoma
IIB
4.077 -0.780 -0.485 1.701 3.228 0.205 -1.649 -1.119
-0.184 1.111 -1.086 pancreas adenocarcinoma
IIA
0.023 -2.387 -1.201 -0.326 -0.817 -1.667 -0.601 -1.308
-0.767 -0.399 -0.275 pancreas adenocarcinoma
IIB
-0.753 -0.958 -1.019 -1.618 1.857 1.518 -1.712 1.638
0.001 -0.512 -0.079 pancreas adenocarcinoma
IIB
-0.075 0.919 -1.323 2.625 -1.556 0.000 -2.878 1.029
-1.924 -1.665 0.146 pancreas adenocarcinoma
IIB
-1.360 0.946 -0.992 -0.765 5.242 3.051 6.568 0.429
-0.116 5.588 1.103 pancreas adenocarcinoma
IIB
-2.342 -0.319 -1.728 0.494 0.405 -0.694 0.095 -1.169
0.261 0.556 -0.293 pancreas adenocarcinoma
IIA
-0.734 0.336 -1.266 0.148 -1.033 -0.527 0.140 -0.990
1.394 -0.257 -1.921 pancreas adenocarcinoma
IIB
0.449 0.527 -0.190 -0.456 -2.563 -0.592 -2.508 -1.514
0.306 -0.172 0.538 pancreas adenocarcinoma
IIB
0.692 1.038 2.152 -3.694 -2.826 -2.368 2.140 1.800

Table35.txt

-1.408 0.068 2.328 pancreas adenocarcinoma
IIB
-1.234 1.026 1.017 0.391 0.496 0.000 -0.984 0.910
1.043 8.190 4.180 pancreas adenocarcinoma
IIA
-1.287 -0.292 0.699 -1.411 -1.183 -2.557 -0.781 -2.887
-0.033 -0.655 -0.771 pancreas adenocarcinoma
IIA
0.163 0.000 1.729 0.000 3.352 -0.647 2.162 0.299
-0.265 -1.164 -0.049 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-1.885 -0.097 -1.376 0.924 3.031 0.000 1.230 -1.818
-0.298 3.203 1.059 pancreas adenocarcinoma
IIB
-0.347 6.265 2.087 0.600 0.392 -0.730 1.649 0.882
1.983 -0.883 -0.747 pancreas adenocarcinoma
IIB
1.302 1.586 -1.023 1.484 0.950 -1.106 0.258 0.644
-0.143 -1.953 -0.376 pancreas adenocarcinoma
IIA
-0.691 -0.989 0.504 0.331 0.176 0.079 -2.698 -1.809
-2.005 -1.784 -0.313 pancreas adenocarcinoma
IIB
-1.856 0.353 -0.926 3.059 0.438 0.865 -0.542 -0.947
-0.378 -1.316 0.973 pancreas adenocarcinoma
IIA
-2.822 -0.370 1.074 4.128 7.898 3.092 -0.017 4.382
-2.311 7.149 4.032 pancreas adenocarcinoma
IIB
0.216 2.550 -1.047 2.226 -0.938 0.529 -0.258 0.253
0.485 2.265 0.855 pancreas adenocarcinoma
IV
-1.421 2.522 4.632 1.688 5.137 0.354 0.321 -0.136
-0.475 -0.113 -0.283 pancreas adenocarcinoma
IIB
-1.181 4.483 -1.333 4.292 10.726 0.374 0.938 4.631
-0.357 7.222 4.915 pancreas adenocarcinoma
IIB
-0.258 -0.731 -3.258 -0.852 -2.014 -0.065 -0.199 -0.842
-1.052 -1.256 0.000 pancreas adenocarcinoma
IIB
-2.751 -1.642 0.986 -0.684 -0.513 0.044 1.099 0.476
0.822 -0.570 -0.864 pancreas adenocarcinoma
IIB
-1.507 0.005 -1.806 -0.198 0.819 -0.144 -2.725 -2.366

Table35.txt

-0.958 -1.255 -0.666 pancreas adenocarcinoma
IIB
-1.499 1.553 0.296 -0.543 -0.266 0.604 -0.571 -1.367
-1.947 0.131 -0.225 pancreas adenocarcinoma
IIB
-1.945 -0.014 -1.513 -0.431 1.827 0.090 0.652 -1.153
-1.326 2.213 0.064 pancreas adenocarcinoma
IIB
-0.117 0.947 -1.660 -1.785 0.240 1.513 -0.257 -0.768
-1.071 -1.209 -0.681 pancreas adenocarcinoma
IIB
-1.025 2.502 3.492 2.481 3.672 -1.598 6.388 -0.480
-2.009 -1.804 -0.269 pancreas adenocarcinoma
IA
0.683 1.828 1.674 -0.602 -0.557 -1.584 -0.195 0.457
0.891 -0.334 2.732 pancreas adenocarcinoma
IIB
-0.027 0.000 -0.110 -0.083 2.443 0.000 0.000 -1.389
-1.436 1.803 2.208 pancreas adenocarcinoma
IV
-2.151 -0.144 -1.225 -2.426 -0.759 -0.987 -0.545 -0.694
-0.395 -0.857 -0.823 pancreas adenocarcinoma
IIB
-2.653 0.460 -1.501 -0.802 0.329 -0.787 2.962 0.227
-0.451 -0.508 0.095 pancreas adenocarcinoma
IIB
-1.927 0.000 -0.861 0.000 0.182 0.000 0.000 0.000
0.000 -0.688 -0.823 pancreas adenocarcinoma
IIB
0.000 0.000 -0.378 0.137 -1.485 0.000 -0.375 0.000
0.000 -0.217 0.000 pancreas adenocarcinoma
IA
0.489 0.000 -1.731 -1.914 -1.912 -0.911 -0.667 -0.700
-1.817 -1.791 -1.429 pancreas adenocarcinoma
IA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IB
-3.090 -0.378 -0.823 -1.222 -0.144 0.000 0.000 0.000
0.000 -0.910 0.137 pancreas adenocarcinoma
IV
0.046 0.000 -0.027 0.000 -0.781 0.000 -0.790 -0.823
-0.227 -1.208 0.000 pancreas adenocarcinoma
IIB
0.101 0.000 -2.680 2.774 0.000 0.163 2.937 -0.798
-0.395 -0.261 0.000 pancreas adenocarcinoma
IIB
-0.116 -1.368 1.511 -0.369 -0.269 0.000 0.366 0.309

Table35.txt

0.366	-0.169	0.000	pancreas	adenocarcinoma	IIB						
-1.468	0.000	0.050	-0.541	-0.984	0.561	-3.310	-0.988	0.542	-3.884	-0.592	pancreas	adenocarcinoma	IIB
-2.462	-0.057	-0.367	-1.537	-0.827	-1.095	-1.169	-1.968	-0.528	-1.742	0.000	pancreas	adenocarcinoma	IIB
-2.758	-0.156	-1.751	0.293	-0.404	-0.395	-0.920	-1.529	-2.767	-1.949	0.089	pancreas	adenocarcinoma	IIB
-1.629	1.292	-1.181	0.962	0.288	-0.585	-0.500	-2.534	-0.592	-0.640	-1.316	pancreas	adenocarcinoma	IIB
-0.540	0.050	3.208	-2.085	-0.265	0.116	2.434	-0.278	0.559	0.513	0.248	pancreas	adenocarcinoma	IIB
-2.648	-3.090	-3.284	0.035	-1.066	0.651	1.855	-0.942	-0.337	0.365	-0.233	pancreas	adenocarcinoma	IV
-1.793	-1.214	-1.734	-1.168	1.147	0.141	-2.031	-3.680	-1.396	-2.805	-2.846	pancreas	adenocarcinoma	IIB
-0.695	0.678	-0.097	1.129	0.541	0.237	0.595	-0.080	-1.405	1.075	-0.941	pancreas	adenocarcinoma	IIB
-1.225	-1.602	-2.650	-1.428	-0.806	0.352	-3.306	-0.482	-0.391	-0.887	-2.074	pancreas	adenocarcinoma	IIB
-2.867	0.000	-1.303	0.050	0.000	0.266	-1.281	0.000	0.865	0.000	0.000	pancreas	adenocarcinoma	IV
-2.716	0.807	0.396	0.091	0.666	-0.376	-1.991	0.650	-0.244	0.394	-0.945	pancreas	adenocarcinoma	IB
-0.679	0.223	-0.508	0.107	1.141	-2.697	-0.434	0.594	0.067	-1.327	0.244	pancreas	adenocarcinoma	IV
-0.071	-0.868	-1.766	0.610	-0.182	-1.265	-0.251	-3.084	0.050	-0.822	-1.810	pancreas	adenocarcinoma	IIB
-1.846	-0.059	-0.692	-1.177	-2.317	0.000	-0.158	-1.091	-1.281	-1.660	-0.443	pancreas	adenocarcinoma	IIB
-0.307	-0.333	-0.621	-2.440	0.124	0.812	0.221	-1.430	-1.323	0.039	-0.396	pancreas	adenocarcinoma	IIB
0.529	0.000	0.000	0.000	0.000	0.000	0.000	0.000						

Table35.txt

0.000	0.000	0.000	pancreas		adenocarcinoma		
			IA				
-0.939	-2.754	-2.253	-1.144	-2.525	0.215	-0.952	-0.387
0.074	-1.297	-0.305	pancreas		adenocarcinoma		
			IIB				
-1.365	-3.090	-1.666	-1.365	1.222	0.169	-0.595	-0.993
-0.921	0.527	0.295	pancreas		adenocarcinoma		
			IIB				
-0.786	0.704	0.168	-0.538	-1.561	0.163	-0.589	0.306
-0.820	-1.067	-0.152	pancreas		adenocarcinoma		
			IIB				
0.081	-0.378	-0.638	0.677	-1.308	-1.080	2.736	-2.296
-0.817	-2.026	-0.039	pancreas		adenocarcinoma		
			IIB				
-0.298	0.000	-0.769	0.000	0.000	0.000	-0.378	-0.872
0.000	-1.107	0.000	pancreas		adenocarcinoma		
			IIB				
-2.625	0.128	-0.444	-0.409	-0.350	-0.705	-0.267	0.211
-0.436	0.137	-0.168	pancreas		adenocarcinoma		
			IA				
-0.622	0.000	-1.158	0.741	0.916	0.000	0.717	-2.044
-0.968	-1.280	-0.848	pancreas		adenocarcinoma		
			IA				
-0.134	0.000	-0.984	-0.216	1.586	0.000	0.202	-3.205
0.119	0.000	-0.072	pancreas		adenocarcinoma		
			IIB				
0.457	-0.243	-2.111	0.034	-0.491	-0.974	0.169	-1.113
-0.569	0.039	1.356	pancreas		adenocarcinoma		
			IIB				
-1.544	-0.302	-0.471	-0.471	-2.059	-0.102	-0.010	-0.405
-0.238	-1.910	-1.274	pancreas		adenocarcinoma		
			III				
-0.596	4.366	3.090	5.444	6.353	3.090	3.612	0.339
0.157	5.582	5.320	pancreas		adenocarcinoma		
			IB				
-0.864	-0.545	-1.510	0.000	-0.902	-1.307	0.868	1.200
-0.201	-1.349	-1.316	pancreas		adenocarcinoma		
			IIA				
-2.186	0.000	-2.050	-0.809	0.823	-0.074	-1.235	-1.322
0.000	-0.675	-2.199	pancreas		adenocarcinoma		
			IIB				
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			III				
-0.261	0.000	0.000	0.000	0.362	0.000	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table35.txt

```
0.000   0.000   0.000   pancreas        adenocarcinoma
                IIA
0.000   0.000   0.000   0.000   0.000   0.000   0.000   0.000
0.000   0.000   0.000   pancreas        adenocarcinoma
                IIB
0.000   0.000   0.000   0.000   0.000   0.000   0.000   0.000
0.000   0.000   0.000   pancreas        adenocarcinoma
                IIB
0.000   0.000   0.000   0.000   0.000   0.000   0.000   0.000
0.000   0.000   0.000   pancreas        adenocarcinoma
                IIA
0.000   0.000   0.000   0.000   0.969   0.000   0.000   0.000
0.000   0.000   0.000   pancreas        adenocarcinoma
                III
0.000   0.000   -1.288  -0.074  -0.526  0.000   0.000   0.441
-0.144  0.218   0.000   pancreas        adenocarcinoma
                III
-0.708  0.000   -1.571  -1.413  -1.078  -0.941  -3.090  -2.049
0.104   -2.737  -0.917  pancreas        adenocarcinoma
                IB
-0.997  0.450   -0.792  -1.316  -1.432  -0.105  -1.016  0.865
0.561   -1.397  -1.709  pancreas        adenocarcinoma
                IIB
-0.328  -0.823  3.285   0.055   2.467   2.111   -0.130  -0.787
-3.176  -4.090  0.292   pancreas        adenocarcinoma
                IIB
-0.580  0.000   -2.013  -0.205  -1.521  0.000   -0.721  -0.408
-2.904  0.014   0.295   pancreas        adenocarcinoma
                IIB
-0.530  0.000   -2.175  -1.589  -0.384  0.000   -1.164  -0.680
-2.645  -1.603  -1.653  pancreas        adenocarcinoma
                IIB
-1.864  0.000   2.041   -0.656  0.000   0.000   -1.316  -3.260
0.540   2.271   0.579   pancreas        adenocarcinoma
                IV
-0.581  -0.433  -1.551  -0.146  -0.634  -0.174  0.349   -0.322
-0.395  -1.978  -0.234  pancreas        adenocarcinoma
                IIA
-1.918  -0.392  -1.369  -0.241  -2.605  0.089   -0.476  -1.030
-1.034  -0.464  -1.842  pancreas        adenocarcinoma
                IIB
-0.496  -0.445  -0.156  -2.004  -1.926  -1.135  -1.686  -1.464
-0.364  -2.242  -0.679  pancreas        adenocarcinoma
                IIB
-2.276  0.000   -0.237  3.703   3.090   0.317   0.487   0.893
0.784   0.399   0.000   pancreas        adenocarcinoma
                IIB
-0.777  0.298   -1.442  0.621   0.286   -0.654  -0.450  -1.602
```

Table35.txt

-1.605 -1.874 0.216 pancreas adenocarcinoma
IIB
-1.329 0.117 1.707 -3.654 5.118 -1.782 -0.191 1.452
-1.327 0.056 1.321 pancreas adenocarcinoma
IIB
-0.174 -1.465 -0.998 -1.368 -0.696 0.218 -0.081 -1.892
0.690 -3.962 0.307 pancreas adenocarcinoma
IB
0.000 0.000 -0.563 -0.425 -0.145 0.000 -1.335 0.000
-1.316 -1.153 0.432 pancreas adenocarcinoma
IIB
0.370 -0.569 -0.930 -0.146 -2.220 -0.092 -1.613 -0.356
-0.929 -0.987 -0.409 pancreas adenocarcinoma
IB
-2.101 1.236 -1.041 -1.166 1.490 -1.340 2.958 0.473
-0.747 1.810 -0.244 pancreas adenocarcinoma
IIB
-0.675 -0.136 -0.584 0.286 -0.282 -0.407 -0.364 0.743
-0.274 0.643 -0.013 pancreas adenocarcinoma
IIB
-0.108 -0.209 -1.650 0.493 -1.132 0.233 -3.060 -1.166
-0.858 -1.667 -0.730 pancreas adenocarcinoma
IB
0.114 2.940 0.358 -0.131 -1.046 2.271 3.245 -0.058
-0.910 -0.892 3.412 pancreas adenocarcinoma
IIA
-2.042 0.700 -3.428 -0.426 -2.603 -0.260 -1.822 -0.981
-1.049 0.579 -0.616 pancreas adenocarcinoma
IV
-2.533 0.000 -0.681 0.897 -1.474 1.180 0.176 -0.133
-0.217 -1.967 -0.087 pancreas adenocarcinoma
IIB
-0.379 -0.505 -0.445 0.000 -0.300 0.000 -2.789 0.000
-2.164 0.137 1.503 pancreas adenocarcinoma
IIB
-1.176 0.000 -2.588 -0.216 0.256 0.208 -3.072 -0.631
-0.007 -0.735 -0.354 pancreas adenocarcinoma
IIB
-0.592 -1.256 -1.224 0.050 -0.481 0.211 -1.142 0.161
-1.390 -0.187 -0.827 pancreas adenocarcinoma
IIB
-0.982 -0.910 -0.533 0.000 1.101 0.268 -0.790 0.000
0.309 0.527 0.000 pancreas adenocarcinoma
IIA
-1.831 -3.564 -1.313 -0.089 -0.070 -0.059 -1.789 -0.382
-1.576 -0.421 -0.026 pancreas adenocarcinoma
IIB
-1.640 -0.724 -0.949 -2.189 -0.022 -2.418 -1.757 0.000

Table35.txt

-0.088 1.857 -2.682 pancreas adenocarcinoma
IIA
-0.561 0.049 -0.456 0.311 -1.153 -0.911 -2.335 -0.687
-1.473 -0.445 0.309 pancreas adenocarcinoma
IIB
-1.501 -1.916 -0.693 -0.791 -0.354 -0.416 -1.241 0.000
-2.228 -0.657 -0.376 pancreas adenocarcinoma
IIB
-1.617 -1.148 -0.645 -0.263 -1.990 -0.514 -2.325 0.000
-1.311 -0.875 -0.529 pancreas adenocarcinoma
IIB
-1.738 -0.730 -1.878 -0.433 -0.892 -0.235 -0.788 0.309
-2.161 0.790 0.595 pancreas adenocarcinoma
IIB
0.130 0.000 -0.813 0.619 -2.373 -3.090 -0.588 0.000
-1.268 -1.316 -2.998 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 -0.144 0.000 0.000 0.000
0.000 -0.505 0.000 pancreas adenocarcinoma
IIB
-0.584 -1.108 -1.110 -1.360 -1.315 -2.519 -0.398 0.000
0.213 0.000 -0.959 pancreas adenocarcinoma
IIB
-1.663 -0.215 -1.172 -1.564 -2.990 0.460 -0.989 0.000
-1.426 0.000 -0.847 pancreas adenocarcinoma
IIB
2.144 0.000 -1.169 -1.360 2.052 -0.681 -0.982 0.015
-0.686 0.000 0.000 pancreas adenocarcinoma
IIB
-1.851 -2.368 -0.612 0.646 0.365 -2.133 -4.161 -1.387
-1.916 -0.420 0.022 pancreas adenocarcinoma
IIB
-0.835 0.000 -0.632 -0.790 -0.144 -0.098 -0.113 0.000
0.251 0.000 0.000 pancreas adenocarcinoma
IIB
-0.985 -0.585 -2.248 -0.204 1.295 -0.621 -0.979 -0.833
-2.751 -0.910 -1.360 pancreas adenocarcinoma
IIB
-0.777 -1.016 -2.503 -0.190 -3.293 -0.410 -1.931 0.000
-0.609 -2.869 -0.618 pancreas adenocarcinoma
IIB
-0.161 -1.169 -1.256 0.000 -0.217 0.218 -1.169 0.000
0.116 0.000 -0.170 pancreas adenocarcinoma
IIB
-2.325 -0.252 -2.696 4.291 5.046 -0.789 -0.902 -1.548
1.019 3.626 3.733 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

Table35.txt

0.000 0.000 0.000 pancreas adenocarcinoma
IIB
0.036 0.000 0.084 -0.004 -1.971 -0.413 -0.895 0.000
-1.651 0.000 -0.910 pancreas adenocarcinoma
IIA
-0.628 1.816 0.000 -1.256 -0.424 -0.720 -0.964 0.000
0.511 0.000 -3.090 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-4.001 -0.701 -2.222 -0.644 -1.272 -0.883 -1.999 -2.459
-2.335 -0.522 -0.848 pancreas adenocarcinoma
IIB
-3.090 -1.214 -1.012 0.000 -1.356 -0.144 0.747 0.000
-0.539 1.347 0.000 pancreas adenocarcinoma
IIB
-0.604 -1.427 -2.714 -0.189 -0.528 0.106 -1.427 0.251
-3.693 4.462 4.358 pancreas adenocarcinoma
IIB
-1.677 -0.303 -1.647 0.333 0.295 -0.435 -0.919 0.000
0.048 0.865 -0.304 pancreas adenocarcinoma
IIB
-0.054 0.919 -1.722 -1.432 3.278 -1.286 -2.439 -0.492
-2.462 5.273 -0.190 pancreas adenocarcinoma
IIB
-1.176 -1.276 0.160 0.000 -0.380 -2.768 -3.108 -0.074
-0.359 -1.126 -0.823 pancreas adenocarcinoma
IIA
-2.419 -2.612 -2.646 2.037 6.610 -0.428 -1.863 3.235
2.909 6.017 3.490 pancreas adenocarcinoma
IIA
-4.848 -1.976 -3.206 -0.686 -2.927 -1.797 -0.871 1.153
-1.484 -0.564 -0.668 pancreas adenocarcinoma
IIA
-2.789 -0.113 -2.194 -1.011 1.468 -0.567 -1.141 0.000
-1.836 -1.407 0.165 pancreas adenocarcinoma
IIB
0.439 0.000 -1.406 0.218 -0.539 -2.682 -1.665 0.000
-0.978 0.000 0.000 pancreas adenocarcinoma
IIB
-1.013 -3.026 1.759 -0.514 2.699 0.958 -2.566 0.250

Table35.txt

-0.078 -0.409 0.373 pancreas adenocarcinoma
IIB
-0.818 0.000 -2.038 -0.613 -0.730 0.000 0.309 0.000
0.001 0.137 0.000 pancreas adenocarcinoma
IIB
-0.660 0.085 -1.050 -1.122 -2.883 0.089 -0.842 -0.455
-0.803 -0.557 -1.151 pancreas adenocarcinoma
IB
-1.857 0.497 -0.660 -1.184 -0.598 -0.240 0.565 0.589
-1.822 2.452 -1.707 pancreas adenocarcinoma
IIB
0.604 -0.455 3.158 -1.036 0.402 0.020 -0.732 0.122
-1.322 0.437 0.288 pancreas adenocarcinoma
IIB
-1.654 -0.486 0.307 1.122 -0.937 -0.740 -2.349 -0.505
-1.461 -0.015 0.829 pancreas adenocarcinoma
IIB
-2.806 -1.199 -1.727 -1.887 -0.087 1.170 -2.322 -0.007
-1.326 -0.603 -0.415 pancreas adenocarcinoma
IIB
-3.649 0.389 -1.076 -1.098 -1.113 -2.693 -2.053 0.000
0.373 0.242 0.576 pancreas adenocarcinoma
IIB
-1.594 -1.059 -1.155 -0.502 -0.509 -2.893 -2.161 2.220
-2.013 1.426 -0.115 pancreas adenocarcinoma
IIB
-1.996 -0.254 -3.248 0.509 -3.440 -2.100 -0.549 -2.049
-0.799 -1.203 -0.846 pancreas adenocarcinoma
IIB
-2.152 -0.172 -1.395 -0.446 -0.620 -1.431 -0.130 2.858
-2.996 -1.039 -1.476 pancreas adenocarcinoma
IB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-0.756 0.000 -1.554 0.000 -0.877 0.000 0.000 0.000
0.224 0.000 0.000 pancreas adenocarcinoma
IIB
-2.850 -1.214 -1.455 -0.074 -1.671 0.397 -2.212 -0.396
-0.422 -0.211 0.595 pancreas adenocarcinoma
IIB
-2.453 -0.153 -1.686 -0.810 -0.971 -1.224 -1.669 -0.925
-0.914 0.492 -0.560 pancreas adenocarcinoma
IIB
-1.414 -1.859 -0.986 -0.210 -1.240 -1.232 -1.260 -4.370
-0.620 -0.246 -2.673 pancreas adenocarcinoma
IIB
-0.751 -1.342 -2.819 -1.212 -1.371 -0.938 -2.713 -1.669

Table35.txt

-0.170 -2.118 -1.499 pancreas adenocarcinoma
IIB
-0.121 -0.498 1.100 -1.499 -0.897 0.672 -1.926 -2.611
-1.795 1.843 1.120 pancreas adenocarcinoma
IIB
-1.178 0.089 -0.956 -0.233 0.020 -1.687 -1.379 0.066
-0.357 -1.268 -1.574 pancreas adenocarcinoma
IIB
-1.430 1.157 0.893 0.220 2.538 -0.175 -0.407 0.643
-0.581 -1.351 -1.602 pancreas adenocarcinoma
IV
-0.630 -0.068 -1.458 -1.929 4.174 0.362 1.208 0.551
-2.467 -0.601 -0.926 pancreas adenocarcinoma
IIB
-1.603 0.595 0.801 -1.627 -1.079 0.832 -3.061 -1.760
-0.847 -0.076 -0.265 pancreas adenocarcinoma
IIB
-0.812 -1.913 -0.893 1.663 -0.180 -0.152 -0.268 -1.447
-0.722 0.389 -0.463 pancreas adenocarcinoma
IIB
-2.082 0.091 -3.085 3.278 1.944 0.000 2.797 1.454
2.560 1.409 0.408 pancreas adenocarcinoma
IV
0.378 2.159 -0.064 -0.305 -1.709 0.765 0.350 -1.291
-0.367 0.739 0.114 pancreas adenocarcinoma
IIB
-2.465 0.595 -0.279 -0.930 -0.905 -3.221 -3.090 -0.446
-1.124 0.729 -0.195 pancreas adenocarcinoma
IIB
-2.708 -0.759 -0.270 -1.435 0.015 0.000 -1.318 -2.490
-0.059 -0.159 -0.848 pancreas adenocarcinoma
IB
0.000 0.000 -0.650 0.000 0.000 -1.341 2.450 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-0.252 0.266 -0.187 0.178 2.047 -1.388 -0.018 -1.411
-0.322 -2.419 0.090 pancreas Sarcomatoid anaplastic
carcinoma with osteoclast-like gianIIB

arising in associated with poorly
differentiated adenocarcinoma
-1.103 2.517 0.180 0.233 0.256 -0.541 -0.224 -4.124
-0.060 -0.828 0.579 pancreas adenocarcinoma
IIB
0.407 0.303 2.085 -0.596 3.383 2.472 3.041 1.203
0.537 -0.442 -1.362 pancreas adenocarcinoma
IIB
-2.531 -0.164 -2.024 -0.469 -1.830 -1.203 -0.929 -0.981

Table35.txt

```
0.391     0.589     -0.572    pancreas              adenocarcinoma
                          IIB
-0.826    5.265     1.424     5.028     8.965     2.781     0.634     0.295
-2.803    3.917     3.050     pancreas              adenocarcinoma
                          IIB
-0.257    -1.551    -1.532    -0.638    0.406     0.637     0.605     -2.028
3.997     -0.385    0.753     pancreas              adenocarcinoma
                          III
-0.558    0.217     -1.288    0.122     -2.858    0.086     3.677     -0.423
-0.471    -1.731    -0.074    pancreas              adenocarcinoma
                          IIB
-1.286    -1.269    0.465     -0.269    0.771     0.979     -0.771    -0.317
0.501     -0.327    -0.591    pancreas              adenocarcinoma
                          IIB
-2.080    -0.790    -0.384    -2.378    0.204     -0.164    -0.608    -1.193
-1.709    -0.607    -1.092    pancreas              adenocarcinoma
                          IA
-0.515    0.137     -2.250    -0.851    -3.626    -1.691    -0.871    -0.582
-0.021    -0.998    -2.637    pancreas              adenocarcinoma
                          IIB
-2.027    -0.162    0.031     -1.984    0.531     -0.241    1.365     -1.067
-1.035    -2.444    0.869     pancreas              adenocarcinoma
                          IIB
-2.407    0.199     0.645     1.724     2.315     -1.483    -0.301    -0.403
-1.255    -1.393    -1.020    pancreas              adenocarcinoma
                          IIB
-2.868    2.052     5.310     0.182     1.142     3.598     4.279     0.232
0.578     1.871     0.669     pancreas              adenocarcinoma
                          IIB
-4.044    -0.740    -1.331    -3.105    -0.380    0.025     -0.748    -1.246
-0.628    0.606     0.551     pancreas              adenocarcinoma
                          IIB
-1.009    -0.001    -3.071    0.543     -0.001    0.833     -0.874    -0.251
-1.995    -1.832    -2.558    pancreas              adenocarcinoma
                          IIB
-1.201    -1.460    -2.794    -0.408    -1.026    -0.572    0.056     -0.408
0.672     2.246     -0.406    pancreas              adenocarcinoma
                          IIB
-2.196    1.808     3.507     2.315     3.088     0.104     -0.805    -0.433
2.775     0.743     2.730     pancreas              adenocarcinoma
                          IB
-2.728    -1.882    -0.408    -0.430    -2.404    -0.027    -0.195    -4.346
-2.448    -2.966    -2.133    pancreas              adenocarcinoma
                          IIB
-0.908    -1.329    -0.765    -1.235    -2.083    -1.805    -2.054    -2.729
-2.491    -0.037    -1.798    pancreas              adenocarcinoma
                          IIB
-0.819    -0.763    -0.887    -0.971    -0.623    -1.008    -2.572    -0.755
```

Table35.txt

-1.146 -0.019 0.247 pancreas adenocarcinoma
IIB
-1.212 0.000 -0.073 2.549 6.882 -0.060 -0.385 2.666
0.581 1.058 -2.781 pancreas adenocarcinoma
IIB
-0.401 -2.100 -1.136 -1.159 -3.058 1.206 -1.202 -1.060
-0.504 -1.020 -2.321 pancreas adenocarcinoma
IIB
-0.660 -1.871 -0.146 1.025 -2.189 0.000 -0.607 -0.356
-1.530 -1.424 -2.712 pancreas adenocarcinoma
IA
1.523 -0.297 -0.864 1.167 1.303 0.024 0.937 -0.447
-3.739 -2.324 -0.307 pancreas adenocarcinoma
IV
1.353 -0.122 -0.221 -0.188 1.505 -1.665 -1.704 0.434
1.057 -0.913 0.346 pancreas adenocarcinoma
IIB
3.077 2.277 5.185 -0.023 0.073 1.619 3.460 6.525
5.440 2.897 -0.140 pancreas adenocarcinoma
IIB
0.243 1.581 -0.927 2.854 7.307 -0.308 0.605 -0.878
0.716 2.759 -1.261 pancreas adenocarcinoma
IIB
2.422 1.774 0.043 -0.489 2.154 -0.085 2.977 0.153
0.054 1.206 -1.486 pancreas adenocarcinoma
IB
-0.759 0.479 2.247 -0.852 4.348 -0.831 -1.697 -2.215
-0.584 -0.349 -0.258 pancreas adenocarcinoma
IIB
0.944 2.656 1.352 1.707 0.276 1.338 2.060 -1.086
-0.963 -0.512 1.090 pancreas adenocarcinoma
IB
-0.298 0.511 -0.117 -0.908 -1.535 -2.193 -2.780 -1.473
-0.329 -1.987 0.235 pancreas adenocarcinoma
IIB
-0.175 0.929 -0.381 2.453 2.125 -1.537 0.046 -1.366
-2.261 -1.345 -1.010 pancreas adenocarcinoma
IB
-1.214 -1.439 -0.391 -1.497 -2.649 -3.090 -1.261 -1.256
-0.545 -1.599 -0.652 pancreas adenocarcinoma
IIB
-0.843 -1.004 -0.544 -2.335 -1.873 0.703 -1.887 -0.853
0.115 -0.912 -0.661 pancreas adenocarcinoma
IV
-2.101 0.989 -1.475 -1.581 3.254 0.531 -1.185 -0.823
-3.007 -1.367 1.362 pancreas adenocarcinoma
IIB
-2.329 0.794 -1.617 -2.128 1.512 0.594 -0.535 -0.685

Table35.txt

-1.089 0.056 0.708 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.050 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-1.656 -1.369 -1.903 -0.910 -0.654 -1.563 -3.071 3.481
-0.776 -0.937 0.036 pancreas adenocarcinoma
IIB
-0.495 -1.457 1.984 -0.836 -1.468 -0.543 -1.465 0.282
-1.865 -0.443 -1.589 pancreas adenocarcinoma
IIB
-1.976 0.680 -0.456 2.514 3.569 0.212 -3.044 -1.907
-0.546 3.192 0.522 pancreas adenocarcinoma
IIB
1.893 0.899 -0.725 -0.302 0.585 -0.193 -1.119 0.322
-0.343 -1.606 0.039 pancreas adenocarcinoma
IV
-0.615 -0.367 2.497 4.574 4.456 1.829 0.635 6.340
3.392 1.024 1.338 pancreas adenocarcinoma
IIB
-2.290 -1.829 -1.295 0.894 2.134 0.018 -2.028 -1.156
0.046 -1.051 -1.410 pancreas adenocarcinoma
IIB
6.922 1.920 5.599 4.408 3.336 0.940 3.090 3.516
0.717 3.450 2.490 pancreas adenocarcinoma
IA
-1.500 2.841 4.225 -1.580 5.685 -0.712 -1.897 -0.835
-0.122 1.833 -1.848 pancreas adenocarcinoma
III
0.871 -1.300 -1.332 -0.577 -1.338 -0.552 -1.168 2.252
2.268 -1.174 -0.058 pancreas adenocarcinoma
IIB
-2.267 -0.990 -0.001 0.524 0.198 -0.574 -1.329 -0.766
-0.547 -2.206 -1.849 pancreas adenocarcinoma
IIB
0.050 0.000 -0.736 0.000 -0.686 -1.360 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-1.142 0.000 0.595 0.000 -1.393 -0.161 0.266 -3.672
0.051 -2.855 0.451 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 -0.541 0.000 0.000 -0.378 0.000
0.000 -0.378 0.000 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.309 0.607 0.000 0.000 0.000
-0.790 0.000 0.000 pancreas adenocarcinoma
IIA
-0.144 -1.169 0.000 0.000 0.000 0.000 0.000 0.000

Table35.txt

0.000	-1.169	0.000	pancreas		adenocarcinoma		
			IIB				
-1.183	0.520	0.340	-0.104	0.429	-0.199	-0.561	0.750
0.374	1.181	-1.261	pancreas		adenocarcinoma		
			IIB				
-1.472	0.137	-2.734	-2.353	-0.265	0.000	-0.215	-1.328
-0.027	-2.626	-0.496	pancreas		adenocarcinoma		
			IIB				
-0.304	0.000	0.000	-0.060	-1.827	0.000	-1.093	0.629
-0.964	-2.373	-0.553	pancreas		adenocarcinoma		
			IIB				
-0.174	-0.442	-1.320	-1.488	-0.643	-3.245	-1.489	-1.232
-0.284	-1.049	-2.236	pancreas		adenocarcinoma		
			IB				
0.000	0.000	0.000	0.000	-1.214	0.050	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
-0.378	-0.823	-1.353	-3.111	0.028	0.000	0.000	0.000
-3.090	-1.269	0.278	pancreas		adenocarcinoma		
			IIA				
-0.536	0.000	-1.212	0.120	-0.221	0.717	2.643	-0.972
-0.318	-0.222	-1.825	pancreas		adenocarcinoma		
			IIB				
0.103	-0.211	-0.552	-0.480	-0.034	-0.094	0.073	-1.380
-0.460	-1.678	0.020	pancreas		adenocarcinoma		
			IIB				
-0.883	0.264	-0.502	1.709	0.439	-1.605	2.211	0.630
-0.781	-0.884	0.011	pancreas		adenocarcinoma		
			IIB				
-0.419	0.000	-0.201	0.000	0.176	0.000	-0.378	0.000
0.000	-1.316	0.000	pancreas		adenocarcinoma		
			IA				
-3.252	-0.438	-0.065	-1.389	-1.246	0.461	-0.325	-0.679
-0.929	0.318	-0.898	pancreas		adenocarcinoma		
			IB				
0.620	0.649	-0.341	-1.283	-2.392	-1.046	-0.172	-1.281
0.261	-0.485	-0.446	pancreas		adenocarcinoma		
			IIB				
-3.193	-1.088	-2.149	-0.282	-1.763	-1.010	-1.498	-0.687
-1.588	-0.890	0.204	pancreas		adenocarcinoma		
			IIB				
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	pancreas		adenocarcinoma		
			IIB				
-2.390	-0.321	-2.403	-0.367	2.686	-1.557	-1.023	0.798
-1.092	-1.595	-0.332	pancreas		adenocarcinoma		
			NA				
0.187	0.000	-0.749	0.113	-0.466	-0.505	0.441	-0.442

Table35.txt

-0.276 0.031 0.259 pancreas adenocarcinoma
IIB
-1.385 0.000 -1.573 -0.322 0.000 0.000 0.000 -0.144
-3.090 -0.367 -0.378 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IV
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-0.966 0.826 -0.583 -0.257 0.569 0.024 -0.327 0.109
-2.234 0.441 -2.301 pancreas adenocarcinoma
IIB
0.069 -1.177 -3.020 -0.568 0.365 -0.149 0.360 -1.195
-0.564 -0.742 -1.012 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IV
-0.489 1.153 -0.251 1.332 4.220 0.148 -1.399 -0.612
1.909 0.168 -0.079 pancreas adenocarcinoma
IB
-3.169 1.518 -0.180 2.769 2.946 -0.376 0.276 1.773
-1.177 0.004 0.901 pancreas adenocarcinoma
IIB
-1.371 1.382 0.139 -0.417 1.493 -0.388 -0.020 0.933
1.758 -0.318 -0.904 pancreas adenocarcinoma
IIB
0.329 0.000 -1.639 -0.395 0.312 0.000 -0.170 0.000
0.366 -0.867 0.460 pancreas adenocarcinoma
IIB
-1.387 -1.107 -2.692 1.250 0.203 1.249 -0.781 0.129
-0.794 -1.256 3.336 pancreas adenocarcinoma
IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas adenocarcinoma
IIB
-1.213 1.856 -0.983 -0.239 -0.073 0.108 -0.758 -0.816
-1.030 1.344 2.819 pancreas adenocarcinoma
IIB
-0.107 -0.341 -1.790 2.878 0.748 -0.233 -0.168 -0.575
0.045 -1.827 -0.559 pancreas adenocarcinoma
IV
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

Table35.txt

```
0.000     0.000     0.000     pancreas              adenocarcinoma
                        IIB
-0.608    -1.195    -1.874    -1.313    -0.394    -0.694    -0.781    -0.912
-3.227    -1.663    -0.791    pancreas              adenocarcinoma
                        IIA
-0.751    -0.010    -0.440    -0.918    -1.463    -1.360    -0.654    -1.045
-0.721    -1.418    -2.328    pancreas              adenocarcinoma
                        IIB
-0.079    -0.217    0.188     -1.292    1.386     -1.927    0.130     -0.301
-0.654    -0.562    0.079     pancreas              adenocarcinoma
                        IIB
0.000     0.000     0.000     0.000     0.000     0.000     0.000     0.000
0.000     0.000     0.000     pancreas              adenocarcinoma
                        IIB
-2.430    1.313     -1.793    1.538     1.919     -0.246    -3.031    0.192
-0.642    -2.403    -1.563    pancreas              adenocarcinoma
                        IIa
-2.312    -0.631    -2.457    -2.303    -2.196    -0.648    -1.588    0.000
-0.142    0.000     -1.219    pancreas              adenocarcinoma
                        IB
-2.234    -1.370    -1.306    -0.080    -0.976    -1.746    -0.536    0.086
-2.088    -0.547    0.218     pancreas              adenocarcinoma
                        IIB
-1.141    -1.319    -1.740    0.000     -2.706    -2.623    -3.926    0.163
-1.745    0.000     0.959     pancreas              adenocarcinoma
                        IIB
0.000     0.000     0.000     0.000     0.000     0.000     0.000     0.000
0.000     0.000     0.000     pancreas              ductal ADK pT3 pN1 G3
                        IIB
0.361     -1.471    -4.321    -1.499    -2.500    -0.745    -2.506    0.230
-2.496    2.372     2.392     pancreas              ductal ADK pT3 pN1 G2
                        IIB
-2.473    0.000     0.309     0.000     0.595     0.000     0.000     0.000
0.000     0.000     0.000     pancreas              ductal ADK pT3 pN1 G2
                        IIB
-0.736    0.000     0.000     0.000     0.000     0.000     0.000     0.000
0.000     0.000     0.000     pancreas              ductal ADK pT3 pN1 G2
                        IIB
0.000     0.000     -0.257    0.000     0.000     0.000     0.000     0.000
-0.217    0.000     0.000     Pancreas (Ampulla)    squamous k (ampulla) pT3 pN1
G3                        IIB
0.277     0.804     1.088     -0.508    -0.822    -0.916    0.283     4.343
6.982     4.956     -0.694    pancreas              ductal ADK pT3 pN1 G2
                        IIB
-2.307    0.401     0.965     6.619     9.155     -1.048    1.295     1.846
1.087     5.979     6.947     pancreas              ductal ADK pT3 pN1 G3
                        IIB
0.000     0.000     0.000     0.000     0.000     0.000     0.000     0.000
```

Table35.txt

0.000 0.000 0.000 pancreas ductal ADK pT3 pN1 G3 IIB
-1.135 1.366 0.953 -1.144 -3.258 -0.665 -4.124 1.224
-1.565 0.220 1.052 pancreas ductal ADK pT3 pN1 G3 IIB
-1.769 0.649 0.428 -0.186 0.807 -1.276 -1.449 0.390
-1.110 -0.395 1.234 pancreas ductal ADK pT3 pN0 G3 IIA
-0.036 -0.339 0.692 -0.385 6.844 -1.025 0.608 1.693
2.728 0.258 -0.290 pancreas ductal ADK pT3 pN1 G3 IIB
-1.367 -1.330 -1.219 1.500 0.453 -0.965 -3.964 -1.749
0.300 -0.099 -3.147 pancreas ductal ADK pT3 pN1 G3 IIB
5.415 -1.196 -1.541 -1.786 -4.024 -1.906 -1.175 3.395
3.442 -2.590 -0.521 pancreas ductal ADK pT3 pN1 G2 IIB
-0.946 -1.472 -1.347 -0.544 -0.442 -0.913 -1.671 -2.086
-2.484 -1.255 -2.353 pancreas ductal ADK pT3 pN1 G2 IIB
-1.347 -2.989 -1.043 -0.089 -0.477 -0.492 -2.571 -1.184
-3.506 -1.836 -1.436 pancreas ductal ADK pT3 pN1 G3 IIB
-2.124 0.005 -0.981 -3.645 -0.672 -1.242 1.954 -1.494
0.463 2.045 -0.253 pancreas ductal ADK pT3 pN1 G3 IIB
-0.130 -0.081 -1.078 -0.563 0.999 -0.317 -0.273 -0.170
0.671 1.261 -2.083 pancreas ductal ADK pT3 pN1 G3 IIB
0.231 0.000 0.000 0.000 0.309 0.000 0.000 0.000
0.000 0.000 0.000 pancreas ductal ADK pT3 pN1 G3 IIB
-2.841 -0.592 -1.464 -1.764 -2.177 -0.022 -2.016 -3.107
-0.799 -0.702 1.675 pancreas ductal ADK pT3 pN1 G2 IIB
-1.262 -1.213 -4.335 3.574 -2.402 -1.208 -2.482 2.146
1.775 4.765 -0.218 pancreas ductal ADK pT3 pN1 G3 IIB
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 pancreas ductal ADK pT3 pN1 G3 IIB
-4.366 1.162 -2.891 -0.685 1.794 0.560 6.088 0.642
0.412 0.300 0.243 pancreas ductal ADK pT3 pN1 G3 IIB
-2.772 -1.068 -1.876 -1.521 -2.676 -0.734 -1.180 0.167
-1.576 -1.367 -0.221 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IA
-0.921 -1.661 -0.813 -1.320 -2.891 -0.046 -3.709 -1.754

Table35.txt

-2.860 -2.836 -2.774 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IB
-3.222 2.515 2.747 0.083 -1.198 -0.322 -1.715 -1.857
-1.317 -0.211 -1.036 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IB
-4.236 0.536 -2.157 0.014 -2.166 0.089 -1.678 0.400
-2.615 -1.162 -1.323 Uterus Endometrioid Adenocarcinoma, Mixed PT1lolid-VilloglandularIB
-1.114 -1.026 -1.437 0.398 -1.270 -0.293 -0.092 1.961
-1.075 -0.496 -1.917 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IB
-3.066 -2.698 -2.320 -1.958 -3.543 -2.374 -4.324 -2.138
-1.809 -3.061 -2.406 Uterus Atypical Complex Endometrial Hyperplasia NA
-2.386 -1.323 -2.330 -2.378 -2.755 -1.752 -0.772 -1.538
-1.990 0.395 -1.323 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IA
-2.926 -1.894 -3.008 5.816 -4.153 2.866 5.753 -1.281
-3.954 -3.358 -0.502 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IA
-2.075 -0.394 -3.911 0.396 -0.627 -1.437 -1.972 -1.096
-0.199 -0.793 0.197 Uterus Atypical Complex Endometrial Hyperplasia no ca
-1.891 -1.225 -0.669 -0.710 -3.485 -1.689 0.041 -0.240
-2.251 -1.197 -0.587 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IA
-1.843 -2.203 -4.426 -0.328 -5.245 -0.795 -0.235 -0.445
-1.698 -2.243 -3.185 Uterus Endometrioid Adenocarcinoma, Villoglandular Pattern IA
-2.691 -1.129 -2.907 -0.787 -2.404 -0.786 -1.004 -0.603
-1.989 -0.689 -1.483 Uterus Atypical Complex Endometrial Hyperplasia NA
-3.464 -1.305 -2.597 -1.245 -2.082 -0.754 0.907 -0.684
-1.802 -3.029 -1.205 Endometrial NA NA
-1.818 -1.586 -1.225 -0.682 -1.737 -1.733 -0.558 -1.006
-0.212 -0.715 -0.334 Endometrial NA NA
-2.121 -0.951 -0.616 5.858 3.159 1.719 7.502 3.450
8.789 -1.207 -0.296 Ovarian Adenocarcinoma IV, G3
-0.066 -1.894 -3.482 -1.606 -2.615 -1.090 -1.866 0.213
-2.738 0.177 -1.383 Ovarian Carcinosarcoma IV, G3
6.167 3.935 3.211 2.842 3.936 -1.038 3.160 2.068
2.029 2.360 1.037 Ovarian Dysgerminoma IA, G3
3.043 -0.502 -0.647 -0.805 1.104 0.372 -1.626 2.263

Table35.txt

4.171 -0.597 1.086 Ovarian Adenocarcinoma
IA, G3
-1.277 0.055 -2.301 -2.640 -2.683 0.002 -2.612 0.786
4.750 -0.890 -1.907 Ovarian Clear Cell Carcinoma
IA, G2
-1.966 -1.057 -2.507 -2.725 0.174 -0.631 -1.941 -1.866
0.402 9.838 11.185 Ovarian Adenoacanthoma
IA, G2
-2.056 -2.683 -0.729 -1.566 -1.176 -0.851 -0.976 0.525
9.722 -1.103 -1.075 Endometrial NA
NA
-0.731 -1.019 -2.341 -2.274 -0.676 0.319 -0.714 -0.254
-1.557 0.537 -1.141 Uterus Endometrioid Adenocarcinoma
IB, G2
-1.666 -2.643 -2.118 0.495 -2.200 4.775 6.138 -0.938
-2.192 9.713 0.127 Endometrial NA
NA
-1.328 -0.598 -0.115 -0.904 -0.541 -0.842 1.834 0.202
-0.044 -2.154 -1.104 Uterus Endometrioid Adenocarcinoma
IB, G1
17.229 5.425 12.336 2.660 5.999 -0.982 6.146 0.344
0.778 -0.534 1.382 Uterus Endometrioid Adenocarcinoma
IB, G3
-2.194 -0.164 -0.224 -1.476 -1.575 -0.141 -1.812 -0.278
0.046 10.087 -2.921 Uterus Villoglandular Endometrioid
Adenocarcinoma IA, G1
7.240 3.027 7.076 -1.341 -1.061 6.245 6.517 2.404
2.001 0.000 5.185 Endometrial NA
NA
0.989 -2.773 4.720 -2.782 9.870 -1.411 -1.381 4.639
3.328 -3.034 3.094 Ovarian Adeno-squamous Carcinoma
IC, G3
16.127 2.019 13.572 6.067 10.641 4.790 11.923 0.369
12.516 2.664 7.125 Uterus Villoglandular Endometrioid
Adenocarcinoma IIIC, G3
-0.490 -0.790 0.429 0.000 -1.814 -0.982 -0.571 -0.150
0.275 0.000 -1.169 Ovarian NA
NA
13.712 6.001 -0.912 -0.475 -1.381 1.411 -2.274 7.169
14.491 1.096 -1.067 Ovarian Papillary Serous
Adenocarcinoma IA, G2
19.305 6.574 17.487 5.723 2.270 -1.326 -2.463 -0.873
-0.925 9.526 -2.353 Ovarian Papillary Transitional Cell
Carcinoma IIA, G2
-0.465 -0.663 -0.576 -0.220 -2.320 0.815 3.439 -1.094
13.811 0.000 0.000 Uterus Villoglandular Endometrioid
Adenocarcinoma IA, G2
19.110 -0.738 3.306 1.605 9.989 0.694 5.195 6.252

Table35.txt

11.094 3.094 3.190 Ovarian Endodermal PT1inus Tumor IA, G2
-0.903 -0.615 -1.275 2.341 7.089 -0.522 -0.967 0.089
-0.984 3.181 3.760 Ovarian Papillary Serous Adenocarcinoma IIIC, G1
13.718 6.580 13.400 3.335 11.276 -2.312 14.619 3.186
6.491 -2.926 -0.310 Ovarian Papillary Serous Cystadenocarcinoma IIIB, G2
-0.763 2.761 -0.139 5.115 0.638 0.480 13.452 0.000
4.849 2.090 -1.878 Ovarian NA NA
2.971 1.092 4.403 -0.562 0.204 0.438 2.480 0.561
2.110 -0.570 0.764 Ovarian Papillary Serous Adenocarcinoma IIIB, G2
4.113 3.349 7.441 7.425 14.555 4.923 10.231 5.945
0.406 4.033 0.429 Ovarian Mixed Carcinoma IC/3
4.187 1.257 5.276 1.191 7.507 2.619 5.017 0.149
3.073 3.202 2.647 Ovarian Serous Adenocarcinoma IA, G2
11.868 3.611 -1.785 2.771 3.827 -0.627 8.873 5.984
14.057 1.700 15.104 Ovarian Clear Cell Carcinoma IIIB, G3
-1.653 4.667 3.141 5.478 -0.357 -0.387 6.622 -1.064
6.034 5.426 -2.185 Ovarian Serous Adenocarcinoma IC, G2
-0.706 -2.254 -0.716 -0.187 -0.321 -0.025 0.284 -1.215
-1.437 0.012 -0.338 Endometrial NA NA
-1.342 -0.914 -1.618 -0.886 -0.990 -0.894 -0.496 7.301
9.931 -0.040 -0.705 Endometrial NA NA
-1.451 0.409 -0.216 -0.725 1.207 -0.296 0.183 1.436
3.333 0.689 1.736 Endometrial NA NA
-0.029 0.921 0.823 -2.003 -1.388 -1.427 1.421 4.496
11.488 -1.612 -1.947 Endometrial NA NA
0.905 0.386 -0.527 0.253 0.882 0.059 1.859 0.798
-0.130 -0.662 0.838 Uterus Endometrioid Adenocarcinoma, Villoglandular Type with PT1qIB, G2
-3.181 -1.053 -1.574 -0.413 -1.184 -0.583 -0.344 -0.843
-2.784 -1.227 -1.554 Endometrial NA NA
-0.144 -1.600 -2.320 -1.277 -1.166 0.057 -1.482 3.585
8.792 -2.169 -0.265 Uterus Endometrial Adenocarcinoma, Villoglandular Type IIIC, G2
-2.249 -1.460 -1.669 0.309 -1.663 -1.825 0.213 5.895

Table35.txt

```
10.718    -1.916    -0.150    Uterus                Endometrioid Adenocarcinoma,
Villoglandular Type          IB, G2
-2.562    -0.908    -1.313    0.826     -2.603    -0.090    -0.975    -0.405
-1.053    -0.602    -0.990    Uterus                endometrioid adenocarcinoma
                              IA
-1.451    -2.753    -0.211    -1.332    -0.982    -1.095    -2.156    4.033
11.115    -0.107    -0.579    Uterus                endometrioid adenocarcinoma
                              II
-3.493    -1.423    -3.019    -0.661    -2.984    -2.364    -0.174    -2.391
-1.799    6.290     -1.229    Ovarian               mucinous adenocarcinoma
                              IA
-2.091    -1.466    -1.548    -1.028    -1.774    0.188     -1.662    -0.363
-2.048    -0.749    -1.814    Uterus                endometrioid adenocarcinoma
                              NEED
16.952    8.851     14.824    14.604    16.813    9.775     14.852    11.703
14.763    10.577    10.197    Uterus                endometrioid adenocarcinoma
                              IA
25.610    9.008     22.471    2.977     5.412     2.986     7.466     11.536
-0.670    -0.248    8.898     Uterus                Serous Adenocarcinoma
                              IC
-1.420    -1.478    -0.718    -2.096    -2.144    -2.388    -0.919    -2.511
-1.628    -0.525    -0.488    Uterus                endometrioid adenocarcinoma
                              IB
-1.174    -1.443    -1.901    -1.271    -3.130    -1.553    1.556     -0.481
-2.443    -2.116    -1.897    Uterus                endometrioid adenocarcinoma
                              IA
-1.929    -1.442    8.380     5.464     1.651     4.703     8.512     4.286
2.090     7.311     2.591     Uterus                serous adenocarcinoma
                              IVB,G3
0.183     -0.936    -1.221    -0.905    -0.938    -0.467    -0.443    -0.575
-0.510    -0.123    1.523     Endometrial           NA
                              NA
-2.845    -2.090    -1.132    -1.514    -3.309    -1.756    -2.567    -1.658
-1.034    -0.643    -0.144    Uterus                endometrioid adenocarcinoma
                              IIIC2
-1.779    -1.271    -0.961    -1.828    -3.002    -1.113    -2.114    -0.717
-1.990    -2.570    0.271     Uterus                endometrioid adenocarcinoma
                              IB
-1.939    -0.708    -3.034    -1.439    -1.631    -0.878    -2.913    -2.772
-0.730    -3.132    -1.798    Uterus                endometrioid adenocarcinoma
                              IIIC2
-3.182    0.000     -0.862    0.000     -0.335    0.000     -0.534    -0.293
-0.573    -0.677    0.000     Uterus                endometrioid adenocarcinoma
                              IB
-3.114    -1.608    -2.337    -1.253    -1.623    -0.788    -1.730    4.604
10.465    5.870     4.642     Uterus                endometrioid adenocarcinoma
                              IB
-2.234    -0.349    -3.240    0.312     -1.149    -1.015    -0.921    -1.583
```

Table35.txt

-2.206 -1.742 -2.507 Uterus endometrioid adenocarcinoma IIIC, G2
-1.688 -1.098 -2.613 0.863 -1.372 -0.959 -2.796 -2.624
-0.666 -0.596 -1.522 Endometrial NA NA
-3.535 -0.126 -5.096 -0.208 -1.508 0.090 -1.405 6.091
11.105 0.021 -3.166 Uterus endometrioid adenocarcinoma IB
-2.839 -1.713 -1.417 0.383 -1.863 5.244 6.535 -0.594
-3.270 -0.955 -0.693 Ovarian micropapillary serous ovarian carcinoma IIIB
1.405 6.535 8.535 5.761 -1.993 -0.900 2.423 2.900
5.738 2.309 -0.499 Uterus serous adenocarcinoma IA
-3.682 -2.232 -3.697 -0.912 -0.506 -0.849 -3.777 -1.695
-3.130 -0.550 -1.627 Endometrial NA NA
-1.590 -1.354 -2.370 0.239 -1.827 -1.177 -3.105 -1.854
3.623 -2.021 -1.063 Uterus endometrioid adenocarcinoma IIIC2
-2.282 -0.199 -1.978 -1.505 -1.282 -1.053 -2.672 -1.007
-2.314 -1.910 -1.638 Uterus endometrioid adenocarcinoma IA
-1.548 -1.349 -2.240 -0.664 -3.191 -0.620 0.608 0.757
-2.372 -1.987 -0.587 Uterus NA NA
-0.680 0.636 -1.090 -0.855 -2.046 -0.520 -1.922 0.328
-1.658 -0.116 -0.998 Endometrial NA NA
-2.219 -1.508 -3.202 -1.087 -3.781 3.479 7.371 1.714
-2.271 -1.567 -0.539 Endometrial NA NA
-2.184 0.805 -1.637 -0.580 -1.985 0.220 -1.730 -0.562
-3.478 -2.683 -1.088 Uterus NA NA
-1.011 -2.058 0.058 8.241 -0.795 1.971 8.132 8.989
8.732 -0.212 7.503 Uterus NA NA
-1.665 -1.245 9.934 -1.901 -0.336 -0.911 13.874 7.862
13.694 9.146 6.565 Uterus NA NA
14.736 5.653 0.847 -0.342 5.365 -0.998 10.943 -0.273
3.915 -1.284 6.850 Ovarian NA NA
-1.326 -0.454 -2.173 -1.375 -2.984 -0.778 -1.086 1.353
-1.468 -0.157 -1.950 Uterus NA NA
-1.203 -2.120 -0.598 0.167 -0.964 0.279 -1.191 0.204

Table35.txt

```
-3.042    -1.134    -1.169    Uterus                NA
                      NA
0.699     6.587     1.542     -1.504    8.563     3.370     7.972     3.140
6.085     2.304     0.429     Uterus                NA
                      NA
-2.393    -0.479    -3.036    -1.783    -1.419    -1.633    -1.959    -0.468
-1.577    0.498     -1.155    Uterus                NA
                      NA
-2.202    -2.366    -2.889    -0.242    -1.967    -0.961    -1.662    -1.526
-2.025    -1.613    -1.201    Endometrial           NA
                      NA
-2.540    0.341     -1.503    -1.451    -1.618    -1.036    0.557     0.038
-0.285    -1.074    -0.461    Endometrial           NA
                      NA
-1.347    -1.822    4.764     -1.098    -3.238    1.401     -2.385    6.835
12.305    0.828     0.469     Ovarian               malignant Brenner tumor
                      IIIA, G3
7.089     -0.363    4.039     -0.943    1.446     -1.812    0.735     2.591
2.973     -2.096    -0.609    Ovarian               Endometrioid Adenocarcinoma,
Villoglandular Type           IV, G1
-1.337    11.211    -2.330    4.107     11.538    2.865     -0.775    5.924
4.949     6.283     3.411     Ovarian               Endometrioid Adenocarcinoma,
PT1olid Type                  IB, G3
-0.933    -0.642    -0.725    -3.512    -1.520    -1.282    -0.673    -0.327
-0.957    9.794     6.068     Ovarian               mucinous cystadenocarcinoma
                      IA, G1
10.168    1.970     12.705    6.839     14.670    7.268     7.243     3.500
6.500     6.651     -1.733    Ovarian               Serous Papillary
Cystadenocarcinoma                    IIIA, G3
-2.228    -1.721    -2.121    -1.981    -2.097    -0.540    -0.177    -2.056
10.236    0.750     0.545     Ovarian               serous papillary
cystadenocarcinoma                    IA, G1
8.652     -0.263    8.912     0.161     2.928     9.356     6.055     2.362
7.003     4.534     2.964     Ovarian               Mucinous Adenocarcinoma,
suggestive of Krukenberg's tumor IIIA, G3
12.035    1.015     8.500     5.141     10.588    7.456     14.468    2.311
4.945     3.324     0.520     Ovarian               endodermal sinus
                      IA, G3
-3.282    -1.719    -1.487    -1.073    -0.556    0.195     -1.428    -0.608
-3.040    -1.004    -1.172    Ovarian               serous papillary
cystadenocarcinoma                    IB, G3
-2.483    0.981     -1.342    -1.611    0.033     -2.198    -1.878    -2.798
-1.596    -1.120    -2.119    Ovarian               mucinous adenocarcinoma
                      IA, G1
-1.195    -0.771    -0.438    -1.045    -0.944    1.359     -1.104    5.149
12.480    -2.008    -1.295    Ovarian               clear cell adenocarcinoma
                      IA, G3
3.064     0.294     6.893     -2.312    -2.170    6.502     11.538    1.290
```

Table35.txt

14.445 9.500 1.271 Ovarian mucinous carcinoma IA, G3
4.678 2.487 5.624 1.779 8.992 1.157 -1.463 6.088
5.404 8.164 3.565 Ovarian serous adenocarcinoma IIIA, G3
-4.018 1.783 7.620 3.792 4.227 0.383 3.382 9.525
14.834 1.491 8.730 Ovarian clear cell adenocarcinoma IA, G3
10.625 0.071 6.383 7.952 12.277 5.403 10.025 6.979
7.800 3.837 4.277 Ovarian serous adenocarcinoma IA, G3
-2.307 -0.357 -0.417 1.117 -1.492 0.019 -0.366 -1.976
-0.966 -0.750 1.261 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IIA, G1
-2.234 -1.091 -0.677 -0.365 -2.020 1.253 -0.471 -0.928
-0.809 0.392 -0.130 Uterus mucinous adenocarcinoma IA, G1
-0.552 0.247 -0.894 -1.779 -0.277 -0.991 0.640 -0.657
-1.761 -1.606 -0.749 Endometrial NA NA
14.248 3.317 7.329 5.675 12.094 3.093 11.516 1.453
10.305 5.523 5.304 Endometrial NA NA
0.529 0.983 -2.088 -1.782 -2.034 -0.945 0.003 -0.636
0.842 -0.461 -0.902 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IB, G1
11.423 6.125 11.008 2.012 2.306 -1.845 -1.218 6.716
16.024 6.943 6.564 Endometrial NA NA
-1.164 -0.228 -3.331 -0.370 -2.767 0.532 -1.253 -1.515
-0.430 -1.157 0.812 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IB, G1
6.006 -0.757 -2.613 -0.235 -1.838 -1.169 -2.220 -0.675
-0.354 -0.188 -0.905 Uterus mucinous adenoca IC, G1
-2.776 1.036 -1.522 0.014 -1.660 -2.214 0.157 -0.948
-1.488 -0.931 -1.331 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IB, G1
-3.720 -0.558 -2.208 0.207 -1.476 -0.735 -1.376 -0.830
-0.262 -0.770 -2.821 Endometrial NA NA
-1.723 -3.038 -0.206 -1.044 -1.189 0.109 -0.626 -0.662
-0.613 -1.398 -3.348 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IA, G1
2.726 -1.677 3.814 -0.589 3.856 -1.362 -1.881 8.051
-0.148 -1.681 4.490 Ovarian Serous IIIC
2.151 -1.718 3.526 3.090 7.545 4.431 14.744 3.777

Table35.txt

17.172	4.348	3.024	Ovarian		Serous		
			IIIC				
0.884	-2.082	-1.710	2.415	1.795	1.008	0.545	-1.634
-0.111	0.098	-0.666	Ovarian		Serous		
			IV				
0.000	-1.122	9.288	0.295	1.010	7.596	9.598	3.815
9.048	0.000	0.000	Ovarian		Serous		
			IIIC				
3.057	5.085	15.635	-1.013	12.953	3.000	5.509	4.673
10.868	3.209	0.165	Ovarian		Serous		
			IIIC				
2.142	-2.028	8.572	9.302	13.764	-0.489	0.001	6.583
12.558	3.570	0.239	Ovarian		Serous		
			IIIC				
-2.627	4.593	-0.930	4.644	2.635	-1.502	-1.173	0.261
2.319	1.400	-1.676	Ovarian		Serous		
			IIIC				
5.317	2.653	4.042	3.090	0.000	4.105	6.127	2.752
7.189	4.100	2.578	Ovarian		Serous		
			IIB				
8.274	-0.826	8.498	4.599	1.384	5.864	2.485	0.435
0.337	1.049	-0.870	Ovarian		Serous		
			IIIC				
4.430	-2.203	8.599	0.000	4.031	2.105	10.837	-0.609
17.987	2.116	3.804	Ovarian		Serous		
			IIIC				
0.000	-1.188	-1.067	0.000	3.090	-2.142	-1.497	-1.006
-1.355	-1.220	0.000	Ovarian		Serous		
			IIIC				
-0.450	5.150	10.733	9.121	10.524	5.256	8.924	-1.268
1.457	0.685	4.456	Ovarian		Serous		
			IV				
3.832	2.665	3.135	6.969	6.076	0.966	5.600	1.988
8.432	3.361	1.766	Ovarian		Serous		
			IV				
10.115	1.765	7.381	4.368	9.114	5.063	9.483	7.750
15.539	-1.393	-1.942	Ovarian		Serous		
			IIIC				
7.429	3.242	3.512	2.149	4.036	0.332	3.008	0.644
7.118	0.628	-1.286	Ovarian		Serous		
			IIIC				
12.590	4.648	-0.400	-0.885	-1.589	1.697	-1.293	4.384
5.062	0.361	-0.639	Ovarian		Serous		
			IV				
4.783	-0.868	8.469	1.592	1.975	-0.690	1.522	1.245
6.356	4.876	3.938	Ovarian		Serous		
			IIIC				
-3.076	-0.393	-3.235	-2.556	-3.623	-1.050	-0.558	-1.430

Table35.txt

-1.915 -2.086 -1.981 Endometrial NA
NA
-2.471 0.319 -3.572 -0.521 -3.155 0.117 -0.764 -1.222
-1.638 -1.687 -1.206 Endometrial NA
NA
-1.497 0.544 -3.265 10.863 -1.129 0.743 -0.909 4.864
10.435 -0.044 -2.324 Endometrial NA
NA
15.320 6.363 11.705 1.926 13.841 -1.011 14.266 2.802
5.636 -1.574 5.139 Ovarian Serous
IIIC
0.199 -0.256 1.060 4.981 5.228 3.003 6.077 -0.330
2.769 3.261 7.560 Ovarian Serous
IIIC
-1.130 3.750 -0.967 -3.113 -0.601 -0.407 -1.952 -1.624
-1.981 -0.462 -0.479 Uterus Mixed adenocarcinoma with
clear cell & serous features IVB
0.000 0.000 0.000 0.282 0.063 -0.277 -2.458 -0.764
-1.648 0.253 -1.847 Endometrial NA
NA
-2.184 -0.817 -1.334 -1.106 -2.177 3.425 -0.053 -1.043
-2.029 -1.715 -1.692 Endometrial NA
NA
11.932 3.740 19.157 5.607 10.170 -0.483 10.406 3.386
14.614 10.786 1.946 Uterus IVB
IVB
11.449 1.556 8.041 1.191 10.972 5.455 -0.762 4.461
8.264 -2.915 -0.021 Ovarian Serous
IIIC
-1.182 -0.441 -2.512 -0.346 -0.179 -2.001 -0.958 0.352
-0.936 -0.710 -1.532 Endometrial NA
NA
16.086 7.703 13.197 8.248 13.347 6.767 8.976 5.872
11.713 -1.907 -2.007 Endometrial NA
NA
-1.686 -1.169 -0.484 1.596 -1.453 3.104 1.846 -0.093
-0.099 -2.129 -0.855 Endometrial NA
NA
-3.297 -0.633 -2.701 -2.621 -0.319 -1.842 -1.104 -1.441
-2.630 -2.022 0.210 Ovarian Serous
IIIC
-2.295 -0.287 1.538 2.839 1.986 1.986 4.991 2.815
0.606 -0.716 2.416 Uterus Serous
IVB
-0.981 -1.956 -2.552 -0.605 -0.677 -1.186 -2.661 -1.540
-1.704 0.058 -0.442 Endometrial NA
NA
-1.901 -1.147 -0.265 3.211 4.079 -0.757 -1.783 2.192

Table35.txt

9.038 -1.613 -2.761 Ovarian Serous
IV
1.314 6.381 4.387 -1.772 -0.044 6.263 4.963 2.511
3.593 1.148 -3.456 Ovarian Serous
IV
2.036 -1.795 -2.773 -0.673 5.484 2.946 11.589 4.508
6.836 -0.105 -1.341 Ovarian Serous
IIIC
5.920 -1.554 8.686 2.875 14.319 -1.634 -0.472 4.427
8.299 -0.547 0.391 Ovarian Serous
IV
0.000 5.390 -2.846 1.720 4.939 1.322 3.501 2.525
10.719 0.687 5.945 Endometrial NA
NA
0.000 1.039 1.396 1.877 -0.836 -0.391 -1.403 -0.543
-1.831 0.000 0.000 Uterus Serous
IIIC2
-3.348 0.300 2.625 0.677 10.130 3.357 -1.184 -2.407
-2.259 -0.939 2.570 Ovarian Serous (also appendiceal
mucinous neoplasm of uncertain maIV
-0.254 -1.113 -0.215 0.847 -2.261 1.006 -1.012 -1.625
-1.324 -1.206 0.378 Endometrial NA
NA
-1.224 1.223 1.125 -0.828 -0.265 -0.675 -0.925 1.052
-1.026 1.048 -0.874 Ovarian Serous
IIIC
0.000 0.595 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Ovarian Serous
IIIC
8.795 -2.308 3.318 7.281 2.176 -2.642 9.555 1.037
7.731 4.049 3.554 Ovarian Papillary Serous
Cystadenocarcinoma IC, G3
-0.148 -1.682 5.767 0.319 4.336 -0.506 3.872 0.000
-1.841 -0.483 0.216 Ovarian Endodermal PT1inus Tumor
IIIB, G3
-1.687 -2.909 -1.512 -1.878 -2.136 0.131 -1.862 -0.504
-0.588 1.441 -0.165 Endometrial NA
NA
-2.718 -0.982 -1.438 -1.603 -0.231 0.434 -0.643 -0.952
-2.831 -1.769 -2.185 Uterus Endometrioid Adenocarcinoma,
Villoglandular Type IC, G2
-2.271 -1.913 -1.947 -0.541 -2.264 -0.259 -0.482 0.030
1.068 -2.063 -1.323 Endometrial NA
NA
-2.483 -1.731 -2.193 -0.583 -2.048 -0.684 -1.137 -0.990
-3.194 -3.409 -0.333 Uterus Endometrioid Adenocarcinoma,
Villoglandular Type IB, G2
-2.709 -1.622 -2.736 -2.330 -3.134 -1.297 -2.225 -1.815

Table35.txt

7.500 0.160 -2.371 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IA, G1
14.906 -2.372 -1.766 -2.964 -1.626 -0.577 -1.591 2.253
7.468 1.156 -0.678 Uterus Carcino-PT1arcoma (Malignant Mullerian Mixed Tumor) IC, G3
-1.258 -0.344 -3.126 0.031 -1.826 -2.812 -2.319 -0.217
-0.635 -1.157 -2.652 Endometrial NA
NA
-2.161 -0.007 -4.275 -0.280 -3.136 -0.733 -2.970 0.307
-0.326 -1.448 -0.904 Endometrial NA
NA
-3.534 -0.015 -1.431 0.715 -3.271 -0.050 -2.521 0.417
-0.777 0.819 -0.428 Uterus Endometrioid Adenocarcinoma, Poorly Differentiated IV, G3
-3.007 -2.508 -4.508 -2.103 -3.016 -2.292 -2.194 1.308
6.882 -2.403 -1.503 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IA, G1
-0.679 0.760 -1.931 -2.088 -0.590 -1.056 -1.736 -2.616
-0.441 -0.359 -1.852 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IB, G1
-2.228 -0.481 -2.627 -3.031 -3.301 -1.053 -0.394 -2.389
-2.211 -1.524 -0.726 Endometrial NA
NA
-0.706 -2.257 -4.925 -1.893 -3.047 -0.784 -0.413 -2.366
-2.291 -1.231 -1.238 Uterus Endometrioid Adenocarcinoma, Villoglandular Type 1A, G1
6.593 7.393 -2.078 1.336 -2.659 -1.449 -0.684 3.767
-1.116 -2.201 -2.069 Uterus Endometrioid Adenocarcinoma, Villoglandular Type IA, G2
-2.373 -0.530 -1.800 -0.616 -1.173 -0.493 -2.235 0.204
-1.664 -1.068 -0.505 Endometrial NA
NA
11.676 4.849 0.092 1.537 3.066 1.713 -0.879 -0.405
1.368 -2.022 1.035 Ovarian serous-papillary adenocarcinoma IIC, G3
-2.362 -1.005 -0.985 -2.398 -1.111 -1.881 -1.533 -1.872
-1.842 -1.389 -0.198 Endometrial NA
NA
2.825 -1.442 -2.091 4.311 0.366 0.152 -1.055 -1.051
-2.204 8.782 7.595 Endometrial NA
NA
-2.372 -2.204 -1.364 -1.043 -2.374 -2.418 -1.427 1.402
1.420 0.050 2.102 Uterus serous-papillary adenocarcinoma II, G3
-2.109 -0.034 0.357 0.715 -1.818 -0.282 -0.855 1.879
2.147 -0.574 0.594 Uterus endometrioid adenocarcinoma IA, G3
-1.666 2.399 0.865 -1.047 -2.069 0.104 -1.157 0.000

Table35.txt

5.813 0.000 0.000 Endometrial NA
NA
-2.921 -1.588 -2.160 -2.859 -3.082 -1.830 -1.684 -0.289
-2.406 -1.392 -1.138 Ovarian granulosa cells tumor
IIB, G2
0.336 -0.174 -3.151 3.884 1.359 0.290 -0.072 0.000
0.627 0.000 0.000 Ovarian serous adenocarcinoma
IIIC, G3
-0.178 -2.234 -0.823 -1.753 -2.133 0.138 -2.335 1.386
1.830 0.000 1.525 Ovarian serous-papillary
adenocarcinoma IIIC, G2
1.272 1.564 4.365 4.461 13.160 9.839 9.124 0.101
-1.200 13.254 0.706 Ovarian serous adenocarcinoma
IIIC, G3
-3.731 0.187 -1.155 -2.063 -3.093 0.998 -2.696 -1.351
-2.198 -0.993 0.119 Endometrial NA
NA
0.140 0.000 0.000 0.000 -0.571 0.000 0.000 0.000
-0.445 0.000 0.163 Uterus endometrioid adenocarcinoma
IA, G1
-2.356 0.885 -3.482 8.783 3.086 1.859 -1.229 0.296
-1.199 -0.404 -0.978 Uterus serous-papillary
adenocarcinoma IIIC, G3
-1.134 0.111 -1.527 -0.200 -3.009 -2.530 -3.677 -2.337
-2.134 -1.758 -1.412 Endometrial NA
NA
-1.912 0.424 -2.295 -0.339 -1.251 -0.531 0.116 -0.891
-2.241 0.060 -0.146 Uterus Serous-papillary
adenocarcinoma IA
-4.087 -0.372 -0.530 -1.325 -3.561 -0.940 12.290 -1.597
-0.564 -1.717 -1.824 Ovarian Serous-papillary
adenocarcinoma IIIC, G1
-3.664 -0.169 -2.309 -1.192 -1.514 -1.156 -2.246 -3.135
-0.946 -0.296 0.399 Uterus endometrioid adenocarcinoma
IA, G1
-3.477 -1.114 -3.935 -1.849 -3.442 -2.526 -2.075 -0.459
-0.287 -0.669 -0.805 Ovarian Serous BL
IA
-0.610 0.000 -1.169 0.000 -2.321 0.000 -3.394 0.000
0.357 -1.214 0.000 Uterus Endometroid adenocarcinoma
IA, G1
3.732 -3.099 -0.074 1.828 -0.419 -1.607 0.934 0.000
2.121 0.000 0.000 Ovarian Serous-papillary
IC, G3
-1.905 -0.237 -2.394 0.231 -2.236 -2.568 -1.186 -0.590
-1.749 -1.241 -0.734 Uterus endometrioid adenocarcinoma
IA, G2
1.194 2.437 6.593 1.806 5.403 7.209 6.687 0.451

Table35.txt

14.243 4.272 3.446 Endometrial NA
NA
-3.862 0.551 0.564 -2.573 -3.244 -1.994 -1.763 0.904
-4.186 -0.857 -1.966 Uterus Endometrioid adenocarcinoma
IB, G2
-2.133 -2.799 -1.998 0.060 -2.623 -1.363 -1.528 -0.088
-1.201 -2.289 0.674 Uterine & Ovarian ENDOMETRIOID LG
IC2 (oc) & IA (ec)
7.305 5.516 7.686 1.327 4.245 3.556 12.561 -2.900
4.845 2.858 -1.630 Uterine & Ovarian Synchronous primary of the
ovary and endometrium IVA
0.000 2.322 0.000 0.175 -0.038 0.561 -0.144 0.000
2.011 0.233 0.000 Ovarian NA
NA
10.237 -0.429 2.521 5.188 10.268 8.037 7.737 6.050
11.098 3.139 4.887 Uterus SEROUS HG + paraganglioma in
lymphnode IA
-1.831 4.159 -0.720 4.490 0.315 -1.153 4.731 4.297
2.289 -0.113 -1.761 Uterus SEROUS HG
IVB
1.309 -1.478 0.121 2.561 1.490 2.735 5.468 0.384
4.829 2.660 -1.473 Ovarian NA
NA
-4.285 -1.110 -4.513 -2.293 -1.918 -1.160 -1.193 -1.473
2.567 0.776 -1.102 Ovarian NA
NA
-3.126 -0.363 -2.374 -0.522 -0.479 -0.431 -0.033 1.406
-0.011 -1.624 0.886 Ovarian NA
NA
6.715 0.155 1.908 -0.976 2.419 0.156 -1.317 -1.620
3.462 3.887 2.725 Ovarian NA
NA
-2.457 -0.128 0.129 -2.402 -2.268 -0.611 -1.119 -2.205
-0.154 0.144 -0.452 Ovarian NA
NA
-2.165 -0.992 -1.632 1.000 -0.510 -0.982 0.137 -0.074
-0.387 -0.595 -3.438 Uterus Endometrioid Adenocarcinoma,
Solid Type IIB, G3
-3.650 -1.023 -3.446 -1.707 -3.653 -2.285 0.152 0.385
-0.257 -1.689 -1.130 Uterus Endometrioid Adenocarcinoma,
Villoglandular type IB, G2
0.358 4.429 -1.608 0.126 3.490 -1.185 -0.483 3.090
8.399 -0.013 3.090 Uterus Papillary Serous
Adenocarcinoma IC, G3
-2.567 -0.455 2.327 -2.364 -2.268 -2.236 -0.248 -1.165
-0.971 -2.359 -0.640 Endometrial NA
NA
0.566 -1.563 -2.326 1.169 -2.121 -2.289 -0.704 -2.359

Table35.txt

-2.232	-0.057	-1.584	Endometrial	NA	NA									
10.414	5.803	5.346	-0.537	-1.669	6.859	-2.370	9.384							
5.548	-1.534	6.596	Endometrial	NA	NA									
-2.291	-0.599	-2.287	-0.158	-4.023	-0.729	-3.277	-1.880							
-1.364	-3.106	-0.207	Endometrial	NA	NA									
-3.020	-0.460	-3.787	-0.654	-2.291	-0.203	-2.505	-0.165							
-1.988	-0.717	-1.442	Endometrial	NA	NA									
-2.829	-1.803	-1.642	-1.035	-2.100	-1.215	-0.126	-0.123							
-2.517	-0.435	-2.199	Uterus	II, G2	mucinous adenocarcinoma									
-3.092	0.226	1.022	-2.077	-1.788	-0.321	0.567	1.096							
0.324	-0.357	-1.176	Uterus	IB, G1	Endometroid adenocarcinoma									
-1.312	-2.409	-0.415	0.335	-3.006	-0.007	-1.185	-0.388							
3.052	-3.090	-3.201	Ovarian	NA	NA									
0.000	0.000	0.000	0.000	0.218	0.000	0.000	0.000							
0.000	0.000	-1.214	Uterus	IA, G2	Endometroid adenocarcinoma									
10.210	-0.220	-2.518	-1.233	-1.182	7.366	8.666	1.497							
1.228	5.591	5.233	Endometrial	NA	NA									
-1.195	-3.233	-2.310	-1.210	-0.862	-2.255	-1.833	-1.222							
-4.095	-0.549	-0.410	Uterus	IA, G1	Endometroid adenocarcinoma									
1.316	-0.955	-0.164	5.743	6.544	-2.285	-1.867	1.044							
1.251	0.628	1.318	Ovarian	NA	NA									
-1.992	-0.822	-2.772	-3.282	-2.184	-1.656	-2.561	-1.848							
-1.522	-0.740	-1.217	Uterus	IA, G1	Endometroid adenocarcinoma									
2.334	0.879	-0.310	0.312	-1.010	-2.519	-1.836	-0.582							
0.278	-0.872	-1.479	Ovarian	NA	NA									
2.257	0.331	-0.625	-0.744	0.427	0.309	3.792	0.218							
2.218	-1.256	1.236	Ovarian	NA	NA									
-3.423	0.342	9.144	-1.836	-0.939	0.398	-1.950	-0.143							
-2.284	-2.350	-0.541	Uterus	IA	Serous-Papillary									
0.563	1.385	2.244	2.715	8.423	5.353	0.191	1.398							
-1.690	-1.117	-1.293	Uterus	IIIA, G2	Serous adenocarcinoma									
-0.265	0.132	-0.607	-1.449	4.043	1.189	4.454	7.597							

Table35.txt

14.349 0.144 -1.385 Ovarian NA
NA
-1.842 -1.797 -3.235 0.209 -2.164 -0.407 -1.973 -1.638
-2.654 -0.253 -2.195 Uterus Endometroid adenocarcinoma
IA, G1
-1.483 -0.533 -1.923 -0.949 -0.570 -1.458 -1.641 0.134
-0.297 5.724 -1.229 Uterus Endometroid adenocarcinoma
IB, G2
-3.002 0.856 -1.693 -1.177 -3.134 -1.098 -2.546 -1.681
-2.668 -1.175 -0.627 Uterus Endometroid adenocarcinoma
IA, G1
-2.414 -1.113 -2.137 0.479 -1.799 -0.028 -1.068 -0.077
-2.362 -0.542 -0.330 Uterus Endometroid adenocarcinoma
IB, G2
-1.657 -0.857 -3.134 -0.809 -2.293 -1.710 -1.905 -0.726
-2.605 -1.082 -1.761 Uterus ENDOMETRIOID LG
IA
-2.195 -0.660 -1.865 -1.407 -0.564 -0.645 -1.741 -0.605
-3.483 -2.430 -1.325 Uterus ENDOMETRIOID LG
IA
1.325 0.178 -1.380 -1.494 -2.280 -0.525 -2.499 0.062
-2.017 0.000 0.000 Uterus ENDOMETRIOID HG
IA
-3.403 -2.045 -1.648 -1.669 -1.268 -1.919 -0.647 1.250
0.091 -3.043 -0.811 Uterus ENDOMETRIOID GRADE 2
IB?
-0.072 -0.698 0.637 -0.605 -1.558 -0.335 -2.577 0.000
-1.395 0.370 -1.714 Uterus SEROUS HG
IIIC2
-0.104 0.275 -1.338 0.727 -0.777 -0.160 -1.731 -1.066
-0.784 -0.052 0.137 Uterus Endometrioid Adenocarcinona,
Villoglandular Type IA, G1
0.623 -1.547 1.703 -0.842 -1.024 0.348 -1.146 -0.982
-0.325 -1.058 -0.507 Uterus Endometrioid Adenocarcinona,
Villoglandular Type IIIA, G2
-0.553 -0.826 -0.844 -0.504 0.518 -0.597 1.225 -0.738
0.312 -0.859 0.614 Uterus Endometrioid Adenocarcinona,
Villoglandular Type IA, G2
-0.803 0.022 -0.511 2.488 -1.088 -1.332 -2.379 0.042
-0.604 -0.516 0.881 Uterus Endometrioid Adenocarcinona,
Villoglandular Type IA, G2
0.136 -1.715 -0.083 0.395 -1.023 -0.796 -1.693 0.420
0.424 -1.359 -0.234 Uterus Endometrioid Adenocarcinona,
Villoglandular Type I, G1
-0.866 5.044 7.498 8.142 15.977 5.902 5.745 -0.115
0.216 9.221 -0.004 Ovarian NA
NA
11.830 7.321 8.637 7.511 12.746 3.348 7.910 -0.290

Table35.txt

5.823 -1.332 4.118 Endometrial NA
NA
9.744 6.783 7.824 6.948 10.624 3.706 7.153 1.775
1.851 -1.557 0.178 Ovarian NA
NA
3.790 5.553 8.839 7.369 16.545 5.280 5.100 9.374
5.516 3.879 6.513 Ovarian NA
NA
-0.121 -0.904 -1.744 -0.751 -0.394 -0.352 -1.366 1.397
-0.675 0.342 -1.996 Ovarian NA
NA
-0.052 7.058 5.592 0.416 0.368 -1.059 0.467 1.403
-1.608 -1.978 1.417 Ovarian NA
NA
11.321 4.338 7.065 7.405 13.750 1.424 3.373 6.953
7.769 -1.910 8.253 Ovarian NA
NA
-0.147 0.585 6.809 0.434 2.016 0.256 2.335 -2.669
0.823 0.815 -0.026 Ovarian NA
NA
8.513 5.831 7.443 5.879 11.833 -0.531 7.634 4.132
3.352 6.507 3.176 Uterus Endometroid carcinoma
III
-1.062 -0.585 -0.268 7.097 -2.215 0.056 -0.017 -1.771
-0.855 0.133 0.198 Uterus ENDOMETRIOID CARCINOMA OF THE
ENDOMETRIUM WITH MUCINOUS DIIA
-0.528 2.004 6.597 6.613 4.914 -0.765 1.787 0.413
-0.497 3.024 2.163 Ovarian NA
NA
-0.332 -0.110 -1.177 -1.533 -1.274 -0.589 -0.184 -0.087
0.385 -2.763 -0.245 Uterus Endometrioid carcinoma with
mucinous features IA
0.166 -1.181 0.084 -0.053 0.372 -0.857 -0.267 0.391
-0.857 0.041 -0.102 Uterus Endometrioid carcinoma
IA
-1.901 -2.048 -1.054 -2.303 -1.495 -1.100 -1.331 -1.247
-1.703 -3.161 -0.039 Uterus Endometroid carcinoma
IA
-1.603 -1.248 -0.743 -0.809 -2.068 -2.077 1.547 -0.385
-1.522 -0.090 0.302 Endometrial NA
NA
3.590 4.176 8.910 1.446 -2.198 2.388 7.526 5.189
6.225 3.306 1.704 Ovarian NA
NA
-2.665 -0.819 0.218 0.244 -1.929 -0.117 1.880 0.505
-1.610 -1.129 -0.787 Ovarian Low grade serous carcinoma
IA
4.367 7.686 11.871 5.777 2.944 3.426 4.979 1.081

Table35.txt

2.231 1.431 6.080 Ovarian NA
NA
4.702 3.518 -1.424 7.344 5.083 6.268 0.106 -0.211
-0.310 -1.954 0.085 Uterus Serous carcinoma
IV
-1.299 -0.595 0.362 -2.390 -1.680 -0.749 -1.352 -2.628
-0.898 -1.605 -3.240 Uterus Endometroid carcinoma w/ focal
squamous differentiation IIIA
-0.649 0.890 0.265 0.019 -2.008 -2.159 0.652 0.542
-0.510 -1.531 1.157 Endometrial NA
NA
12.175 5.292 2.384 1.268 -1.876 0.029 -0.386 1.593
6.142 8.823 5.922 Uterus High grade serous carcinoma
IB
10.607 5.308 -1.428 3.044 8.484 0.207 -0.192 0.069
2.819 9.462 2.381 Uterus High grade serous carcinoma
IB
5.071 3.618 3.541 -0.692 -0.647 2.209 -1.536 0.687
2.675 -0.415 4.155 Ovarian NA
NA
-1.866 2.558 7.540 0.235 -0.746 -1.685 -1.306 -0.893
-2.159 0.549 -2.690 Uterus HG Serous carcinoma with focal
endometrioid differentiatioIB
0.373 -1.595 0.741 -0.563 -0.183 0.626 0.001 -1.674
-1.193 0.165 0.644 Uterus Endometrioid carcinoma
IA
-2.394 -1.014 -0.730 -1.462 -1.863 -2.450 -0.768 -0.057
-1.712 -1.068 -1.402 Uterus Endometrioid carcinoma
IA
9.108 6.570 7.514 5.693 8.628 4.505 3.413 5.389
5.680 0.770 -2.102 Ovarian NA
NA
4.991 4.283 2.758 2.684 5.620 1.575 2.291 1.738
3.690 0.554 -2.824 Ovarian High grade serous carcinoma
IIIC
-1.978 -2.967 -0.107 0.655 1.280 -0.459 -1.576 -0.017
-1.244 -0.572 -0.399 Uterus Endometrioid carcinoma
IIIA, G2
-2.966 -0.363 -1.516 0.246 -0.212 0.089 -1.389 -2.905
-1.329 -0.896 0.310 Uterus Endometrioid carcinoma
IIIA, G2
0.136 -1.448 1.180 0.771 -1.443 -0.586 -0.028 -1.020
-0.951 -0.590 -2.226 Uterus Endometrioid carcinoma
IB
-1.444 0.705 -2.780 0.543 -0.342 -1.279 0.827 -1.930
0.508 0.613 -2.274 Endometrial NA
NA
2.138 -0.650 -0.706 0.721 -2.519 -1.845 0.249 -1.133

Table35.txt

-0.621 -1.086 1.426 Uterus Endometrioid carcinoma IA, G1
2.682 -0.448 -0.128 0.174 -0.669 -0.725 -0.421 0.500
-0.648 -1.404 -0.651 Uterus Endometrioid carcinoma IA, G1
-2.484 -1.607 -0.125 0.186 -0.165 0.310 -0.730 0.052
-0.031 0.123 -1.449 Uterus endometrod ca w/ squamous differentiation IA, G2
15.466 3.357 14.247 1.145 -1.045 -1.704 4.522 8.723
16.013 9.915 8.499 Uterus endometrod ca w/ squamous differentiation IA, G1
5.229 -0.543 -0.153 -1.958 -2.749 1.646 -0.508 4.368
15.251 0.000 1.121 Ovarian NA NA
-0.238 -1.769 -0.703 1.002 -2.875 3.606 6.138 0.185
-1.890 0.626 -1.879 Uterus Endometrioid carcinoma IA, G1
-2.578 -1.359 -3.950 -1.619 -1.516 2.351 2.899 -0.605
-1.264 -1.268 -2.776 Uterus Endometrioid carcinoma IA, G1
-2.575 -2.782 -0.293 -1.259 -0.918 -0.510 -0.404 0.636
0.853 -0.769 -1.229 Ovarian NA NA
-1.172 1.510 4.388 -0.775 -1.898 0.761 -0.290 -1.430
-1.275 1.158 -1.990 Uterus Endometrioid carcinoma IA, G1
-1.261 -1.125 -2.389 -1.646 -1.088 -2.143 -1.559 -1.065
-0.479 -0.120 -0.458 Uterus endometrod ca w/ squamous differentiation IA, G1
-0.622 -0.845 0.860 -0.626 -1.334 -0.187 -1.617 1.614
-1.186 -2.514 -0.115 Uterus endometrod ca w/ squamous differentiation IA, G1
-3.530 -1.320 -3.152 -3.164 -3.001 -0.938 -0.240 -1.041
0.360 -1.796 -0.610 Uterus ENDOMETRIOID GRADE 2 IA
-1.073 0.470 -2.851 -1.358 -1.733 3.930 2.508 -0.783
-1.426 1.214 -2.180 Ovarian NA NA
2.400 8.236 7.575 0.238 0.294 5.180 7.513 4.620
5.112 7.162 6.359 Uterus SEROUS HG IIIA OR B?
-2.484 1.696 -1.599 0.324 0.339 -1.793 -0.631 -0.407
-0.256 2.685 -0.370 Uterus HIGH GRADE IB
1.976 3.629 -1.840 -0.524 -0.305 0.418 -1.217 -0.647
-1.570 8.431 1.064 Uterus HIGH GRADE IB
-1.794 -1.045 -1.777 -2.140 -1.765 -1.200 -1.654 0.000

Table35.txt

-3.093 -0.540 -1.735 Ovarian GRANULOSA CELL TUMOR + EIN IC2
10.090 0.008 -0.594 -0.557 -0.760 0.432 -1.072 -0.572
-0.403 -0.002 -0.089 Uterus ENDOMETRIOID LG IA
-3.511 -2.526 -2.376 -1.640 -0.203 -0.499 -1.940 -1.116
-2.349 -1.602 -1.120 Uterus ENDOMETRIOID GRADE 2 IB
-1.122 -1.302 1.457 -0.301 0.085 0.930 0.459 -0.384
0.450 -0.605 1.705 Uterus SEROUS HG IIIC2
3.469 -1.417 -1.078 -1.296 -3.753 -0.986 -2.578 -1.409
0.926 1.330 0.492 Uterus ENDOMETRIOID HG IIIC2
-2.218 -0.036 -0.587 9.615 19.750 -1.951 -1.169 3.679
-0.570 2.997 4.793 Uterus ENDOMETRIOID LG IIIC2
-1.995 -3.564 -1.876 -1.030 -1.944 -0.755 -1.665 0.915
-1.596 -1.240 -1.959 Uterus ENDOMETRIOID LG IA
-2.151 -2.859 0.189 0.952 -3.222 0.014 -1.657 -0.246
-0.913 -1.590 -0.872 Uterus ENDOMETRIOID LG IA
-1.125 7.086 4.349 2.495 5.969 3.014 5.859 -0.010
12.936 8.213 7.962 Uterus SEROUS HG IIIC1
-1.964 -0.018 -0.772 -1.207 -0.113 -1.179 -1.815 -1.291
-0.608 0.191 0.838 Endometrial NA NA
-1.439 -0.986 -0.538 -0.104 -3.805 -2.714 -0.832 -0.790
-3.224 -1.274 -1.411 Endometrial NA NA
-0.489 -0.590 -2.886 -0.788 -0.508 -0.542 -0.408 0.277
-0.254 -1.091 0.137 Uterus Endometrial Adenocarcinoma, Villoglandular Type IB, G2
-1.924 -0.036 -0.558 0.614 -1.545 0.230 -1.034 -0.666
-1.256 -0.136 -1.008 Endometrial NA NA
4.165 -0.458 -1.787 -1.894 -4.756 -1.237 -1.278 -1.019
-0.158 -1.664 1.361 Uterus Squamous Cell Carcinoma, Clear Cell Type IB, G3
-1.133 -1.711 -1.255 -2.487 -1.013 -0.333 -1.192 -1.558
-1.558 0.902 -1.726 Endometrial NA NA
-2.193 -0.831 -0.963 -1.540 -0.356 0.079 -0.795 -0.653
-0.378 0.317 -1.037 Endometrial NA NA
-0.726 6.509 -0.631 0.581 -0.883 0.735 0.017 -0.835

Table35.txt

-1.055 0.088 -1.934 Endometrial NA
NA
9.930 9.608 1.640 9.084 13.305 -0.357 -0.561 5.741
2.624 11.508 -0.821 Endometrial NA
NA
-0.373 -0.873 -0.434 -1.869 -0.157 -0.495 -1.328 -0.579
-1.490 -0.380 0.991 Uterus ENDOMETRIOID LG
IIIC1?
-1.192 -0.542 0.322 -1.214 0.538 0.115 0.356 -0.892
-1.203 0.473 -1.037 Uterus ENDOMETRIOID GRADE 2
IIIC1
12.613 7.170 4.803 5.818 12.482 0.445 -0.639 6.603
7.151 10.487 9.053 Ovarian NA
NA
11.717 6.295 11.792 7.183 11.923 5.083 8.648 8.976
7.738 7.701 7.098 Uterus ENDOMETRIOID GRADE 2
II
-1.505 -0.712 0.577 -1.484 -0.732 0.361 -1.870 -0.540
-0.831 1.103 -0.537 Uterus ENDOMETRIOID HG
IIIC1
-0.972 6.090 2.870 0.480 15.099 5.021 -0.300 -1.133
-0.894 0.685 1.163 Uterus SEROUS HG
IIIC2
-2.329 -1.674 1.322 0.279 -0.242 0.396 -1.125 0.404
-0.628 0.104 -0.519 Uterus ENDOMETRIOID GRADE 2
IIIC2
0.504 0.210 -1.072 -0.355 -0.245 1.070 -0.784 1.421
-0.684 -0.927 0.475 Uterus ENDOMETRIOID LG
IIIC1
-3.854 -1.120 3.478 0.941 -1.516 -0.523 -2.877 -0.886
-1.729 0.106 -0.746 Ovarian NA
NA
-2.504 -1.097 -2.613 -1.177 -2.006 -1.571 -1.195 -1.052
-1.780 -1.635 -0.420 Uterus ENDOMETRIOID LG
IA
-0.999 0.000 -0.213 0.000 -0.505 0.000 -1.169 0.441
-0.710 0.000 0.000 Uterus ENDOMETRIOID LG
IA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Ovarian NA
NA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Uterus ENDOMETRIOID GRADE 2
II
7.991 2.306 8.286 -1.703 1.184 -0.414 6.529 0.137
10.157 4.259 2.792 Uterus endometrium: predominantly
high grade sarcomatous componenII at least (sarcoma) IIIC

Table35.txt

with epithelial component (30-35% of tumor = HGSC).

-0.727	-0.278	-2.046	0.297	-3.059	-3.703	-1.089	1.860
-3.467	-2.347	0.729	Uterus		ENDOMETRIOID LG		
			IA				
-2.925	0.382	-1.785	-0.836	-1.603	-0.792	-0.373	-2.773
-0.036	-1.310	-2.317	Uterus		ENDOMETRIOID GRADE 2		
			IA				
-3.161	-0.808	-1.810	2.012	8.539	2.076	-1.322	1.998
4.061	2.516	6.829	Ovarian		NA		
			NA				
-0.852	-2.290	-2.655	-0.982	-2.364	-1.417	0.353	-1.336
-0.007	-0.767	-0.579	Uterus		ENDOMETRIOID LG		
			IA				
-0.177	3.531	4.638	1.553	1.154	-2.769	-3.127	-1.701
-1.652	11.795	10.820	Endometrial		NA		
			NA				
-0.235	-1.031	-1.821	4.965	0.427	-1.258	-0.280	-1.512
-1.633	-1.456	-2.789	Uterus		ENDOMETRIOID LG		
			IB				
4.370	-1.342	-0.213	3.643	5.958	4.418	4.304	0.771
-2.178	0.000	3.500	Uterus		ENDOMETRIOID LG		
			IA				
5.759	-0.210	-2.310	0.972	-2.453	4.160	6.826	0.755
9.015	7.432	0.199	Uterus		SEROUS HG		
			IIIC2				
-0.163	0.516	-3.551	-1.248	-0.210	-1.055	-0.861	-0.481
-1.315	-1.273	2.246	Uterus		ENDOMETRIOID LG		
			IIIC1				
-1.870	-0.851	-2.551	-0.922	-0.931	-2.167	-2.380	-1.935
-2.127	-0.528	-1.353	Uterus		ENDOMETRIOID HG		
			IA				
-0.586	-0.261	-1.280	-0.066	-1.231	1.373	2.639	-1.787
-1.013	-1.116	-0.448	Uterus		ENDOMETRIOID LG		
			IIIA				
1.085	-0.105	-0.658	-0.210	13.876	-2.108	-0.495	5.399
11.230	-0.518	5.554	Endometrial		NA		
			NA				
-1.240	-0.977	-0.430	-1.344	-0.239	-0.808	-0.687	0.746
-0.930	-1.228	-1.402	Endometrial		NA		
			NA				
-1.609	-0.251	-1.718	-1.705	0.059	-0.880	-0.149	-1.439
-1.203	-2.483	-0.962	Uterus		UNDIFFERENTATIED HG		
			IIIA				
13.245	-0.728	7.229	-0.892	-1.142	-2.132	8.083	6.479
2.717	7.172	8.093	Endometrial		NA		
			NA				
-2.939	-1.274	-3.151	-2.451	-1.665	-1.168	-0.312	-0.663

Table35.txt

-2.512 0.089 0.029 Ovarian Serous papillary borderline tumor of ovary. NA
-4.023 -1.047 -1.667 -1.916 -1.467 -1.298 -1.971 -1.641 0.399 -0.823 -2.316 Uterus Endometrioid carcinoma IC, G1
4.259 2.916 6.811 -0.881 -2.648 2.927 4.023 7.215 -0.351 8.145 6.892 Uterus HG serous carcinoma II
19.620 9.145 15.043 11.723 -0.083 6.042 9.237 -0.259 6.247 -1.651 3.618 Ovarian NA NA
-1.440 0.006 3.865 0.896 2.612 1.056 -0.151 0.124 1.255 0.200 0.419 Ovarian HG serous carcinoma IVA
2.165 0.316 1.594 4.442 10.488 0.331 -0.531 -1.214 2.984 2.144 -1.854 Uterus HG serous carcinoma IB
-0.901 0.357 -3.539 0.615 -4.239 5.836 10.439 0.564 -2.068 0.195 0.355 Uterus HG serous carcinoma IB
-1.885 -1.079 -2.050 0.100 -1.871 -1.636 -1.886 -0.115 3.539 -0.774 0.565 Endometrial NA NA
6.806 -0.566 -2.627 1.127 -0.992 -0.051 -1.693 1.570 1.761 1.091 2.427 Ovarian NA NA
-2.225 0.254 -3.183 -2.048 -1.178 -1.746 -0.898 0.813 -1.793 -0.621 -0.578 Uterus endometrod ca w/ squamous differentiation IA, G1
-4.058 -0.155 -1.668 -1.440 -1.412 -0.624 -0.756 3.150 8.222 -1.653 0.046 Ovarian NA NA
22.408 2.751 16.674 -0.395 10.100 2.301 1.782 6.902 1.894 8.770 10.359 Ovarian NA NA
0.324 -0.057 -0.982 -1.129 -2.858 -1.538 -0.536 0.521 -1.879 -1.268 -1.916 Endometrial NA NA
0.310 0.842 -0.439 0.257 -1.509 1.602 -0.096 2.896 4.169 0.406 0.431 Endometrial NA NA
13.110 -1.590 -2.869 3.676 14.108 10.408 2.594 1.305 5.656 -1.302 -0.739 Ovarian NA NA
-0.749 -0.315 -1.657 -0.181 -1.071 -0.190 -0.291 -1.346 -1.654 -1.115 -0.928 Endometrial NA NA
18.456 6.164 15.704 2.160 15.979 9.356 13.167 1.584

Table35.txt

11.800 0.615 10.389 Ovarian NA
NA
-0.349 -2.026 -0.990 -0.192 -1.320 -0.922 -2.503 2.454
5.669 -1.720 -1.796 Endometrial NA
NA
-0.202 -1.203 -0.979 0.831 -5.349 -1.552 -0.696 0.579
-1.445 -1.124 -1.885 Endometrial NA
NA
-0.593 -1.004 -2.999 -2.028 -1.113 4.106 5.379 -2.300
-1.290 -0.559 -2.249 Endometrial NA
NA
-2.699 -0.783 -1.636 -0.031 -2.686 -0.926 -0.472 -0.566
-2.028 -1.113 0.758 Endometrial NA
NA
1.531 -1.438 -0.687 0.256 -1.001 -1.650 0.308 -1.337
0.975 -0.454 2.600 Ovarian Endometrial Adenocarcinoma,
Villoglandular Type IIA, G2
9.594 -2.128 5.518 0.019 6.457 2.213 6.927 0.086
8.267 0.291 0.228 Ovarian NA
NA
-1.493 -2.017 -0.597 -1.359 -2.446 -1.215 -1.152 -1.957
-0.364 1.456 -0.874 Ovarian NA
NA
0.000 0.834 -1.712 0.428 -1.825 -0.673 0.442 0.000
0.369 0.000 0.063 Ovarian NA
NA
2.327 -1.350 0.280 4.104 -0.931 -0.871 -1.649 -1.019
6.687 -1.590 -1.308 Ovarian Mixed Germ Cell- Sexcord
Stromal Tumor IIIA, G3
1.193 -0.005 1.555 1.726 -1.104 0.000 0.899 -1.183
0.310 0.919 0.178 Ovarian NA
NA
-0.835 -0.917 -0.630 -0.467 -2.074 -1.342 0.436 -2.022
-0.993 -0.360 -1.054 Ovarian NA
NA
5.137 -1.263 3.124 1.330 2.357 0.000 2.504 3.090
4.967 -1.399 4.165 Ovarian NA
NA
0.636 -2.110 2.897 0.258 1.353 -0.790 -0.858 -0.531
0.073 0.040 0.354 Ovarian NA
NA
-0.713 0.293 -3.041 -1.859 1.120 1.447 4.770 -1.005
2.562 -4.532 0.443 Ovarian NA
NA
-0.438 -1.346 -2.257 -0.487 -0.715 -1.826 0.354 -0.812
14.679 0.170 5.697 Ovarian NA
NA
-0.628 -0.652 -0.669 -1.460 -1.018 -1.141 -0.190 3.090

Table35.txt

16.199 0.173 -2.543 Ovarian NA
NA
-2.889 0.299 -1.902 -0.671 -1.864 -0.961 -3.405 -0.690
-0.988 -0.658 -0.318 Ovarian Granulosa Cell Tumor
IA, G2
-1.188 -2.545 -0.007 -2.630 -1.890 1.166 2.504 -0.256
-1.273 -2.098 -0.326 Endometrial NA
NA
-3.425 -1.042 -2.617 -0.572 -1.453 -2.789 -1.163 -2.334
-2.002 0.430 -1.679 Uterus ENDOMETRIOID LG
IA
-1.392 -0.273 -3.194 -0.942 -2.184 -0.108 -1.243 -1.184
-4.242 -0.988 0.119 Endometrial NA
NA
-2.060 -0.332 -1.726 -0.713 -1.444 0.250 -0.715 0.092
-2.352 -0.614 -0.505 Uterus ENDOMETRIOID LG
IA
-1.892 0.818 -2.212 -1.116 -2.232 -0.656 -0.950 6.059
10.084 0.858 -2.042 Uterus ENDOMETRIOID LG
IA
-0.945 -0.680 0.236 -1.063 -1.145 0.804 -1.333 -0.660
-1.435 -0.980 -1.721 Endometrial NA
NA
-2.074 -0.870 -1.319 0.162 -1.943 1.301 -3.331 -1.389
-1.928 -2.122 0.565 Endometrial NA
NA
-1.170 0.583 -2.703 -0.096 -1.879 0.086 -0.611 -2.767
-1.284 -1.681 -0.207 Endometrial NA
NA
13.367 7.229 -0.604 0.434 5.058 1.013 12.418 1.716
6.893 0.665 1.187 Uterus SEROUS HG
IVA
12.720 -0.182 10.011 2.052 2.448 4.473 7.266 5.339
7.392 7.825 3.197 Ovarian NA
NA
-0.698 0.214 -1.133 -1.456 -0.972 -0.616 0.036 -1.090
0.922 -1.266 -0.748 Endometrial NA
NA
-3.311 3.090 0.000 -2.007 -2.265 0.775 0.335 4.918
9.692 -2.051 0.870 Ovarian NA
NA
5.175 4.771 4.215 2.850 6.478 -0.859 3.079 3.267
4.134 4.687 3.484 Endometrial NA
NA
-3.388 -1.286 -1.333 -0.784 -1.747 -2.100 -2.267 -3.276
-3.451 -1.356 0.547 Endometrial NA
NA
12.715 1.987 10.878 3.191 4.136 -0.814 10.478 6.660

Table35.txt

13.677 3.420 0.648 Endometrial NA
NA
-1.221 -2.439 -1.007 1.515 2.112 2.511 3.695 0.031
-1.428 -0.735 -0.979 Uterus ENDOMETRIOID LG
IA
-2.269 -1.036 -1.437 -1.878 -0.518 3.644 4.420 -0.780
-1.044 -1.667 -0.552 Endometrial NA
NA
-0.698 -2.369 -2.287 -1.975 -2.366 0.707 -1.962 -0.356
-0.824 -1.326 -0.894 Endometrial NA
NA
-1.689 -0.211 -1.446 -0.333 -1.956 -1.976 -2.016 -1.540
-0.896 0.384 0.040 Endometrial NA
NA
-1.783 -2.655 -2.668 -2.024 -1.527 5.991 6.433 0.009
-1.074 -1.066 0.437 Endometrial NA
NA
-3.586 -1.288 -2.788 -0.699 -0.033 -2.256 -2.530 -1.353
-1.227 0.905 -0.999 Uterus ENDOMETRIOID LG
IA
-1.704 -2.748 -2.058 0.061 -3.063 -0.698 -2.822 0.165
-0.782 0.301 -0.574 Uterus endometrioid grade 1
IA
4.214 0.104 -2.405 3.090 -0.414 -1.477 3.214 -0.546
-0.305 -1.837 -1.887 Ovarian uterine carcinosarcoma/HG
serous carcinoma IIIA
-2.067 -0.731 -0.899 -0.491 -1.721 0.191 -2.649 -2.338
-1.749 -0.424 -0.833 Uterus Endometrioid carcinoma
IB
-1.954 -0.823 -1.802 2.919 0.000 -0.698 6.830 0.139
12.189 0.000 0.000 Ovarian serous
IIIC
-3.399 -1.074 -3.439 -0.363 -1.221 0.559 -1.713 0.389
0.073 -0.822 -2.452 Uterus Endometrioid carcinoma
IA
-2.570 -1.927 -2.273 -2.237 -1.430 -1.610 -1.329 -1.127
-1.880 -0.621 -1.743 Uterus Endometrioid carcinoma
IA
-2.435 -0.722 -0.623 -0.391 -1.101 -2.695 -1.931 -2.534
-1.350 -2.843 -3.336 Uterus Endometrioid carcinoma
IB
-4.265 -1.610 -0.885 -0.801 -2.674 -1.589 -0.347 -1.938
-1.795 -0.362 -2.407 Uterus Endometrioid carcinoma
w/squamous differentiation IA
-2.314 -1.588 -2.768 -1.403 -1.056 -0.503 -2.133 -0.503
-1.241 -2.140 -1.415 Uterus Endometroid carcinoma
IA
2.301 7.423 4.464 -2.224 -1.089 1.761 6.329 -1.360

Table35.txt

2.903 -0.966 2.442 Uterus HG adenocarcinoma w/extensive poorly differentiated componIB

in some areas while other areas have HG endometroid appearance

10.118 0.188 1.290 -0.089 -1.507 3.121 2.385 1.169
14.508 4.627 6.178 Uterus HG serous fallopian tube carcinoma metastatic to uterus anIIIC
-1.515 -0.709 -3.068 -0.896 -0.761 -0.203 -1.904 -1.422
-3.998 -2.175 -0.754 Uterus Endometrioid carcinoma
IA
-1.172 -2.720 1.909 0.530 6.016 -0.138 10.470 -0.633
6.968 5.341 6.046 Ovarian HG serous carcinoma involving colonic serosa IIIC
-0.204 -2.359 -1.557 -0.633 0.780 -1.065 -1.669 -0.890
3.290 1.704 -0.857 Uterus HG serous and panc ca
IIIC
-1.019 -0.804 -1.755 -1.107 -0.735 -1.968 -0.735 8.952
14.877 -0.859 -0.981 Uterus Endometrioid carcinoma
IA
-2.737 -1.315 -2.363 -1.420 -3.802 -1.063 -2.614 -2.680
-1.647 -0.479 -0.870 Uterus Endometrioid carcinoma
IA
-3.679 -0.496 -0.620 -1.591 0.573 -1.502 -0.896 1.058
-0.037 -1.365 -2.057 Ovarian NA
NA
-0.063 -1.878 0.952 -1.405 5.535 1.236 1.314 3.659
8.100 3.742 -1.651 Ovarian NA
NA
-1.953 -1.392 -2.934 -1.292 -3.275 -1.956 -0.804 -0.882
-1.988 -2.426 0.099 Ovarian serous borderline tumor of the ovary
IA
13.724 0.565 6.961 4.210 3.704 -0.881 2.646 6.340
9.108 -3.133 4.524 Ovarian NA
NA
1.263 0.000 0.865 0.651 -1.745 0.000 0.875 -2.921
-0.497 0.000 0.000 Endometrial NA
NA
-0.262 -1.395 0.945 0.506 -2.372 -0.862 -1.511 0.558
6.185 -0.101 0.881 Ovarian NA
NA
-1.261 0.000 0.000 6.004 5.678 3.359 0.006 0.612
-2.106 0.000 0.000 Ovarian NA
NA
-2.251 -1.323 -2.232 -2.928 -2.486 -1.284 1.381 -2.054
-2.622 -2.413 -0.773 Ovarian Serous borderline tumor
NA
1.950 10.453 8.061 4.992 2.613 0.000 6.526 1.782

Table35.txt

10.421 4.677 2.507 Ovarian HGSC with STIC III
-2.225 0.228 10.053 -1.259 -1.148 -2.116 -1.238 -3.069
-0.647 -1.223 -1.119 Ovarian NA NA
2.749 -1.149 0.000 -1.906 -1.178 0.000 1.456 0.000
1.860 -2.567 1.876 Ovarian NA NA
9.887 1.070 5.601 2.900 4.983 3.532 9.271 -0.421
5.853 3.803 0.720 Ovarian NA NA
-2.244 -1.377 -2.096 -1.750 -2.959 -1.252 -0.198 -1.450
-0.811 4.472 5.887 Ovarian low grade serous carcinoma arising w/in a background of seIIIA
-2.625 -0.931 0.000 1.813 0.653 9.748 4.061 -0.272
0.918 7.412 1.938 Ovarian NA NA
-1.418 -1.963 -2.854 -0.036 -0.098 0.249 0.000 -1.184
-1.711 0.000 -3.090 Ovarian NA NA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Ovarian NA NA
-3.463 -0.452 -3.178 -0.971 -2.726 -0.718 -0.819 0.068
-2.603 -2.030 -2.568 Endometrial NA NA
-2.440 -0.625 -2.303 1.051 -2.310 -2.463 -1.708 0.092
1.884 -1.825 -1.197 Endometrial NA NA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Ovarian NA NA
-1.910 -0.161 -1.171 0.147 -2.640 -0.414 -3.032 -2.371
-3.835 3.367 0.042 Endometrial NA NA
-0.573 -0.936 -3.819 -0.963 -1.684 0.509 -2.206 -0.058
-0.799 0.573 5.210 Endometrial NA NA
-1.090 -1.901 -1.713 -0.295 -1.256 -0.103 0.624 -0.400
-0.350 -1.553 -4.393 Uterus adeno ca, endometrial endometrioid type (grade II), with pIA
-3.371 -2.289 -2.020 -1.825 -1.783 0.242 -0.651 -1.817
-2.112 -1.405 -1.938 Endometrial NA NA
10.465 1.138 -1.002 1.367 -0.888 -0.125 5.072 1.655
-2.186 -0.590 -1.481 Ovarian NA NA
-2.210 0.000 3.090 -1.835 -0.902 1.589 0.728 0.000

Table35.txt

5.533 0.000 -0.467 Ovarian NA
NA
0.069 -0.727 -0.658 1.473 -0.718 1.678 -0.620 0.670
-1.422 -0.236 -0.581 Uterus Benign, Nabothian cysts,
endometrium proliferative type NA
-1.729 -2.387 -1.605 0.219 -1.615 -0.995 -2.252 -0.702
0.163 -0.674 -0.615 Endometrial NA
NA
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 Endometrial NA
NA
12.287 -0.370 -1.321 -1.824 -1.047 -1.444 -2.053 -1.593
-0.394 5.098 3.845 Endometrial NA
NA
-2.066 -1.628 -0.468 -1.710 -0.982 -0.055 -1.476 2.144
-1.021 -0.138 -2.659 Ovarian NA
NA
-1.680 -3.673 -3.780 -1.007 -2.647 -2.281 -0.654 -0.587
-1.904 -0.100 -2.526 Endometrial NA
NA
2.608 3.456 3.993 -1.630 -1.327 2.855 -2.533 0.000
3.090 -0.956 0.000 Uterus Controversial Moderately
differentiated adenocarcinoma mosNA

primary, LVI, 1/6 LEFT PELVIC LN
pos, left tube endometriosis, both O epithelial incl
-2.787 -0.857 -2.214 -1.628 -1.842 -0.715 -3.090 -0.552
-1.692 -1.071 -1.459 Endometrial NA
NA
7.086 0.000 2.623 3.152 5.056 0.000 2.099 -0.026
10.892 3.623 0.593 Ovarian NA
NA
0.185 5.029 5.606 9.933 8.665 -0.982 -1.883 2.825
8.240 2.981 1.991 Endometrial NA
NA
-1.922 -0.207 -1.813 -1.486 -2.148 1.007 -2.523 -2.402
-2.494 -0.875 -0.672 Endometrial NA
NA
-0.355 -0.920 -0.971 -0.843 -3.286 -2.484 -2.810 -0.999
-1.558 -0.588 -0.657 Endometrial NA
NA
-1.434 -1.085 -3.716 -0.983 -3.993 -2.947 -2.409 -1.973
-1.414 -0.698 -1.257 Endometrial NA
NA
-2.633 -1.132 -3.428 -2.006 -1.186 -1.244 -1.528 0.595
-1.428 -0.874 -1.305 Endometrial NA
NA
-2.794 -0.187 -1.499 0.000 -3.525 -5.345 -0.793 0.000

Table35.txt

-2.740 -1.093 0.000 Endometrial NA
NA
8.074 6.057 7.038 3.992 3.013 3.462 0.518 3.650
6.631 3.528 0.602 Ovarian HG serous carcinoma of both ovaries IIIC
0.000 6.337 3.090 3.321 -0.357 -0.091 1.065 0.388
6.450 0.098 -0.588 Ovarian NA
NA
-2.687 3.671 -1.566 -0.439 5.206 -1.617 -1.115 0.376
10.492 4.070 2.312 Endometrial NA
NA
-2.360 -1.410 -1.168 -0.843 -1.714 -2.144 -1.551 0.247
-4.507 -1.885 -0.683 Ovarian NA
NA
-2.366 3.505 3.662 -0.228 -3.336 -0.198 2.188 2.751
2.150 -2.328 -0.198 Endometrial NA
NA
-1.172 -0.871 0.236 -0.232 -0.734 -1.147 2.406 -1.087
-0.420 -0.022 -0.453 Colorecatal adenomas NA
NA
0.440 -0.931 1.184 0.164 -0.666 0.000 -0.196 -0.097
-0.205 -0.797 -0.881 Colorecatal adenomas NA
NA
-0.282 6.425 5.368 6.832 7.501 1.920 -0.402 1.126
0.187 -2.885 -1.346 Colorecatal adenomas NA
NA
-1.093 8.127 5.353 6.754 7.878 1.174 -1.469 3.810
-1.161 -1.589 -1.465 Colorecatal adenomas NA
NA
-1.259 -1.749 -3.925 -0.286 -0.028 -0.866 -1.187 0.635
-0.757 2.323 -0.419 Colorecatal adenomas NA
NA
0.323 0.504 -0.111 -1.189 -0.060 -1.365 -0.147 -0.437
-1.299 0.817 0.245 Colorecatal adenomas NA
NA
-0.427 -2.789 -0.275 -1.037 0.599 -0.463 0.327 1.297
-0.305 0.280 -1.092 Colorecatal adenomas NA
NA
0.362 -0.954 -0.579 -0.383 3.017 -1.008 1.368 -1.330
0.138 0.744 0.803 Colorecatal adenomas NA
NA
-0.772 2.169 -0.429 2.803 3.942 1.710 0.022 -1.413
1.287 6.639 2.832 Colorecatal adenomas NA
NA
0.127 5.044 2.579 0.878 -1.018 -0.969 -2.256 -0.775
1.685 0.940 -0.839 Colorecatal adenomas NA
NA
-0.197 -0.939 -0.410 -0.860 -0.676 -1.009 -1.994 3.541

Table35.txt

1.477 4.176 -1.307 Colorecatal adenomas NA
NA
-2.304 3.180 -1.296 -1.208 -0.015 -0.394 -1.083 -2.508
-1.813 0.306 1.591 Colorecatal adenomas NA
NA
0.531 -1.203 -1.111 -1.060 -0.290 0.940 -1.333 0.327
-1.385 0.297 -0.226 Colorecatal adenomas NA
NA
-0.798 0.643 -0.334 -2.922 0.362 -0.123 0.057 -0.051
-3.124 0.400 -0.246 Colorecatal adenomas NA
NA
-1.618 -1.395 -0.968 1.207 -0.077 -1.190 0.990 0.135
-0.763 -0.881 -1.350 Colorecatal adenomas NA
NA
-1.153 -0.620 -0.919 3.808 6.056 -0.811 -0.845 3.846
3.381 -1.083 -0.704 Colorecatal adenomas NA
NA
0.118 -1.178 -1.805 -1.271 0.536 -1.076 0.779 -1.110
0.822 0.078 -0.792 Colorecatal adenomas NA
NA
-0.724 -0.108 -0.380 0.513 0.794 -0.654 0.673 -0.807
-0.016 -2.038 -0.120 Colorecatal adenomas NA
NA
-0.563 -0.036 -2.526 -0.592 -0.313 0.000 1.765 -0.773
-2.925 1.109 0.153 Colorecatal adenomas NA
NA
-1.102 0.948 -0.386 0.505 -0.130 0.000 -1.535 -1.493
-0.539 -3.231 -1.702 Colorecatal adenomas NA
NA
-1.152 -0.192 -2.160 0.160 -0.379 1.401 0.479 -4.517
-1.949 0.269 1.720 Colorecatal adenomas NA
NA
-2.435 6.171 0.839 1.244 1.954 -1.714 -0.851 5.279
3.047 2.076 5.274 Colorecatal adenomas NA
NA
-0.161 -1.830 -0.240 -1.386 -0.384 0.967 -0.469 -1.488
-0.225 1.113 -1.037 Colorecatal adenomas NA
NA
0.691 -1.191 -0.630 -0.265 -0.383 6.858 -0.240 -0.843
1.101 1.124 0.036 Colorecatal adenomas NA
NA
5.553 -0.064 -1.005 -0.747 8.516 -0.119 1.876 -0.481
-1.132 0.403 0.530 Colorecatal adenomas NA
NA
-0.917 -1.376 -0.407 -1.281 -0.302 -0.390 2.023 -1.119
-2.576 0.522 -1.499 Colorecatal adenomas NA
NA
0.434 -0.016 -1.909 -0.824 10.565 -1.148 0.504 2.371

Table35.txt

0.639	1.056	-0.832	Colorecatal adenomas	NA	NA					
0.771	0.000	0.000	-0.935	0.670	-0.925	0.717	0.000	-0.376	-0.002	-0.858
Colorecatal adenomas	NA	NA								
-0.953	-0.018	-1.725	-0.675	-2.282	0.322	-0.766	-0.526	1.341	0.333	-1.271
Colorecatal adenomas	NA	NA								
-1.688	0.224	4.564	0.163	-0.810	0.454	2.276	2.258	3.303	0.974	-1.062
Colorecatal adenomas	NA	NA								
-1.853	0.366	-0.753	0.511	-3.311	0.871	0.204	-0.432	0.388	0.200	-1.056
Colorecatal adenomas	NA	NA								
-1.338	-1.292	-0.533	5.511	7.663	-1.717	-0.586	2.465	3.636	0.276	0.085
Colorecatal adenomas	NA	NA								

Grade	TCGA equivalent
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Table35.txt

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Table35.txt

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Table35.txt

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G1-G2	HNSC
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Table35.txt

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Table35.txt

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Table35.txt

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Table35.txt

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Table35.txt

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G3	STAD

Table35.txt

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G3	OV
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Table35.txt

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Table35.txt

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Table35.txt

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Table35.txt

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Table35.txt

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G2	PAAD

Table35.txt

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Table35.txt

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Table 36. Plasmas

Genome Wide Aneuploidy Score	Official Name	reads	uids	chr1p	chr1q	chr2p	chr2q	chr3p	chr3q	chr4p	chr4q	chr5p	chr5q	chr6p	chr6q	chr7p	chr7q	chr8p	chr8q
0.57626138	PANC 303 PLS	13122805	7455633	-0.944	-0.116	-1.394	-0.176	0.198	-0.262	1.399	2.830	1.476	1.595	-1.431	2.310	1.041	1.793	-0.322	2.328
0.088062391	PANC 304 PLS	10644674	1651113	-0.889	1.392	-0.604	0.976	-0.628	1.463	-0.185	1.282	0.464	1.084	-1.148	0.823	0.553	0.513	-0.888	-1.243
0.785913513	PANC 305 PLS	14138799	11360279	-0.689	-0.865	-1.688	-0.123	0.747	2.236	0.508	3.028	2.961	1.382	-2.495	1.793	0.174	2.796	-0.716	0.923
0.324064665	PANC 306 PLS	14574611	3313397	-1.015	-0.437	-1.634	-1.698	-1.033	0.157	0.640	1.479	2.150	1.615	-2.243	1.679	0.741	1.641	1.043	-0.025
0.018610499	PANC 307 PLS	11811266	5284352	-0.633	-0.213	-1.696	0.071	0.311	0.982	-0.997	-0.303	-0.209	1.194	0.039	1.345	-0.752	0.745	-0.664	0.948
0.01696031	PANC 308 PLS	13071777	2774002	0.065	0.719	0.285	0.354	-0.425	1.342	1.029	1.202	-0.548	0.905	-0.366	1.460	-1.302	1.454	-1.118	0.422
0.618815583	PANC 323 PLS1	10643881	3770749	1.333	1.112	-0.103	-1.409	-1.019	0.953	-1.225	-1.933	-0.173	1.909	-0.324	-1.453	1.844	0.459	-0.463	0.788
0.077366184	PANC 333 PLS1	12882061	8642782	1.261	-0.040	-0.485	-0.377	-0.315	0.238	0.255	0.634	0.221	0.887	-0.029	-0.365	-0.036	0.844	-0.179	0.828
0.048291578	PANC 335 PLS1	11983641	4923107	-1.175	-0.236	0.630	0.421	-0.653	1.568	-0.360	0.668	0.193	-0.093	-0.777	-0.986	1.221	1.260	-0.555	0.370
0.298979503	PANC 336 PLS1	10619796	8884929	-0.450	-0.405	-1.553	-0.406	1.086	1.103	-0.464	3.005	2.407	0.776	-1.599	1.162	-0.611	0.695	-0.543	2.452
0.809882501	PANC 336 PLS 2	8984725	6730121	-1.552	-0.945	-2.637	0.672	1.531	1.618	1.378	4.521	1.839	1.226	-1.514	1.715	-0.489	1.916	-0.399	2.543
0.283753932	PANC 339 PLS1	12400327	7375924	0.280	0.282	-0.614	0.699	-1.141	0.267	1.013	2.469	-0.096	-0.207	-1.413	1.106	-0.644	1.979	0.372	2.026
0.810018853	PANC 339 PLS 2	12299124	10509832	-1.045	-0.230	-1.859	0.408	0.819	1.345	2.014	3.534	2.472	0.131	-1.566	1.013	-1.574	2.600	-0.904	2.201
0.05095987	PANC 343 PLS 1	12271521	5419679	-1.258	1.692	0.009													

Table36.txt

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     0.494      -0.371     2.370      -0.389     0.366      0.784      0.311
-0.625     -0.525     -0.699     -0.047     -0.570     0.652
0.327383412     PANC 344 PLS1     13439600   6151985    -0.092     1.232
-1.010     0.242      0.047      1.608      -0.719     0.632      1.595      -1.652
    -0.707     1.555      -1.256     0.777      -1.704     2.179
0.123410597     PANC 345 PLS1     13303606   6545397    0.698      0.026      0.565
     1.013      -1.534     -0.523     0.106      1.037      0.774      0.629
-0.703     1.111      -0.744     0.213      -0.063     1.775
0.051901944     PANC 346 PLS1     12515948   5700068    -0.672     -0.466
-1.359     0.677      0.847      0.893      0.602      0.522      0.179      1.656
    -0.533     0.737      0.664      -0.742     -1.017     1.500
0.114260567     PANC 347 PLS1     11677261   6875071    -0.391     1.145
-1.132     0.969      0.590      0.392      -0.211     0.694      1.304      0.345
    -0.593     0.810      -1.061     0.455      -0.635     1.361
0.05638501      PANC 348 PLS1     11339306   5761965    -0.609     0.112
-0.678     1.538      -0.322     -0.145     -0.562     0.892      0.977      0.914
    -0.402     -0.492     -0.026     0.237      -0.791     0.151
0.286125528     PANC 349 PLS1     11950107   2218847    0.022      1.587
-0.940     1.745      -0.341     0.008      -0.070     -1.144     -1.255     0.746
    0.630      -1.589     -0.286     -0.521     -1.179     -0.260
0.060066773     PANC 350 PLS1     12193116   5317421    -1.055     -0.404
-1.499     1.126      -0.571     1.133      -0.687     1.681      0.947      1.846
    -0.798     1.504      0.294      0.120      -1.897     0.809
0.328013889     PANC 352 PLS1     11339490   4747816    1.239      0.384
-2.311     -0.106     0.112      1.111      -1.460     -1.037     -1.941     -0.150
    2.050      -0.252     0.039      0.191      -0.190     0.636
0.544246079     PANC 353 PLS1     10242753   7662894    -0.786     0.400
-2.165     0.354      0.709      0.482      1.400      1.862      1.898      -0.014
    -1.894     0.985      -1.135     1.620      -1.046     2.126
0.158182533     PANC 354 PLS1     13012628   2493447    -0.302     1.078      1.214
     1.620      1.079      0.123      -0.695     -0.234     -0.346     0.965
0.117      -1.279     1.101      0.148      -1.495     -0.179
0.063841717     PANC 355 PLS1     14095204   3569318    -1.850     0.320      0.908
     -0.469     -0.097     0.956      0.052      1.933      0.560      1.515
-0.621     0.855      0.143      0.624      -2.192     0.178
0.132741206     PANC 356 PLS1     13154516   2646677    0.100      1.530      1.840
     1.719      0.932      1.048      0.418      1.048      0.232      -0.423
-0.474     -0.008     -0.660     0.469      -1.144     0.592
0.153388823     PANC 357 PLS1     15262046   3900100    0.803      0.792      0.593
     1.187      -1.690     0.806      -0.521     0.441      0.694      0.081
0.225      0.757      0.776      1.584      -0.539     -0.251
0.108407402     PANC 358 PLS1     16427937   3809204    -0.391     0.016      0.660
     -0.475     1.329      1.573      -0.284     0.878      -1.062     0.855
-0.887     0.691      -0.651     -0.044     -1.312     1.726
0.411134368     PANC 359 PLS1     10013958   7442672    -0.308     0.177
-1.604     0.078      0.273      0.427      0.706      2.085      0.663      -1.089
    -2.108     0.737      -1.509     1.617      1.133      2.203
1               PANC 361 PLS1     12398338   10476736   0.043      -0.483
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Table36.txt

-0.957 0.696 -0.776 1.757 0.419 0.800 1.411 1.893
-0.758 0.402 -1.337 -2.317 -5.948 4.383
0.106340952 PANC 362 PLS1 11738580 7462756 -0.323 0.201
-1.870 1.641 0.596 0.498 0.625 1.457 0.382 -0.171
-0.969 0.109 -1.923 0.765 -2.322 0.457
0.185146645 PANC 363 PLS1 12657409 6352227 -1.962 0.390
-1.861 -0.115 1.675 0.973 0.110 0.744 0.106 0.219
-0.284 0.796 0.838 1.812 -0.631 1.177
0.188548086 PANC 364 PLS1 11510062 6908571 0.409 0.799 0.107
0.686 0.965 1.590 -0.836 0.915 0.923 1.305
-1.597 -0.210 0.372 -0.780 -1.483 0.755
0.018515887 PANC 372 PLS 13730168 3282207 -0.610 0.695 0.272
1.236 -0.274 0.309 0.198 0.286 0.043 0.379
1.293 1.298 -0.710 1.108 -0.749 0.250
0.74799686 PANC 373 PLS 12695361 11200161 -1.406 -0.777
-2.408 1.835 0.737 1.764 0.194 3.014 1.296 0.727
-1.543 1.055 -1.256 2.902 -0.563 1.144
0.483554685 PANC 375 PLS 17351456 4573490 -0.669 1.240 0.502
0.669 -0.867 2.081 -0.314 1.644 0.881 0.457
-1.413 1.677 0.484 1.441 -0.752 -0.853
0.74925863 PANC 376 PLS 10821066 8286794 -1.262 -1.598
-2.061 0.651 0.664 1.469 0.637 3.976 2.411 1.719
-2.693 1.583 -0.998 2.109 -0.384 2.213
0.398746709 PANC 377 PLS 9680570 1405404 -2.013 0.144
-2.337 -0.281 0.510 1.160 -0.008 1.924 -0.230 0.532
-0.851 1.796 0.195 2.174 -0.741 3.451
0.426631744 PANC 378 PLS 10372706 1856550 -0.215 1.963
-1.892 -0.142 0.899 0.428 -0.724 1.034 -1.638 0.133
1.447 -0.232 1.528 -1.348 -0.342 -0.187
0.774862503 PANC 381 PLS 11509298 8689140 -0.649 -0.190
-2.081 0.701 1.140 0.694 1.767 3.309 1.550 0.966
-1.019 1.198 -0.310 2.279 -1.474 1.826
0.468634731 PANC 382 PLS 10439613 8295404 -0.791 -2.203
-2.288 -0.207 0.737 0.612 1.094 2.233 1.037 -0.449
-1.865 0.585 -1.284 2.054 2.061 1.558
0.05065382 PANC 383 PLS 12638785 6719193 0.070 -0.326
-1.269 0.551 0.032 -0.247 -0.336 0.418 -0.602 -0.656
-1.063 0.258 -2.601 0.977 0.046 0.674
0.246533519 PANC 384 PLS 14532910 4785638 -1.187 0.446
-0.983 1.344 -0.180 1.082 -0.662 2.738 1.607 0.498
-0.494 2.188 0.018 1.244 -0.694 0.103
0.441394015 PANC 385 PLS 12060403 7228709 -0.433 -0.969
-0.724 0.429 0.609 1.313 0.435 2.203 2.482 0.770
-0.856 0.942 1.529 1.250 -0.268 1.356
0.198291071 PANC 386 PLS 15279460 4559445 -0.795 -0.102 0.464
1.072 -0.448 0.415 0.763 3.178 0.407 0.318
-2.177 1.165 1.242 0.889 -1.003 1.048
0.208224558 PANC 387 PLS 14272408 4037652 1.080 1.386 0.584

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     0.906      -1.316     1.204      -1.135     -0.588     -1.418     1.696
-0.696     -0.872     1.714      -0.289     -0.615     -1.260
0.636914621     PANC 388 PLS      11359427   6713267    -0.620     -1.240
-1.538     0.046      1.385      1.758      0.697      1.914      2.668      1.893
    -1.376     -0.362     1.385      2.912      -1.371     1.374
0.202274389     PANC 389 PLS      9582212    6906608    -0.158     1.463      0.175
     1.313      0.022      0.686      -1.315     -0.510     -1.355     -0.325
0.201      0.159      -0.716     -0.182     -0.515     1.356
0.053077914     PANC 390 PLS      10619957   5503001    -0.591     0.370
-1.826     -0.132     0.575      0.385      0.605      0.936      0.926      -0.210
    0.061      0.596      -1.289     2.442      0.031      0.097
0.573147622     PANC 391 PLS      13854519   7383890    -0.422     0.059
-2.915     0.373      1.350      0.658      1.532      1.672      0.043      1.230
    -0.737     0.457      -1.816     2.602      -1.270     0.917
0.011621108     PANC 392 PLS      13404691   3228266    -0.184     0.540
-1.136     1.138      0.351      0.800      0.866      -0.126     0.612      1.052
    -1.006     0.876      -0.268     0.231      0.531      1.021
0.294743649     PANC 393 PLS 1    14791953   3619871    -0.949     1.011
-0.668     -0.103     1.361      2.482      -1.292     -0.303     -0.549     1.580
    -0.653     -0.333     0.837      0.296      -1.812     1.706
0.041073949     PANC 394 PLS 1    13486093   7021339    0.397      0.202
-0.430     0.207      0.122      2.531      0.655      0.257      -0.317     0.838
    -0.448     -0.220     -0.313     -0.132     -0.491     1.096
0.089177044     PANC 395 PLS 1    11933935   5215342    -0.205     0.512
-0.403     1.015      1.189      -0.687     -1.075     -1.024     -0.313     0.527
    -0.590     -0.021     -0.604     0.007      -0.557     1.123
0.73577671      PANC 396 PLS 1    13948112   12227918   -1.216     -0.384
-2.282     0.424      1.760      1.190      1.613      3.013      1.215      0.562
    -1.914     1.375      -1.127     1.181      -0.537     2.333
0.198766537     PANC 397 PLS 1    13060322   8032079    -2.283     -0.302
-1.207     0.544      0.629      1.322      0.973      1.447      0.149      -0.268
    -0.860     0.059      0.747      1.204      -0.325     1.764
0.136168019     PANC 398 PLS 1    13710843   12249633   -0.227     0.203
-0.568     0.354      0.865      0.989      0.506      0.960      1.628      -1.325
    -0.959     0.673      -1.170     1.963      -0.856     1.116
0.312269302     PANC 399 PLS 1    14903105   13899626   -0.292     0.161
-0.919     0.535      0.743      0.848      0.497      1.185      0.213      -0.380
    -1.267     -0.142     -1.487     1.757      -0.644     1.805
0.154113741     PANC 400 PLS 1    12685885   6189324    0.208      -0.570
-1.608     0.599      1.964      -0.114     0.502      0.328      0.716      -0.056
    -1.944     -0.035     -2.449     1.370      -1.184     0.451
0.123989827     PANC 401 PLS 1    11302778   6696403    -0.793     -0.766
-1.479     1.035      0.595      1.037      0.061      0.895      0.264      0.220
    -0.860     0.470      -1.553     1.742      -1.109     0.920
0.100682064     PANC 402 PLS 1    10989985   6731366    -1.547     0.620
-1.937     0.594      0.562      0.372      0.833      1.651      1.227      0.051
    -1.322     1.314      -1.435     1.228      -0.860     -0.182
0.051766286     PANC 403 PLS 1    15685874   4694056    -0.486     1.274
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Table36.txt

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-0.951 0.198 1.029 0.083 0.535 -1.141 0.168 -0.227
0.188 0.818 -0.557 0.461 1.696 0.519
0.147852092 NL PLS 545 12887551 5714899 -0.044 -0.620
-0.714 0.670 -0.498 0.720 0.312 0.511 -0.226 -1.649
0.338 2.623 0.561 0.768 -1.778 1.778
0.018757669 NL PLS 546 11351570 6118316 -0.642 0.082
-1.188 -0.522 -0.041 -0.156 0.132 1.459 0.537 0.539
-0.678 1.849 1.154 0.032 0.527 0.913
0.45535146 NL PLS 547 12401409 4053750 -0.968 -1.354
-0.978 0.388 1.705 -0.712 -0.031 -2.139 -0.077 0.010
0.431 -1.697 0.459 -0.518 2.585 -0.211
0.023219086 NL PLS 548 13967540 3385827 -0.125 1.042
-0.992 -1.001 -0.709 -0.137 0.894 0.427 1.059 0.437
-1.438 0.700 0.817 2.289 -1.094 0.661
0.496680087 NL PLS 549 13264202 3428496 -0.508 -1.399 0.710
-1.897 1.899 -0.119 2.302 2.860 0.634 -1.369
-0.607 0.539 0.069 -0.883 0.276 0.036
0.282862385 NL PLS 550 14458820 3716033 1.447 -1.950 0.079
1.662 1.476 0.572 0.793 2.003 0.784 0.335
-0.073 -0.383 -1.976 -1.025 0.364 -0.158
0.260130347 NL PLS 551 12864558 4396354 0.008 0.916 1.369
2.806 0.394 0.374 1.439 -0.241 -0.939 -0.671
0.169 0.885 -0.585 1.227 -0.797 0.901
0.326683805 NL PLS 552 12162136 3427274 -1.601 -1.880
-0.881 1.365 -1.546 1.239 0.013 0.138 -0.705 1.842
0.070 1.542 -0.328 2.255 -0.320 0.541
0.030371753 NL PLS 553 14369316 3859596 0.165 0.048 0.388
0.444 -0.429 0.740 -0.841 1.479 -2.368 -1.382
-0.789 0.281 0.039 0.495 -0.306 0.066
0.067158231 NL PLS 554 10814249 4490637 -0.144 1.628 0.559
1.944 -0.656 1.231 0.700 0.310 -0.724 0.041
0.533 0.115 1.001 1.601 -1.446 0.211
0.161898662 NL PLS 555 13307620 4338696 0.632 1.954 1.335
-1.398 -0.413 1.311 -0.864 -0.385 -0.876 0.927
-0.127 1.246 -0.117 0.614 -2.172 -0.216
0.022181013 NL PLS 556 13378304 4803328 0.606 0.592
-0.394 0.582 -0.438 0.499 -1.187 -0.441 0.416 1.847
-0.101 0.105 -1.438 -0.219 -0.298 0.100
0.135811991 NL PLS 557 15575536 3662849 0.326 0.516
-1.928 -0.956 -2.116 0.696 0.162 -0.728 -0.888 0.342
-0.202 -0.115 0.545 1.381 -1.183 1.151
0.108849552 NL PLS 558 14146590 3139357 0.446 -0.417
-0.457 1.127 -0.731 1.018 0.598 1.919 1.738 0.160
-0.477 0.958 -0.558 0.651 -1.197 0.984
0.199455234 NL PLS 559 12810242 2922903 1.790 0.054
-0.019 0.637 -0.645 1.209 0.557 -1.657 -1.260 -0.075
0.945 -0.823 -0.671 -0.294 1.545 -0.269
0.009274582 NL PLS 560 12983447 2741480 0.055 -0.418 0.356

Table36.txt

-0.988 -0.214 0.454 0.227 -0.855 -0.062 0.737
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0.277 0.779 -0.479 0.094 0.516 1.631
0.005382929 NL PLS 562 13340725 2856418 1.005 -0.559
-0.051 -0.069 0.072 -0.401 -0.257 0.555 0.683 0.528
-1.112 -0.037 0.435 -0.261 0.512 -0.859
0.296917503 NL PLS 563 13709293 4971436 0.392 2.356
-0.822 0.941 -1.229 0.342 0.538 0.847 -0.531 -1.129
-0.616 1.600 1.439 1.387 -0.612 0.877
0.15854789 NL PLS 564 14432547 7327456 0.661 -0.157
-0.822 -0.311 -0.276 1.429 1.628 1.413 0.766 1.196
-1.690 0.774 -0.644 2.615 -0.562 0.177
0.346722903 NL PLS 565 15709280 3054026 -0.248 0.923 0.637
-0.943 0.907 -0.917 -0.328 -1.942 -1.760 0.760
0.638 2.730 -0.786 0.757 -0.985 -0.544
0.327165449 NL PLS 566 11959538 3960043 0.283 -0.763
-1.118 -0.630 -0.576 0.779 1.338 0.636 -0.429 -1.288
-0.572 0.441 0.530 -0.265 0.952 2.759
0.411175922 NL PLS 567 13011656 2800985 0.632 -0.711
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-1.434 1.370 -1.425 1.637 0.840 0.830
0.306350252 NL PLS 568 15176450 2742651 -0.346 -0.810
-1.995 0.945 0.278 -2.553 1.249 -0.955 -1.464 0.645
-0.789 0.770 0.356 -0.297 1.904 0.952
0.45554818 NL PLS 569 14985820 2431298 0.415 -0.686 0.448
0.986 1.115 1.874 0.502 2.355 -1.334 2.667
-0.550 1.887 -0.357 0.723 -0.223 1.736
0.023520445 NL PLS 570 13451463 5819420 -1.181 0.089 0.586
1.328 0.050 0.415 0.391 0.532 -0.779 0.386
-1.454 -0.606 -0.461 -0.406 1.142 0.824
0.372568956 NL PLS 571 13379329 4406416 0.963 0.673
-0.706 2.550 0.793 0.788 -0.058 -1.937 -1.230 0.364
1.347 -0.408 -1.589 -0.915 -1.374 0.624
0.043549645 NL PLS 572 13510902 4855900 0.405 0.809 0.643
-1.199 1.426 -0.049 -1.062 -0.081 0.017 0.198
2.121 0.274 0.622 -0.980 -0.330 1.586
0.407108227 NL PLS 573 15147907 3748744 0.018 -1.799
-0.982 -0.555 1.644 -1.255 0.886 1.869 1.531 0.442
1.006 0.039 0.530 0.696 2.326 -0.740
0.046367192 NL PLS 574 11004177 5116353 -0.542 -0.473
-1.326 -0.068 -0.937 -0.221 1.682 2.081 1.156 1.624
-0.317 0.670 0.448 0.873 -0.591 0.568
0.10224961 NL PLS 575 13342371 1787128 -0.565 -1.018
-0.755 -1.415 -0.940 -0.182 1.771 1.219 0.107 0.924
-0.333 0.344 0.960 0.472 0.596 -1.317
0.069412385 NL PLS 576 13529982 3221789 -0.446 -0.568

Table36.txt

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-1.030 1.363 -0.424 0.928 0.136 -0.098
0.036587563 NL PLS 578 14098414 2220482 -1.466 -0.321 1.264
-0.795 -0.996 -1.278 -0.617 1.926 -0.491 1.098
0.645 0.313 0.797 1.298 -0.408 0.592
0.43905817 NL PLS 579 14091078 2696476 0.353 3.329 0.589
1.468 0.134 1.847 -0.641 -1.517 -2.422 -0.256
1.119 0.720 0.244 -2.366 -0.802 0.530
0.2833817 NL PLS 580 14943359 4062625 -0.124 0.042 0.452
1.029 0.920 -0.975 -0.623 -2.477 -1.718 -0.769
0.377 -0.956 -0.798 -1.178 0.447 0.834
0.063252699 NL PLS 581 15215007 3965029 0.012 -0.582
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-0.102 0.112 0.335 0.714 -0.147 -1.410
0.077034936 NL PLS 582 13807424 5431338 -0.086 1.090
-0.970 -0.346 -0.719 0.268 0.529 1.016 -0.423 -0.531
0.594 1.118 -0.121 1.224 -0.911 -0.376
0.037762537 NL PLS 583 15421384 3842764 0.409 0.425
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1.352 -0.230 0.714 -0.507 -0.642 -0.890
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0.274 -0.446 -1.511 -0.089 1.507 1.002
0.16268351 NL PLS 585 13615593 2536656 0.726 0.619 1.301
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0.256 -1.272 0.162 -0.370 0.425 0.010
0.072512427 NL PLS 586 11053523 5323230 -0.615 -0.780
-0.092 -0.198 2.436 0.088 0.573 -1.011 -0.109 -0.248
-1.407 -1.381 -0.976 0.665 1.091 -0.701
0.035696078 NL PLS 587 14512109 2791030 0.165 0.126
-0.070 0.982 -0.539 0.705 -0.351 -1.221 -1.393 0.331
0.569 -0.324 -0.513 0.514 0.559 2.394
0.306805695 NL PLS 588 13625663 5688761 0.265 -1.613
-1.160 0.768 -1.110 -0.201 -1.440 -0.635 -1.108 2.461
-0.040 0.338 -1.731 0.364 1.028 1.139
0.04107827 NL PLS 589 17529296 3396426 -0.300 -0.845
-0.208 0.594 -0.098 1.049 0.110 0.601 2.457 0.739
-1.005 -0.159 0.610 -0.593 -0.403 -0.187
0.438484239 NL PLS 590 15142512 3324125 -0.526 0.339
-0.502 0.085 0.280 0.045 -1.548 0.837 0.290 0.791
0.082 1.207 0.518 0.133 -2.254 1.304
0.239249473 NL PLS 591 14493351 3485797 0.740 0.457
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0.316 -0.836 -0.718 1.131 0.810 0.324
0.117874168 NL PLS 592 14636889 2115726 2.462 1.952

Table36.txt

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-0.611 -0.382 -1.202 -0.767 -0.845 -0.058 0.338
-0.749 -0.809 -0.570 1.092 0.165 -0.236
0.052940954 NL PLS 594 13106976 4140158 0.730 1.039 0.807
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0.249 0.294 0.145 -0.635 -0.829 -0.386
0.05402336 NL PLS 595 18313045 4489158 -1.198 0.577 0.186
1.026 -0.722 -1.417 0.067 -0.413 -1.585 0.506
0.245 1.065 -1.318 0.101 1.654 -0.077
0.047071825 NL PLS 596 2490814 256586 0.616 0.096 1.601
0.233 -0.599 -2.552 0.271 0.015 -0.833 -0.645
0.052 1.342 0.085 -0.613 1.299 0.737
0.072987365 NL PLS 597 14554619 3395853 0.602 0.099 0.692
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0.254839558 NL PLS 598 14932304 3423438 1.414 1.560
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-0.321 2.168 -0.012 1.217 -0.694 1.222
0.109986644 NL PLS 599 13746961 4649900 -2.078 -0.168
-0.434 -0.025 0.840 1.251 0.267 1.578 1.445 1.220
-0.050 1.259 -0.655 0.637 0.356 -1.324
0.532223227 NL PLS 600 14524297 1856933 0.463 -1.268 1.204
0.048 1.254 -0.179 0.469 1.267 0.695 -0.983
-0.955 -0.797 0.808 -0.396 1.642 -0.165
0.233786103 NL PLS 601 14141447 2925654 -0.025 1.757 0.509
1.225 -0.436 0.959 -0.459 -0.208 -0.579 0.817
-0.166 0.516 0.742 0.558 -1.811 -0.019
0.350998896 NL PLS 602 14586518 3616018 0.145 0.999 0.189
1.664 0.016 1.669 -0.620 2.271 1.615 -1.528
-0.864 1.498 -2.049 1.140 -0.335 1.361
0.03433866 NL PLS 603 15116942 3129128 -1.066 -0.713
-1.199 0.676 -0.398 -0.231 -0.030 0.301 1.099 -0.231
-2.104 0.014 -0.661 0.066 0.973 -0.623
0.348879003 NL PLS 604 13475602 3514562 0.245 -1.483
-0.177 -0.275 1.271 0.014 -0.095 -1.039 -0.553 0.912
1.434 -1.704 0.840 0.987 2.361 0.058
0.443573226 NL PLS 605 16631952 3082923 2.346 0.429
-0.562 1.313 -0.271 -0.707 -1.108 -2.849 -1.960 -0.453
2.362 0.877 1.748 -0.087 0.395 -1.108
0.249882372 NL PLS 606 15630521 2862293 -2.196 -1.644
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0.627 1.583 -0.851 -1.145 0.413 0.596
0.032910798 NL PLS 607 14666200 5984316 -1.306 -0.994
-1.526 0.694 -1.346 -0.368 0.059 1.547 1.106 -0.783
-0.418 1.671 -0.331 1.056 0.747 1.256
0.039506253 NL PLS 608 13305656 9123492 -0.457 -0.516

Table36.txt

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0.42770281 NL PLS 609 12559246 3601334 0.141 1.668 0.606
1.560 0.294 0.932 -1.042 -2.070 -2.352 0.687
2.345 -2.306 0.349 0.126 -0.685 -0.104
0.137315366 NL PLS 610 17372470 3562385 -0.626 -0.448
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-0.268 0.779 -0.285 0.998 -0.013 -0.365
0.634549683 NL PLS 611 12648406 4375248 -1.200 -0.184
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-0.416 1.214 -0.432 0.629 -1.848 -1.010
0.095030004 NL PLS 612 13388841 3955227 -1.501 0.217
-0.575 -0.145 -0.371 0.034 -0.965 -1.301 -0.842 0.043
0.234 1.498 1.611 -1.333 0.227 -0.128
0.034409326 NL PLS 831 14067407 2721504 0.075 -0.011 0.296
0.177 0.195 0.706 -1.200 0.309 -0.322 1.599
-0.376 -0.587 0.936 0.002 -0.161 0.680
0.215262681 NL PLS 832 16493319 8703338 1.204 2.325 0.943
0.360 -0.381 0.661 -0.114 -0.225 -0.858 -2.108
1.550 -0.077 -0.018 -1.133 -1.532 -0.297
0.062313654 NL PLS 833 11123480 1203597 -1.532 0.861
-0.234 -0.883 -0.494 1.863 0.161 0.240 0.980 1.852
-1.503 -0.278 -0.589 0.711 1.083 0.641
0.010805897 NL PLS 834 17774564 4309640 -1.159 0.173
-1.297 0.261 0.349 0.815 0.742 0.845 1.378 -0.023
-0.095 0.581 0.323 0.252 0.003 0.683
0.093480255 NL PLS 835 16754991 3424311 -0.391 -1.728 0.711
0.068 0.404 0.793 -0.103 -0.128 -0.535 0.736
-0.575 0.615 -0.153 2.135 -0.436 1.895
0.038871587 NL PLS 836 14581125 2462680 -0.263 0.263
-0.869 -1.043 0.329 -0.173 -0.208 -0.375 -0.443 0.207
0.912 -0.282 -0.571 -0.059 0.632 1.476
0.252537887 NL PLS 837 14727139 2162374 -0.148 1.746 0.990
1.689 0.798 1.866 -1.970 -1.018 -1.698 0.461
1.231 0.875 -0.296 0.407 0.865 -2.421
0.017729152 NL PLS 838 15490993 2524081 -0.729 -0.469 0.778
1.303 -0.883 0.324 -0.112 0.402 0.146 0.055
-1.022 -1.216 0.944 0.606 0.749 0.648
0.01210002 NL PLS 839 15293754 2442317 -0.905 1.023
-0.217 0.383 0.158 -1.056 0.731 0.254 -0.495 0.488
0.020 0.918 1.039 0.657 -1.135 0.047
0.075030482 NL PLS 840 13728196 2354006 -1.887 0.041 0.639
0.143 1.127 1.473 0.415 0.747 0.228 0.206
0.032 0.814 -0.349 -0.326 -0.293 0.950
0.10376592 PANC 425 PLS 14233718 4799314 0.281 1.483
-0.406 -0.414 -0.291 1.536 -0.425 -1.235 -0.338 0.194
0.143 0.590 0.887 0.897 -2.552 -0.264
0.282639733 PANC 426 PLS 14540885 6728010 -0.637 -0.939

Table36.txt

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0.780 1.437 0.000 0.227 -0.800 1.424
0.800734708 PANC 428 PLS 13946071 10633096 -1.061 -1.575
-3.775 0.391 0.798 1.362 0.691 3.244 2.477 1.830
-2.403 1.308 -0.259 2.200 -0.063 2.211
0.780756186 PANC 429 PLS 14081502 3595246 -1.365 0.060 0.818
-1.020 1.242 2.331 -2.578 -2.717 2.123 4.340
-0.542 -0.501 1.911 2.979 -0.815 1.844
0.138887913 PANC 430 PLS 14796757 4963308 -0.333 0.598
-1.556 0.206 -1.666 0.658 -0.567 1.487 -0.194 2.058
-1.493 2.022 0.146 -0.074 -1.528 1.291
0.102792146 PANC 431 PLS 15899425 3820726 -0.180 0.216 1.096
-0.142 0.557 1.166 -1.229 0.372 -1.589 0.216
-0.344 -1.272 1.131 1.116 -0.132 1.439
0.313660461 PANC 432 PLS 16054763 4298820 0.076 0.752 0.003
0.512 -0.253 0.696 -0.061 0.699 -1.085 2.807
-0.490 0.451 -0.705 1.386 -0.023 1.601
0.051976898 PANC 433 PLS 14728601 6848218 -0.976 1.142
-1.274 0.478 -0.822 1.014 0.158 1.147 0.422 0.827
-0.473 1.234 0.695 0.027 -2.272 1.130
0.109015251 PANC 434 PLS 15296768 3660429 0.133 -0.160
-0.201 0.784 0.334 0.954 0.112 -0.191 0.080 0.966
0.368 -0.439 -0.719 -0.359 0.177 0.453
0.394466054 PANC 435 PLS 15094402 3864712 -0.680 -0.515
-2.136 -0.742 0.437 1.569 -0.222 2.041 0.961 3.552
-1.754 0.233 -0.763 1.272 -0.849 0.460
0.187798615 PANC 436 PLS 13882118 7796196 -0.513 -1.186
-2.673 1.027 -0.712 0.280 -0.738 1.362 0.711 1.040
-0.834 0.434 -0.213 0.247 0.160 1.118
0.701635452 PANC 437 PLS 15661106 3281014 -1.969 -0.962 0.589
0.114 -0.842 0.347 -0.503 2.141 0.567 3.750
-1.559 1.237 -0.470 -0.443 -0.360 2.324
0.258380575 PANC 438 PLS 15494440 6741941 -1.351 0.723
-0.308 -0.008 -0.339 1.258 -0.483 2.762 0.755 2.464
0.794 2.151 -1.015 0.820 -1.607 0.624
0.226588527 PANC 439 PLS 16337694 4486715 1.533 1.862 0.009
-1.002 0.359 -0.914 -0.159 0.200 0.293 0.563
-0.894 -0.709 1.055 0.147 -1.299 1.254
0.328530693 PANC 440 PLS 15816023 8044434 -1.189 -0.035
-1.211 1.542 0.549 1.054 -0.021 2.389 0.630 1.150
-0.932 1.584 0.707 1.848 -1.879 1.824
0.367792915 PANC 441 PLS 14472858 5199311 -0.264 0.487
-1.083 -0.226 -0.587 1.476 1.389 2.096 0.308 1.598
-0.916 0.539 0.558 0.911 -0.004 2.096
0.276181104 PANC 442 PLS 16103203 5128135 -1.671 0.277

Table36.txt

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0.858 -1.132 1.049 0.165 -1.091 1.031
0.531597153 PANC 444 PLS 14635373 6950060 -0.943 0.447
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-1.881 -1.007 0.774 2.324 -0.431 2.258
0.379943392 PANC 445 PLS 14382524 6184039 -0.713 -0.360 0.794
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-1.312 -0.859 -1.163 -0.658 -0.091 1.959
0.110760931 PANC 446 PLS 14176902 11717079 -0.817 0.253
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-1.454 1.146 -1.342 1.576 0.844 1.996
0.485834911 PANC 447 PLS 14806404 4701816 -1.254 0.085 0.749
0.549 -1.025 2.723 0.828 0.810 0.106 2.893
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0.707398621 PANC 448 PLS 15005800 9083574 -2.009 -0.371
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-1.246 1.507 0.179 2.356 -1.912 1.586
0.674832945 PANC 449 PLS 11887421 9035018 -2.181 -0.357
-1.289 0.879 1.842 1.153 1.340 3.560 2.287 0.618
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Table36.txt

| | | |

Table36.txt

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Table36.txt

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0.466584843 NL PLS 559 15454025 3401914 2.155 -1.640
-0.544 1.664 -0.468 1.492 -0.156 -1.878 -1.767 0.580
0.726 -0.810 -0.760 -0.244 0.107 0.429
0.310435954 NL PLS 560 14960586 2994435 1.519 -1.444
-0.599 0.386 0.797 0.649 -0.532 -2.368 -0.783 -1.622
-0.273 -0.954 0.031 0.084 0.727 2.066
0.455377387 NL PLS 561 13695540 3687602 -0.102 0.809
-0.279 -2.326 2.041 -0.657 -0.923 3.787 1.541 -1.325
0.602 0.977 0.021 0.912 0.346 1.251
0.021872398 NL PLS 562 13797933 4061484 0.589 0.219 0.078
0.090 0.796 -1.377 0.237 -0.625 1.492 0.539
0.410 -1.247 -0.299 -0.226 0.151 -0.520
0.016107395 NL PLS 563 14003820 5269169 0.152 0.313
-0.204 -0.795 0.266 0.389 0.831 0.661 -1.511 0.667
0.499 0.227 0.058 1.468 -0.482 0.300
0.039758875 NL PLS 564 13923647 7587652 0.020 -0.944
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-0.346 1.057 -0.452 1.313 -0.901 0.423
0.107032466 NL PLS 565 15203181 3350989 -0.243 1.420
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0.361 -0.396 -0.149 0.602 -0.525 -1.447
0.583404106 NL PLS 566 14092202 4278811 0.154 -0.190
-1.062 0.564 1.042 -0.300 2.098 1.528 -0.462 -1.796
0.252 -0.731 -1.212 -0.698 1.034 2.207
0.378163064 NL PLS 567 15238284 3081890 0.270 -0.043
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-1.298 0.848 -0.647 0.724 -0.191 1.928
0.465237552 NL PLS 568 14898105 3042188 0.347 0.086
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0.247 -1.192 0.731 0.521 0.962 0.815
0.47267622 NL PLS 569 13588216 2863048 0.334 0.095 0.585
0.544 1.537 0.708 -0.340 1.651 -0.753 2.872
0.257 2.377 0.031 0.839 -0.330 1.063
0.381287646 NL PLS 570 12944297 5877867 -0.609 -1.738
-0.601 -0.261 1.698 -1.401 0.701 2.642 1.688 0.284
-1.440 1.135 -1.072 -0.756 0.511 0.321
0.460894661 NL PLS 571 14213177 4680882 2.011 0.131 1.378
0.835 0.154 -0.397 -0.846 -1.158 -1.925 -0.145
1.321 -0.900 0.025 -2.403 0.564 -0.572
0.191389414 NL PLS 572 15253938 5464748 -0.428 -0.432 1.440
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0.009 0.608 0.855 -0.794 -0.179 2.219
0.325819228 NL PLS 573 14477352 4018470 1.258 -1.722
-0.579 -0.579 0.783 -1.192 0.657 1.160 0.321 0.485
0.302 1.327 0.383 -0.197 2.212 -0.574
0.016674416 NL PLS 574 13029827 5488700 0.024 1.022

Table36.txt

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-0.897 0.090 -0.930 0.720 0.685 0.469
0.060920722 NL PLS 578 12700615 2397485 -1.259 0.757 1.112
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1.415 -0.848 0.486 0.343 1.556 0.451
0.507942188 NL PLS 579 12976746 2741338 0.917 2.736 0.048
-0.169 0.685 0.898 -2.114 -1.185 -2.290 0.072
2.128 -1.077 0.817 -1.294 1.448 2.141
0.202321276 NL PLS 580 14371656 4396736 -0.824 1.413 1.329
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-0.989 1.078 0.150 -0.258 -1.990 -1.009
0.019728573 NL PLS 581 15672750 4236994 -0.159 0.528 1.176
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1.269 1.533 -0.930 -1.032 -0.357 -0.947
0.073925183 NL PLS 582 13828100 5735560 -0.118 0.569
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0.081571689 NL PLS 584 16147120 4943800 -0.036 -0.321 1.198
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-0.071 0.039 -0.118 0.572 2.070 0.269
0.151567785 NL PLS 585 12983369 2741422 2.108 -0.616
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1.463 -1.061 -0.763 -0.521 0.722 0.414
0.230002822 NL PLS 586 12733998 5828006 0.003 1.270 0.128
0.871 1.081 0.293 -0.028 -1.474 0.266 0.759
-1.380 -0.272 -1.864 0.725 -1.337 0.554
0.289740088 NL PLS 587 13420225 2782821 0.022 0.454 0.302
1.482 -0.732 0.042 -2.230 -3.543 -1.580 1.175
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0.035625547 NL PLS 588 15447060 6189455 -0.339 -1.361 0.770
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0.107 0.940 -1.108 -0.654 0.103 0.649
0.215247531 NL PLS 589 15061414 3418232 1.748 0.330
-0.001 -0.704 1.291 0.681 1.730 2.356 2.136 -0.511
-0.830 0.431 -0.387 -1.945 -1.277 -0.332
0.149187631 NL PLS 590 13851942 3397062 0.349 -0.670

Table36.txt

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2.053 0.736 -0.140 0.888 -0.607 1.038
0.091402692 NL PLS 593 12377359 2127958 1.203 0.382
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0.045377758 NL PLS 594 14767607 4661880 -1.162 0.061 1.172
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0.065012441 NL PLS 595 14506822 4477388 -0.627 0.657 0.015
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0.059519271 NL PLS 597 15715817 3794755 -0.525 0.137
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0.512303075 NL PLS 598 14888438 3695653 1.057 1.254 0.422
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2.324 -1.504 0.305 -0.643 -1.614 0.287
0.38281749 NL PLS 602 8010959 1218669 -0.600 1.075 1.717
2.585 0.200 -0.080 -0.173 0.404 -0.403 -1.203
1.661 1.206 0.603 0.083 1.236 -0.418
0.307439305 NL PLS 603 13440125 3141129 -1.388 -0.946 0.513
-0.975 0.136 -1.014 0.032 0.889 1.094 -0.488
0.682 -1.025 0.514 -0.593 2.237 0.818
0.227350222 NL PLS 604 15301668 3830270 0.110 -0.430 1.068
-0.449 0.642 -0.061 0.763 -0.294 -1.265 1.199
1.284 -0.620 0.877 0.466 1.560 1.892
0.609204036 NL PLS 605 16498634 3272385 3.581 0.513 0.371
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1.755 -0.548 -0.568 -1.110 1.147 -0.411
0.254504961 NL PLS 606 14893520 3010875 -1.974 -2.260 0.608
0.469 -0.679 0.068 1.127 1.532 2.052 0.138
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0.025324333 NL PLS 607 14849290 6344638 -1.036 -0.976

Table36.txt

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0.099774665 NL PLS 608 15163733 10277368 -0.278 0.431
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0.781602238 NL PLS 611 15662031 4985636 -0.739 -2.719
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-1.698 1.753 -0.403 0.847 0.581 -1.236
0.020752595 NL PLS 831 14188681 3019977 0.216 1.540 1.188
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0.036140869 NL PLS 833 11848740 1360837 0.081 0.376 0.812
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0.030346584 NL PLS 834 17772132 4714518 -1.359 0.445 0.113
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0.125246369 NL PLS 836 12372558 2723878 0.767 1.541
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0.456 0.054 -0.134 1.193 -1.161 0.260
0.106008994 NL PLS 837 12815327 2758077 -2.033 0.915
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1.250 1.473 0.151 -0.830 -0.574 -1.177
0.078438296 NL PLS 838 12935938 2702292 -0.648 1.167 1.284
0.517 0.681 0.012 1.700 1.047 0.586 -1.306
-1.016 -0.729 1.288 -0.978 -0.225 0.092
0.010389248 NL PLS 839 14132300 2694168 -0.309 0.904 0.137
0.974 -0.407 1.551 0.793 -0.705 -0.529 -0.919
0.046 2.388 1.580 -0.551 0.153 -0.409
0.094153066 NL PLS 840 13520897 2606121 -0.447 0.893 0.227
1.206 -0.886 0.997 1.378 -1.152 -0.112 0.355
0.877 0.683 -0.976 -0.497 0.178 1.499
0.03343698 NL PLS 841 13406234 8480055 1.078 1.232 0.981
0.227 0.237 0.441 0.442 0.386 -0.201 0.156
-0.765 -0.258 -0.240 -0.046 -0.317 0.607
0.033513687 NL PLS 842 15877217 4122477 -0.955 0.760 0.439
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0.542786523 NL PLS 843 14153713 7890199 0.506 1.008

Table36.txt

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0.097262841 NL PLS 844 12532120 2585857 -0.241 1.883 1.191 0.250 -1.049 0.635 -0.464 -1.632 -1.898 0.777 0.266 -0.249 -0.001 -0.233 -0.264 0.123
0.022445309 NL PLS 845 13692032 1926071 0.452 0.505 1.391 0.957 0.673 0.671 -0.468 -0.863 0.806 1.143 0.023 -1.585 0.236 -0.456 -1.438 -0.879
0.295670773 NL PLS 846 11778456 1278020 -0.116 1.942 0.612 3.062 -0.164 -0.193 -1.649 -0.893 -0.909 1.839 -0.299 -2.049 -0.281 0.805 -0.634 -0.037
0.206353077 NL PLS 847 13055814 1999823 0.376 2.174 0.804 0.289 -1.113 1.255 -0.478 -2.039 -1.864 0.386 1.094 -1.157 0.107 -1.715 -1.069 0.089
0.119416533 NL PLS 848 14630937 3385034 -0.276 0.037 0.519 0.884 -0.763 1.194 0.184 -0.502 -1.505 1.272 1.310 -0.543 -0.344 -0.453 0.041 0.086
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0.304336768 NL PLS 850 14198889 2521525 -2.172 -0.171 1.638 -0.075 -0.903 0.388 0.784 1.202 0.333 1.455 -0.723 2.055 0.197 0.330 -1.221 -0.625
0.049429441 NL PLS 851 13014502 2520764 0.931 -0.978 1.306 -0.073 0.339 0.530 -0.495 -0.271 -1.183 1.130 -0.280 -1.620 -0.731 1.550 0.009 0.073
0.002758076 NL PLS 852 12970505 2478607 -1.176 -0.279 -0.957 -0.017 0.710 0.015 0.024 0.428 0.475 1.291 -0.781 0.960 0.243 0.049 0.410 -1.090
0.066622958 NL PLS 853 12146690 2406813 0.263 1.470 1.812 -0.894 1.404 0.521 -0.119 -1.552 -1.016 -0.720 2.460 -0.588 -0.873 -0.272 -0.052 0.605
0.119612219 NL PLS 854 13974691 1661646 1.149 1.316 1.021 -1.341 -1.803 0.462 0.365 -0.734 -0.606 0.064 -0.662 1.378 0.765 1.042 -0.789 -0.212
0.044176341 NL PLS 855 13717642 2418560 0.535 0.687 0.665 0.412 -1.349 1.223 -0.261 0.067 0.371 -0.316 -0.156 0.906 0.226 0.320 -0.555 1.415
0.078774177 NL PLS 856 13252963 2016720 -1.431 -0.338 1.386 0.786 -0.450 1.682 1.536 -1.396 -0.479 -0.024 -0.887 0.711 0.435 -0.839 1.469 0.441
0.701289918 PANC 682 PLS 2 13360681 9649368 -1.793 -1.085 -1.425 0.001 0.169 0.097 1.145 4.032 1.815 1.546 -2.006 2.624 -0.419 1.006 0.144 1.924
0.463115824 PANC 682 PLS 3 13845585 9781491 0.008 -1.561 -1.819 0.154 0.162 0.642 1.880 3.438 1.868 0.672 -2.350 2.487 -0.148 1.089 0.692 1.517
0.154949043 PANC 707 PLS 2 15101625 10626246 -0.702 -1.241

Table36.txt

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0.105856968 PANC 750 PLS 2 14781179 10972024 -1.875 -0.830
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0.030576925 PANC 945 PLS 1 14023466 4151647 -1.302 0.734 0.304
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1 PANC 946 PLS 1 17168483 7618860 -11.000 11.000
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-1.978 -2.551 -0.677 -11.000 3.830 11.000
0.200310126 PANC 947 PLS 1 13871960 4653199 0.143 2.060
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-0.382 0.780 0.453 -0.165 -0.060 1.561
0.109669403 PANC 948 PLS 1 13131541 3496870 0.330 -0.670
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0.417938493 PANC 949 PLS 1 13762492 1891063 1.472 0.890 1.085
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0.140067911 PANC 950 PLS 1 13962838 2550726 -0.312 -1.148
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0.359976529 PANC 951 PLS 1 14276264 3792191 -1.279 1.284
-0.649 -0.098 -0.765 2.524 -0.146 2.424 -0.365 1.197
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0.747459995 PANC 952 PLS 1 13245799 6844815 -0.953 -0.676
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0.499590853 PANC 953 PLS 1 13964772 8407433 -0.311 -1.310
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-1.225 0.790 0.809 0.964 -0.533 1.349
0.291862553 PANC 954 PLS 1 13393749 2159268 -0.282 -0.169
-0.644 0.032 -1.525 1.185 -0.704 2.510 0.227 2.226
-1.952 2.833 0.155 1.251 -0.163 0.923
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0.160566836 PANC 956 PLS 1 12970698 6100208 -0.580 -0.605
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-1.611 1.660 -2.255 1.059 0.710 1.781
0.093870108 PANC 957 PLS 1 13160403 2667270 0.035 1.344 0.322
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-0.547 0.043 0.058 -0.507 0.962 -1.592
0.081678803 PANC 961 PLS 1 12676785 2727283 -1.214 -0.239

Table36.txt

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0.106713782 PANC 968 PLS 1 14275993 6701890 -1.492 -0.109
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0.845 -0.039 0.077 0.564 0.018 1.033
0.020561131 PANC 970 PLS 1 14145852 8976982 -0.940 1.140 0.783
-0.786 -0.596 1.144 0.132 1.493 0.960 -0.185
-0.268 -1.382 -0.175 -0.495 0.176 -0.085
0.801148887 PANC 971 PLS 1 13081025 4931530 0.687 0.990
-0.197 -0.696 0.369 1.230 -1.746 -5.543 -2.361 2.175
-1.478 -1.849 1.015 0.987 -0.145 0.763
0.100529325 PANC 972 PLS 1 12599400 2797086 -0.057 0.193 0.661
0.835 0.726 1.493 -0.620 1.451 0.307 -0.013
-0.590 0.680 0.412 0.313 0.367 -0.732
0.652066284 PANCA 1010 PLS 1 12872930 3989197 2.142 2.076 0.399
0.532 -0.100 0.028 -2.094 -1.378 -1.237 -0.131
1.442 -0.719 0.088 -0.783 -0.297 -0.623
0.326721858 PANCA 1011 PLS 1 14820190 7984038 -0.303 0.178
-0.351 -1.095 -0.105 1.686 0.569 3.095 0.978 2.245
0.019 0.370 -0.961 -0.456 0.003 2.173
0.028907658 PANCA 1012 PLS 1 14389852 3704890 -0.602 0.913
-0.234 1.034 0.641 1.278 -0.245 2.044 0.586 -0.007
-1.802 2.293 0.275 0.755 -0.511 -0.022
0.376520587 PANCA 1013 PLS 1 13265144 6854390 1.019 1.712 0.243
0.333 -0.575 2.156 -0.748 1.105 -0.321 0.514
-0.347 -0.362 0.001 -0.337 -0.283 0.692
0.688426305 PANCA 1014 PLS 1 12873594 9415214 -1.262 -0.017

Table36.txt

-0.873 0.301 -1.356 0.743 0.605 2.665 0.253 2.550
-1.219 1.102 -0.947 1.427 0.672 1.644
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0.198950893 PANCA 1018 PLS 1 14636297 7549389 -1.634 -0.977
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-1.061 1.805 -0.162 0.853 0.472 1.105
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0.387 -0.769 0.290 -0.426 0.251 -0.120 2.067
-1.200 2.219 -0.758 0.049 -0.385 0.394
0.035175281 PANCA 1020 PLS 1 13669106 8431143 -0.604 -1.257
-1.242 0.326 -0.308 0.055 0.312 1.016 1.060 -0.035
-1.333 2.436 -1.747 -0.013 0.465 1.224
0.133918944 PANCA 1021 PLS 1 14712271 11359679 0.124 0.100
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-2.095 1.626 -1.350 0.834 0.741 1.900
0.126076818 PANCA 1022 PLS 1 12849071 9012996 0.257 -0.587
-2.138 0.618 -0.077 0.321 1.301 2.587 0.887 1.542
-2.003 0.829 -0.616 1.701 0.225 1.007
0.058817443 PANCA 1023 PLS 1 12339235 4646068 -1.002 -0.382
-1.110 0.418 0.798 0.058 -0.082 1.129 1.645 -0.522
-1.564 1.769 -0.198 0.207 0.836 1.879
0.0269054 PANCA 1024 PLS 1 14348328 3530496 -0.415 0.182
-1.332 0.059 -0.979 1.255 0.786 0.947 1.662 0.341
0.065 0.350 0.228 0.042 -0.707 0.112
0.203109076 PANCA 1025 PLS 1 13647225 6010627 -1.693 -0.143
-0.853 -0.429 0.420 1.534 3.375 0.843 1.708 1.575
-1.292 0.209 -0.783 -0.526 -0.563 1.195
0.081554091 PANCA 1028 PLS 1 13488172 4883260 -1.399 2.059
-0.306 -0.627 -0.204 0.445 -0.151 -0.155 -0.130 1.752
-0.847 1.487 -0.218 0.399 -0.323 0.398
0.202366661 PANCA 1029 PLS 1 14507697 10297552 -0.708 0.999
-1.892 0.062 -0.080 -0.642 1.057 2.465 1.330 -0.207
-1.705 1.170 -0.063 0.354 -0.678 2.417
0.063068916 PANCA 1030 PLS 1 12014622 7159663 -0.291 0.096
-2.440 -0.092 -0.824 0.517 -0.247 2.038 0.706 -0.044
-1.570 0.901 -0.777 1.558 0.548 1.441
0.033842916 PANCA 1031 PLS 1 13657349 4050374 -0.404 1.056 0.503
0.189 -0.632 0.443 0.455 1.231 1.250 0.555
-0.787 0.730 0.287 0.024 0.602 0.373
0.011610706 PANCA 1032 PLS 1 13056300 5606912 -0.119 -0.544
-0.496 0.692 -0.397 -0.137 0.252 1.264 1.111 0.420
-1.853 0.383 -0.209 0.993 2.004 0.881
0.335894872 PANCA 1033 PLS 1 12985876 2912012 -0.515 0.578 1.426

Table36.txt

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    -1.681     0.955      -0.460     0.192      0.189      0.885
0.009045053     PANCA 1035 PLS 1  13212651   5770487    -0.875     -0.097
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    -0.953     2.176      -0.679     -0.496     -0.362     0.815
0.312900169     PANCA 1036 PLS 1  15425315   3626880    1.022      2.029      0.501
     1.625      0.047      1.206      -1.739     -1.538     -1.016     1.410
-0.933     0.786      -0.365     -0.579     -1.462     -0.537
0.398794681     PANCA 1037 PLS 1  14590244   12207809   -1.120     -0.839
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    -1.976     2.317      -1.496     1.879      0.851      1.032
0.041160429     PANCA 1039 PLS 1  12841252   7065382    0.384      1.064
-0.847     0.692      0.439      0.829      -0.347     -0.285     -0.604     -1.342
    1.121      0.771      0.115      -0.889     -0.142     1.500
0.143968407     PANCA 1040 PLS 1  14642142   7819264    0.544      0.133
-0.509     0.166      0.215      0.913      -0.374     0.753      -0.343     -1.539
    0.399      -0.440     0.265      -0.271     -1.913     0.813
0.344195059     PANCA 1041 PLS 1  13862913   1436924    0.603      1.446      1.398
     0.548      -0.991     2.181      0.514      -0.492     -2.227     0.223
1.741      0.172      -0.533     -1.184     1.725      0.561
0.298812536     PANCA 1042 PLS 1  11949445   6256880    -0.563     0.105
-1.995     0.666      -0.438     -0.670     -0.215     2.807      1.207      1.587
    -1.759     2.771      -1.221     1.279      0.866      0.962
0.008063059     PANCA 1043 PLS 1  13290219   3466480    -0.074     -0.849
-0.411     0.266      0.154      1.555      -0.453     0.309      -0.213     0.530
    -0.828     0.707      0.702      0.509      -0.221     0.861
0.23198133      PANCA 1044 PLS 1  14316550   6400753    -0.855     -0.115
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    -1.682     1.397      0.082      1.204      0.143      1.607
0.049290263     PANCA 1045 PLS 1  15269267   11129632   0.779      0.431
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    -0.927     0.550      -0.360     -0.095     -0.379     1.551
0.459684798     PANCA 1047 PLS 1  13961156   3456796    -1.209     0.839      0.253
     0.809      0.444      2.379      -1.257     1.475      0.064      2.052
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0.800853822     PANCA 1048 PLS 1  12960246   11774769   -0.423     -0.604
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    -2.765     1.315      -1.321     3.193      0.016      3.297
0.573593031     PANCA 1050 PLS 1  13407191   10117516   -1.575     -0.508
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    -1.648     1.529      -1.463     2.914      0.188      1.022
0.435975738     PANCA 1051 PLS 1  13073229   9370638    -0.935     -1.250
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    -2.599     1.760      -1.159     2.491      0.012      1.563
0.29384739      PANCA 1052 PLS 1  13982505   5405952    0.623      0.553      0.811
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Table36.txt

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-1.408 -0.515 0.844 0.674 1.092 4.164 3.474 -0.060
-2.297 2.764 0.513 0.875 -0.969 0.491
0.271578926 PANCA 1054 PLS 1 13990220 9859994 -1.401 -1.689
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-0.670 0.870 -0.782 0.076 -0.693 1.582
0.103562274 PANCA 1055 PLS 1 14381404 2890865 0.468 2.177
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-0.324 0.104 0.499 -0.173 -1.474 -0.237
0.068067733 PANCA 1056 PLS 1 13009272 6950252 -0.818 0.504 0.122
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-1.022 0.959 0.469 1.295 -0.780 1.226
0.522093708 PANCA 1057 PLS 1 13587592 3486960 1.525 1.687
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0.190927235 PANCA 1059 PLS 1 13691704 4247203 1.926 1.860
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0.465 -1.846 -0.550 0.350 -1.043 0.158
0.226757477 PANCA 1060 PLS 1 11923321 8355033 -1.373 0.558
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0.062077113 PANCA 1061 PLS 1 21008377 12459236 -0.552 -1.023
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-1.220 1.255 0.428 -0.574 0.556 2.357
0.070542096 PANCA 1062 PLS 1 15502467 4480094 -2.039 1.110
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-0.643 1.031 -0.160 0.453 -0.346 1.231
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-1.269 -0.101 -1.050 1.591 -0.149 0.068 0.303 1.742
0.033 0.913 0.598 0.576 -1.772 0.420
0.187070281 PANCA 1064 PLS 1 13727718 9583409 0.247 -0.022
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0.487347185 PANCA 1065 PLS 1 13606426 4072916 0.811 2.683 0.050
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1.465 -0.196 0.208 -0.060 -0.792 1.482
0.649744875 PANCA 1067 PLS 1 14711550 10628980 -1.632 -1.190
-1.409 -0.598 -0.645 -0.527 1.570 3.700 2.279 1.943
-1.294 0.671 -0.469 0.666 0.924 1.166
0.061155023 INDI 001 PLS 1 4239292 2269425 -0.020 0.174
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-0.919 1.130 -0.551 1.737 0.046 0.714
0.015837031 INDI 002 PLS 1 3439098 1348486 -0.596 0.242

Table36.txt

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0.040406828     INDI 003 PLS 1    3195961    1960909    -0.552     0.094
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    -1.819     0.168      -0.038     -0.206     0.773      0.895
0.24186071      INDI 004 PLS 1    3558812    2130912    -0.810     0.613
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    -0.435     1.040      -0.102     1.161      2.399      1.346
0.468626309     INDI 005 PLS 1    3940680    2430314    1.211      2.805
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    1.573      -1.096     -1.728     -1.380     0.516      0.725
0.749196544     INDI 006 PLS 1    4211859    2374559    1.293      2.306      1.931
     1.554      3.429      -0.654     -0.138     -2.141     6.371      -1.883
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0.015157346     INDI 007 PLS 1    3644084    2334145    -0.054     0.892
-0.679     0.371      0.996      0.198      0.873      0.691      0.146      -0.136
    0.574      -0.927     0.501      0.710      0.258      0.530
0.396856041     INDI 008 PLS 1    3820097    2243413    0.690      2.378      0.728
     -0.414     -1.371     2.771      -0.439     -2.886     -1.182     0.971
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1               INDI 009 PLS 1    4548035    2357898    -0.155     11.000
-1.231     -0.308     -0.073     3.095      -0.977     -0.692     0.042      1.137
    1.405      -1.014     -0.751     -11.000    -0.578     2.022
0.186951108     INDI 010 PLS 1    3952634    2480467    -0.479     0.939
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    -0.171     0.712      -2.033     0.736      0.099      1.687
0.114455541     INDI 011 PLS 1    3450322    1857802    -0.779     1.200
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    0.561      0.867      -0.098     -0.679     1.778      -0.375
0.237511132     INDI 012 PLS 1    3506091    2154946    -2.348     -0.170
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    -0.904     -1.211     -0.330     1.215      1.357      1.227
0.095539063     INDI 013 PLS 1    3786054    2416561    -0.071     0.971      0.023
     0.592      1.643      1.211      -0.981     0.210      0.016      -0.281
0.774      -0.882     1.568      -0.001     0.182      0.948
0.512844034     INDI 014 PLS 1    3962457    2005500    -1.321     0.409
-1.277     -1.006     0.508      0.505      0.409      2.538      2.808      -1.647
    -0.692     -1.027     -0.488     -0.042     1.479      2.488
0.36315633      INDI 015 PLS 1    4088148    2453117    -1.682     -0.027
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    0.758      -0.575     -1.040     1.627      2.076      1.911
0.059838795     INDI 016 PLS 1    4318653    2461509    0.786      1.632
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    1.161      -0.731     0.635      -0.009     1.218      1.119
0.44474974      INDI 017 PLS 1    4135965    2199189    -1.541     0.074
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    -0.484     -0.554     1.499      1.795      0.075      2.171
0.294188633     INDI 018 PLS 1    3925080    2130340    -0.012     1.641      1.560
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Table36.txt

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-1.447 1.080 -1.301 1.363 1.671 1.616
0.509296753 INDI 020 PLS 1 3874713 2246638 1.431 2.093
-1.103 -1.330 -0.283 2.005 -0.708 -2.708 -1.556 1.591
1.753 -2.643 1.084 1.420 0.386 -0.363
1 INDI 021 PLS 1 3728502 2311488 -1.197 -0.607 2.897
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3.141 -3.229 0.827 -0.685 -1.752 11.000
0.701683948 INDI 022 PLS 1 4402900 2098545 0.143 1.286
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2.062 1.089 -0.037 0.800 -1.964 3.380
0.542685428 INDI 023 PLS 1 4067797 2443513 -1.267 -0.293
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-0.358 0.032 0.852 1.664 -0.009 1.191
0.278333179 INDI 024 PLS 1 4644818 2278599 -0.339 -0.413
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-0.959 1.887 -1.055 1.538 0.017 0.941
0.119825277 INDI 025 PLS 1 4499917 1863327 -1.170 0.443
-0.424 0.657 1.115 1.114 0.292 2.255 1.733 0.572
-1.423 0.434 -1.788 1.631 -0.439 1.309
0.01958615 INDI 026 PLS 1 4395374 2301520 0.557 0.539 0.762
-0.351 0.011 1.277 -1.118 0.665 -0.574 -0.237
-0.200 -0.248 -0.819 0.801 1.622 0.619
0.042124006 INDI 220 PLS 1 4723473 3165355 1.727 1.791
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-0.672 -0.133 -0.813 0.217 0.064 0.399
0.397815173 INDI 224 PLS 1 4516898 3517667 -0.288 0.313
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-1.538 1.175 0.031 1.282 0.051 2.830
0.046500166 INDI 227 PLS 1 4059504 1772099 0.212 0.638 0.790
-0.975 -0.082 0.812 -1.210 0.668 0.375 -0.842
-1.313 -0.275 -2.182 0.561 -0.067 0.662
1 INDI 231 PLS 1 3897450 2489922 -4.201 4.577 1.034
0.226 -4.994 0.904 0.540 2.834 1.481 -0.906
1.458 -5.117 -1.865 -1.251 0.490 11.000
0.054270857 INDI 235 PLS 1 4053066 1989843 0.721 0.492
-0.433 0.326 2.163 1.344 -0.458 -0.604 -0.988 1.586
0.263 0.137 0.236 0.969 0.547 0.845
0.257357276 INDI 239 PLS 1 4710813 2174418 -1.155 -0.575
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-2.744 0.487 -0.838 2.203 -0.709 0.935
0.233167584 INDI 242 PLS 1 4048526 2219124 -1.451 0.950
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0.168315475 INDI 246 PLS 1 4007747 1335098 -2.868 -0.991

Table36.txt

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0.194857092 INDI 252 PLS 1 4585125 3246089 0.259 0.998
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-0.723 -0.708 -0.272 1.767 0.419 1.670
0.017496606 INDI 257 PLS 1 3496702 2312579 -0.181 -0.016
-1.796 1.110 -0.248 -0.658 0.608 1.192 1.517 0.605
-1.454 0.697 -1.778 1.029 0.562 0.980
0.119370727 INDI 264 PLS 1 4667468 2110263 1.102 0.306 1.103
0.151 0.403 0.237 -0.669 -0.268 -1.096 -0.394
1.597 -2.071 0.352 0.604 -0.140 0.318
0.258238552 INDI 266 PLS 1 3877609 2885455 -0.832 -0.041
-1.504 0.160 0.917 0.426 1.814 1.345 1.862 -0.354
-1.112 1.293 -1.277 0.018 2.905 0.647
0.150517716 INDI 269 PLS 1 4645885 3149760 -0.705 1.271
-0.895 -0.554 -0.248 2.128 0.042 1.685 0.061 -0.460
-1.288 0.591 -0.693 1.345 1.191 1.438
0.050086216 INDI 273 PLS 1 4102411 2385984 -0.211 -0.853
-0.072 0.189 -1.001 0.318 0.210 1.468 1.755 0.999
-1.104 1.044 -0.903 0.370 0.412 1.618
0.045231782 INDI 283 PLS 1 4392096 2622367 -1.152 -0.867
-0.236 -1.028 -0.222 0.048 -0.774 1.019 0.798 0.124
-1.028 0.470 0.841 0.514 -0.767 1.461
0.239608214 INDI 285 PLS 1 4561436 2351559 -1.368 2.088
-0.500 -0.530 0.952 1.186 -0.401 0.594 0.916 0.193
0.476 0.049 0.162 -0.429 -0.592 0.951
1 INDI 288 PLS 1 3864195 2156269 -3.035 3.461 4.654
-1.836 0.011 8.041 1.874 -5.368 2.625 -2.097
3.385 -0.278 1.326 5.421 -1.728 3.265
0.291627423 INDI 291 PLS 1 3393058 2186404 -1.262 -0.178
-0.726 1.544 0.946 -0.603 0.728 2.652 1.117 -0.039
-1.902 0.562 -2.449 1.371 1.600 0.892
0.046105834 INDI 292 PLS 1 3860849 2509536 -1.000 1.703 0.154
1.530 0.633 -0.524 0.892 1.457 0.343 -0.825
-0.020 0.973 -1.982 1.978 -0.241 -0.011
0.107423292 INDI 324 PLS 1 4217320 1691537 -0.029 -0.339
-0.749 0.467 0.948 0.895 0.613 2.387 2.354 0.700
-1.935 1.195 -2.126 1.511 1.373 0.869
0.024308975 INDI 326 PLS 1 3882123 1858041 0.972 1.129 0.267
0.496 1.127 1.274 -1.267 0.195 0.945 -0.333
0.809 -0.836 -1.471 0.359 -0.200 0.296
0.095247124 INDI 413 PLS 1 4243741 2872949 -1.307 0.385
-1.012 -0.203 1.673 0.909 -0.044 0.135 1.790 0.541
-1.191 2.011 -1.120 1.309 0.873 -0.366
0.029616101 INDI 414 PLS 1 2018897 1173965 0.215 1.583

Table36.txt

-0.918 -0.314 -0.345 0.185 0.070 -0.379 0.024 -0.683
2.075 -1.497 1.423 1.310 -0.365 -0.399
0.034252068 INDI 415 PLS 1 2064062 1371213 -0.584 0.961
-0.570 -1.139 -0.252 -0.233 0.172 -0.533 2.527 0.377
-0.584 0.947 -0.503 0.395 0.114 1.613
0.382444724 INDI 417 PLS 1 2601552 1851698 2.007 1.879
-0.517 1.056 0.094 0.308 -1.204 -1.508 -1.628 -1.733
2.261 -1.554 -0.060 -0.589 0.993 1.364
0.344808784 INDI 491 PLS 1 2262430 1573018 1.587 2.764 0.476
0.407 -0.276 -0.555 -0.589 -1.871 -1.372 0.561
1.172 -0.417 -1.432 -0.327 0.135 1.057
0.128675529 INDI 492 PLS 1 2556742 1549150 1.350 -0.279
-0.283 2.299 -0.312 0.856 0.188 -1.210 -0.693 -0.208
1.053 -0.030 -0.175 -0.951 -0.376 1.086
0.210553685 INDI 494 PLS 1 2619838 1698679 -0.457 1.075
-1.096 -1.017 0.433 0.495 0.236 1.239 -1.267 1.399
-1.074 -0.173 0.249 -0.745 0.880 2.234
0.025599273 INDI 495 PLS 1 3499299 2276748 0.125 1.362
-0.364 0.505 2.126 1.110 0.201 -0.236 -0.445 0.259
0.035 0.294 -0.611 1.223 0.286 0.329
0.096008202 INDI 496 PLS 1 3869861 2344569 1.405 2.522
-0.788 -0.369 1.170 0.984 -0.471 -0.861 -0.819 -0.764
-0.942 0.136 -1.207 -0.645 0.306 0.736
0.075398083 INDI 497 PLS 1 3478246 2076278 -1.432 1.002 0.091
0.439 2.144 0.918 0.616 1.061 1.253 0.099
0.219 0.277 0.340 1.287 0.759 0.142
0.055907236 INDI 499 PLS 1 3966299 2705486 0.009 0.226
-0.511 -0.899 0.221 -0.036 -0.218 0.870 0.040 -0.905
0.628 -0.756 0.219 0.480 1.810 0.637
0.14349173 INDI 503 PLS 1 3749427 2205595 0.469 0.647
-0.860 -1.377 0.882 1.221 -1.006 0.836 0.733 0.399
-0.307 0.818 -1.064 -0.012 0.049 2.320
0.075424002 INDI 505 PLS 1 4423287 3247075 -0.171 1.381
-1.669 1.204 0.799 1.101 0.749 -0.791 -0.839 -0.271
-0.706 0.526 0.313 0.120 -0.682 0.305
0.300092625 INDI 507 PLS 1 2723221 1148382 -2.094 0.372
-1.336 0.569 1.041 -0.164 0.923 2.565 2.316 1.633
-0.877 0.316 -0.125 0.277 0.247 2.446
0.050970783 INDI 513 PLS 1 4202908 2685614 -0.124 1.382
-0.250 0.262 0.391 0.663 0.055 0.610 -0.331 0.495
-0.750 1.297 0.258 1.256 -0.036 1.811
0.133748255 INDI 519 PLS 1 3791256 2484855 -0.357 0.206
-2.144 0.331 0.130 -0.731 0.667 2.151 1.080 -0.944
-0.740 0.415 -1.090 0.259 -0.252 0.755
0.017435909 NL PLS 841 4307106 1706418 0.071 0.514 0.419
0.571 0.372 -0.420 2.076 0.000 1.397 -0.335
-0.724 1.860 -0.147 1.114 -0.141 0.985
0.193856199 NL PLS 842 4137097 1552423 0.392 0.437 0.503

Table36.txt

-1.773 -1.250 0.266 -0.440 0.197 0.520 -0.935
-0.169 1.752 0.817 2.414 1.415 0.499
0.767713011 INDI 077 PLS 1 13558220 9618158 -1.492 1.436 0.726
-0.180 0.076 1.930 0.249 0.998 2.486 2.955
-0.518 -0.994 1.629 2.419 -0.753 2.847
0.176894485 INDI 078 PLS 1 10824849 7613209 -0.261 0.708
-0.286 -0.074 0.265 0.473 0.931 1.907 1.796 0.941
-0.661 0.131 1.090 2.118 -1.408 1.719
0.569409694 INDI 079 PLS 1 11822086 8973463 -0.079 -0.253
-1.510 0.262 -0.193 0.964 0.599 1.965 1.510 1.314
-1.182 0.706 0.624 2.155 -1.415 2.804
0.089952818 INDI 080 PLS 1 9963344 4878506 0.226 -1.283 0.395
-0.549 -0.796 0.131 0.240 1.598 0.422 0.306
-0.785 -0.055 -1.052 1.562 0.765 2.557
0.581690552 INDI 081 PLS 1 10881072 7943446 -1.479 -0.500
-0.385 -0.856 -0.713 -0.382 0.819 1.251 0.928 2.078
-0.493 -1.036 1.351 2.019 0.637 0.827
0.61022706 INDI 129 PLS 1 13561324 10975347 -1.118 0.601
-0.136 0.414 -0.370 1.595 0.067 3.479 0.913 1.566
-2.351 -0.029 -0.410 3.661 0.199 1.617
0.595795358 INDI 147 PLS 1 13436722 11389092 -1.859 -1.050
-1.737 0.402 1.666 0.784 1.213 2.671 3.210 0.065
-1.559 0.773 -1.641 0.225 1.970 1.024
0.422033864 INDI 149 PLS 1 11191494 9197061 -1.546 -1.180
-1.262 -0.034 0.638 -0.880 1.485 2.779 2.612 0.246
-0.407 1.392 -0.188 0.327 0.913 0.941
0.735942997 INDI 151 PLS 1 16279540 10562917 -1.744 -1.560
-1.543 0.595 -0.865 0.143 0.682 3.191 2.273 1.222
-2.116 2.248 -0.484 1.655 0.203 2.006
0.603717745 INDI 153 PLS 1 13130455 8901352 -1.690 -0.410
-1.453 -0.704 1.087 0.394 1.509 1.660 2.581 1.298
-2.086 0.787 -0.506 0.952 0.931 1.788
1 INDI 166 PLS 1 11899593 10256264 -0.004 1.783 1.588
2.262 -4.628 -3.897 -4.529 -11.000 1.899 -1.821
3.636 4.794 11.000 5.922 -11.000 11.000
0.674727068 INDI 167 PLS 1 12626115 9486203 -2.852 -0.816
-1.387 -0.145 0.766 0.646 1.450 2.367 1.651 1.608
-1.765 0.985 -1.589 1.929 1.502 2.053
0.377360978 INDI 168 PLS 1 9595428 6811739 -1.018 0.073
-1.116 0.518 1.258 0.042 0.710 1.884 0.784 0.387
-0.374 -0.137 -0.764 0.648 0.504 1.370
0.251303846 INDI 171 PLS 1 8894013 7704112 -1.457 0.275
-0.144 1.446 -1.155 0.200 0.639 0.993 1.767 -1.184
1.055 0.466 0.811 0.187 1.971 -0.951
0.650760929 INDI 172 PLS 1 9287021 8033551 -0.850 0.248
-0.216 0.291 0.711 1.836 0.799 3.330 1.849 0.444
-0.625 -0.091 -0.910 2.854 -0.602 2.010
0.28505319 INDI 173 PLS 1 9469686 6362292 -1.382 -0.215

Table36.txt

-0.734 0.445 0.501 0.844 0.799 2.566 0.966 0.219
-1.142 1.267 -2.058 0.658 0.466 1.700
0.647230553 INDI 176 PLS 1 14185849 11021628 -1.091 -0.860
-0.524 0.512 0.723 1.646 0.682 3.771 1.627 0.879
-0.745 1.900 -1.954 1.332 1.812 1.757
0.760044195 INDI 177 PLS 1 12191480 10481645 -0.406 0.514
-0.583 0.474 -0.209 2.254 0.675 3.207 1.533 2.009
-1.030 0.595 -1.730 2.547 -2.302 1.604
0.372375447 INDI 182 PLS 1 12488059 10448879 0.484 0.048 0.841
1.170 0.446 2.160 -0.431 1.199 1.522 1.456
-0.573 1.216 0.197 2.028 -2.494 1.231
0.190458012 INDI 190 PLS 1 10799035 9151462 -1.549 0.560
-0.095 0.857 -1.013 0.611 0.367 1.533 2.268 0.190
-0.049 0.796 -0.164 1.232 0.043 0.456
0.596569682 INDI 205 PLS 1 11731765 10277322 -0.895 0.739 0.296
1.508 0.076 2.013 -0.790 2.381 1.219 1.130
-1.810 0.703 -0.452 2.705 -1.016 2.320
1 INDI 208 PLS 1 11501022 9836789 -1.363 0.925
-0.265 0.638 -0.372 1.768 -0.600 1.660 1.578 2.237
-1.042 0.908 -0.626 1.789 -2.540 11.000
0.294986581 INDI 214 PLS 1 10225900 7132998 -1.927 -0.188
-0.472 0.002 0.843 1.211 0.145 2.143 1.979 0.694
-0.234 -0.264 0.966 1.961 -1.232 1.424
0.74407556 INDI 215 PLS 1 11300817 9240368 -1.833 -0.122
-3.038 0.175 -0.296 1.075 0.201 4.832 0.042 0.943
-1.776 1.547 -1.736 2.527 0.471 1.545
0.792164461 INDI 219 PLS 1 12507304 10447515 -1.938 0.534
-3.698 0.245 -0.144 0.950 1.588 3.770 1.134 1.495
-1.424 0.512 -0.723 3.038 -0.011 2.023
0.116650086 INDI 238 PLS 1 12560965 7192232 -0.111 0.719
-1.099 -0.635 0.262 0.107 0.570 1.425 1.274 0.266
-2.296 1.955 -0.153 1.169 0.586 2.352
0.807058572 INDI 249 PLS 1 9271391 4579910 -1.453 -0.391
-0.101 -1.442 1.857 -0.611 2.155 3.880 3.277 -0.059
-2.073 -0.836 -0.692 -0.531 1.958 0.930
1 INDI 272 PLS 1 13644810 8686978 -5.637 11.000 0.442
1.736 -5.289 0.821 0.846 1.943 0.827 2.872
-0.760 -4.612 0.869 2.619 -2.314 4.634
0.146790422 INDI 295 PLS 1 11047240 4176451 1.206 0.835 1.930
-0.076 0.162 1.087 -2.593 0.295 -1.201 -0.784
0.177 0.285 0.579 -0.006 -0.659 2.392
0.307018455 INDI 296 PLS 1 11084090 5296994 -0.545 0.251 0.011
-0.186 1.430 0.404 -0.889 2.983 0.566 1.080
-0.697 0.044 0.299 0.568 -0.687 1.585
0.114424752 INDI 298 PLS 1 11152352 6168638 0.625 1.708 0.889
1.029 1.300 0.914 -0.646 -1.214 -1.938 0.155
0.391 -1.233 0.448 -0.055 -1.327 0.920
0.82892208 INDI 299 PLS 1 12325235 7767342 -2.260 -1.092 0.663

Table36.txt

-0.163 1.429 0.171 1.482 3.026 2.107 1.717
-0.801 1.663 0.987 2.720 -1.338 2.400
0.099776151 INDI 302 PLS 1 11451092 4790046 -0.815 0.330 0.394
0.205 1.281 0.706 1.168 0.291 0.930 1.366
-0.221 -0.473 -0.473 1.119 -0.384 0.812
0.104622728 INDI 303 PLS 1 9920101 5440637 -0.273 -0.260
-0.935 -0.098 0.681 0.220 0.509 1.857 1.644 -0.623
-2.515 -0.943 0.560 0.492 0.029 -0.021
0.815343044 INDI 304 PLS 1 11459565 8889152 -2.069 -0.702
-1.441 0.070 1.319 0.147 1.656 4.831 3.348 0.343
-2.162 1.779 -1.700 0.856 1.471 1.466
1 INDI 305 PLS 1 11553691 9290762 -5.368 2.222
-0.510 0.691 -4.489 -3.213 -0.542 -2.291 2.168 -5.500
11.000 0.184 3.081 6.061 -0.548 5.361
1 INDI 306 PLS 1 9616486 5885640 -3.834 5.173 1.876
2.775 3.622 11.000 4.043 -4.428 -11.000 -11.000
-2.666 -3.192 11.000 11.000 -11.000 11.000
0.497036333 INDI 307 PLS 1 9965219 7300474 -0.516 0.508
-0.306 -0.262 0.479 0.268 0.823 2.829 1.170 -0.205
-0.546 1.068 0.740 1.792 -0.873 1.479
0.624771696 INDI 308 PLS 1 11678686 10463043 -1.746 -0.612
-1.087 0.752 1.582 1.367 0.848 3.718 2.038 0.111
-0.368 1.428 -2.327 1.334 0.669 1.502
0.670106076 INDI 309 PLS 1 10106373 8630974 -1.721 -0.990
-2.080 0.814 1.394 0.341 1.234 3.753 2.823 -0.235
-1.315 1.613 -2.207 0.108 1.569 1.760
0.802883318 INDI 310 PLS 1 9445336 8271533 -1.777 -0.645
-1.284 0.150 2.076 0.945 1.732 4.970 2.196 -0.141
-2.265 1.745 -2.362 1.486 0.956 0.989
0.726549715 INDI 311 PLS 1 12370291 9640398 -1.683 -0.448
-1.747 0.351 1.596 0.956 1.066 3.886 1.944 0.806
-1.939 1.015 -1.557 1.778 0.548 1.974
0.763734297 INDI 314 PLS 1 9183557 4919781 -1.314 -1.626
-0.464 0.425 0.549 0.192 2.129 4.514 2.660 0.658
-3.145 0.902 -1.499 1.205 0.562 0.779
1 INDI 341 PLS 1 9220020 5230571 -11.000 11.000 2.530
1.920 1.105 1.402 1.332 -4.496 1.372 0.163
0.516 -4.825 7.509 1.696 -4.015 11.000
0.138998128 INDI 367 PLS 1 15389926 7585945 0.363 0.835
-0.986 1.476 0.894 0.707 -0.590 -1.131 -0.058 0.166
-0.005 0.312 1.149 1.731 -1.665 0.543
0.133223759 INDI 375 PLS 1 10224055 3134877 -0.956 1.186
-0.363 -0.857 -1.403 -0.004 -0.368 1.162 -0.285 -0.017
-0.742 1.373 -1.034 1.235 -0.552 1.947
0.068676171 INDI 387 PLS 1 9839158 3890818 -0.546 1.918 0.378
0.360 -1.569 0.424 0.365 -0.553 -0.909 0.965
0.265 -0.165 0.053 0.322 -1.089 1.280
1 INDI 391 PLS 1 13016876 6949109 3.445 11.000 2.437

Table36.txt

1.524 -3.222 6.389 3.893 -11.000 2.542 0.429
2.686 -6.839 3.792 5.151 -1.835 -0.491
1 INDI 393 PLS 1 9746262 5451665 -1.535 4.946
-2.612 -1.596 4.723 5.666 11.000 -0.763 -0.217
-11.000 3.673 5.681 -1.641 -0.996 -5.080 11.000
0.872171276 INDI 401 PLS 1 10884434 6953341 -3.538 3.645
-1.191 0.727 -1.403 0.799 1.312 2.694 0.792 1.994
0.864 -3.968 1.403 2.999 -1.530 1.541
0.684035415 INDI 406 PLS 1 9835781 6224340 -1.868 2.240
-0.846 -1.597 0.446 0.802 1.197 1.229 2.935 0.201
-2.158 0.307 -0.111 1.601 1.126 2.671
0.420150373 INDI 418 PLS 1 12769843 6691227 -0.805 0.501
-0.273 -0.363 0.563 -0.095 0.458 3.603 -0.155 1.196
-0.438 0.537 -0.140 1.378 0.177 1.322
0.442215244 INDI 419 PLS 1 10506814 7944912 -0.812 -0.193
-0.946 -0.186 0.847 0.005 0.918 1.850 2.332 -0.923
-0.785 0.433 -1.249 1.255 0.005 1.926
0.842801982 INDI 420 PLS 1 9433762 3975949 -1.642 0.539 0.360
0.379 1.155 0.759 2.320 2.875 1.590 -11.000
-0.133 1.948 -1.238 -4.471 4.555 7.595
0.098201091 INDI 421 PLS 1 11073793 5795564 0.130 -0.382
-0.528 0.705 0.306 0.345 1.144 1.468 1.581 1.639
-0.376 1.156 -0.325 1.464 -0.346 1.153
0.476962142 INDI 422 PLS 1 12581568 5782029 -1.353 0.488
-1.260 0.651 0.355 0.710 1.486 3.817 1.142 1.908
-1.463 1.520 -0.931 0.930 0.176 0.482
0.337612669 INDI 423 PLS 1 11559563 6086842 -1.027 0.116
-0.896 0.334 0.160 0.664 1.120 1.390 1.934 1.905
-2.171 1.064 -1.548 2.306 1.026 1.237
0.429972657 INDI 427 PLS 1 14762669 7243717 -0.511 -0.101
-1.339 0.136 -0.003 0.326 0.778 2.713 0.632 2.057
-3.599 2.235 -0.380 1.531 0.558 1.165
0.130205635 INDI 428 PLS 1 11941804 6244785 -1.259 -0.892
-0.296 0.118 -0.038 0.776 0.203 2.878 0.753 -0.569
-1.835 2.338 -1.161 0.420 1.684 1.844
0.623796536 INDI 429 PLS 1 11599869 7782190 -1.392 -0.074
-1.407 -0.346 -0.074 -0.121 0.443 3.686 3.089 1.882
-1.964 1.280 -0.940 2.124 -0.593 1.023
0.228981225 INDI 430 PLS 1 11571251 6131157 -0.409 0.499
-1.623 0.551 -0.185 -0.111 0.366 3.322 1.906 0.410
-0.765 0.899 -1.233 0.653 0.462 1.623
0.660282795 INDI 431 PLS 1 9792673 3935403 -2.304 1.032
-1.177 -0.480 0.641 -0.121 0.688 3.237 2.656 1.267
-1.166 1.922 -0.550 0.149 1.506 1.896
0.335071877 INDI 432 PLS 1 11234321 9004101 -0.997 -0.267
-2.898 -0.015 0.109 0.079 1.174 2.714 1.678 -0.613
-2.790 0.572 -0.856 1.470 1.432 1.391
0.263379573 INDI 433 PLS 1 15201015 12243096 -0.865 -0.029

Table36.txt

-2.065 -0.453 0.180 -0.466 1.227 1.529 2.244 0.685
-2.586 0.836 -2.263 1.071 0.959 1.900
0.077801885 INDI 434 PLS 1 10487689 3628223 -0.683 0.293 0.887
0.895 1.010 0.577 0.891 0.391 0.386 1.219
-0.345 -0.925 0.311 0.793 -0.840 1.717
0.168782229 INDI 435 PLS 1 12425905 7663554 -0.332 0.789
-0.966 0.687 -0.925 0.620 -0.272 -0.358 1.076 1.202
-1.662 1.062 -0.318 2.266 0.573 0.259
0.565281656 INDI 436 PLS 1 13233874 7064094 -1.114 0.187
-0.343 -0.321 -0.620 0.085 0.921 3.312 1.057 2.823
-1.902 0.368 -0.928 2.165 0.056 0.622
0.257160484 INDI 437 PLS 1 12676573 9541503 0.607 -0.311
-1.893 -0.003 0.511 0.073 1.764 1.540 1.895 -0.595
-1.077 0.464 -0.778 1.773 0.793 1.519
0.478472849 INDI 438 PLS 1 10746778 6861608 -1.799 -0.686
-1.089 -0.289 0.066 -0.552 0.330 2.854 1.863 0.388
-1.084 2.148 -0.707 1.489 0.332 2.258
0.341843513 INDI 439 PLS 1 9720829 6255536 -0.576 -0.451
-0.634 -0.447 1.146 0.609 2.194 2.708 2.824 -0.251
-1.702 0.889 -1.501 1.258 0.755 1.798
0.59798683 INDI 441 PLS 1 12413927 9276429 -1.899 -0.269
-1.449 -0.317 1.501 0.331 0.664 2.253 1.852 1.134
-1.353 0.573 -2.213 1.207 1.581 1.061
0.717896159 INDI 444 PLS 1 11231691 10108941 -1.798 -0.907
-0.938 0.739 1.227 0.239 0.826 3.451 3.280 -0.267
-2.515 0.536 -2.565 1.303 1.888 1.281
0.541209093 INDI 446 PLS 1 9615923 7285752 -1.516 -0.387
-1.194 0.202 0.549 1.609 0.828 3.151 1.250 0.689
-1.518 1.048 -0.904 2.338 -0.075 1.810
0.679036843 INDI 450 PLS 1 9450534 5835601 -2.540 -0.300 0.411
0.468 0.473 1.361 0.178 2.040 0.312 1.854
-0.454 0.437 -0.381 2.772 -0.309 1.436
0.513207045 INDI 452 PLS 1 11501943 5858042 -2.276 -0.289
-0.653 0.042 -0.252 -0.224 1.798 1.261 1.114 1.830
-2.279 0.514 -0.422 2.635 1.180 1.458
0.08004133 INDI 456 PLS 1 12273285 8999173 -0.735 -0.126
-0.843 0.831 -0.169 0.657 0.580 2.218 1.887 0.754
-1.738 0.726 -2.356 0.822 0.092 1.264
0.31092728 INDI 461 PLS 1 9646399 4354493 -2.060 0.101
-1.374 0.753 -0.273 -1.006 1.510 2.722 1.649 1.251
-1.777 1.546 -1.115 2.466 0.507 1.038
0.863762695 INDI 463 PLS 1 13322369 6210744 -2.032 0.068
-0.118 0.621 -1.198 -0.971 0.706 -2.404 2.740 -0.163
-0.432 0.771 0.571 3.621 -1.782 4.641
0.727892018 INDI 464 PLS 1 10346496 9011808 -0.688 0.048
-0.748 0.085 -0.412 0.675 0.873 3.189 3.093 1.583
-1.341 0.550 -0.064 2.315 -1.218 2.879
0.655785909 INDI 466 PLS 1 11574682 7043239 -0.790 -0.417

Table36.txt

-1.075 1.394 -0.023 0.142 0.084 2.528 1.040 1.673
-3.378 1.722 -2.500 2.358 2.080 1.623
0.259703737 INDI 467 PLS 1 11114635 8243151 -1.120 -0.257
-1.261 0.091 -0.246 -0.371 0.660 2.720 0.602 -0.275
-2.135 1.002 -2.839 1.781 0.805 1.459
0.721392728 INDI 468 PLS 1 10736749 8881124 -0.879 -0.384
-0.902 1.187 1.415 0.715 0.902 4.293 2.430 0.036
-2.927 2.070 -3.585 1.297 1.329 1.244
0.803054542 INDI 470 PLS 1 11071781 5843570 -1.432 -0.176
-0.858 1.442 1.257 2.137 0.461 4.274 1.840 1.313
-3.544 1.880 -3.057 2.551 1.105 1.410
0.065033631 INDI 472 PLS 1 12276119 6516559 -1.712 -0.636
-0.557 1.224 -1.319 0.250 0.100 2.328 0.484 0.987
-2.164 1.672 -0.948 0.307 0.002 0.150
0.567607323 INDI 475 PLS 1 11354067 8392298 -0.378 -0.089 0.208
-0.519 0.332 0.600 0.675 0.951 2.187 2.458
-0.353 0.333 1.600 2.290 -1.687 1.846
0.022524997 INDI 477 PLS 1 10985729 4604207 -0.920 -0.970 0.494
-0.647 0.865 1.904 -0.543 -0.042 1.184 1.083
-0.070 0.020 0.004 1.001 -0.153 1.494
0.762317781 INDI 481 PLS 1 10517641 9026347 0.084 0.034
-0.402 -0.918 0.089 0.812 0.569 1.633 2.759 2.326
0.347 0.585 -0.123 3.399 -4.441 1.882
0.822545512 INDI 482 PLS 1 12527085 9881276 -1.113 0.434 0.265
-0.161 -0.207 0.762 1.189 3.521 3.659 2.237
-1.286 -0.237 0.988 3.671 -0.873 1.437
0.05368791 INDI 483 PLS 1 10977381 4021046 -1.749 -0.116 0.294
-0.122 -0.297 0.485 1.457 1.342 0.192 0.434
-1.039 -1.065 -0.563 0.961 0.766 -0.074
0.076832799 INDI 486 PLS 1 12540041 6510294 -2.590 0.330
-1.126 -0.371 -0.795 0.352 0.543 0.539 0.295 0.660
-0.794 0.887 0.700 1.259 0.723 0.937
0.850971955 INDI 543 PLS 1 10935565 4600102 0.421 0.545 1.963
1.315 -1.268 4.261 -0.805 -2.394 2.544 -2.026
0.492 -2.859 1.958 3.107 -1.229 -0.241
0.064691507 INDI 545 PLS 1 9722445 4705715 -0.055 2.281
-1.030 0.836 0.188 1.253 0.386 -0.253 -0.754 0.038
1.623 -0.136 0.374 0.475 -0.627 -0.010
0.057242775 INDI 546 PLS 1 9198044 5045007 -0.123 2.263
-0.553 -1.119 0.193 -0.629 0.107 -1.057 0.551 0.610
0.264 -1.083 -0.718 0.897 -1.023 1.842
0.011104134 INDI 549 PLS 1 10993154 4450145 -0.244 0.951 0.200
-0.173 0.198 0.805 0.894 -0.726 0.623 -0.810
0.814 -0.762 -0.027 0.693 0.706 0.567
0.077764307 INDI 550 PLS 1 9946291 3142624 0.097 -0.613
-0.828 0.558 1.022 -0.094 -0.303 2.724 1.585 0.107
-0.364 -0.349 -0.115 0.954 0.989 -0.507
1 INDI 552 PLS 1 11721078 8294650 3.916 2.072

Table36.txt

-1.647 -1.929 -3.665 0.274 0.802 -3.463 4.740 -2.499
2.956 2.300 -0.469 -1.387 -2.660 11.000
0.088854245 INDI 557 PLS 1 9175042 2987588 0.699 1.905 0.777
1.437 0.060 0.899 -0.685 -0.250 -0.606 -1.199
1.447 -0.604 0.229 0.889 -0.206 1.812
0.524018604 INDI 558 PLS 1 11341563 5929836 -2.931 -0.311
-1.150 0.386 0.097 0.649 0.092 3.587 2.262 0.556
-2.178 1.831 -0.682 1.850 -0.171 1.520
0.360674652 INDI 560 PLS 1 10735343 4496068 -0.902 0.751 1.103
-0.133 0.123 1.149 0.656 2.458 0.923 2.274
-0.998 1.701 -1.171 -0.117 0.775 1.115
0.629775164 INDI 562 PLS 1 10954772 8789694 -1.401 -0.385
-1.050 0.318 0.810 0.888 1.508 1.394 2.297 1.031
-1.165 -0.769 -0.721 2.204 -0.071 1.756
0.481014134 INDI 563 PLS 1 11296901 7541485 -1.357 -0.501
-1.423 0.375 0.104 0.871 2.168 1.830 2.130 1.003
-1.161 -0.359 -1.194 1.764 -0.618 1.654
0.016553187 INDI 564 PLS 1 12084289 5727312 0.102 1.303 0.570
0.151 0.622 1.433 -0.864 0.215 0.024 0.262
-0.868 -0.139 0.454 0.497 -0.392 1.007
0.70738114 INDI 567 PLS 1 11816052 5273198 -1.092 1.817 1.035
0.588 0.394 1.328 0.576 0.578 1.137 -0.174
-1.215 0.179 1.990 0.906 -0.276 1.516
0.129938608 INDI 570 PLS 1 12243522 6337104 0.217 0.142
-0.056 0.645 0.285 0.594 -0.382 1.728 0.567 0.716
1.203 0.073 -1.332 -1.088 0.014 1.016
0.231584727 INDI 572 PLS 1 12847416 7386997 -0.604 -0.555
-0.068 0.248 -1.738 0.608 0.090 1.977 1.894 1.138
-0.573 0.463 -0.745 0.817 0.041 1.895
0.188785869 INDI 573 PLS 1 12296632 4266238 -1.892 0.548 0.366
0.184 -0.635 -0.400 -0.244 1.740 0.912 0.863
-1.136 0.345 0.460 1.559 0.608 1.970
0.053420265 INDI 574 PLS 1 12026503 5755072 -0.506 0.942
-0.402 -0.173 -0.053 0.794 1.127 2.086 1.278 -0.136
-1.205 1.246 -0.192 0.166 0.010 1.148
0.207766612 INDI 576 PLS 1 9950371 3639584 -0.903 0.975 0.767
0.469 0.113 1.386 0.358 2.908 -0.246 0.846
-0.500 -0.622 0.557 0.262 -0.775 1.081
1 INDI 580 PLS 1 12236338 10428784 -11.000 11.000
-1.216 -1.028 -0.577 -0.420 -11.000 0.309 0.994 -0.684
-1.793 -0.043 11.000 1.232 -1.389 11.000
0.75000306 INDI 581 PLS 1 11156983 6377975 -1.959 -2.437
-0.933 0.014 -0.095 -0.234 0.028 2.680 1.338 1.052
-2.066 2.041 -1.085 2.124 -0.252 3.046
0.48887042 INDI 582 PLS 1 12914414 9588014 -2.112 -1.114
-1.568 -0.169 -0.573 -0.029 1.374 2.370 2.124 1.515
-2.547 1.824 -0.967 2.058 0.545 1.260
0.594913784 INDI 583 PLS 1 12937047 7679976 -1.911 -2.049

Table36.txt

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-2.345 1.051 -2.182 1.545 1.127 1.516
0.230910382 INDI 584 PLS 1 12594116 6462552 -1.350 -1.423 0.162
-0.613 -0.346 1.134 2.777 1.744 2.655 0.716
-0.766 1.151 -1.232 0.793 0.322 0.976
0.181721955 INDI 586 PLS 1 13339574 10379556 -1.894 -0.174
-2.003 0.096 0.619 0.228 0.236 2.558 1.786 1.128
-1.205 0.167 -1.727 0.630 0.594 1.350
0.388396548 INDI 587 PLS 1 13538551 6966451 -1.390 -0.421
-1.032 -0.312 0.022 1.018 0.678 2.944 0.620 1.322
-2.122 1.980 -0.815 1.101 -1.033 1.288
0.809431372 INDI 590 PLS 1 10472123 7712323 -2.513 -0.535
-0.295 1.428 0.593 1.139 1.548 3.646 2.279 1.385
-3.258 2.076 -1.807 2.712 0.546 2.025
0.855041186 INDI 591 PLS 1 10202492 6731326 -2.095 -0.219
-0.817 0.552 -0.352 1.996 0.892 3.017 2.641 2.483
-1.735 1.851 -0.557 2.777 -2.206 2.199
0.485483975 INDI 594 PLS 1 11661873 9297201 -1.421 -1.065
-2.102 -1.066 1.066 -0.462 1.806 2.208 1.784 0.496
-1.967 0.798 -0.751 0.776 1.469 0.973
0.110134588 INDI 598 PLS 1 10940861 6636238 -0.484 1.220 0.603
0.287 -0.125 1.084 -0.706 1.320 0.123 0.615
-0.044 -0.217 -1.769 -0.931 0.530 2.415
0.820299082 INDI 599 PLS 1 10872941 4852094 -1.486 -1.882
-1.353 0.097 1.460 -0.545 2.233 3.965 4.323 1.686
-2.206 1.537 -0.334 1.527 1.422 0.972
0.592623171 INDI 600 PLS 1 10821891 7556646 -1.380 -0.073
-1.399 -0.223 1.332 0.109 0.545 1.534 3.511 1.633
-2.312 0.796 -1.444 1.553 -0.291 1.035
0.11567663 INDI 602 PLS 1 11024773 4556116 -1.040 -0.442
-0.120 -0.734 0.809 -0.201 1.437 2.298 1.271 0.229
-0.697 1.173 -1.323 0.423 -0.716 0.894
0.15055306 INDI 605 PLS 1 10186723 7189943 -0.335 0.054
-0.158 -0.773 0.732 -0.340 0.200 2.500 2.537 0.614
-1.052 1.113 -1.438 1.303 0.123 0.764
0.467302657 INDI 608 PLS 1 11211596 7745301 -1.675 -0.610
-0.762 0.125 -0.548 0.734 0.122 2.333 2.532 1.960
-1.673 -0.491 -0.765 1.190 -0.760 1.433
0.380216721 INDI 609 PLS 1 10714634 4190985 -1.053 -0.618
-1.630 -0.271 1.204 1.133 0.866 2.990 1.382 0.298
-1.810 1.737 -1.023 -0.099 -0.323 1.353
0.096233542 INDI 611 PLS 1 12730347 6875302 -1.859 -0.385
-0.815 -0.235 0.576 0.202 0.844 1.865 1.339 0.992
-1.920 0.277 -1.661 1.256 0.748 1.199
0.020568049 INDI 612 PLS 1 11169569 6135499 -1.102 -0.441
-1.380 -0.384 0.304 -0.717 -0.150 2.402 1.207 0.533
-1.309 1.153 -0.683 0.206 0.840 0.893
0.348758899 INDI 614 PLS 1 12284598 9161072 -0.236 0.012

Table36.txt

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-3.319 -0.113 -0.214 1.575 0.424 1.444
0.676231329 INDI 615 PLS 1 11449602 6933346 -2.235 -0.980
-0.639 -0.256 0.366 0.108 1.792 3.843 2.326 0.411
-2.372 1.396 -0.686 2.005 1.145 0.954
0.135917589 INDI 617 PLS 1 11406767 5017464 -0.575 -0.542
-0.097 -0.780 0.822 0.289 1.031 3.101 0.733 0.583
-1.962 -0.254 0.333 0.302 -0.169 1.406
0.738464157 INDI 618 PLS 1 10617824 8876925 -1.624 -0.477
-2.468 0.462 0.385 0.771 0.622 3.404 1.786 0.612
-1.936 0.473 -0.285 3.790 0.312 1.960
0.561338103 INDI 620 PLS 1 11295709 5800789 -1.691 -0.584
-0.766 -0.539 -0.218 0.541 0.246 3.112 1.377 0.893
-2.533 1.092 -1.044 0.863 0.093 2.894
0.280480422 INDI 621 PLS 1 8876388 3263249 -1.431 -0.893
-0.605 0.073 1.987 -0.117 0.930 1.859 0.979 1.838
-0.597 1.474 -0.724 1.444 0.132 1.132
0.511351964 INDI 622 PLS 1 10758506 9233233 -0.135 1.029
-0.044 1.080 0.166 1.441 -0.037 1.375 0.848 2.243
-0.477 0.615 0.958 2.481 -1.159 2.149
0.838158732 INDI 636 PLS 1 10045304 7952129 -1.392 1.958
-1.511 0.245 1.329 1.497 0.124 4.045 2.026 0.266
-0.343 -1.170 -1.069 3.513 0.298 2.479
0.514170617 INDI 639 PLS 1 10248016 7285435 -0.501 -0.031
-2.057 0.064 0.885 0.933 0.498 3.216 0.623 1.076
-1.640 0.668 -2.741 2.291 0.515 1.351
1 INDI 645 PLS 1 10993723 8670864 0.224 4.251
-1.767 -3.069 0.677 2.878 -1.208 -2.152 0.363 0.320
3.084 -1.055 -3.449 4.150 0.656 11.000
0.773127174 INDI 652 PLS 1 8976164 5482961 -1.745 -1.839
-1.179 0.378 1.234 0.924 0.877 3.662 3.294 0.756
-1.713 1.475 -0.489 1.564 0.777 1.764
0.008576145 INDI 653 PLS 1 10022455 5527098 -1.183 0.932 0.137
0.524 0.374 1.923 0.273 1.349 0.349 0.049
-0.175 1.410 -0.698 0.558 0.101 0.250
0.449163851 INDI 661 PLS 1 11632364 9762791 -0.810 0.315 0.601
0.109 0.071 1.344 0.154 2.709 1.285 2.557
-0.660 0.020 -0.466 2.696 -0.666 1.652
0.654175532 INDI 669 PLS 1 12170050 10287209 -0.724 0.317
-0.687 0.784 0.145 2.375 -0.470 1.567 1.698 1.845
-1.167 1.411 1.172 2.496 -0.959 1.689
0.103838183 INDI 671 PLS 1 10815565 2759084 0.717 0.576
-0.845 -0.702 1.325 0.807 -0.002 1.236 -0.326 0.401
-0.707 -0.853 -0.847 0.695 -0.396 -0.877
0.061639546 INDI 674 PLS 1 9296832 3630495 -0.458 1.789 1.370
0.810 0.128 -0.171 -0.708 -0.859 -0.257 1.016
1.665 -1.543 1.317 -0.950 -0.126 0.363
0.071306964 INDI 676 PLS 1 8492977 3135298 0.819 0.929

Table36.txt

-0.275 1.191 0.853 0.465 -1.337 0.526 -1.247 -0.415
0.485 -0.965 -0.576 0.165 0.426 -0.463
0.407872199 INDI 681 PLS 1 8069583 3060517 -0.601 1.638 1.312
-0.241 -0.210 0.532 -1.018 -2.356 -1.103 0.855
1.621 -1.454 1.000 -0.033 -0.358 2.099
0.198147159 INDI 684 PLS 1 9398853 3469511 0.014 1.574 0.148
0.318 -0.736 0.860 -1.162 -1.251 -0.907 0.477
0.016 -1.114 1.383 1.619 -1.377 0.300
0.129414055 INDI 687 PLS 1 11168684 6824763 -0.410 1.094
-0.937 0.350 0.313 1.090 1.369 -0.404 0.734 0.617
0.195 -1.674 0.564 0.497 -0.061 2.010
0.068295055 INDI 690 PLS 1 8350145 3963368 -0.822 1.188 0.252
0.620 -0.001 2.331 -0.445 -0.560 0.306 -0.542
0.859 -0.521 1.904 0.118 0.565 0.257
0.15008217 INDI 691 PLS 1 8430172 4346213 -2.026 0.499 0.076
1.048 -0.237 1.330 0.153 -0.490 0.423 1.244
0.157 -0.793 1.844 1.262 1.245 1.022
1 INDI 693 PLS 1 13603295 7671827 11.000 5.505 4.821
1.573 -11.000 11.000 -4.644 2.158 11.000 -11.000
2.594 6.859 -4.330 0.246 -6.134 11.000
0.218204301 INDI 694 PLS 1 7715174 4091525 -0.550 1.618
-0.659 0.417 0.796 1.498 -0.678 0.964 -0.657 1.688
0.881 0.086 0.221 -0.623 -0.842 0.295
0.051432128 INDI 696 PLS 1 7991187 2626556 -0.122 0.583
-1.126 -0.311 -0.547 0.445 0.455 -0.036 -0.127 -1.321
-0.035 -1.319 0.365 0.519 -0.789 0.544
0.12828898 INDI 700 PLS 1 10958975 3639893 0.201 0.153
-0.978 -0.071 0.093 1.310 -0.018 -0.709 -1.913 1.119
0.409 -1.055 0.457 0.800 -0.459 0.744
0.884559197 INDI 738 PLS 1 11602600 7717035 2.619 4.793 1.068
-0.056 -4.855 2.983 -2.807 -0.779 2.156 3.943
-0.695 -4.334 1.124 2.271 -1.543 2.668
1 INDI 760 PLS 1 11162715 9545833 -0.891 7.223
-1.114 -0.475 -1.172 0.095 -0.817 0.060 6.491 11.000
-2.055 -0.351 -0.593 1.332 -5.850 11.000
0.23793882 INDI 771 PLS 1 12669347 8906338 -1.234 1.336
-2.172 1.034 1.279 0.802 -0.165 2.085 -0.264 1.499
-2.342 0.568 0.404 1.250 -0.332 0.421
0.083437076 INDI 775 PLS 1 9203664 8099294 -0.952 0.667
-0.099 -0.209 -1.143 0.525 0.658 2.407 0.629 -0.540
0.355 0.409 -0.978 1.340 1.132 0.899
0.584075739 INDI 778 PLS 1 9610521 7414151 -0.835 -0.522
-1.843 0.866 0.953 1.369 -0.278 4.018 -0.498 0.952
-1.398 1.358 -2.944 2.110 0.660 1.368
0.594050668 INDI 846 PLS 1 9112143 3304180 -2.381 -0.501
-0.481 -1.146 1.971 -1.449 0.315 3.240 1.877 0.772
-2.158 1.188 -0.722 1.813 -0.312 1.775
0.690005095 INDI 847 PLS 1 11439577 9757113 -0.874 -0.568

Table36.txt

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-0.960 0.873 1.419 3.211 -1.038 2.346
0.068012864 INDI 848 PLS 1 200822 173545 0.122 -0.590
-0.642 -0.513 2.124 -0.778 0.127 1.085 0.007 0.604
-0.315 -0.168 -1.554 2.147 -0.226 2.133
0.259047689 INDI 849 PLS 1 9342987 2566730 -1.998 -0.436 0.318
0.640 1.730 -0.557 0.705 0.921 0.115 2.182
-1.177 -0.288 -0.449 1.421 1.241 -0.866
0.018758971 INDI 854 PLS 1 270653 123370 -0.589 0.574
-0.475 0.094 0.079 0.047 0.945 1.538 0.836 -0.117
-1.498 0.660 -1.082 0.533 1.518 -0.710
0.24880234 INDI 855 PLS 1 11697748 6597859 -1.111 0.531 0.194
-0.124 -0.094 0.871 0.932 1.168 1.382 0.533
-0.562 0.091 1.171 2.079 -0.711 1.057
0.801276458 INDI 861 PLS 1 10369766 8612470 -1.480 -0.073
-0.656 -0.020 0.489 0.354 0.931 3.405 2.531 1.567
-1.731 0.622 -0.125 3.357 0.106 2.585
0.498466998 INDI 864 PLS 1 10374201 8253336 -0.457 0.643 0.092
0.261 -0.333 1.726 0.689 0.963 1.024 1.812
-0.313 -0.122 2.004 2.836 -1.454 2.031
0.410015841 INDI 868 PLS 1 9290721 7842270 0.229 0.380 0.551
0.467 0.078 1.943 -0.012 1.840 1.055 1.896
-0.942 0.432 -0.254 1.914 -1.253 1.513
0.014346517 INDI 894 PLS 1 12433548 6154491 -0.687 0.298
-0.897 -0.549 0.149 0.824 0.824 0.300 1.509 0.738
0.393 0.405 0.397 0.732 -0.529 0.098
0.574713188 INDI 901 PLS 1 10661046 7921770 -1.163 0.687
-0.717 1.301 -0.744 1.161 0.205 2.126 0.489 1.220
-2.630 -0.451 1.408 0.778 -0.359 3.360
1 INDI 075 PLS 1 33164208 4175638 0.823 2.771 3.982
3.543 -2.373 11.000 0.757 -11.000 -3.078 -2.096
2.919 -0.517 -1.157 4.337 -2.145 -3.157
0.057762985 INDI 244 PLS 1 29447550 6148713 0.088 1.443 1.586
-0.211 -0.894 -0.004 -0.050 -0.096 -0.734 1.689
-0.517 0.037 -0.033 -0.388 0.311 -0.774
0.11751485 INDI 245 PLS 1 207369 109744 -0.560 2.116 1.082
-0.883 -1.569 -0.823 -0.023 -0.042 0.565 0.696
-2.054 0.256 0.514 2.220 0.131 0.114
0.079697498 INDI 248 PLS 1 32680768 5980498 -0.202 1.080 0.782
0.804 0.597 -0.184 0.400 -0.019 -2.215 0.695
1.058 -0.981 1.269 0.224 -1.771 0.072
0.040097189 INDI 250 PLS 1 35118762 6310300 -0.036 1.895 0.337
0.268 0.515 0.663 0.639 -0.540 -1.359 1.788
-0.173 -0.023 0.067 0.700 -1.244 0.276
0.849421757 INDI 256 PLS 1 34711855 5179613 0.095 2.353 1.605
-1.308 -0.412 1.832 -1.387 -2.524 -1.696 0.128
0.108 -2.730 0.765 0.815 -0.419 5.572
0.050983459 INDI 258 PLS 1 338965 268878 0.270 1.842

Table36.txt

-0.903 -0.337 0.837 -1.447 -0.730 -0.869 0.751 -0.356
-0.034 -1.334 0.715 0.589 0.158 -0.596
1 INDI 263 PLS 1 157297 116561 0.627 0.270
-5.792 -6.256 -0.241 5.432 -11.000 -11.000 0.805 1.883
1.078 11.000 3.987 11.000 -5.643 -1.110
0.034533168 INDI 271 PLS 1 40377341 6081426 -0.002 0.921 0.160
0.988 -1.053 0.082 0.621 -0.655 0.344 1.775
0.232 0.395 0.616 0.583 0.196 0.625
1 INDI 278 PLS 1 30257052 6723889 -3.827 1.465
-0.400 -2.316 -3.847 11.000 -0.725 -11.000 -1.285 -5.239
2.048 -11.000 0.040 6.162 0.242 11.000
0.706860296 INDI 279 PLS 1 35985736 6107556 1.897 1.442 1.108
1.246 0.124 1.481 -1.700 -1.635 -2.307 -0.099
1.764 -1.141 0.428 -3.485 0.300 -0.169
0.292511522 INDI 281 PLS 1 29003529 4878041 -1.504 0.505
-0.640 -0.291 0.141 0.175 -0.478 2.263 1.228 2.950
-1.786 0.086 -0.558 1.653 -0.281 0.494
0.221668304 INDI 293 PLS 1 36563252 4341753 0.805 0.809 1.256
0.501 -1.956 0.955 0.582 1.738 -1.379 0.037
-0.634 -0.455 0.393 -0.292 -1.380 -0.378
0.043683319 INDI 388 PLS 1 32854273 4423021 -1.139 -0.422
-0.129 1.233 -0.113 2.196 -0.311 -0.657 0.638 2.377
0.521 1.123 0.097 0.685 -1.118 -0.335
1 INDI 510 PLS 1 37332995 6285843 1.421 2.727 2.704
2.451 2.118 5.606 4.634 -11.000 0.918 -11.000
6.084 -6.544 11.000 -5.220 -2.269 11.000
0.010275488 INDI 537 PLS 1 35613096 8269619 -1.083 0.146 0.364
-0.244 -0.081 1.555 -0.199 0.900 0.400 0.038
-0.985 0.066 -0.134 1.796 0.626 0.236
0.252043897 INDI 699 PLS 1 39349250 4903979 0.186 0.526 1.910
0.515 -0.782 1.378 -1.008 -0.402 -2.303 1.730
0.211 -0.624 0.025 -0.671 0.774 1.164
0.044776006 INDI 702 PLS 1 304282 215776 -0.848 0.373 0.460
1.146 0.253 0.336 0.963 2.607 1.672 -0.683
-0.410 0.630 -0.966 0.412 -0.709 0.468
0.283246805 INDI 703 PLS 1 36981012 4880379 -1.347 1.046 0.395
1.433 -0.679 1.098 0.458 3.839 -1.130 0.705
-0.381 0.802 0.221 1.265 -0.731 0.805
0.150007517 INDI 706 PLS 1 313993 101739 1.072 0.361
-0.731 -0.707 2.789 -1.156 -0.369 0.570 -1.682 -1.227
0.610 3.682 -0.192 0.729 0.527 -0.083
0.039097835 INDI 707 PLS 1 35335143 5850793 0.530 0.200
-0.304 0.744 1.294 0.379 -0.128 2.414 1.166 -0.340
-1.327 0.085 -0.624 -0.590 0.120 1.150
0.24112885 INDI 730 PLS 1 603399 200109 -1.606 0.377 0.194
0.919 -1.751 3.812 0.520 -0.013 -0.533 -1.217
0.383 -1.286 -0.539 1.778 1.149 4.441
0.044235674 INDI 736 PLS 1 33031244 6395602 -1.510 -1.250 2.000

Table36.txt

-0.004 0.158 1.929 0.594 0.555 0.480 0.070
-0.172 -0.413 0.917 -0.324 0.342 -0.434
0.038580119 INDI 740 PLS 1 220201 137605 -0.170 2.109
-1.279 0.832 -0.703 -0.565 -1.128 0.540 1.349 -0.174
1.029 0.817 0.387 1.651 -1.633 0.894
0.171838037 INDI 741 PLS 1 534753 437851 -1.761 -0.463 0.251
0.941 0.258 -0.765 1.685 2.807 -1.019 -0.009
-1.575 -0.457 0.185 0.552 1.409 2.043
0.090033921 INDI 742 PLS 1 41510757 5002598 0.052 1.748 0.875
0.732 0.498 1.974 -0.698 -1.039 -0.799 1.421
0.439 0.108 1.364 -0.130 0.218 1.108
0.047684458 INDI 888 PLS 1 270596 114557 0.461 0.210
-1.576 -0.990 -1.903 1.463 0.736 1.051 -0.254 0.647
-0.743 -0.387 0.325 0.526 0.073 1.908
0.158355776 INDI 895 PLS 1 306859 274786 0.842 2.735 0.642
-0.995 0.705 0.074 1.464 0.989 -0.525 -0.135
-1.065 1.937 1.819 0.928 -0.616 -0.101
0.008973631 INDI 896 PLS 1 32297749 3914456 0.857 0.170 0.787
-0.702 0.057 0.929 -1.165 -1.321 -0.074 0.518
0.322 0.851 1.559 0.581 -0.236 -0.423
0.077782187 INDI 899 PLS 1 31696082 3955307 0.985 0.833
-0.712 0.301 -0.515 0.827 -1.087 -2.868 -1.463 -0.019
-0.606 -0.559 0.432 1.073 -0.162 0.293
0.041952148 NL PLS 841 9160701 1983207 -0.409 1.101
-1.181 -0.162 1.815 0.239 0.815 0.318 1.431 0.478
0.530 0.332 -0.839 1.491 1.455 0.723
0.040555341 NL PLS 842 9750249 1758590 -0.127 -0.066 0.952
0.726 -0.538 1.465 -0.528 0.544 0.374 -0.557
-0.675 -0.843 0.481 0.545 0.816 1.087
0.011616764 NL PLS 914 9569231 2048667 -0.836 -0.303
-0.289 0.339 -0.014 0.811 -0.946 0.463 0.246 2.091
0.479 0.099 -1.121 0.062 -0.600 1.327
0.039829468 NL PLS 915 10764005 2292701 0.397 0.230 0.262
-1.545 0.569 1.059 0.150 -1.292 0.203 0.053
-0.077 0.605 1.123 -1.453 -0.373 0.337
0.063655155 NL PLS 916 6083914 4564477 -0.272 -0.689
-1.155 1.068 -0.674 0.069 -0.535 0.774 -0.182 1.120
-0.764 1.346 -0.763 0.097 -1.296 1.800
0.071105216 NL PLS 917 10552936 2945291 -0.617 -1.000
-0.866 1.464 1.367 1.028 -0.350 1.507 -0.001 0.536
0.336 0.792 -0.522 1.545 0.001 -0.070
0.366191751 NL PLS 918 9580700 2100769 -1.205 1.621 0.905
-0.112 0.293 1.282 -0.703 0.227 -0.827 0.565
1.561 -0.033 -1.043 -1.130 -1.141 2.203
0.357259639 NL PLS 919 10583848 2476233 -0.446 0.661 1.084
-0.546 0.669 0.774 2.405 1.334 -0.045 -0.404
-1.019 0.834 -0.428 -0.664 1.020 1.762
0.205605788 NL PLS 920 5970272 2856939 -1.434 -1.052

Table36.txt

-0.046 -0.640 -0.296 0.223 -0.016 -1.102 0.176 -0.510
-0.663 0.164 1.153 0.025 0.475 1.473
0.175140498 NL PLS 921 11233721 2095801 1.571 0.959 1.225
1.460 -2.047 -0.177 0.836 -2.107 -0.701 -1.504
0.765 0.563 -0.433 -0.471 1.005 -0.538
0.025249825 NL PLS 922 10306511 3009115 -0.502 -0.351
-0.491 0.023 0.859 1.998 0.413 0.544 0.001 -0.074
0.201 2.871 0.251 0.919 0.093 -1.067
0.068151947 NL PLS 923 11132267 2550453 0.618 -1.607 0.055
0.985 0.343 0.291 -0.243 0.531 0.254 1.391
0.517 -1.258 -0.019 -0.173 -0.197 -0.367
0.017937574 NL PLS 924 8218223 1367750 0.099 1.526
-0.624 0.668 0.200 -0.137 0.682 -1.061 -1.050 -0.366
1.995 -0.280 1.447 0.780 0.359 -0.348
0.224981221 NL PLS 925 6856102 3236746 1.819 0.449 0.149
0.203 -0.377 0.267 -0.626 -2.763 -0.646 -0.489
1.653 -1.172 -1.882 -0.759 0.439 0.914
0.112178367 NL PLS 926 11254657 3029456 -1.538 -0.329
-0.353 0.100 1.460 0.423 0.663 1.122 1.466 -0.255
0.106 1.211 -0.710 1.040 -1.495 -0.949
0.018171148 NL PLS 927 9461099 1668228 -0.742 -0.139
-0.907 0.501 0.814 0.607 -0.670 -0.684 1.257 -2.016
0.435 0.279 -0.072 0.167 0.896 1.768
0.230505747 NL PLS 928 8753332 1769529 1.244 0.602 1.640
0.549 -0.261 -0.712 -1.207 0.249 -1.151 -0.190
1.436 -0.906 0.075 -0.669 -1.947 -0.404
0.519087837 NL PLS 929 7318064 3625686 -2.115 -1.832 0.815
0.188 -0.131 1.244 2.141 3.287 2.721 -0.908
-1.321 1.536 1.338 -1.438 -0.038 1.630
0.091249116 NL PLS 930 9636549 3001548 0.276 1.061 0.535
0.346 0.713 1.076 -0.099 0.090 -0.150 -1.026
0.306 0.124 -0.320 -0.475 -0.632 0.607
0.020578393 NL PLS 931 6831988 3813262 1.012 0.845 0.349
-0.003 -0.489 0.655 0.366 0.022 -0.391 -0.256
2.568 0.545 0.743 0.184 1.450 -0.199
0.163947782 NL PLS 932 8503512 1701494 -0.259 -0.880 0.247
0.452 0.870 0.879 2.176 3.325 1.375 0.059
0.333 0.027 0.422 0.395 -0.357 1.209
0.059388196 NL PLS 944 11093173 2161104 -0.278 0.669 0.113
-0.369 -0.299 0.687 0.954 -0.607 -0.019 1.486
0.145 -1.000 -0.201 0.731 0.199 -0.034
0.039326637 NL PLS 945 11170626 2626543 -0.984 -0.150
-0.432 0.747 2.099 1.476 0.668 0.094 0.297 0.616
-1.369 -0.196 0.491 -0.167 -0.977 -0.272
0.12559143 NL PLS 946 11429122 2558450 0.244 2.168 0.184
-0.723 -1.180 -0.584 0.534 -0.398 -1.545 0.486
0.026 -0.662 0.102 -0.345 -0.293 0.903
0.256452757 NL PLS 947 6722207 3315353 0.259 2.110 0.899

Table36.txt

0.460 1.422 1.137 -1.736 -1.386 0.068 0.201
-0.377 -0.214 1.593 -0.466 -0.968 -1.834
0.051951961 NL PLS 948 11360063 2581642 0.633 -1.459 0.404
0.406 -0.745 0.592 1.718 -0.464 -0.402 0.109
0.487 1.346 1.412 0.188 -1.531 -0.063
0.045048438 NL PLS 949 9694374 1937319 0.078 -1.327
-0.406 -0.025 0.689 0.015 -0.898 0.706 -0.882 0.251
-0.084 -0.439 0.403 -0.039 0.077 -0.873
0.025275738 NL PLS 950 6841599 3791038 0.718 1.372 0.683
0.336 -1.819 1.092 -0.552 1.674 1.444 -0.918
-0.408 1.114 -1.204 1.077 0.721 -0.661
0.074599644 NL PLS 951 11995903 2172586 0.434 -0.499
-1.696 -0.163 1.033 0.069 1.570 -1.016 1.206 0.334
-1.111 -0.360 -0.303 -0.351 0.422 1.432
0.066888224 NL PLS 952 10574836 2584881 0.764 0.227
-1.196 -0.372 1.074 -0.385 0.580 -0.589 1.212 0.275
-1.628 -0.631 -0.452 -1.030 0.230 1.367
0.036251525 NL PLS 953 5732762 2490114 0.272 -0.310
-0.590 1.036 0.753 0.944 -0.024 1.190 1.861 -1.419
-0.467 0.938 -1.560 1.777 -0.479 0.710
0.02741204 NL PLS 954 5961761 3226227 -1.370 0.924 0.244
0.321 -0.155 -0.714 -0.253 1.561 1.737 0.594
-0.848 0.569 -0.441 -0.229 1.740 -0.891
0.226061785 NL PLS 955 9405880 1682232 0.590 -0.505
-0.064 1.899 0.687 -1.957 -0.820 -0.198 -0.332 1.038
-3.044 -0.145 0.015 0.377 0.686 -0.912
0.109259571 NL PLS 956 7646218 2835154 0.999 -0.939 0.755
-1.044 -0.796 1.331 -0.198 0.472 2.135 0.476
-1.516 0.508 -0.152 0.973 0.178 0.379
0.096682344 NL PLS 957 8695797 2082911 0.177 1.430
-0.962 1.522 0.068 -0.093 0.571 1.966 0.200 -0.378
0.951 0.708 -0.428 -0.171 -0.334 -2.021
0.062663354 NL PLS 958 8899849 1583180 -0.293 -1.390 1.008
-0.266 0.893 -0.029 1.909 1.422 -1.033 1.394
0.788 1.450 1.005 -0.548 -0.490 -1.654
0.024502858 NL PLS 959 6059090 3092625 0.119 -1.501 0.461
0.580 0.679 1.032 0.951 1.010 0.783 0.808
-1.153 0.956 -1.440 1.278 -0.043 1.817
0.058478688 NL PLS 960 9515003 1825321 0.204 1.798
-0.754 0.270 0.371 0.405 0.113 -2.398 -0.339 -2.189
0.759 1.022 -0.096 -0.215 -0.509 0.340
0.022687291 NL PLS 961 8797545 2042266 0.571 -0.847
-0.514 -0.471 -0.666 1.662 -0.399 -0.585 -0.621 -0.071
0.923 -0.039 -1.497 -0.504 0.693 -0.417
0.086849111 NL PLS 962 10170841 1979600 -0.590 -0.964
-0.678 -0.821 0.823 1.324 1.366 1.172 0.583 3.032
-0.749 -0.534 -0.444 0.352 -0.381 0.814
0.050460516 NL PLS 963 9599810 2013558 0.835 -0.276

Table36.txt

-0.421 0.242 1.153 0.686 0.354 0.595 -0.320 -0.216
0.244 0.282 -0.428 1.028 0.773 0.149
0.11070652 NL PLS 964 10725717 2410606 1.960 1.083 0.412
1.118 0.258 -0.485 -0.101 -1.030 -0.862 -1.118
1.094 -0.569 -1.332 -0.964 0.895 0.420
0.100875483 NL PLS 965 10690573 2344793 -0.338 -0.837 0.413
0.608 0.981 0.244 0.308 -0.302 -0.955 0.247
-0.880 0.774 -0.482 0.193 1.081 -0.895
0.094550973 NL PLS 966 11585480 2899371 1.028 1.162
-1.694 0.874 -0.606 0.597 -0.637 0.949 1.014 0.125
0.332 0.445 -0.343 -1.120 0.159 0.804
0.340106956 NL PLS 967 8658975 1314924 -1.120 -2.298 0.185
1.058 -0.243 0.124 -0.602 -1.755 -1.076 1.737
-0.935 -1.826 0.782 1.334 1.241 1.142
0.152380228 NL PLS 968 6130107 2674984 -1.706 0.448 0.745
-0.578 -1.612 2.251 1.752 1.086 0.926 -1.054
-3.001 -0.427 -0.137 0.405 -0.987 1.064
0.485783164 NL PLS 969 8576203 2138188 1.090 0.373 0.397
-0.609 -0.637 -0.332 -0.735 0.954 -1.355 1.198
0.953 -0.984 0.761 1.589 0.720 1.521
0.176998516 NL PLS 970 8470879 1761929 -0.608 0.080 0.436
-0.163 0.798 0.111 0.452 0.206 1.230 0.746
-1.615 1.661 -0.610 0.174 0.934 0.869
0.14870754 NL PLS 971 8010027 1413021 -0.986 -1.355 1.632
0.789 -0.267 1.583 0.760 2.595 0.177 -0.620
-0.719 0.062 -0.862 1.309 -0.340 -0.336
0.032084995 NL PLS 972 5350961 2456794 0.194 -0.201 1.504
-0.532 -0.132 0.547 -0.390 -0.815 1.565 0.338
-0.857 1.209 -0.319 -1.011 0.995 0.277
0.044192151 NL PLS 973 6526599 3200657 0.145 -0.198
-1.559 0.504 0.910 1.011 -0.123 -0.228 -1.258 0.596
0.874 -0.597 0.509 0.139 -1.098 -0.427
0.030685758 NL PLS 974 9013181 2029887 -0.601 1.091 0.045
0.554 1.048 -0.339 -0.748 -0.603 0.181 0.404
0.178 0.320 -1.150 -0.480 0.157 0.211
0.028339058 NL PLS 975 10493869 2103163 0.710 1.601 0.195
-0.722 -1.214 1.039 0.439 0.912 -0.715 0.893
0.729 -0.082 0.116 0.861 -1.597 -0.525
0.249455957 NL PLS 976 11002580 2501238 -2.120 0.545 1.950
0.723 0.508 -0.377 -0.144 0.266 2.640 -0.412
0.178 1.492 -0.443 0.914 0.564 0.800
0.174124966 NL PLS 977 9024100 2742090 -1.018 -0.002
-0.233 0.332 -0.855 -2.089 0.581 -0.043 0.275 -0.090
0.271 -0.177 -1.973 1.117 0.217 1.490
0.289747881 NL PLS 978 11318711 2540364 0.802 0.950 1.801
-0.443 0.497 0.191 -0.509 -0.613 -1.719 -0.174
1.506 -0.831 -0.085 0.186 -2.819 0.728
0.13078208 NL PLS 979 11016217 2520339 0.402 -0.737 1.211

Table36.txt

```
     0.218      0.450      -2.425     0.496      0.844      0.829      0.509
-1.892     1.012      0.400      1.274      1.088      -1.124
0.371072166     NL PLS 980        6581251    3809877    -1.075     -0.547
-0.750     -0.511     0.336      -1.468     0.607      2.485      0.619      0.691
    -0.268     2.916      -0.937     2.290      -0.716     1.011
0.398779443     NL PLS 981        9496881    2205575    -1.021     0.842
-0.740     1.017      1.783      1.822      1.917      1.293      0.097      1.213
    -0.956     1.920      -0.081     0.569      -0.029     2.018
0.07039575      NL PLS 982        9366276    1850541    0.619      0.277      0.950
     0.618      0.568      1.313      -0.222     -0.412     -0.752     0.206
-0.005     -0.591     1.134      0.494      -0.608     -0.786
0.137088111     NL PLS 983        10325395   2145590    1.931      -0.497     1.391
     -1.560     -0.116     -0.115     0.722      -1.628     -0.067     -0.994
-0.706     -1.153     1.676      -0.019     0.525      1.011
0.264218794     NL PLS 984        10173270   2394995    0.916      1.576      0.447
     0.075      -0.247     1.348      -0.202     -1.225     -1.903     -0.380
2.746      -2.395     -1.784     -0.533     0.092      0.853
0.070412327     NL PLS 985        7585724    4161994    1.475      -0.661
-0.104     1.151      0.460      -0.025     -1.027     -0.657     -0.006     -0.325
    0.358      0.530      -0.193     -0.750     -0.638     1.087
0.039733444     NL PLS 986        8729828    1745256    -0.894     0.346      0.664
     0.141      -0.867     -0.098     -0.319     -0.570     -1.015     2.114
0.242      0.208      0.415      -0.088     -0.763     0.185
0.056902821     NL PLS 987        11293895   2467948    0.116      0.632
-0.296     1.674      -0.828     -0.197     1.081      1.538      -0.701     -0.357
    -0.884     0.954      0.505      -0.611     0.727      -1.402
0.071411216     NL PLS 988        9674783    2749665    0.420      0.896      0.481
     -0.312     -0.978     -0.037     0.414      0.381      1.437      0.238
0.087      0.507      0.518      1.307      -0.974     1.158
0.056476705     NL PLS 989        4630382    2361149    0.629      0.922
-0.601     1.169      -0.485     -0.213     0.712      0.907      -0.863     -1.050
    0.922      -1.491     -0.885     1.693      1.701      -0.164
0.243442916     NL PLS 990        11171477   2114731    0.514      0.052
-0.806     -0.284     -0.264     1.018      -0.619     0.899      -1.991     -0.063
    0.165      -1.456     1.756      -0.426     -2.050     -0.023
0.048843609     NL PLS 991        12685933   2302200    -0.513     0.150      0.290
     0.834      -0.901     -0.346     0.703      0.494      -1.306     0.092
-0.228     0.716      1.228      2.223      0.019      0.415
0.005785505     NL PLS 992        9422278    2444103    -0.741     0.420      1.560
     -0.031     1.781      0.006      -0.476     -0.548     -0.015     0.830
-0.600     0.643      -1.213     0.013      0.373      -0.310
0.018154683     NL PLS 993        7165271    3540714    0.958      0.198
-0.217     0.670      0.552      0.238      0.762      0.962      -0.745     0.297
    0.795      1.748      0.386      0.443      0.106      -0.098
0.060523572     NL PLS 994        10849086   1854438    0.792      -1.518     0.528
     -0.294     0.757      0.801      1.055      0.968      0.068      -0.298
0.509      0.225      -0.243     0.324      1.029      0.495
0.411338529     NL PLS 995        11495044   3085759    0.031      1.209
```

Table36.txt

-0.631 0.340 0.438 -0.050 -0.455 -2.455 -1.082 -0.517
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0.029067992 NL PLS 996 11336257 2252505 0.199 -0.285
-0.029 0.372 2.177 -0.632 0.642 0.498 0.893 1.998
-0.371 0.122 -0.296 0.741 -0.016 0.304
0.032039183 NL PLS 997 11565524 2112149 0.737 -2.061 0.932
1.122 0.313 0.210 0.685 -0.239 -0.737 0.595
0.013 -0.162 -0.197 0.246 -0.463 0.184
0.04233761 NL PLS 998 9235605 1818459 0.389 -1.920 0.737
1.228 -0.617 1.754 0.153 0.337 0.611 0.515
0.206 1.711 -1.113 0.325 0.216 0.971
0.119349481 NL PLS 999 9335662 2184622 -1.274 -0.129
-0.646 0.977 1.665 0.445 1.329 0.421 0.895 1.430
-1.266 -0.276 0.554 2.695 0.096 -0.745
0.016853402 NL PLSA 1000 11258677 2962490 1.141 0.145 0.797
-1.213 0.066 -1.248 -1.069 -0.473 0.871 -0.118
0.677 -0.787 -0.876 0.183 -0.301 1.090
0.192275934 NL PLSA 1001 8731517 1315838 -1.028 -0.872 0.454
-1.414 1.848 2.083 -1.575 -0.891 -1.335 -0.158
1.946 0.935 0.111 -1.383 -0.473 -1.980
0.236670586 NL PLSA 1002 10755595 1979261 0.053 2.163
-0.695 1.174 0.002 0.450 1.903 2.309 -0.673 0.634
-1.968 1.976 -0.278 -0.208 1.318 0.895
0.203567898 NL PLSA 1003 11592752 2285987 -1.187 1.732
-0.795 0.064 0.699 1.144 -1.472 0.189 -1.961 0.847
-0.531 0.647 -0.762 2.267 -0.765 0.632
0.102800906 NL PLSA 1004 10513886 2628950 0.164 -0.398 0.621
-0.925 0.340 0.058 -0.729 -0.924 -1.032 0.173
1.258 0.918 0.506 -0.262 -0.283 1.112
0.08060398 NL PLSA 1005 9873327 1814560 1.700 1.158 0.560
-1.575 -0.588 0.052 -0.337 -1.128 0.948 0.658
1.248 1.682 0.062 0.660 1.116 1.133
0.035555316 NL PLSA 1006 9698975 2040465 -1.406 -0.428
-0.126 0.589 -0.044 -0.514 0.680 -0.141 0.537 1.228
-1.337 0.517 0.428 0.617 -0.398 -0.687
0.073177558 NL PLSA 1007 8892428 2185438 0.124 -0.937
-0.868 2.415 -0.446 0.820 -0.946 -1.112 0.755 -0.763
-0.543 0.209 0.106 -1.495 1.208 0.368
0.033121923 NL PLSA 1008 10246515 2407537 -0.869 0.946
-0.881 0.709 0.130 0.021 -0.526 1.008 1.419 -0.036
1.072 1.567 0.634 0.774 -0.236 -1.259
0.106163545 NL PLSA 1009 10284501 1423419 0.006 0.114 0.827
-0.802 -1.642 -2.061 0.169 1.717 0.957 1.007
1.136 0.129 -1.345 1.936 0.377 0.055
0.143105975 NL PLSA 1010 8705340 2104009 -1.143 -0.226
-0.417 1.904 0.964 0.803 -1.533 0.646 -0.974 0.286
-0.064 0.019 1.498 0.139 -1.188 0.493
0.051092284 NL PLSA 1011 10687615 2073679 1.444 -0.170 0.566

Table36.txt

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0.378 -0.242 1.056 0.417 0.303 -0.094
0.022967296 NL PLSA 1012 9795547 1341194 -0.065 -0.115
-0.199 -0.534 0.500 0.084 -0.162 0.362 -1.442 -0.068
-0.565 1.086 -0.278 1.927 0.841 -1.066
0.188766111 INDI 117 PLS 1 14136026 6951880 0.183 -1.101
-1.744 0.291 0.304 0.059 -0.055 2.799 1.435 0.634
-1.945 1.686 -2.408 1.436 1.330 0.847
0.036725947 INDI 284 PLS 1 14249806 6626752 -0.378 -0.111
-2.337 -0.675 -0.149 -0.360 0.193 0.984 1.298 -0.114
-1.663 0.515 -0.617 1.841 1.152 1.159
1 INDI 331 PLS 1A 13686853 3298868 -1.898 7.130 3.505
4.550 -1.427 2.429 -2.229 -6.807 0.786 -0.463
2.493 -11.000 1.140 5.436 1.717 4.852
0.350303722 INDI 333 PLS 1A 11668615 2941891 1.366 1.129 1.671
1.136 -0.012 2.004 -1.398 -0.698 0.661 -1.528
0.848 0.086 0.243 -1.657 -0.625 1.704
1 INDI 335 PLS 1A 12638983 2277195 -2.461 -0.887
-0.999 -1.164 -0.775 -0.311 -0.998 -0.988 -0.753 -1.154
0.657 -0.992 -1.958 -0.629 11.000 11.000
0.425158542 INDI 336 PLS 1A 16365263 5629136 1.047 0.227 0.220
0.981 -1.542 -0.082 -1.099 0.580 -2.550 -0.154
0.308 -2.072 -1.382 -0.787 0.054 1.101
0.027374341 INDI 342 PLS 1A 12557715 3217683 -1.489 0.762
-0.525 -0.579 -0.950 -0.338 -0.826 0.827 0.263 -0.400
-1.136 0.917 -1.297 1.518 0.084 1.053
0.012018604 INDI 346 PLS 1A 14914834 5112215 0.329 -0.776
-1.540 0.301 0.750 -0.521 0.275 0.365 1.123 0.503
-0.956 1.838 -0.083 0.137 0.043 0.404
0.661448554 INDI 353 PLS 1A 14450386 4675676 -0.522 0.051
-0.865 1.844 -1.132 2.642 -0.309 3.060 0.932 1.060
-1.084 0.981 -1.537 0.631 -0.028 2.589
0.107783125 INDI 355 PLS 1A 12597770 5694986 0.570 -1.417
-1.108 -0.212 0.597 -0.527 0.754 1.588 0.333 -0.428
-0.833 1.329 -0.341 0.905 -0.353 1.640
0.364312899 INDI 357 PLS 1A 13330675 4357613 -0.527 0.076
-0.316 -0.694 0.192 0.668 0.065 1.260 -0.059 0.282
-1.330 0.312 0.513 1.929 -0.659 0.713
0.006037237 INDI 358 PLS 1A 14328754 4345934 0.683 0.229
-0.169 0.643 0.023 0.849 0.553 0.939 0.889 0.466
1.150 -0.626 -1.378 -0.157 -0.270 0.137
0.251158424 INDI 360 PLS 1A 13373346 6539699 1.517 1.748
-0.510 0.675 0.534 0.747 0.096 -0.513 0.409 -1.440
1.134 -1.744 -1.551 -0.333 0.575 1.874
0.117300981 INDI 364 PLS 1A 14630027 4248070 -0.782 -0.249
-0.660 0.430 -0.180 0.218 0.275 0.305 -0.597 0.923
-1.457 1.457 0.356 1.472 -0.396 1.010
0.038428525 INDI 369 PLS 1A 11910707 5807528 -0.048 0.397

Table36.txt

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-2.058 0.752 -1.010 0.579 0.510 0.533
0.251735267 INDI 371 PLS 1A 13918611 5023007 1.416 0.416 1.012
1.336 0.779 0.715 0.118 0.121 -0.765 -2.041
-1.281 -0.942 0.828 -0.641 -0.255 1.354
0.457641337 INDI 372 PLS 1A 15219162 9462255 0.032 -0.339
-1.277 0.529 -1.437 -0.098 0.766 1.453 1.352 1.822
-1.438 -0.245 -0.518 1.930 0.596 2.366
0.139141034 INDI 373 PLS 1A 13505802 6152277 0.226 -1.165
-1.655 -0.568 -0.114 0.497 0.576 1.602 0.595 -0.271
-1.539 0.199 -1.089 0.273 0.102 3.385
0.394067144 INDI 381 PLS 1A 12395884 2555396 -1.456 -0.416
-0.367 1.950 -0.280 1.055 0.294 2.503 2.405 1.133
-1.788 -0.323 0.100 1.031 -0.001 2.245
0.019138205 INDI 383 PLS 1A 14149481 5828793 0.028 -0.048
-0.934 0.770 -0.357 -0.373 -0.035 1.957 0.955 -0.028
-1.189 0.047 -1.964 -0.533 0.704 1.228
0.019872033 INDI 389 PLS 1A 12602657 2832722 -1.972 0.859 1.546
0.416 0.342 1.597 0.064 -0.010 0.153 -0.015
0.212 0.392 0.857 0.786 -0.663 -0.072
0.028579597 INDI 392 PLS 1A 12043191 2251577 -0.428 0.526 0.078
-0.367 0.555 1.514 -0.452 0.514 0.427 0.116
-2.196 0.165 1.273 1.224 -1.105 -0.950
0.226241362 INDI 394 PLS 1A 14462072 5072854 0.238 -0.082
-0.299 -1.036 1.055 0.428 1.595 0.366 0.095 0.495
-0.924 -0.835 -1.595 1.467 -0.333 1.363
0.12705959 INDI 395 PLS 1A 14087840 2867706 -2.014 -0.099
-0.098 -0.123 0.614 1.004 0.018 1.595 1.096 1.667
-0.185 1.220 -0.214 1.288 0.051 0.171
0.180551104 INDI 403 PLS 1A 12682776 4190820 1.279 1.028 0.246
0.031 0.387 -0.597 0.186 -1.619 -1.959 0.915
1.127 -1.791 -2.037 -1.195 -0.583 1.180
0.013161804 INDI 405 PLS 1A 12261572 3500927 -1.136 -0.212
-0.085 -0.181 0.999 1.867 1.149 0.036 0.166 0.291
-0.443 0.433 0.147 1.168 -0.627 1.025
0.587238301 INDI 624 PLS 1 12289445 5328558 -0.771 -1.009
-1.118 -0.126 2.319 -0.117 -0.013 2.144 2.235 0.166
-2.472 1.950 -1.092 0.774 1.443 0.879
0.260810039 INDI 635 PLS 1 11224774 3844743 0.378 0.011
-0.838 -1.189 1.052 0.560 -0.656 0.481 1.263 -0.123
-0.423 -0.176 -1.361 1.759 -0.091 1.535
0.158241793 INDI 640 PLS 1 15219688 6000787 -0.974 -1.147
-1.527 -0.433 0.362 1.339 -0.795 -0.420 1.405 0.001
-0.372 -0.357 0.471 2.604 0.494 0.188
0.322335918 INDI 643 PLS 1 12905544 4789347 -0.930 -1.684
-1.715 -0.487 1.430 1.393 0.452 2.064 0.514 0.164
-1.089 1.258 -1.107 1.937 0.322 2.493
0.770526604 INDI 644 PLS 1 15570170 5747093 -1.454 -2.161

Table36.txt

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-3.148 1.254 -1.776 2.589 0.842 1.385
0.867446032 INDI 647 PLS 1 13145802 5511182 -2.392 0.471
-0.681 0.872 -0.744 -0.913 -0.359 -0.454 4.344 -0.366
-0.397 2.179 1.055 3.185 -1.952 7.407
1 INDI 648 PLS 1 15140339 7478222 -11.000 3.394 2.889
3.847 3.504 4.627 -3.889 -2.648 11.000 -7.034
3.036 4.440 3.392 4.037 -11.000 4.008
0.227959644 INDI 649 PLS 1 13632758 6556744 -0.891 -0.362
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-1.679 -0.664 -1.480 1.659 0.845 0.923
0.472125535 INDI 650 PLS 1 11977011 4242142 -0.466 -0.631
-2.538 -0.406 0.656 0.645 0.416 2.021 2.698 0.394
-1.827 0.410 -0.920 2.089 0.804 1.485
0.295730752 INDI 651 PLS 1 12161113 5219042 -2.210 -1.834
-1.466 -0.670 0.896 -0.188 0.401 0.906 2.346 1.143
-1.585 1.109 -1.619 0.815 1.365 0.585
0.698968946 INDI 654 PLS 1 13746351 6098880 -0.690 -1.053
-1.898 0.288 1.041 0.791 -0.447 3.019 2.069 1.378
-2.435 0.632 -1.053 1.068 1.655 2.438
0.756851112 INDI 655 PLS 1 13305699 5011144 -2.834 -0.158 0.624
-0.303 0.010 0.251 1.852 2.184 2.245 0.833
-1.672 1.258 0.923 2.541 -0.718 1.954
0.831440135 INDI 657 PLS 1 15551274 6691209 -2.498 -0.089
-1.057 -0.290 -0.104 2.247 0.006 0.546 2.854 1.691
-1.737 -0.190 2.186 2.316 -1.338 3.095
0.05832433 INDI 658 PLS 1 10983225 2984745 -0.795 -0.950
-0.267 -1.236 0.380 -0.078 0.783 -0.126 1.143 2.466
-1.331 1.058 -0.309 0.624 0.177 1.194
0.576525833 INDI 660 PLS 1 15997537 6581418 -1.754 -0.111
-0.738 -1.350 1.006 0.389 1.011 0.510 0.009 2.427
-0.331 -0.472 0.632 1.133 -0.924 2.284
0.680825417 INDI 708 PLS 1 10597262 3020316 -1.413 0.126
-0.782 -0.834 0.127 0.028 -0.232 1.367 0.042 1.940
-0.587 -0.339 -0.598 2.604 0.541 1.854
0.030408332 INDI 718 PLS 1 12587962 4879435 0.093 0.122 0.155
-0.544 0.767 0.185 0.611 0.128 0.936 -0.493
-0.869 0.388 -2.026 1.036 0.983 0.919
0.312715517 INDI 720 PLS 1 13025935 5796808 -1.771 0.791
-1.088 -1.216 0.739 0.712 0.793 2.244 1.024 0.798
-1.104 0.336 -1.562 0.810 0.977 2.442
0.103473513 INDI 721 PLS 1 14512175 2823118 -0.390 -0.262
-0.552 -0.629 0.096 -0.883 0.633 2.828 -0.362 1.933
-0.727 0.100 -0.940 -0.486 0.086 1.138
0.12819612 INDI 722 PLS 1 13234903 3119851 0.250 -0.085
-1.133 -0.105 -0.567 0.072 0.211 1.566 -0.031 0.509
-0.848 0.336 0.595 1.185 -0.912 0.078
0.100568939 INDI 723 PLS 1 12359335 2748058 -0.736 1.233

Table36.txt

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0.007 1.542 -0.878 1.066 -1.017 0.652
0.155772498 INDI 724 PLS 1 14026893 5251729 0.874 1.114 0.174
-0.645 0.149 0.639 1.289 -0.996 -0.551 -0.063
0.888 -0.455 1.362 1.137 -0.052 2.100
0.053829241 INDI 725 PLS 1 10699299 2545641 -0.484 2.745 0.854
-0.254 0.839 0.905 -0.437 1.415 1.381 -0.306
0.618 0.195 -0.444 -0.214 -0.874 0.399
0.38573755 INDI 726 PLS 1 10500220 4565619 -1.360 -0.345
-1.303 0.963 1.064 1.083 0.663 2.302 2.211 -0.694
-0.960 -0.030 -1.247 0.617 1.172 1.618
1 INDI 727 PLS 1 14421175 7099962 -11.000 -11.000 6.056
7.218 -0.408 8.126 -5.205 -11.000 -4.918 -11.000
11.000 5.346 11.000 -6.464 -5.573 11.000
0.068575107 INDI 729 PLS 1 11671261 3706666 1.251 1.257
-0.829 0.143 1.101 -0.936 -0.582 0.832 -0.328 -0.932
-0.187 -0.163 -0.935 0.653 0.538 0.519
0.074938707 INDI 731 PLS 1 11859443 2801647 -2.016 -0.568
-0.782 -0.415 1.645 1.533 -0.240 1.137 0.185 1.047
-0.756 2.043 0.512 0.326 0.781 -1.018
0.09914623 INDI 744 PLS 1 12862357 8040058 -0.221 0.851
-1.391 -0.433 1.565 -0.130 0.862 1.490 1.575 -0.491
-0.795 0.418 -0.682 0.224 -0.297 0.359
0.633321929 INDI 745 PLS 1 14731552 7433354 -1.327 -0.845
-2.178 -1.244 -0.032 0.319 0.123 0.701 1.546 0.711
-1.496 -0.652 -0.185 2.122 0.341 1.826
0.748966715 INDI 746 PLS 1 15445486 8533658 -1.158 -0.867
-2.299 -0.768 0.075 0.072 1.189 1.994 1.765 0.884
-2.390 0.748 -1.097 2.061 0.999 2.574
0.321053125 INDI 747 PLS 1 12162616 3443374 -1.510 -0.713
-0.618 0.125 0.399 0.282 1.559 2.739 -0.062 2.478
-2.274 0.408 -0.379 0.498 -0.005 1.482
0.85369624 INDI 748 PLS 1 11173006 4651579 -2.477 -1.602
-1.542 1.969 1.547 0.681 1.944 6.568 3.412 1.010
-1.540 2.050 -1.818 1.949 -0.155 2.307
0.690862839 INDI 749 PLS 1 13318102 4622630 -0.742 -1.534
-1.586 -1.906 1.045 -0.182 1.205 3.274 2.101 1.325
-1.769 0.483 -0.761 1.880 1.189 0.922
0.125412261 INDI 750 PLS 1 8645937 1944826 -0.098 -0.700
-0.682 -0.978 0.297 0.073 1.037 1.224 0.522 1.937
0.027 -0.647 -0.166 1.432 0.294 0.795
0.246655676 INDI 751 PLS 1 9605342 1267755 -1.454 1.446 2.110
0.289 0.753 1.767 1.128 2.159 1.336 1.025
-0.475 -0.202 -0.884 0.368 -0.530 2.643
0.650272284 INDI 752 PLS 1 14056971 4920422 -1.213 -1.968
-1.993 -1.046 1.279 -0.775 0.407 3.263 2.139 -0.449
-1.984 1.731 -2.797 1.457 0.108 2.632
0.058685236 INDI 758 PLS 1 14054973 4927159 -0.908 -0.485

Table36.txt

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0.554633636 INDI 761 PLS 1 12942365 6498134 -0.665 -1.799
-0.846 0.314 1.059 -0.201 0.970 1.535 -0.431 2.021
-1.589 -0.423 0.746 2.156 0.478 2.015
0.053084415 INDI 763 PLS 1 13923618 4995467 -0.229 -0.634
-0.856 -0.880 -0.626 -0.232 0.350 0.951 -0.124 1.915
0.040 -0.457 0.872 0.685 0.462 1.301
0.45218467 INDI 764 PLS 1 9062118 2318294 -0.323 0.241
-1.027 -1.525 -0.241 0.791 0.843 -0.336 -2.159 0.011
-0.549 0.541 1.581 3.375 -2.289 0.201
0.80129494 INDI 765 PLS 1 14042304 9459016 -0.923 -0.394
-0.553 0.294 0.053 0.825 -0.231 4.712 1.212 2.070
-1.419 0.155 -1.071 2.487 -0.971 2.493
0.28913541 INDI 767 PLS 1 7952766 1711335 -1.448 0.769
-1.072 0.328 1.446 1.632 -0.138 1.073 0.582 1.257
-2.127 1.934 -1.895 1.440 -1.035 0.995
0.367337829 INDI 768 PLS 1 10084836 3891212 -2.414 0.020
-0.653 0.368 -0.300 0.902 0.728 2.247 2.209 0.830
-0.249 0.819 -0.320 2.005 1.268 1.211
0.053229999 INDI 769 PLS 1 8234147 1978881 -0.414 -0.681
-1.271 -0.240 -1.117 0.555 -0.818 2.231 -0.190 1.321
0.971 0.825 -0.090 0.549 0.937 0.146
0.057613132 INDI 770 PLS 1 14568618 5528943 -1.102 -0.798
-1.240 -1.605 0.510 0.216 -0.595 0.669 1.239 0.638
-1.652 0.579 -0.587 1.192 2.210 0.146
0.664165962 INDI 772 PLS 1 9863688 2974991 -0.079 -1.481
-1.761 0.493 1.187 -0.477 1.330 3.277 0.060 1.237
-1.720 -0.369 -2.301 0.361 0.220 1.346
0.19720193 INDI 773 PLS 1 11845318 3381366 -1.643 -1.415
-0.703 -0.465 0.306 -0.842 0.797 1.356 0.592 0.577
-0.100 -0.379 -0.720 0.838 1.332 0.622
0.087049561 INDI 774 PLS 1 10569815 2404841 -0.501 0.788 0.079
0.374 -1.557 0.234 -0.184 -0.485 0.855 -0.587
0.824 -0.778 1.600 -0.196 0.915 -1.556
0.336057049 INDI 777 PLS 1 16012616 11054312 -0.705 -0.239
-0.632 -0.044 1.228 1.365 1.109 2.383 1.213 -0.021
-0.234 0.477 -3.403 1.024 0.765 1.261
0.112217529 INDI 779 PLS 1 8901414 2986474 0.140 0.390
-1.121 -1.376 -0.265 0.811 -0.276 1.753 -0.605 2.168
-1.300 -0.336 -1.533 0.555 1.091 0.475
0.048042419 INDI 780 PLS 1 9356132 2829409 -1.059 -2.036 0.381
0.062 0.471 0.990 0.368 1.253 0.153 -0.963
-0.238 -0.548 -1.327 0.589 0.901 1.183
0.08715613 INDI 781 PLS 1 7856122 1535473 -0.519 -0.488
-1.623 -0.877 -0.234 -0.407 0.766 -0.003 1.123 -1.657
-0.237 -1.167 1.194 0.977 -0.179 0.076
0.779125349 INDI 782 PLS 1 14446569 5728837 -0.174 1.683 0.657

Table36.txt

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-2.798     -1.753     -1.281     0.763      -1.137     1.105
0.253739293     INDI 783 PLS 1    10852578   3717813    1.321      1.516
-0.467     -0.607     0.197      0.723      -1.313     -2.546     -1.763     0.476
    1.797      -2.019     0.089      -0.974     0.145      0.746
0.028301273     INDI 785 PLS 1    8177211    2339386    0.520      1.071      0.568
     -0.633     1.747      0.622      -0.845     1.137      0.810      0.113
-0.604     0.340      -0.065     0.448      0.137      -0.541
0.050122115     INDI 787 PLS 1    14724764   3464792    -0.575     0.400
-2.055     -0.299     -0.341     0.452      0.393      1.378      1.477      0.628
    0.034      0.608      0.956      1.086      -0.821     1.876
0.131385039     INDI 788 PLS 1    14967689   5205531    0.480      0.381
-1.968     -0.765     1.004      -0.671     1.499      2.288      1.346      -1.386
    -0.980     0.397      -0.177     0.057      0.910      1.142
0.038181873     INDI 789 PLS 1    13703270   3722126    0.595      -0.582
-0.588     -0.941     -0.230     1.623      0.232      -0.451     0.639      1.329
    -0.931     1.331      -2.144     0.437      -0.523     0.920
0.032410294     INDI 790 PLS 1    12365978   2077160    -0.543     -0.184
-0.816     -0.404     1.222      0.334      0.221      1.083      -1.020     0.104
    0.205      -0.999     0.326      0.409      -0.177     -0.184
0.052041392     INDI 791 PLS 1    14212193   3051009    -1.230     -0.106
-0.011     -1.030     1.220      0.793      -0.001     0.613      2.261      1.020
    -0.596     -0.120     0.213      1.447      1.705      1.314
0.605204292     INDI 793 PLS 1    13226579   5519446    -1.343     0.449
-2.113     -0.828     -0.191     0.450      2.245      3.095      1.546      1.264
    -2.508     0.961      -0.822     1.508      1.013      1.973
0.156446246     INDI 794 PLS 1    12233996   5270922    -0.765     -0.746
-1.816     -0.634     0.599      0.333      1.964      2.779      1.128      -0.936
    -1.307     2.246      -1.290     0.401      0.788      1.154
0.067088308     INDI 795 PLS 1    12999302   4874578    0.147      -0.346
-0.245     -0.334     0.257      -1.196     0.646      1.783      0.984      -0.461
    -1.291     1.635      -0.532     1.321      -0.234     0.048
1               INDI 798 PLS 1    15109263   9013795    -0.293     -0.876
-0.194     -0.004     0.668      3.181      1.289      -0.576     1.636      0.924
    -1.612     -4.680     2.791      2.021      -3.468     6.259
0.236757502     INDI 802 PLS 1    14018427   7371508    0.226      0.861
-1.428     -0.162     -0.359     0.361      0.245      2.062      0.806      -0.174
    -0.646     0.537      -0.954     1.275      1.140      2.379
1               INDI 804 PLS 1    12772001   7256465    -6.937     -3.215     5.545
     11.000     -1.425     -0.144     -2.128     -4.407     -2.854     11.000
-2.911     -4.015     -1.545     4.675      -11.000    11.000
0.307507892     INDI 805 PLS 1    12025491   2976283    -1.060     0.487
-1.321     -1.376     -0.609     0.464      1.572      1.146      1.413      1.222
    0.524      -0.499     0.935      1.868      0.733      1.326
0.039206854     INDI 806 PLS 1    9169085    2758398    0.245      1.561      0.771
     0.285      0.767      1.074      -0.145     0.947      0.385      -0.294
-0.219     0.460      -2.250     -1.101     0.004      0.028
0.305209017     INDI 808 PLS 1    12257921   4640670    -1.574     0.096
```

Table36.txt

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0.102141712 INDI 809 PLS 1 9159410 2106980 -1.480 -0.776 0.880
0.251 1.617 0.335 0.167 0.820 -0.157 0.173
-1.609 2.185 -1.506 0.126 0.334 0.358
0.334325295 INDI 810 PLS 1 10377640 3078379 -1.115 -0.824
-0.777 -0.738 0.695 -0.194 0.348 2.529 1.568 0.567
-1.291 -0.331 -0.609 0.380 1.181 0.549
0.056711512 INDI 811 PLS 1 16256455 6634686 -0.664 0.784
-0.569 -0.001 -0.259 0.901 -0.964 1.364 0.767 1.107
-1.984 1.485 -0.259 0.280 0.935 2.083
0.486642457 INDI 812 PLS 1 12643278 3243593 -1.848 1.472
-0.132 0.294 1.633 0.638 -0.994 0.678 1.751 2.348
0.506 0.090 -1.434 -0.027 0.291 1.244
0.123641476 INDI 815 PLS 1 12449655 3895120 -0.926 0.794
-0.014 -0.150 0.062 -0.972 0.029 1.002 0.829 1.935
-0.898 0.088 -1.174 1.674 0.597 1.340
0.07834674 INDI 816 PLS 1 9542773 2702402 -0.460 1.161
-0.783 -0.636 -0.968 1.004 0.811 1.710 0.828 -0.040
-1.725 0.709 -2.284 0.745 1.267 1.663
1 INDI 818 PLS 1 12703144 5591665 0.788 0.982
-0.023 -3.070 0.851 4.817 -0.120 3.400 2.218 -0.579
-0.293 -2.988 -2.515 0.536 -0.631 6.711
1 INDI 819 PLS 1 11551796 2449452 -0.346 6.723
-0.983 -1.232 -0.223 2.588 -1.969 -0.439 -1.226 1.274
-1.039 -1.783 6.266 2.597 -0.493 -0.139
1 INDI 820 PLS 0 13890928 4117765 -4.678 -3.734
-2.634 2.264 1.590 2.253 -4.869 -11.000 1.496 6.917
0.983 2.121 2.315 2.662 -3.490 2.090
1 INDI 821 PLS 1 10342657 2140252 0.035 1.989 0.747
0.344 2.189 0.458 1.113 2.887 0.433 -11.000
0.476 0.174 -0.632 1.594 1.024 3.117
0.181387758 INDI 823 PLS 1 14348901 4131174 1.086 1.046
-0.531 0.333 0.051 2.709 -1.287 -0.395 0.081 0.717
0.799 -0.606 -0.349 -0.014 -0.313 -0.357
0.075786344 INDI 825 PLS 1 10940329 3820950 0.607 1.132
-0.196 -0.380 2.201 -0.454 -0.172 1.124 0.167 -0.620
-0.411 0.672 -0.689 0.949 0.152 1.301
0.021140672 INDI 826 PLS 1 12897236 3343296 -0.554 -0.744
-0.239 0.818 0.677 0.325 1.248 0.706 0.676 1.354
-1.203 0.680 -1.669 -0.021 0.781 1.090
0.2857671 INDI 827 PLS 1 8935817 2484655 -0.258 1.756
-0.716 -1.403 -0.995 2.182 -1.973 1.143 -0.915 1.572
-0.691 -0.418 -1.039 1.346 0.306 0.156
0.082983598 INDI 828 PLS 1 13186596 3529563 -0.275 0.331
-1.164 0.717 0.351 0.303 0.169 -0.020 1.280 0.308
-0.607 0.260 -0.711 0.283 1.716 2.398
0.068975517 INDI 829 PLS 1 11247548 4396989 -0.551 -1.943 0.424

Table36.txt

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0.193089922 INDI 831 PLS 1 12353841 4646277 -0.499 -0.680
-1.027 -0.217 0.666 -0.553 -0.333 1.833 2.489 1.378
0.019 1.716 -0.960 0.808 -0.273 2.265
0.097367966 INDI 832 PLS 1 12775019 4487424 -0.087 -1.169 0.388
0.380 1.055 1.232 -0.155 1.858 -0.286 -0.347
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0.380653852 INDI 833 PLS 1 12751825 2976242 -1.883 -0.458
-1.010 -0.519 0.739 -0.528 1.203 1.730 1.522 -1.561
-2.687 0.873 -1.659 1.748 1.357 0.902
0.083831574 INDI 834 PLS 1 11868017 2098884 0.458 0.618
-0.303 -0.275 -0.663 1.403 -0.413 -0.296 1.322 0.772
-0.106 -0.472 -1.501 1.510 0.934 1.171
0.110737163 INDI 835 PLS 1 12424009 2880159 -1.586 0.523 0.140
-0.497 -0.479 -0.926 0.298 0.244 1.019 -0.274
-1.218 1.139 -2.016 1.197 0.407 1.686
0.218133924 INDI 837 PLS 1 15639531 4753784 -0.323 1.085
-0.335 -0.298 0.171 -0.307 -0.032 -0.729 -1.703 0.179
0.470 -0.406 -1.352 0.450 -0.527 2.033
0.062075872 INDI 838 PLS 1 11108900 4094700 0.664 0.698 0.251
-0.499 0.552 -0.376 -0.192 0.687 0.151 -0.892
-1.405 1.722 -1.879 -0.201 0.731 1.259
0.492838958 INDI 839 PLS 1 13831409 2929114 -0.302 1.676 0.081
0.531 0.737 0.783 -0.103 -0.726 -1.823 0.321
0.129 -1.171 -0.632 0.932 -1.605 1.631
0.127172399 INDI 840 PLS 0 13130050 5043555 -1.155 -0.092
-1.301 0.126 -0.157 -0.012 -0.165 2.023 0.653 2.398
-1.464 0.679 -0.623 1.551 0.063 0.595
0.070628778 INDI 841 PLS 1 17597362 6042015 -0.736 0.245 0.249
0.440 0.143 0.514 -0.926 0.830 2.838 -0.341
-1.176 1.216 -0.823 0.981 -0.795 1.345
0.016835589 INDI 842 PLS 1 11576152 2415949 -1.457 -0.191
-0.251 -0.068 -0.030 1.293 -0.654 0.795 0.988 0.241
-1.673 0.598 -0.859 1.565 1.282 0.767
0.035431255 INDI 845 PLS 1 14628643 3275612 -0.400 0.585
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-1.609 1.396 -0.625 1.053 0.997 1.603
0.350422677 INDI 862 PLS 1 12679868 6289455 -1.087 -0.751
-0.510 -0.567 -0.585 0.252 1.498 1.055 1.631 0.123
-1.408 -0.546 -1.384 2.734 0.324 2.404
1 INDI 904 PLS 1 11989847 5791736 -1.203 0.421
-1.167 0.135 0.102 1.118 0.411 2.890 1.787 1.041
-1.865 0.875 -1.869 0.853 -0.320 2.333
0.439469728 INDI 905 PLS 1 16519216 9022260 -1.059 0.029

Table36.txt

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-1.715	3.378	-0.040	2.712	0.737643088	INDI 907 PLS 1	17608692	8967910	-2.473	-0.656
-1.697	-0.161	0.397	1.482	1.229	4.112	0.747	0.831	-2.178	1.691
-1.204	1.834	-0.600	2.692	0.554939191	INDI 908 PLS 1	13887392	8907177	-1.475	-1.116
-1.511	-0.084	-0.025	-0.063	1.558	1.425	1.353	1.967	-2.080	1.515
-0.643	1.900	0.567	2.133	0.519593435	INDI 909 PLS 1	15495271	8534908	-1.732	-0.770
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-1.373	1.804	-0.048	2.491	0.512601321	INDI 910 PLS 1	13615873	8234048	-1.328	-1.091
-1.347	-0.243	-0.393	0.082	1.205	2.680	1.844	0.397	-2.425	2.332
-0.817	2.749	-0.294	2.240	0.713464872	INDI 911 PLS 1	14956088	6751128	-1.934	-1.528
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-0.490	1.985	-0.486	2.691	0.653638519	INDI 912 PLS 1	14831618	9817654	-1.441	0.539
-2.535	0.532	-0.560	0.013	1.116	1.752	0.813	1.993	-2.383	0.902
-0.744	2.622	0.740	1.603	0.600980346	INDI 913 PLS 1	17349058	9537148	-1.412	0.144
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-0.067	1.106	-0.530	1.929	0.843388739	INDI 914 PLS 1	12793339	8309047	-1.785	0.476
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1.546	1.677	0.541	4.580	0.052797962	NL PLS 841	13001956	2370284	-0.065	0.926
-1.451	1.312	0.064	-0.098	0.672	0.166	-0.014	-0.602	0.122	0.855
-0.423	1.026	1.594	1.455	0.072946017	NL PLS 841	9530114	2165016	0.774	-0.048
-0.053	0.688	-0.030	-1.139	-0.499	0.334	0.438	-0.188	-0.260	-0.679
-1.690	1.355	0.855	1.937	0.10627693	NL PLS 842	12226636	2000598	-0.868	-0.050
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-0.618	-0.808	0.673	-0.112	0.149085442	NL PLS 842	10165671	1907408	-1.651	0.142
-1.612	0.534	-1.583	1.291	-0.301	0.636	0.244	-0.275	0.044	1.462
1.250	-0.026	0.229	0.627	0.048662897	NL PLS 879	9295466	1959958	0.508	0.422
0.447	0.087	0.644	-0.794	-0.391	0.811	-0.442	0.343	0.453	-1.232
0.607	-0.803	-2.335	-1.670	0.117389705	NL PLS 879	8333576	1739062	-0.735	1.030
-0.028	0.570	1.022	0.755	0.446	0.320	-3.179	0.439	1.932	-1.993
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Table36.txt

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2.542 -0.003 0.627 -1.148 0.676 -0.046
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-0.152 -0.384 -0.641 -0.982 -1.145 -1.295
0.352914411 NL PLS 882 10611861 2682215 0.778 0.648
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-0.422 -0.055 0.609 -0.612 0.575 1.027
0.024732494 NL PLS 883 10385209 2789015 0.439 0.233
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0.965 -0.002 -1.725 1.171 -1.025 -1.061
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0.022491753 NL PLS 885 11514741 2906456 -0.316 -0.819 0.462
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0.017731147 NL PLS 886 10146950 4105980 0.700 -0.032
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-1.612 1.143 -0.299 -0.043 0.733 0.369
0.018292195 NL PLS 887 10994171 3866745 -0.330 1.166
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0.660 1.722 -1.048 1.256 -0.307 -0.040
0.050460479 NL PLS 888 9079932 3278971 0.261 1.000
-0.729 -0.637 0.884 -0.791 -0.308 0.758 0.268 1.459
0.210 0.568 -0.309 1.471 0.085 1.628
0.074548638 NL PLS 889 10222566 1463967 -0.695 -1.039 0.283
1.449 -0.721 0.703 0.193 0.622 2.000 0.505
0.739 0.055 0.356 0.484 0.604 0.650
0.41819625 NL PLS 933 10560495 2741870 -1.065 -1.051
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-0.035 -1.306 0.562 0.283 -1.920 1.126
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Table36.txt

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0.2455061 NL PLS 936 10570936 5211328 -0.456 -0.257
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-1.446 1.224 -0.164 1.921 -0.141 0.298
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0.040514725 NL PLS 937 9049336 2456947 -0.506 0.130 0.508
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-0.705 -0.919 0.054 -1.178 0.040 -0.171
0.045785772 PANC 482 PLS 1 11904277 2606551 -0.883 1.131
-1.143 1.284 -0.445 -0.052 0.723 0.380 0.293 -0.426
-2.458 1.862 0.251 0.840 0.022 1.653
0.163944322 PANC 483 PLS 1 10753293 4000932 -2.388 -0.418
-1.641 -0.277 0.300 0.790 1.654 1.504 0.156 0.923
-0.595 0.443 -0.092 0.596 0.227 1.565
1 PANC 484 PLS 1 10915979 4040945 -0.627 -0.597
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-2.111 1.214 -0.794 1.461 0.877 1.694
0.066031873 PANC 485 PLS 1 11620942 1509605 -1.378 1.721
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-1.006 0.726 0.595 0.970 -1.878 2.337
0.061327054 PANC 486 PLS 1 12571432 2484477 -0.212 0.559 1.266
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1.231 1.244 1.148 -0.728 -0.600 1.036
0.031079002 PANC 487 PLS 1 12309100 2690311 0.588 1.598
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1.558 1.603 -0.009 0.524 -1.088 0.344
0.312380208 PANC 488 PLS 1 11908919 4855077 -0.789 -0.012
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0.581224649 PANC 490 PLS 1 11437108 4429748 -2.103 -0.662 0.359
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-0.791 0.970 0.735 1.462 -0.539 3.217
0.125591251 PANC 491 PLS 1 13135062 3150432 -0.037 0.754 0.940
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-1.433 1.208 -0.641 0.940 -0.578 -0.649
0.177383856 PANC 492 PLS 1 12325125 3533498 0.989 2.562
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0.372924482 PANC 493 PLS 1 9657357 5835538 -0.803 0.465

Table36.txt

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0.168676336     PANC 548 PLS 1    10311637   1631420    -1.140     1.731
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0.959 0.993 1.610 -2.099 1.357 1.090 1.542
0.293 0.079 1.034 0.242 -2.094 -0.686
0.019937796 PANC 648 PLS 1 7523575 1472271 -0.526 -0.889 0.723
-0.123 -0.024 -0.156 2.181 0.867 1.285 1.225
-1.876 0.137 0.302 1.260 -0.258 -0.278
0.098694177 PANC 649 PLS 1 10868511 4575592 -0.223 0.114
-1.395 1.020 -0.023 0.534 -0.316 2.490 0.877 -0.196
-1.079 2.180 -0.432 0.654 -0.518 1.141
0.092203253 PANC 650 PLS 1 9464103 3314823 -1.807 -0.299
-1.385 -0.764 0.007 -0.212 0.261 2.103 0.770 -1.088
-0.495 -0.063 -1.282 -0.654 1.238 1.091
0.844065732 PANC 651 PLS 1 9999330 5718787 -1.667 0.321
-2.626 0.512 0.807 0.923 2.142 4.497 2.712 1.789
-1.395 1.871 -0.243 1.767 0.283 1.635
0.185784036 PANC 652 PLS 1 9008555 2085113 -1.678 0.125
-1.047 1.205 1.179 -0.071 -0.477 3.532 -1.235 0.532
-0.146 -0.286 -0.248 0.941 0.505 0.157
0.130473186 PANC 653 PLS 1 8778255 1394024 -1.463 0.868
-0.011 -0.658 -1.017 1.797 1.417 1.157 1.052 2.328
-1.007 0.896 -0.449 1.422 -1.106 0.288
0.033410123 PANC 654 PLS 1 11052308 4123851 0.561 0.459
-1.152 -0.208 1.125 0.992 -1.711 0.676 -0.769 1.010
-1.033 1.606 -0.122 -0.333 -0.078 1.209
0.019903651 PANC 655 PLS 1 8328228 2136244 -0.311 1.257 1.322
1.001 -0.182 1.282 -0.509 0.067 -0.100 -0.172
0.861 0.090 0.819 -0.188 -1.633 -0.694
0.045096482 PANC 656 PLS 1 8407307 872129 -0.641 -0.366
-0.522 0.639 -0.128 1.365 0.096 1.585 0.332 -0.530
0.243 1.419 0.622 -0.273 -1.245 0.561
0.035317323 PANC 657 PLS 1 9134804 2878099 0.408 -0.146 0.174
0.227 -0.626 0.058 -1.202 1.661 0.668 0.662
-0.084 1.045 -2.004 -0.526 -0.657 0.242
1 PANC 658 PLS 1 10070919 2787896 -0.660 -1.153
-1.474 -0.694 -0.725 -0.580 0.919 1.013 0.354 0.478
-2.696 -0.211 -1.082 0.187 0.360 0.511
0.018015728 PANC 659 PLS 1 9601030 3605770 -0.448 1.423
-1.002 0.880 1.688 1.316 0.549 0.462 -0.317 1.462
0.470 0.845 -1.403 -0.983 -0.778 0.293
0.028727098 PANC 660 PLS 1 8691144 1420518 0.430 -0.256 0.536

Table36.txt

```
     0.410      -0.559     0.870      0.931      0.605      -0.759     1.739
0.667      -0.573     -0.235     0.740      -0.698     1.071
0.550108663     PANC 661 PLS 1    10289724   7248350    -2.126     -0.473
-2.169     -0.496     0.752      1.083      1.531      2.971      2.661      0.585
    -1.856     3.073      -0.505     0.167      1.338      0.786
0.055518825     PANC 662 PLS 1    9642226    2670316    0.143      -0.054     0.083
     0.398      -0.060     -0.188     -1.135     0.694      1.307      0.706
-0.762     0.827      -0.705     0.759      0.744      0.439
0.498909244     PANC 663 PLS 1    9133264    4781659    -1.648     -1.227
-2.574     0.461      0.524      0.320      1.468      3.023      2.107      1.196
    -2.106     3.699      -1.266     0.691      0.678      0.573
0.141417256     PANC 664 PLS 1    8896543    1538292    -1.371     -0.810
-0.946     0.863      -0.777     0.690      0.934      0.644      1.314      1.765
    -2.535     1.175      0.812      1.578      0.431      0.113
0.047066874     PANC 665 PLS 1    9658101    4389457    0.151      -0.909
-0.970     0.354      1.289      -0.396     -0.698     1.568      -0.110     1.108
    0.190      -0.206     -0.590     -0.756     -0.067     0.916
0.711558989     PANC 666 PLS 1    10371611   5384052    -2.118     -0.444
-2.353     -0.978     -0.049     -0.023     1.338      3.124      2.595      3.441
    -2.240     2.574      -1.308     1.000      1.450      0.969
0.716748116     PANC 667 PLS 1    12009339   4595257    -2.283     -0.608
-1.922     -0.034     0.576      1.846      0.679      3.394      1.148      1.625
    -2.085     1.390      0.343      1.781      0.785      1.777
0.501041661     PANC 668 PLS 1    11109432   4455501    -1.389     -0.421
-1.362     1.039      -0.587     0.708      0.360      2.635      0.819      2.536
    -0.805     1.622      -0.784     1.122      0.076      1.570
0.483584194     PANC 669 PLS 1    11977734   3638779    -1.391     -0.435
-0.021     1.437      0.049      1.143      0.841      2.834      0.094      2.014
    -1.190     1.663      -0.681     0.972      -0.382     0.130
0.101272302     PANC 670 PLS 1    7429330    701281     0.195      2.307      0.055
     -0.492     2.132      0.939      0.334      0.843      0.891      -0.170
0.003      -1.332     0.603      0.265      0.088      -1.588
0.045276245     PANC 671 PLS 1    9915356    4467572    -0.049     -0.272
-0.741     -0.386     0.316      1.603      1.240      1.109      -0.709     0.153
    -0.746     1.614      -1.012     0.217      -1.082     1.932
0.08516035      PANC 672 PLS 1    9729306    2596620    0.523      1.340      0.888
     1.008      -0.586     0.798      -0.789     -0.128     -1.088     0.619
1.777      -0.515     0.451      -0.333     -0.560     0.512
0.302521637     PANC 673 PLS 1    11107668   3191906    -0.681     0.972
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    0.055      0.868      0.337      2.942      -1.110     1.328
0.350396708     PANC 674 PLS 1    8977062    4511509    -0.813     -2.029
-2.075     0.571      0.372      -0.398     -0.028     1.866      0.621      1.305
    -1.948     2.536      -0.819     0.390      -0.312     1.772
0.163969605     PANC 675 PLS 1    7821392    1663209    -0.955     -0.474
-1.397     0.420      -0.401     0.599      0.060      0.464      3.042      1.286
    -1.715     0.748      1.523      -0.158     -0.290     0.940
0.025749046     PANC 676 PLS 1    10717907   2810880    -0.035     0.117
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Table36.txt

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0.085520485 PANC 677 PLS 1 9279389 4464692 0.048 0.445 0.017
0.023 -1.389 0.448 -0.796 0.818 0.466 -0.822
-1.233 0.706 0.069 0.826 0.623 2.482
0.224070776 PANC 678 PLS 1 10327754 3451132 -2.375 -0.118
-1.053 0.507 -0.389 -0.117 0.172 1.438 0.649 1.438
-0.612 2.605 -1.035 0.550 0.974 1.999
0.016840862 PANC 679 PLS 1 8505586 1665732 -0.591 1.764 0.392
1.885 0.021 1.034 -0.064 -0.646 0.267 -0.069
-0.251 0.349 0.138 -0.071 0.954 0.647
0.115273659 PANC 680 PLS 1 7861364 1332200 0.311 0.450
-0.011 0.182 -0.419 0.286 -0.264 -1.115 -0.538 1.257
-0.500 0.580 -0.286 0.730 -0.427 -0.381
0.235503672 INDI 915 PLS 1 9952477 2962358 0.725 1.908 0.313
-0.655 0.522 1.407 -1.478 -3.247 -0.653 -0.245
1.375 -2.068 -0.889 -0.268 -0.145 -0.015
0.439860518 INDI 916 PLS 1 2340134 1726372 0.947 0.705
-2.179 1.182 -1.407 0.078 0.787 1.187 -0.711 1.036
-2.139 -1.460 -1.581 0.326 -0.112 2.462
1 INDI 917 PLS 1 2351153 1676439 0.545 0.687
-2.408 0.005 -4.964 -0.095 0.723 0.907 1.211 -0.168
2.679 -0.899 -1.074 0.799 -0.586 11.000
0.036860793 INDI 918 PLS 1 2613998 1521976 -1.270 -0.002
-0.928 -0.679 -0.147 -0.661 1.265 1.825 0.887 -0.264
0.118 -0.049 -0.686 0.564 0.547 0.601
0.096691866 INDI 919 PLS 1 11735858 3313917 -0.978 -0.653 0.407
-0.572 -1.290 0.182 -0.445 -0.483 -0.423 1.156
0.111 -0.492 0.150 1.070 1.763 0.946
0.711696192 INDI 920 PLS 1 10813974 3209144 -2.569 -0.794
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-3.411 -0.561 -0.694 0.628 1.070 0.592
0.256083484 INDI 921 PLS 1 11493662 3185284 2.076 0.126 0.005
0.775 -0.929 -0.494 -0.070 0.385 -2.531 1.752
0.167 -1.093 -1.445 -0.128 -0.638 0.896
0.02739911 INDI 922 PLS 1 11416289 3625654 0.069 -0.858 0.077
0.597 -0.424 -0.289 0.556 1.464 1.359 -0.557
-2.265 0.430 -1.338 0.182 0.747 0.213
0.329688069 INDI 923 PLS 1 2177110 1366641 0.974 0.812
-0.308 -0.529 -2.646 0.138 -0.906 -1.258 -2.569 1.201
1.090 -1.741 0.492 -0.068 0.267 1.341
0.079929777 INDI 924 PLS 1 10972340 3059478 1.165 1.003 0.319
-0.954 -0.190 0.196 0.030 -0.649 -1.760 -0.250
0.910 0.322 -0.379 -0.550 -1.034 0.343
1 INDI 925 PLS 1 2359395 1695671 -0.292 11.000 2.435
5.204 -3.314 -2.353 -1.990 0.240 -2.031 -4.914
-0.343 3.064 11.000 11.000 1.133 6.978
0.016000698 INDI 926 PLS 1 12200341 2840428 -0.542 -0.631

Table36.txt

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-1.141 0.560 0.078 1.008 -0.090 2.423
0.185666272 INDI 927 PLS 1 11442120 1895302 1.196 1.253 0.447
1.531 -0.717 -0.829 -0.954 -1.378 -1.283 1.726
0.752 0.319 0.198 -1.443 0.324 0.855
0.265219253 INDI 928 PLS 1 12079236 3330261 -1.583 -0.411
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-1.264 0.374 0.012 -0.307 0.879 1.750
0.064985435 INDI 929 PLS 1 2086023 1503055 0.689 -0.214
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-0.771 0.975 -1.597 1.565 1.533 1.413
0.107580592 INDI 930 PLS 1 10466887 3382013 -1.430 0.196 0.190
1.125 -0.891 1.360 0.369 0.512 1.723 1.373
-1.137 0.537 -1.467 1.204 -0.347 0.936
0.007165144 INDI 931 PLS 1 9967713 3599706 0.101 0.323
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-1.329 0.543 -0.742 0.742 0.646 0.920
1 INDI 932 PLS 1 11541471 3528688 1.125 3.892 1.027
3.664 2.960 4.430 1.362 -3.531 0.342 -0.825
1.549 2.865 -2.974 -0.202 -3.004 11.000
0.072765056 INDI 933 PLS 1 2248379 1418141 0.442 1.956
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0.028067125 INDI 934 PLS 1 11681439 3855958 0.475 1.439
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0.069340623 INDI 935 PLS 1 1912642 1422459 -1.614 -1.012
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-0.091 0.621 -0.768 0.437 0.446 0.640
0.109208494 INDI 936 PLS 1 2107860 1509080 -0.203 0.426
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0.504 -0.159 -1.077 0.575 1.337 1.405
0.054914212 INDI 937 PLS 1 2140759 1516657 -0.793 0.749
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-0.603 1.126 -0.639 -0.462 0.844 1.131
0.062759784 NL PLS 531 1735293 994146 -0.623 -0.780
-0.317 -0.193 -0.884 0.202 0.297 0.443 0.739 0.071
-0.285 1.255 -0.486 1.872 2.392 -0.035
0.0567841 NL PLS 532 1737348 1134771 -0.232 -1.016
-1.303 -0.241 1.035 -0.642 1.358 2.349 1.814 0.001
-0.509 1.591 -0.832 -0.591 0.455 0.477
0.407030477 NL PLS 533 1719020 847352 -0.369 -3.271
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-1.349 3.003 -2.470 2.055 0.781 1.317
0.104592096 NL PLS 536 1835897 880394 -0.018 -0.455 0.923
-0.612 0.646 0.719 -0.355 1.621 -0.976 1.608
1.265 0.087 -1.779 0.484 -0.177 1.613
0.143714411 NL PLS 538 10917916 984801 1.050 -0.186

Table36.txt

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-0.115 -1.838 0.411 -1.893 -0.793 -0.458
0.01505321 NL PLS 542 9554092 898113 0.457 -0.242
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0.543 -0.021 0.567 -0.923 0.854 -0.537
0.042742941 NL PLS 543 1575675 774490 -0.447 0.142 0.195
0.983 -0.433 -0.841 1.188 2.358 0.175 1.419
-1.142 0.058 -1.392 0.843 0.991 -0.118
0.311714988 NL PLS 544 1542914 950179 0.475 -1.988
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-1.541 1.244 -0.820 0.333 1.934 2.039
0.098906724 NL PLS 545 1575170 1001362 0.757 -1.007
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-1.745 2.444 -0.625 -0.329 -0.137 0.709
0.044085589 NL PLS 546 1585060 936441 -1.073 -0.098
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-2.134 1.585 -0.079 0.644 1.468 0.558
0.119153948 NL PLS 547 1662165 913393 -0.478 -1.726
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-1.160 -0.376 -1.544 -1.394 0.633 -1.325
0.012883343 NL PLS 548 9493490 1756307 -0.299 0.925 0.256
-0.745 0.876 -0.268 1.140 0.890 -0.077 0.707
-1.089 0.496 -0.106 1.014 -1.628 0.048
0.601931124 NL PLS 549 9339560 1666978 -0.060 -3.040 0.508
-0.095 2.972 0.002 1.454 2.866 2.470 -0.866
-1.373 0.307 -1.314 -1.124 0.952 0.935
0.403422521 NL PLS 550 1290096 660726 0.621 -1.906
-1.475 0.773 3.402 0.216 1.191 4.098 0.912 -1.216
-0.194 2.585 -2.377 -1.618 0.714 2.372
0.221655218 NL PLS 551 1773697 849826 -0.156 -0.708
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-0.471 1.119 -0.083 0.339 1.023 1.720
0.053258437 NL PLS 552 1389053 778687 -0.295 -1.400
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-0.425 0.805 0.130 -0.038 0.949 0.506
0.149849595 NL PLS 553 1439894 730342 -1.088 -1.657 0.708
-0.162 0.535 -0.746 0.831 2.979 0.689 -0.324
0.188 -0.074 -0.964 0.791 -0.036 0.860
0.071106263 NL PLS 554 1295053 720005 -1.100 0.639
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-0.145 0.967 -0.709 0.241 -0.219 0.773
0.03197879 NL PLS 555 1366259 702266 0.480 -0.458
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-0.491 -0.082 -0.019 1.891 0.209 0.537
0.060679885 NL PLS 556 1502802 814203 0.032 -0.836

Table36.txt

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0.15162052 NL PLS 558 9265371 1154262 1.200 -0.389 1.471
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0.381290068 NL PLS 559 9888878 704204 3.462 0.260 0.750
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2.265 -0.324 0.623 1.209 1.141 1.579
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0.114703564 NL PLS 562 9692278 1264305 1.658 -0.160
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0.070946576 NL PLS 563 1534254 822662 0.870 0.480 0.654
0.783 0.189 -0.210 0.165 0.475 -0.398 0.794
0.822 0.106 -0.807 -0.565 0.526 0.160
0.086974367 NL PLS 564 1678459 1061240 0.603 -0.494
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-1.084 -0.173 0.273 2.914 -1.012 0.481
0.059807502 NL PLS 565 7598210 618904 0.149 -0.091
-0.026 0.785 -0.213 0.366 1.217 0.155 -2.162 0.311
-0.490 1.846 -1.868 -0.225 -1.383 -1.286
0.437289447 NL PLS 566 8477303 894892 -0.461 -1.586
-0.493 -0.075 -0.473 -1.375 2.328 2.242 -0.423 -2.346
-0.047 1.118 -0.491 -0.639 1.507 2.725
0.008235305 NL PLS 567 9077873 444080 1.265 -0.028 1.048
0.420 -0.354 0.121 -0.260 0.304 0.331 -0.345
0.189 1.855 -0.164 -0.264 0.183 0.393
0.056204531 NL PLS 568 11806243 748079 0.197 -0.446
-1.277 0.687 -0.838 -0.312 -0.118 -0.146 -0.399 -0.240
0.101 1.363 -0.139 -0.371 1.880 -0.408
0.08828534 NL PLS 569 7893915 605291 -0.385 -0.009
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0.223366252 NL PLS 570 1591545 813883 0.010 -0.790
-0.339 -1.507 0.317 -0.358 1.506 3.098 1.909 -0.587
-2.357 1.666 -0.216 0.113 0.128 1.418
0.280227187 NL PLS 571 9061379 1126657 0.981 0.493 1.315
1.510 0.519 -0.312 -2.134 -1.175 -1.092 0.813
1.665 -0.093 1.294 -1.541 -2.060 -0.324
0.168262314 NL PLS 572 9619924 1228194 0.115 -0.477 0.052
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Table36.txt

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0.076963966 NL PLS 575 8463683 576489 -0.733 -0.956 0.950
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0.227592087 NL PLS 577 1595485 706725 -0.413 -1.202
-0.958 1.129 0.098 -2.714 -0.751 -0.085 1.518 0.904
-1.638 0.004 -1.044 0.641 0.946 1.359
0.040353024 NL PLS 578 10029773 1139749 -1.278 -1.125 0.923
0.118 -0.407 -1.924 0.006 -0.890 -1.427 0.008
0.410 0.219 -0.656 0.483 1.595 0.682
0.151274511 NL PLS 582 1414517 803450 -1.349 -0.220
-1.289 -0.479 -0.545 0.671 1.699 1.888 0.647 -1.287
-0.188 0.273 -2.189 1.297 0.097 0.145
0.23181663 NL PLS 584 8204294 473538 -0.386 -2.064 0.088
0.236 0.457 1.709 0.670 0.401 -2.025 -0.280
-0.280 -0.138 -0.288 -0.885 1.884 2.491
0.092927695 NL PLS 585 9322776 529620 0.006 -1.413 0.329
-0.035 0.570 0.157 0.504 -0.874 2.234 -1.213
0.490 0.572 -1.540 1.844 0.454 2.008
0.031035555 NL PLS 586 8677564 490488 1.736 -0.802 0.536
2.064 -0.848 -0.324 0.393 1.041 -0.779 -0.164
-0.449 0.460 0.211 0.754 1.130 -1.488
0.069166254 NL PLS 588 8753747 377489 1.991 0.089 0.924
-1.548 1.209 0.121 0.768 -0.086 -0.237 0.277
0.686 -0.211 0.502 -0.926 0.479 0.169
0.022502843 NL PLS 594 7485226 584614 0.950 0.563 0.934
0.351 0.832 0.022 -0.068 -2.027 -0.498 -1.151
1.309 0.820 -0.511 -0.907 0.187 0.656
0.011264654 NL PLS 595 9202981 393544 -0.268 -0.700
-0.198 1.280 -0.944 -0.465 -0.503 -1.485 -0.481 0.836
0.774 -1.031 -0.700 -0.089 0.132 -0.701
0.148640777 NL PLS 599 9920772 487774 0.754 -0.545
-0.020 2.016 0.992 1.691 0.028 2.591 0.960 -1.339
0.183 0.490 -1.174 -0.141 -0.473 -0.129
0.266072782 NL PLS 601 9184453 759395 1.668 -0.569 0.629
1.144 1.227 1.639 1.962 2.578 -0.373 -0.717
0.091 1.065 0.505 -0.860 -1.457 0.047
0.024575316 NL PLS 602 10091068 501973 0.195 0.470
-0.508 1.148 0.414 0.116 2.010 0.454 0.124 0.182
-0.799 1.247 -0.849 -0.557 -0.309 0.721
0.01065849 NL PLS 607 9578318 746827 0.872 -0.965 0.554

Table36.txt

```
     0.614      -0.736     0.289      -1.228     0.091      0.082      -0.515
0.215      1.481      -0.906     0.468      1.175      -0.822
0.235538349     NL PLS 608        9355284    714126     2.166      0.025
-0.319     2.318      -0.054     -1.043     1.047      -0.373     -0.949     -0.110
    0.609      -0.834     0.466      0.720      -1.975     -2.038
0.143779048     NL PLS 609        10005931   1340362    0.884      -0.404
-0.065     0.113      1.475      -0.417     -0.933     2.890      1.856      1.365
    -0.448     -0.021     -0.725     0.557      1.056      1.418
0.072840716     NL PLS 613        9141852    720966     1.014      1.262
-1.558     1.166      -0.091     1.285      -1.452     -0.058     -0.361     -0.321
    3.023      -0.027     -1.852     0.543      -0.409     0.495
0.068636463     NL PLS 614        8826045    626972     0.934      0.619
-0.436     -1.137     -0.081     0.754      -0.018     -0.576     -1.006     0.699
    1.096      0.465      1.126      1.195      0.073      -1.726
0.00828221      NL PLS 617        8707244    593851     0.305      -1.170     0.533
     0.311      0.653      1.003      1.460      0.588      0.409      0.526
-0.026     0.929      -0.573     0.552      0.198      -0.923
0.019845961     NL PLS 618        9005713    550612     0.265      -0.718
-0.016     -0.107     0.030      -0.491     0.605      -0.132     0.478      -0.544
    -0.516     0.727      1.610      0.349      -0.591     -0.559
0.174434726     NL PLS 620        9273318    1088489    -0.690     -2.142     0.118
     -0.513     0.250      -1.188     0.766      1.156      1.950      -1.360
-0.564     0.204      -0.277     0.610      1.452      1.179
0.051562187     NL PLS 622        7853132    432652     -0.571     0.107      0.515
     1.454      -0.295     3.127      -0.439     0.712      1.100      -0.261
0.082      0.865      -1.103     0.096      -0.493     0.938
0.07699903      NL PLS 623        8611500    384739     1.086      -0.529     0.173
     0.523      -0.117     0.192      0.485      1.034      -1.069     -0.201
0.934      0.167      0.659      -1.278     2.117      0.677
0.089869409     NL PLS 625        10058960   477192     -0.895     1.866
-0.445     -0.393     -0.932     1.839      1.686      0.708      -0.624     0.780
    0.261      -0.216     0.183      0.174      0.034      0.473
0.038747852     NL PLS 626        9235038    500924     -1.370     -0.157
-0.569     1.440      0.069      0.184      -0.014     -0.284     -1.760     -0.303
    0.715      0.543      -0.344     0.332      0.255      -0.085
0.172784211     NL PLS 627        9785983    667525     -0.715     -1.129     0.397
     0.855      -0.631     1.526      0.009      -0.390     -1.463     -1.471
1.023      1.127      -0.206     0.649      0.673      -0.058
0.171059228     NL PLS 627        8674556    508489     0.552      1.484      0.812
     0.674      -0.825     1.460      0.389      -1.227     -1.189     -0.796
0.921      0.600      -2.073     -1.087     0.244      0.094
0.048109044     NL PLS 628        8775004    1246670    0.289      -2.002     0.788
     -0.615     0.429      -1.739     -0.570     0.958      1.210      0.410
0.295      0.343      0.902      0.629      0.365      -1.176
0.022254519     NL PLS 628        1198596    606864     0.026      0.636      0.739
     1.458      0.516      -1.631     -0.969     1.322      1.159      -0.038
-1.238     0.796      0.367      0.598      0.369      -1.425
0.068375885     NL PLS 865        10852566   615552     -0.811     0.664      1.762
```

Table36.txt

1.349 -1.922 0.848 -0.734 -0.676 -0.991 1.063
1.102 0.958 0.543 -0.807 -0.989 -1.657
0.04889982 NL PLS 866 7074630 374036 0.908 0.631 1.280
-1.834 -0.525 1.597 0.152 0.873 -2.055 0.540
1.953 -0.458 -1.114 0.137 1.710 -1.057
0.050664526 NL PLS 873 7732489 486891 1.293 0.349 0.355
-0.026 -1.005 -0.210 0.370 0.566 -1.764 0.150
0.363 -0.735 -1.409 -0.142 0.684 -1.398
0.129671854 NL PLS 874 7660573 438379 -1.079 0.049 1.293
-0.270 -0.271 -2.025 -0.017 0.606 1.083 0.154
0.814 0.285 -0.851 1.201 0.167 2.723
0.178355739 NL PLS 875 9372250 455926 1.459 1.312 0.392
-1.079 1.227 -0.020 -0.456 0.681 -1.033 1.253
-0.588 -1.080 0.102 -1.894 0.226 0.908
0.049848873 NL PLS 876 8034227 313146 -0.362 -0.221 1.404
-0.579 -0.511 -0.734 0.517 0.854 0.071 -0.121
-0.345 0.868 -1.240 -0.790 -0.643 0.879
0.027418214 NL PLS 877 9075149 678827 -1.205 0.376
-0.287 -0.493 -0.064 0.290 0.759 -0.128 0.038 0.649
-0.605 2.090 -0.322 0.254 -1.202 1.927
0.161932748 NL PLS 878 9671977 466657 0.440 1.577 0.069
-1.354 0.364 -0.468 0.148 0.146 0.279 2.234
2.852 0.446 0.240 -1.134 -2.212 -0.433
0.208847332 NL PLS 879 11858098 621073 -0.397 -1.136 0.699
-0.279 0.644 1.752 0.007 2.756 -0.213 0.191
0.616 -2.329 -0.363 -0.720 -2.436 1.374
0.009262955 NL PLS 880 9344847 588542 -0.490 0.487
-1.532 1.670 -0.411 0.265 0.884 -0.794 1.161 -0.164
0.030 1.291 1.465 0.287 0.536 0.051
0.072252369 NL PLS 881 10173933 411072 1.022 0.043
-0.774 -0.152 -0.157 -0.714 0.150 -0.473 0.694 1.073
0.325 -1.848 -0.536 -0.977 1.016 -0.344
0.019700166 NL PLS 882 12751611 703997 1.077 -0.220 0.636
-1.051 0.007 -0.342 -0.636 -2.110 -0.528 0.527
0.756 0.164 -1.139 1.274 0.036 0.316
0.123730074 NL PLS 883 8552026 576934 -0.484 1.200
-0.450 -1.124 -0.474 -1.206 -1.580 0.228 2.150 2.137
-1.615 1.494 -0.345 -0.918 -0.020 0.095
0.126509127 NL PLS 884 14179578 772445 1.316 1.808 0.045
-0.363 0.258 1.034 -0.704 -0.295 -2.488 -1.144
0.882 -2.190 1.541 -1.115 -0.369 -1.336
0.086393037 NL PLS 885 12096091 624094 0.207 -1.089 0.884
1.025 0.459 0.888 -1.639 -1.184 -0.229 -0.618
-0.181 1.184 -1.972 1.699 0.934 0.110
0.09908762 NL PLS 886 10787008 1674296 -0.676 -0.467 0.143
0.841 1.043 0.371 0.521 0.982 -0.050 1.429
-0.163 -0.439 0.248 0.227 -0.046 0.491
0.223617172 NL PLS 887 12129110 1039129 0.422 0.519 0.811

Table36.txt

0.891 -0.057 0.083 -1.983 1.185 -1.572 0.083
1.164 0.271 -1.380 1.093 0.319 -0.117
0.018981693 NL PLS 888 11195616 1072317 -0.632 1.035
-0.284 -1.095 0.076 1.057 0.604 0.309 0.148 0.261
1.924 0.103 0.993 0.216 -0.255 0.935
0.016882404 NL PLS 889 8501091 445273 1.377 1.141
-1.252 0.726 -0.791 1.056 -0.677 0.785 -1.194 0.393
0.500 -1.197 -0.101 -0.323 -0.379 -0.385
0.026428006 NL PLS 890 10736106 1755458 1.075 0.704 1.259
1.065 -0.158 0.671 -0.080 0.389 -0.828 -0.513
-0.763 -0.919 -0.741 -0.420 0.462 -0.535
0.065380673 NL PLS 891 10351129 1367327 0.574 2.245 0.442
1.124 -0.318 0.512 -1.155 1.775 1.150 -0.339
0.469 -0.501 -0.046 0.761 -1.159 -1.457
0.020204308 NL PLS 892 9803645 1685757 0.922 -1.086 0.283
0.437 1.459 -0.393 0.202 0.289 0.149 0.509
0.801 -1.250 -0.656 1.584 -2.139 -0.161
0.371544716 NL PLS 893 10777732 1287714 0.833 1.998
-0.442 -0.867 1.229 -1.739 -0.722 -0.493 -1.489 0.215
-0.640 0.565 -0.120 -0.066 -2.829 0.853
0.054632293 NL PLS 894 11184905 703683 1.125 0.602
-1.545 -0.360 1.691 2.518 -0.319 -1.086 0.629 1.408
-0.134 0.369 0.493 -0.233 -1.340 -0.655
0.189364605 NL PLS 895 11540685 860218 1.564 0.762 0.294
-0.728 -1.942 0.377 0.763 0.214 -0.919 0.851
1.121 -0.101 -2.397 0.378 -0.596 0.789
0.081048833 NL PLS 896 8519633 337102 -0.402 -0.568 0.807
-1.010 2.099 0.184 0.176 1.302 0.518 -0.762
0.290 0.843 -2.104 -1.124 -0.870 -0.328
0.11921526 NL PLS 898 11082955 572264 0.232 1.562 0.253
0.790 -0.497 0.783 0.941 -0.744 -1.511 -0.972
1.274 -1.082 2.436 0.249 0.762 -0.280
0.013473865 NL PLS 899 8193544 460863 0.752 0.678
-0.180 0.765 -0.407 1.266 -0.812 0.724 -0.548 -1.919
-0.604 -0.110 -1.480 -0.226 0.101 0.213
0.027286302 NL PLS 900 10276628 572400 0.121 0.417 0.829
1.508 1.239 1.189 -0.814 0.302 -0.621 -0.847
-1.011 -0.115 -0.795 -0.948 -0.660 0.360
0.200744183 NL PLS 901 11427039 642045 -0.334 -0.465 1.234
0.340 0.730 -0.654 0.710 2.054 -0.407 0.225
-1.055 -0.750 0.018 -2.037 -0.180 1.021
0.334299618 NL PLS 902 10762419 917697 1.314 1.869 0.737
-1.085 -0.368 0.589 -1.984 -1.424 -1.337 -1.200
-0.718 -1.778 2.892 -1.736 -2.313 0.344
0.092309178 NL PLS 903 11725756 630656 0.355 1.040
-2.176 1.336 -0.598 1.792 -0.561 0.254 -1.385 0.409
-0.796 -1.689 -0.349 -0.188 -0.033 0.088
0.175149295 NL PLS 904 10345008 593964 0.795 0.017 1.618

Table36.txt

```
     3.069      0.806      -0.792     -0.731     -1.397     0.688      -0.992
0.495      -0.151     1.553      -0.869     -0.924     1.027
0.070652051     NL PLS 905         9163824    345603     2.164      0.665      0.425
     1.111      -0.585     -0.017     1.098      -0.539     -3.297     0.483
-0.969     -0.264     -0.483     0.762      0.013      -0.152
0.009300783     NL PLS 906         10221837   1396066    -0.295     0.306      1.541
     -0.322     -0.295     1.180      0.163      -0.411     -0.348     -1.199
-0.744     1.198      -0.336     0.009      -0.400     0.758
0.038309494     NL PLS 907         9156073    474142     -0.394     1.212      0.724
     -0.488     -0.640     0.904      0.541      -0.447     -3.091     -0.246
1.089      -0.102     0.189      0.082      -0.035     0.676
0.035415097     NL PLS 908         7730013    284425     1.235      1.075      0.174
     -0.467     -1.033     -0.147     1.065      0.983      -0.671     0.406
-0.123     2.589      0.571      0.035      -0.229     -0.499
0.258707167     NL PLS 909         12262906   631589     0.638      1.123      1.315
     0.242      0.151      0.980      0.024      -1.540     -2.073     -0.547
1.604      -0.089     -1.373     -0.768     -0.067     1.826
0.049672245     NL PLS 910         10715613   574208     0.295      1.046      1.014
     0.130      -0.463     0.028      -1.188     -0.766     -2.306     -1.478
0.956      -0.129     0.568      0.425      0.626      -1.618
0.057134357     NL PLS 911         8547603    342913     1.553      1.106      0.592
     -1.042     1.768      0.673      0.088      -1.571     -0.474     -0.475
-0.003     -0.187     -1.610     0.501      0.814      0.103
0.018411771     NL PLS 912         8744368    454864     0.278      0.553
-0.049     -1.519     0.057      -1.450     -0.361     1.515      1.028      0.416
    -1.223     0.607      -0.049     1.733      -0.861     0.306
0.142192129     NL PLS 913         9455645    317502     0.659      0.341      0.249
     1.287      -2.585     0.094      1.506      0.498      -0.255     0.148
0.915      -0.375     -0.347     -1.062     0.431      0.820
0.060554139     NL PLS 933         8934707    481777     -0.425     -1.064     0.302
     0.032      0.223      0.268      1.188      0.960      1.097      2.451
-0.406     -0.824     0.748      0.771      -2.057     0.129
0.169830551     NL PLS 934         14278409   1231684    -0.759     -1.552     1.588
     0.676      -0.592     1.131      1.489      1.599      -0.033     1.079
-2.036     -1.446     1.003      0.516      -0.545     -0.065
0.147739598     NL PLS 935         12711366   1058392    -1.831     -1.525     0.207
     0.884      -0.603     0.838      0.395      1.293      0.039      1.724
-0.628     0.844      1.138      2.020      -1.025     1.410
0.117631497     NL PLS 936         11843954   1686591    -0.167     1.492      0.781
     1.091      -1.083     -0.016     -0.104     2.799      -0.374     2.277
-0.480     0.161      0.323      0.027      -0.092     -0.709
0.056403959     NL PLS 937         12193218   658656     -0.710     -0.505     1.306
     0.871      0.369      -1.899     1.605      0.511      0.958      1.271
-2.425     -0.480     1.028      0.004      0.050      -0.280
0.022506971     NL PLS 938         8964262    1790182    -0.042     -1.731     1.166
     1.206      -1.077     1.021      0.325      0.852      -0.667     0.873
-0.504     -0.308     -0.614     -0.065     0.064      0.384
0.027909237     NL PLS 939         1876528    1010840    -0.298     -0.246
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Table36.txt

-0.326 -0.957 -1.011 1.056 0.349 1.529 0.015 -0.305 -0.277 1.474 -1.089 0.862 -0.876 1.821
0.089909663 NL PLS 940 8378624 1386678 -1.601 -1.021 0.700 0.980 -0.243 1.555 1.707 1.988 2.496 -0.264
-0.429 -0.106 0.101 1.147 -0.490 0.396
0.102764817 NL PLS 941 1765813 894757 -0.180 -0.218
-0.762 -0.326 -0.439 -0.987 1.742 1.705 1.810 0.363 -0.354 -0.073 -1.136 0.728 -0.523 2.043
0.076034164 NL PLS 942 1676500 1250719 -1.026 -0.372
-1.686 0.463 0.825 -0.778 -0.873 1.673 2.101 0.391 -1.543 0.771 -0.213 0.492 -0.894 1.023
0.021689005 NL PLS 943 8228107 1416441 -1.023 1.395 0.271 0.269 0.575 -0.818 -1.073 -0.192 -0.496 1.426
0.319 -0.536 1.009 0.974 -0.568 -0.140
0.095292227 NL PLSA 1160 14291489 2498969 0.105 0.057 0.757 1.526 -1.039 1.643 0.625 0.379 -1.791 -0.203
-1.051 -0.230 -1.587 1.086 0.283 1.084
0.033477936 NL PLSA 1161 15098116 2815672 0.192 -1.294 1.084 0.861 -0.302 0.616 -0.368 -0.642 -0.205 -0.579
-0.214 0.504 0.566 0.682 0.626 0.057
0.016846926 NL PLSA 1162 14202224 1936329 -0.806 -0.731 2.917 0.765 0.312 0.095 -1.020 -0.538 0.467 0.093
-0.731 -0.852 0.440 -0.670 -0.817 -0.641
0.033650545 NL PLSA 1163 14843905 2734131 -1.119 0.032
-0.669 -0.157 0.754 0.002 0.220 1.389 0.402 -0.041 -1.407 1.252 -0.796 0.319 1.638 -0.077
0.009015975 NL PLSA 1164 14392618 2957048 0.080 0.749 0.851 -0.861 0.814 0.089 -0.831 1.089 0.526 1.152
0.796 0.530 -0.574 0.829 -0.968 0.688
0.056948886 NL PLSA 1165 14931663 2349629 -0.939 1.892
-0.476 -0.348 -0.841 0.678 -0.380 -0.357 0.745 -1.293 1.504 1.283 -0.825 -0.805 -0.350 0.220
0.189810352 NL PLSA 1166 10386390 1603401 -0.859 0.511 0.525 0.451 -1.168 -0.888 -0.605 -1.430 -0.398 -1.658
1.670 -1.018 2.674 -0.628 1.182 -1.630
0.147688785 NL PLSA 1167 15307812 1998108 0.172 -1.975 0.859 1.773 -0.465 -0.499 -0.714 0.827 0.011 1.209
0.023 0.759 0.876 1.538 1.020 -1.229
0.025938946 NL PLSA 1168 16506747 1331992 -0.269 0.939
-0.998 -0.586 -0.044 0.478 0.409 -0.389 -0.675 0.321 1.111 2.373 -0.436 1.253 0.041 -0.623
0.009878984 NL PLSA 1169 15691795 2653511 -0.616 0.616
-0.656 1.638 -0.750 -1.531 -0.513 0.908 0.268 0.695 -0.197 0.905 -0.242 0.682 -0.544 -0.822
0.032032228 NL PLSA 1170 13167872 1476115 -0.076 0.844
-0.231 1.618 -1.752 -0.166 0.859 0.729 -0.532 1.472 -0.165 0.676 0.917 -0.971 -0.913 -0.207
0.005299729 NL PLSA 1171 14284431 1509164 -0.110 0.416

Table36.txt

-0.266 -0.654 0.139 1.281 -0.438 -0.815 -0.126 0.730
-0.819 -0.507 -0.063 -0.378 1.297 -0.029
0.03996462 NL PLSA 1172 15295846 3442737 -2.093 -0.411
-0.095 0.700 0.297 0.592 1.596 1.718 2.565 1.274
-0.380 -0.086 -0.730 -1.233 -0.380 -0.071
0.077066121 NL PLSA 1173 15637789 3607640 -0.145 0.599 0.210
-1.212 0.068 -1.517 -0.443 3.382 1.098 -0.486
-1.670 1.268 -0.286 0.445 0.167 1.220
0.427392512 NL PLSA 1174 15356154 1585448 1.885 0.803 2.479
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0.048817507 NL PLSA 1175 17228913 1637880 0.819 0.437
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0.628 0.608 -0.052 -1.189 -0.472 1.782
0.148543416 NL PLSA 1176 13506496 2448403 0.377 -0.296
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-1.397 -0.071 0.019 2.067 0.787 -0.408
0.024864173 NL PLSA 1177 15168793 3501212 -1.763 0.694
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-0.141 1.588 0.716 0.780 2.032 0.594 0.107
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0.055071572 NL PLSA 1182 15128654 2393450 -0.134 0.119
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1.429 -0.874 0.474 0.398 -1.587 -1.070
0.017558981 NL PLSA 1185 17335536 804892 -0.722 0.501
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0.075259608 NL PLSA 1208 10062686 2512720 0.607 1.998 0.279
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-0.146 -0.502 -1.286 -0.278 -0.358 2.174
0.032554916 NL PLSA 1210 7976068 2004159 -1.810 0.284
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Table36.txt

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0.063 0.466 -0.352 0.399 -2.033 -1.334
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0.216876482 NL PLSA 1217 8909553 1164217 0.702 1.455 2.226
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0.165358392 NL PLSA 1220 9476741 2650181 1.896 1.622 0.044
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0.895 -0.183 -0.555 -1.683 1.324 -0.750 0.590
0.992 -0.288 -0.708 0.291 -0.731 0.417
0.040364718 NL PLSA 1224 1788739 1033950 -0.318 -1.405
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0.642 -0.373 -0.020 1.894 3.197 0.050 -0.495
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Table36.txt

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Table36.txt

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Table36.txt

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0.229915015 NL PLSA 1281 14006445 1445955 -0.990 0.685 1.858
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Table36.txt

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-0.198 2.105 -0.889 0.403 -0.417 -0.457
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-0.386 0.368 -0.143 0.133 -1.096 0.406
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Table36.txt

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-0.493 1.582 0.337 1.317 0.573 0.372 -0.028 -1.414
0.340 1.781 -0.946 0.242 -1.760 -0.016
0.087179687 NL PLSA 1311 9010299 2661507 -0.042 -0.508 0.450
0.515 -0.729 -0.707 -0.148 1.673 0.300 1.113
-0.602 -0.586 -1.027 1.826 0.285 0.397
0.104599075 NL PLSA 1312 2012765 1003063 -0.396 0.435
-0.625 0.745 -0.744 0.077 1.144 -0.888 -0.919 -0.909
-1.010 -0.465 0.751 0.395 0.795 -0.158
0.324369768 NL PLSA 1313 1635761 1157134 -0.906 -2.152
-0.361 1.150 0.350 -0.218 1.334 4.568 2.114 -0.433
-1.313 1.397 -1.454 1.034 1.570 1.178
0.392176296 NL PLSA 1314 1828648 929672 -1.533 -0.768
-0.764 0.544 1.277 1.563 0.042 1.464 1.147 -0.638
-1.510 -0.743 -2.346 -0.065 2.917 2.723
0.011373054 NL PLSA 1315 1709585 899069 1.184 0.187
-0.862 -0.551 0.134 -0.429 0.427 0.796 1.585 -0.044
-1.433 1.778 -0.457 1.122 0.232 -0.048
0.037332802 NL PLSA 1316 1641027 1277581 -1.507 0.240 0.582
1.025 -0.337 -0.062 1.342 2.044 1.061 -0.087
-0.319 0.758 -1.489 1.328 0.747 0.368
0.122260915 NL PLSA 1317 9408781 2916013 -0.834 0.578 1.034
-0.171 0.862 -0.075 0.320 1.821 1.233 1.620
-1.543 0.211 -2.009 -0.059 0.941 -0.160
0.006700437 NL PLSA 1318 8482621 1403776 0.209 -0.767 1.380

Table36.txt

0.086 0.461 0.466 1.163 1.533 0.900 -0.207
0.182 0.365 -0.311 -1.298 -0.128 -0.245
0.009014345 NL PLSA 1319 8986893 2717011 -0.700 -0.573 1.810
0.494 0.065 -0.822 1.061 0.165 1.983 0.049
0.495 0.151 -1.263 0.098 -0.192 -0.679
0.497936377 NL PLSA 1320 9692074 2809903 1.199 0.977 0.237
1.086 -0.400 0.186 -0.408 -0.460 -2.873 -0.815
0.809 -1.680 0.402 -0.715 1.018 0.454
0.032156001 NL PLSA 1321 8944364 1570150 -0.156 2.117 0.065
-1.021 0.229 1.792 -0.071 -0.723 -0.778 1.272
0.543 0.421 1.385 0.807 -0.184 -1.021
0.042750858 NL PLSA 1322 1937920 871894 0.952 0.191 0.185
-0.502 0.142 0.824 -0.304 -0.441 -0.339 -0.234
-0.961 -0.738 -0.935 -0.234 1.104 -0.227
0.130537458 NL PLSA 1323 1835169 892861 -0.305 -2.010
-2.069 -1.149 -0.606 0.625 1.098 1.173 1.835 -0.195
-1.707 1.166 -0.213 0.188 0.902 0.168
0.016183817 NL PLSA 1324 8824591 1380146 0.354 0.415 0.666
0.295 -0.606 0.654 0.173 -1.075 -1.017 0.542
0.403 0.341 -0.638 -1.106 -0.992 1.064
0.109374283 NL PLSA 1325 9967755 1677860 0.075 0.179
-0.417 0.370 0.086 0.201 1.251 0.299 1.540 1.298
-0.134 -0.142 -0.140 -0.196 -0.385 0.706
0.061947989 NL PLSA 1326 1889469 991712 -0.314 -0.220 0.074
-0.115 0.902 -0.236 -0.224 0.129 1.263 0.645
0.824 -0.885 0.743 1.228 -1.597 0.009
0.06620655 NL PLSA 1327 9281550 1684835 0.451 -1.374
-0.780 -0.569 -1.283 -1.438 -0.433 -0.864 0.602 1.299
-0.572 -1.024 0.509 1.250 1.728 -0.656
0.02138385 NL PLSA 1401 10009204 3449398 1.097 -0.076
-0.202 0.570 -0.750 1.352 0.081 -0.399 -0.647 -0.342
0.424 -0.317 1.184 -0.359 -1.134 0.715
0.129147613 NL PLSA 1402 8874761 1737630 -0.390 -1.018 1.038
0.469 -0.052 0.894 1.293 1.615 -0.359 1.223
0.656 0.652 0.902 1.406 -1.713 0.056
0.139781074 NL PLSA 1403 1799750 1200805 1.870 0.334
-2.187 -0.320 -0.526 -0.120 -0.819 0.340 -0.295 0.570
0.178 -1.105 0.019 1.088 0.064 0.462
0.364797232 NL PLSA 1404 8921382 2412648 0.202 0.247
-0.597 -1.570 1.347 -0.474 1.512 2.109 -0.223 -0.584
-0.136 0.052 0.135 -0.277 -0.363 1.086
0.032846371 NL PLSA 1405 2444375 1028090 0.753 -0.106
-0.275 0.940 -0.570 0.707 0.107 0.159 -0.470 -0.552
0.219 -0.014 -1.625 -0.077 -0.558 -1.186
0.027958914 NL PLSA 1406 1686630 1189086 0.733 0.687
-0.751 -0.147 0.030 -0.839 0.524 0.528 0.414 -0.377
0.312 1.492 -1.281 -0.471 0.921 0.048
0.163454175 NL PLSA 1407 1647589 954431 -0.102 -1.027 0.322

Table36.txt

0.895 2.162 1.530 1.915 1.547 -0.216 -0.176
-0.714 1.136 0.398 0.254 0.120 1.076
0.005746511 NL PLSA 1408 9028883 2069587 0.559 0.320 1.161
0.651 0.495 0.371 -1.341 -0.260 -0.055 -0.534
-0.201 0.141 -0.624 0.574 0.618 -0.203
0.037925597 NL PLSA 1409 9898910 3131357 -0.983 1.496 1.099
1.442 0.080 -0.001 0.127 0.317 -0.896 0.649
-0.200 -1.492 0.480 0.203 -0.618 -0.184
0.164437729 NL PLSA 1410 9007943 1602516 -0.518 0.289
-0.135 -0.600 0.279 -0.545 1.011 3.219 0.856 0.944
-1.401 -1.056 -0.288 -0.286 1.287 0.556
0.175275663 NL PLSA 1411 9688514 2336784 0.983 -0.467 0.743
1.929 0.116 1.182 -0.161 -0.097 0.078 1.770
0.842 1.312 -0.588 0.170 -1.834 -0.968
0.059850671 NL PLSA 1412 2393300 1110277 -0.262 -1.410
-0.994 0.381 -0.460 -0.946 -0.627 1.566 -0.042 0.532
-0.251 1.633 -2.089 1.385 -1.109 -0.150
0.122600149 NL PLSA 1413 1624504 1196228 -0.100 0.087 0.269
0.790 0.088 -1.688 -1.197 0.561 -0.248 1.530
0.283 -0.869 -1.474 0.535 -1.698 1.151
0.400589489 NL PLSA 1414 1880535 979555 -0.901 0.078
-1.895 -0.681 -1.714 -0.270 1.495 0.792 2.239 1.590
-2.111 0.588 -0.069 1.321 0.373 1.631
0.029835929 NL PLSA 1280 18526270 2999112 0.533 -0.643 0.152
-0.861 0.406 0.984 1.346 0.175 0.764 -0.837
0.013 -0.164 0.318 0.160 1.341 0.889
0.093489294 NL PLSA 1280 20271323 2883886 -0.587 -0.411 0.683
1.521 1.486 0.665 -0.130 0.700 0.199 0.961
0.405 -1.169 0.220 0.691 -0.600 1.578
0.01987041 NL PLSA 1280 21447524 3284785 -1.235 -1.352 0.227
1.487 0.159 -0.287 1.023 0.296 -0.381 -0.047
1.531 1.461 -1.138 -0.446 -0.026 0.243
0.026236818 NL PLSA 1280 20419976 2923364 -0.441 0.342
-0.357 -0.253 -0.217 -0.970 1.174 -1.661 -0.300 2.007
0.522 -0.370 1.216 -0.057 -1.284 -0.802
0.091877882 NL PLSA 1280 15867350 2911990 -1.442 -0.763 0.280
-0.534 -0.728 1.705 0.605 0.899 1.110 1.360
-1.323 -0.438 0.363 2.088 -0.912 0.349
0.04285112 NL PLSA 1280 14929105 2674840 -0.081 -0.458 0.065
-0.692 0.727 0.375 -0.519 0.403 0.207 0.220
-0.359 -1.077 0.569 1.145 -0.843 0.360
0.01447704 NL PLSA 1280 18853158 2836386 0.055 -1.141 1.741
0.826 0.681 -0.146 0.225 1.948 1.615 -1.067
0.493 0.384 -0.612 0.732 -0.063 -0.134
0.040485987 NL PLSA 1280 15497784 2830459 -0.419 0.155 0.522
0.733 -0.156 0.667 -0.955 2.220 1.563 0.160
-0.547 0.537 1.313 1.391 0.686 -0.037
0.012240643 NL PLSA 1280 21445125 3098725 -0.448 -0.281 0.768

Table36.txt

0.137 0.266 0.661 -0.172 0.979 -1.990 -0.494
-1.678 0.570 0.420 0.341 -0.356 0.157
0.028940014 NL PLSA 1280 13827777 2694804 -0.868 0.359 1.814
-0.326 -1.133 2.261 0.651 0.964 0.775 -0.251
-0.929 0.173 0.043 0.852 -1.034 0.392
0.056089009 NL PLSA 1280 18355979 3156614 -1.157 0.545 1.519
1.765 0.230 -0.504 0.686 -0.495 1.195 -0.538
-1.433 -0.562 0.959 0.442 -0.406 -0.137
0.041647159 NL PLSA 1280 19908151 3092045 -1.173 -0.010 1.292
-0.024 0.333 1.473 0.372 0.066 0.615 -0.759
-1.383 -0.366 0.778 0.780 0.037 0.444
1 INDI 276 PLS 1 10561193 7069993 -2.046 2.783
-0.764 0.548 -2.132 7.144 -0.123 -2.037 11.000 -2.306
3.053 1.347 0.338 2.141 -4.764 3.203

chr9p chr9q chr10p chr10q chr11p chr11q chr12p chr12q
chr13q chr14q chr15q chr16p chr16q chr17p chr17q
chr18p chr18q chr19p chr19q chr20p chr20q
0.585 -3.359 -1.031 -0.412 0.121 0.496 -0.083 -1.953
0.929 0.800 -1.738 -2.489 -1.384 -1.150 -1.736
0.746 0.061 0.440 -1.540 -1.273 -1.082
1.462 -0.766 0.106 -2.101 -1.395 -0.169 0.333 0.016
0.030 0.309 -1.981 -2.386 -0.385 -0.229 1.128
0.387 -0.071 1.876 0.819 -1.264 0.976
2.831 -1.442 -1.894 -0.101 0.845 1.241 -2.048 -0.655
-1.221 1.444 -2.478 -2.462 -1.140 -3.040 -1.525
-0.452 0.572 -1.034 -0.988 -0.795 -0.287
0.443 -1.698 -0.552 -1.665 -0.041 0.478 0.602 0.927
2.260 -0.122 -1.318 -1.348 -1.329 -0.550 -0.551
0.151 0.532 2.404 1.295 -0.810 -0.421
1.302 -0.526 -0.656 -0.492 0.522 1.118 -0.518 0.325
1.216 0.759 0.158 -0.811 -1.303 -1.057 -1.010
0.624 -0.401 -0.412 -1.791 -0.468 -0.242
-0.837 -0.785 -0.255 -0.669 -0.469 0.438 -0.384 0.445
-0.502 -0.149 -1.808 0.654 0.450 -1.641 0.094
-0.773 -1.010 0.040 -0.095 -1.389 -0.486
-0.767 -0.035 1.522 -0.262 -1.138 -0.315 1.931 0.279
-0.459 -1.019 0.729 -3.226 -2.301 0.910 0.538
0.837 -1.594 2.528 2.441 0.737 0.334
1.018 -0.428 1.434 0.667 -0.218 1.306 -1.565 -0.200
-2.121 1.088 -0.367 -1.179 0.796 -0.647 -0.713
0.589 0.248 -1.027 0.198 -1.427 0.681
0.392 -1.856 0.590 -0.093 -1.491 -0.715 1.536 -0.024
0.849 0.655 0.008 -1.541 -0.424 -0.330 -0.535

Table36.txt

-0.404	-0.149	1.326	1.595	-0.314	0.281		
0.113	-0.233	-0.483	-0.876	1.805	2.243	-1.191	-0.966
-0.893	0.854	-0.899	-0.090	-0.036	-2.648	-1.497	
-1.026	0.556	-0.350	-0.489	-1.542	-0.197		
1.613	-2.136	-0.647	-2.909	0.889	1.009	-1.865	-0.635
0.750	0.066	-2.444	-1.831	-1.675	-2.946	-3.099	
0.076	1.055	0.108	-1.781	-2.761	-0.907		
0.798	0.172	0.958	-0.209	0.138	0.509	-2.038	-0.538
-1.803	-0.053	-1.860	0.337	0.241	-1.589	-0.971	
0.545	0.614	-0.192	0.435	-2.109	0.327		
2.810	-1.948	-1.305	-1.379	0.659	0.766	-3.102	-0.317
0.174	1.305	-3.518	0.094	0.135	-2.445	-2.935	
-0.166	0.946	0.456	-0.038	-2.117	0.064		
0.446	-2.017	0.354	-1.350	-0.216	0.617	0.436	-0.655
0.840	0.476	-0.062	-1.533	-1.100	0.304	0.157	
1.292	-0.666	1.442	1.171	-1.034	0.159		
-1.127	-1.360	-0.600	0.190	0.505	2.434	0.142	-0.756
-0.721	1.110	1.209	-0.428	0.940	-2.145	-1.712	
-0.855	-0.506	-0.146	0.828	-1.265	-0.646		
-0.523	-1.166	0.666	0.602	1.706	-0.194	-0.255	0.423
-2.203	0.012	0.621	0.531	-0.088	-1.056	-1.268	
-0.545	-0.325	-0.610	0.073	0.330	-0.492		
1.158	-0.471	-0.047	-1.747	-0.153	0.905	0.044	0.397
-0.538	-0.040	-1.474	0.229	-1.146	-1.497	-0.839	
-0.947	1.313	-0.652	-0.602	0.351	-0.745		
0.520	-1.332	0.279	0.155	0.760	0.576	-0.565	-1.492
-0.990	-0.251	-0.481	0.646	-0.295	-2.426	-1.339	
-0.743	1.516	0.069	0.524	-0.309	-0.703		
0.043	-1.440	-1.802	0.402	-0.897	-0.329	0.950	-0.528
-0.006	1.135	-1.124	-1.022	-0.200	-0.901	-1.282	
0.307	1.259	0.907	-0.925	0.251	0.577		
0.695	-0.944	0.585	0.612	-0.198	0.290	1.696	-0.152
-1.411	0.365	0.461	-1.181	-1.311	-0.201	0.709	
0.854	-1.358	2.011	1.367	1.488	1.778		
0.079	-0.900	-1.588	-1.153	-0.278	0.596	-0.409	-0.914
0.432	0.926	-0.822	-1.224	0.198	-1.398	-0.770	
0.677	0.554	0.500	1.996	-0.433	0.269		
0.246	1.587	0.903	-0.314	1.382	2.134	-1.233	-1.575
-1.121	-0.082	0.531	1.194	0.963	1.097	-0.327	
-0.492	-0.578	-0.310	1.267	0.056	-0.480		
2.249	-0.715	0.028	-1.456	0.389	1.252	-1.864	0.206
0.183	0.991	-1.763	-1.918	-1.997	-2.356	-1.642	
0.453	1.445	0.696	0.057	-1.603	0.264		
-0.373	-0.954	-0.556	2.197	0.019	0.559	0.048	0.701
0.631	-1.546	-0.614	-0.176	-1.543	0.001	-1.316	
0.744	0.589	1.006	1.495	-0.191	-0.363		
0.812	-1.745	-0.749	0.356	0.276	0.111	0.446	1.379
0.589	-0.329	-2.487	-0.563	-0.556	0.183	-0.146	

Table36.txt

0.019	-0.403	1.177	-0.221	-0.713	-0.804		
0.210	-0.235	0.670	0.139	0.207	-0.838	-0.270	0.046
-0.872	-0.087	-1.897	-2.311	-2.451	-0.167	-0.502	
0.058	-0.214	0.096	-2.223	-0.165	-0.339		
-1.204	-1.875	-0.980	-0.207	0.608	-2.136	0.955	-1.065
0.019	-1.198	-0.896	-1.096	-0.433	-0.229	0.811	
-0.660	0.565	1.996	2.020	-0.090	-1.210		
-0.039	-0.502	-0.703	-1.005	-0.652	-0.726	-0.431	-1.280
1.145	1.151	0.655	-1.709	-1.912	-0.598	-1.257	
-0.377	0.081	0.348	-1.100	-0.864	-0.287		
-0.203	0.617	0.050	-0.395	0.860	1.795	-0.622	-1.029
-0.338	0.475	-1.911	0.353	0.027	-1.109	-2.350	
0.904	1.152	0.336	0.592	0.007	0.877		
0.403	0.160	-0.412	0.558	0.511	0.866	11.000	0.997
-0.412	-1.304	-0.663	0.316	-0.193	-2.024	-2.065	
0.188	1.349	-0.308	0.838	-0.536	0.574		
0.531	-0.185	0.567	-0.628	0.353	1.509	-0.637	-0.277
-1.931	0.799	-0.251	-0.003	-0.223	-0.713	-0.893	
0.443	-0.090	0.372	0.368	-1.168	0.459		
0.124	-1.022	-0.281	0.718	1.022	1.347	-0.452	-0.841
0.942	-0.342	-1.512	0.283	-0.339	-0.786	-1.520	
-0.405	-0.560	0.636	0.034	-0.239	-0.414		
-0.550	-0.914	1.044	-0.057	-0.030	-1.229	0.350	-0.912
-1.721	-0.027	0.679	-1.551	-0.613	-1.195	-1.090	
0.174	0.103	1.727	2.192	0.163	-0.602		
0.598	-0.916	-0.066	-0.527	-1.009	0.106	-0.711	0.925
-1.613	-0.443	-0.809	-0.798	-0.080	0.386	-0.884	
0.038	-1.073	0.897	-0.181	0.307	0.564		
1.569	-1.113	-0.958	-2.111	0.798	1.232	-2.210	0.163
0.663	1.223	-2.350	-1.458	-1.086	-2.654	-2.932	
-0.113	0.739	0.787	-1.429	-2.093	-1.212		
1.121	-2.115	-1.497	-2.251	0.081	-0.913	0.003	0.538
2.627	1.340	-3.083	-2.933	-0.498	-0.712	-0.537	
-0.766	0.294	1.152	0.572	-1.755	-1.852		
1.375	-1.169	-0.790	-1.383	0.299	1.010	-2.448	0.413
0.484	0.146	-2.223	-0.546	-0.521	-2.954	-3.452	
-0.376	0.703	-0.141	-1.332	-1.347	-0.506		
1.678	-1.283	-1.918	-0.958	-0.659	0.650	-0.027	-0.540
-1.204	1.269	-0.942	-0.672	0.486	-0.115	-0.747	
0.339	-0.180	-0.746	0.015	-0.897	-2.868		
0.245	-1.260	0.399	1.506	-1.602	-1.039	0.863	-1.226
0.972	-1.553	0.643	-0.344	2.605	0.592	2.222	
-0.032	-1.246	2.139	0.298	1.759	-0.185		
2.625	-2.887	-1.091	-1.503	0.951	0.514	-2.396	0.199
0.726	0.349	-2.958	-2.213	-1.552	-2.920	-3.294	
0.733	0.192	0.047	-0.333	-1.789	-1.139		
2.039	-0.905	-0.251	-1.104	-0.161	1.641	-1.300	-0.513
-0.351	-0.542	-0.668	1.001	0.603	-1.473	-2.135	

Table36.txt

-0.406	1.006	-0.043	1.057	-0.939	0.756		
0.437	1.260	1.318	-0.023	0.562	1.946	-1.038	0.441
-0.448	0.249	-0.290	-1.331	-0.403	0.201	-0.688	
0.771	0.950	-0.161	0.121	0.032	1.058		
1.164	-2.341	-0.635	-0.734	-0.755	-0.757	-0.994	-0.110
0.872	1.698	-1.234	-1.683	-0.278	-0.793	-2.147	
0.083	-0.901	1.139	0.560	-0.551	-0.918		
2.929	-2.492	-0.451	-0.417	-0.601	-0.360	-1.381	0.366
1.705	-0.515	-2.439	-0.934	-0.863	-3.410	-1.513	
-0.637	0.259	-0.888	-0.325	-0.612	-1.129		
-0.076	-2.075	-0.659	-1.563	-1.282	-0.304	0.113	-0.055
0.987	-0.136	-2.262	-2.154	-0.818	-0.414	-0.798	
0.402	0.455	2.181	1.018	-1.044	-0.571		
-0.364	-0.996	1.512	-0.217	-1.236	-0.635	2.953	1.428
-0.065	0.682	0.208	-1.618	-0.458	0.378	0.808	
0.207	-0.725	1.529	0.427	-0.666	-0.545		
0.391	-1.931	-0.586	-1.121	0.561	0.965	0.092	0.273
-0.351	-1.160	-0.863	-2.421	-0.418	-1.175	-2.415	
-0.059	0.336	1.847	1.083	-0.762	-0.485		
0.553	1.262	1.001	0.673	-0.109	1.443	0.288	-0.423
-1.923	0.278	0.506	-0.953	-0.727	-0.971	-0.591	
1.292	-0.160	-0.424	-0.456	0.091	1.706		
1.626	-0.083	0.367	-1.833	1.796	0.142	-1.513	-0.487
0.992	1.319	-0.561	-0.432	0.042	-0.828	-0.995	
-0.458	-0.879	0.149	-0.188	-1.003	0.785		
1.746	-2.253	1.403	-0.342	1.876	0.651	-0.908	0.314
0.007	0.530	-2.028	-0.852	-1.816	-2.235	-2.416	
0.292	0.297	0.248	0.455	-1.397	-0.680		
-0.434	-0.727	-0.902	-0.901	-0.937	-0.197	-0.158	-0.270
0.205	0.343	0.534	-1.369	-1.384	-0.196	0.768	
-0.343	0.014	-1.322	-1.377	0.017	0.384		
1.694	-1.802	-0.568	-0.201	-0.110	-0.948	2.308	-0.341
1.066	-0.172	-1.060	-2.679	-1.283	0.223	0.377	
0.605	0.193	0.261	1.337	-0.402	-1.551		
-0.018	-0.609	0.560	-0.134	0.477	0.449	-1.187	0.255
-1.624	0.058	-1.065	-1.334	-0.014	-0.484	0.178	
0.847	0.421	1.578	0.105	0.052	-0.223		
-0.218	-0.075	1.283	2.102	0.148	-0.878	-0.156	-0.791
-0.560	0.129	-0.810	-0.785	0.497	1.054	-0.028	
0.720	-0.696	1.043	1.948	-0.429	0.165		
1.257	-0.910	-0.977	-1.435	0.997	1.201	-2.105	0.465
0.005	-0.016	-2.996	-1.151	-0.246	-3.238	-3.260	
-0.519	1.217	-0.340	-0.450	-0.930	0.296		
0.634	-1.137	0.472	-0.739	1.091	1.338	-1.039	0.222
0.954	-1.242	-0.708	-2.022	0.203	-1.809	-2.252	
0.072	-0.198	0.330	1.277	-0.274	1.310		
0.168	0.033	0.412	0.306	0.748	1.510	-0.787	-1.085
-0.854	0.690	-1.351	-0.659	-0.260	-1.990	-1.744	

Table36.txt

-0.399	0.783	0.292	-0.840	-1.745	0.230		
1.867	-1.080	-0.546	-0.133	0.611	0.636	-1.271	-0.659
-0.211	0.884	-1.927	-0.409	0.093	-1.937	-2.006	
0.411	0.777	1.006	1.036	0.211	0.677		
0.128	0.398	1.151	-0.302	0.911	1.647	-0.851	-0.695
0.017	0.425	-0.874	-0.437	-0.562	-0.649	-2.255	
0.162	-0.105	0.193	1.548	0.013	0.329		
-0.740	-1.126	-0.948	-0.190	1.726	0.736	-0.034	0.105
-0.273	1.351	-2.748	0.159	0.307	0.001	-1.970	
1.152	0.321	0.687	0.435	-1.771	-0.190		
1.392	-1.656	0.719	-0.567	-0.257	1.493	-0.414	0.492
-1.015	0.743	-1.890	-0.585	-0.441	-1.857	-0.746	
0.839	-0.863	-0.703	0.608	-0.167	-0.233		
0.144	-1.028	0.587	0.524	-1.810	1.016	-0.699	-0.353
-0.751	0.078	-0.873	-0.606	-0.493	-0.039	0.156	
0.005	-0.689	0.986	0.833	-0.551	0.116		
-0.088	-0.721	-0.021	-0.381	-0.023	1.087	-0.024	-0.401
0.671	0.699	-0.592	0.631	-0.011	-1.662	-1.495	
0.812	0.390	-0.909	-0.269	-0.886	0.526		
-0.370	-2.104	-0.270	-2.347	1.024	0.681	-0.658	0.589
1.005	-0.585	-2.040	-0.539	-1.680	-1.621	-2.071	
1.596	-0.327	0.234	0.538	-3.529	-0.298		
0.267	-0.743	-0.371	-1.564	1.287	2.010	-1.216	0.516
-0.459	-0.615	-1.065	-0.257	-0.166	-1.305	-0.737	
-0.400	-1.007	0.655	1.960	-0.693	0.419		
0.316	-0.922	0.099	-1.043	0.310	1.076	-0.737	0.010
0.113	-0.095	-1.577	0.342	-0.082	-1.062	-1.228	
0.074	-0.037	0.654	0.525	-0.216	-0.713		
-0.085	2.432	0.344	0.415	-0.774	0.102	-1.621	-0.865
-0.203	-1.529	-0.738	-0.233	0.690	-0.728	0.996	
-0.307	-0.063	-1.959	-1.060	-0.086	0.779		
0.086	-0.106	0.069	-0.932	1.149	0.574	0.904	0.843
0.126	-0.251	0.550	0.795	-0.335	-0.513	-1.161	
-1.316	-1.248	0.293	-0.586	-0.930	-0.675		
1.670	-1.306	0.487	0.141	-0.560	-0.145	-1.276	-0.512
-0.018	-0.048	-1.515	0.243	-0.190	-1.176	-1.904	
-0.155	-1.313	0.006	-0.148	-0.956	-0.321		
-0.894	-0.411	-0.348	0.150	-1.196	-0.824	0.770	-1.146
1.234	-0.512	0.051	-1.917	-0.830	-1.343	-0.403	
1.135	0.422	-0.724	0.194	-0.037	-1.520		
0.618	-3.259	-2.122	0.073	1.499	-0.435	-1.138	0.126
1.145	0.245	-1.041	-2.470	-0.345	-2.003	-2.093	
-0.052	0.620	1.182	-0.893	-0.883	-1.120		
0.814	-1.094	-0.721	-0.328	1.113	-0.125	0.288	0.839
-0.692	1.337	-0.264	-0.231	-0.961	-0.707	-0.429	
-0.322	0.088	0.105	1.980	-0.774	0.349		
0.785	-2.880	-0.966	0.301	-1.215	0.455	-0.364	0.332
0.704	-1.498	-2.214	-2.605	-0.478	-0.978	-0.217	

Table36.txt

0.923	0.619	0.523	0.337	-1.519	1.066		
1.431	-1.665	0.176	-1.788	1.047	0.525	-2.269	-0.656
0.663	1.661	-2.478	-1.349	-0.617	-1.459	-2.437	
0.244	0.792	-0.675	-2.090	-2.225	-0.674		
-1.586	-1.140	1.481	-0.177	-0.287	-1.849	4.302	-1.957
-0.147	1.249	-2.086	0.223	0.403	-1.414	-1.063	
-0.041	-2.308	-0.151	0.370	1.050	1.085		
-0.495	-1.555	-1.177	-0.303	0.017	0.865	-1.214	1.088
1.106	0.991	-2.019	-1.882	-0.864	-1.303	-1.552	
-0.701	-1.499	-0.415	-0.762	-0.458	-0.964		
1.164	-1.472	-1.029	-1.554	0.995	-1.646	1.892	1.601
0.182	-0.496	0.366	0.137	0.480	-0.303	-0.268	
1.366	-0.493	0.826	-0.224	-0.510	-1.544		
-1.007	-0.113	1.248	1.388	-0.947	1.622	-0.156	-0.001
-0.556	0.608	1.086	-0.214	-0.392	0.235	-0.244	
-0.910	0.354	-0.394	-2.161	0.485	-0.801		
-0.826	0.891	-0.586	1.164	0.196	-0.220	-0.565	-0.251
0.422	0.813	0.388	0.270	-1.265	-0.375	0.238	
-0.303	-2.606	-0.153	0.782	-1.310	-1.458		
-1.270	-1.304	-0.005	0.253	-0.384	0.164	-0.549	-0.032
0.337	-0.826	-0.635	0.403	-0.478	-0.822	-0.071	
1.299	-0.232	1.533	0.522	-0.340	-1.667		
-0.885	0.585	1.230	0.995	-0.147	0.297	-0.655	-0.873
0.497	0.077	0.860	2.191	1.226	0.643	-0.141	
0.591	-1.395	2.525	4.320	0.895	1.373		
0.903	-0.666	-0.926	-0.762	-0.640	-0.361	0.453	0.288
1.966	-0.408	0.037	-1.187	0.043	-0.662	1.519	
0.311	-0.253	-0.638	0.347	-0.191	0.339		
2.041	-0.033	-0.899	0.097	0.919	-0.198	-0.320	-0.205
0.678	-0.648	-0.653	0.576	0.599	-1.079	-0.532	
1.859	2.384	-2.164	-2.250	-0.475	-0.354		
-0.318	0.131	-0.206	0.868	1.564	0.282	0.152	1.103
-1.045	-0.047	-1.166	1.516	-0.198	-1.258	-0.626	
-0.617	0.066	-4.066	-2.266	-0.148	-0.053		
-0.709	0.225	1.097	-0.470	-0.465	-0.524	-1.010	-1.503
-0.581	-0.273	-1.216	-0.138	-1.460	0.397	0.396	
-0.810	-0.251	-2.337	-1.521	-0.236	1.439		
0.803	0.125	-1.369	0.858	-0.460	-0.020	0.050	1.435
-0.324	1.076	-1.565	-1.013	-0.523	-0.183	0.073	
-0.410	-0.062	-0.899	0.372	1.378	-1.589		
0.460	-0.398	0.334	-0.506	2.195	0.735	-0.216	0.080
0.492	0.759	-0.016	-0.410	-0.121	-1.106	0.437	
-0.697	0.080	-0.487	0.650	0.856	-1.745		
-1.493	0.167	1.146	-0.533	-0.979	-0.837	0.236	0.179
-0.231	0.532	-1.194	-2.568	-0.944	0.259	0.557	
-1.258	-0.788	-1.476	0.828	-0.586	-0.602		
-0.215	0.480	0.488	-1.210	1.739	-0.890	-0.274	0.848
1.878	-1.220	0.237	-2.034	-0.185	0.844	0.695	

Table36.txt

-0.223 -1.049 -0.139 0.320 -0.330 -0.047
-0.120 -1.046 -0.711 -0.335 0.204 -0.480 1.281 1.167
-0.195 0.468 0.007 -0.362 0.339 -0.621 1.251
1.739 -1.588 0.474 1.361 -0.224 -0.080
-0.179 0.011 0.487 -0.358 -0.368 1.256 0.246 0.686
-0.409 1.564 0.151 0.925 -0.091 0.768 -0.140
0.426 0.040 -0.451 0.116 1.548 1.272
-0.349 1.497 -1.699 0.437 -0.293 0.537 0.557 0.054
0.204 0.205 0.466 -1.688 -1.668 -1.603 -1.210
-1.265 0.934 -0.776 -2.980 -0.405 -0.874
-0.988 1.421 0.815 0.499 -1.655 -2.289 0.481 -0.193
-1.232 -0.014 3.071 1.529 0.093 1.613 2.463
0.897 -1.079 1.097 1.191 0.128 0.943
1.225 0.285 -0.027 0.583 0.025 -0.387 -0.352 0.695
-1.511 -0.025 -0.216 1.168 1.111 0.161 -0.789
0.584 -0.881 1.162 0.347 0.229 -0.025
0.637 -0.364 -0.644 -0.228 0.785 0.203 0.139 -1.562
0.993 0.582 -0.899 0.308 0.763 -1.226 -1.937
0.496 0.229 -2.878 -0.466 0.499 -1.091
0.283 -0.749 0.598 -0.056 0.953 0.942 -0.134 -0.703
-0.145 -0.047 1.008 0.139 -0.529 0.952 1.324
1.408 0.338 0.195 0.752 0.419 0.105
1.044 -0.581 -0.288 -1.854 -0.026 -1.177 0.951 -0.483
0.541 0.331 -1.238 -1.600 0.225 -0.139 -0.093
-0.718 -0.804 2.693 1.714 0.195 -1.481
1.361 -0.273 -0.231 0.239 -0.211 0.597 -2.366 0.085
-0.360 0.731 -0.303 -0.946 -0.385 0.583 -1.748
-0.059 -0.042 -0.723 0.282 -2.461 -0.208
-0.131 -0.234 1.627 0.747 -1.055 -0.034 1.019 0.458
-0.357 0.467 0.530 0.104 1.478 2.639 2.106
-1.425 -2.821 1.661 1.522 0.648 -0.780
0.958 0.396 -1.340 0.208 -0.093 1.541 -1.044 0.400
-0.124 0.551 0.157 -1.234 0.280 -0.330 -1.342
-0.698 1.989 -2.237 -1.628 0.416 -0.039
0.715 1.258 1.157 -3.434 -0.132 0.306 0.923 0.854
-1.005 -2.107 2.149 0.044 1.602 0.476 0.168
0.291 -0.258 -0.650 -0.560 -0.434 1.004
0.561 2.796 0.366 0.046 0.182 0.069 -1.004 0.283
-0.910 -0.598 -0.107 1.499 1.722 1.111 -0.008
-0.165 -0.759 0.033 1.268 0.600 0.297
-2.844 -1.898 -0.877 -0.340 -1.068 -0.593 -0.579 0.965
-0.029 -0.836 -1.451 0.026 -1.696 -1.915 0.543
0.238 0.637 -2.558 -3.000 0.333 -0.623
1.372 -0.497 0.166 -0.717 -0.302 -0.303 0.646 -1.478
-0.011 0.196 0.164 0.990 0.800 -1.219 -0.063
-0.130 0.334 -0.168 -0.079 -0.246 0.866
-0.689 1.467 2.112 0.125 -0.617 0.907 0.784 -0.534
-1.100 0.738 -0.275 -1.156 -1.045 -0.720 1.241

Table36.txt

-0.531 0.025 0.486 0.127 -0.087 1.325
-0.869 0.255 0.558 -0.058 -0.709 0.596 -1.062 0.669
-0.101 0.186 0.621 -0.265 0.143 -0.340 -0.817
-0.501 0.404 -0.240 -1.843 -0.948 -0.406
0.881 0.448 -1.184 -1.599 0.186 0.866 -0.037 0.223
-0.512 -0.027 -0.478 1.092 0.658 1.295 -2.121
2.388 0.932 -0.119 0.892 -0.606 1.054
0.739 -1.166 -0.979 -2.405 0.602 -0.086 -1.934 -0.110
0.939 -0.546 0.084 -1.117 1.229 -0.404 -0.635
-0.635 0.914 -1.402 -0.899 -0.489 -0.201
1.462 -0.770 -0.338 -1.061 -0.697 -0.624 0.553 1.267
0.081 -1.006 1.339 2.692 -0.244 1.027 1.269
-1.189 -0.506 0.187 1.689 0.843 -0.094
1.162 -0.551 -1.192 -0.904 0.138 -0.921 -0.614 0.789
0.008 0.523 -1.066 -0.105 -0.102 -0.627 -1.498
0.087 2.032 0.283 -0.304 0.415 -1.726
1.361 -0.502 -0.913 0.094 -0.442 -0.145 0.674 0.556
0.846 0.205 -1.372 0.944 -0.868 -0.400 -0.839
-0.054 0.388 -0.862 0.650 -0.730 1.400
-0.002 -0.129 -2.081 -0.604 -0.537 0.923 -0.242 -0.027
1.249 0.120 0.033 0.267 0.422 0.586 0.653
0.271 -1.290 -0.063 1.499 -0.090 -0.736
-1.143 -0.069 1.777 0.151 -0.379 -1.080 2.081 0.434
-0.202 -1.025 0.510 -0.990 -1.200 -0.001 2.062
-0.466 -0.850 0.901 0.948 -0.025 -0.640
-0.866 0.470 0.487 0.969 0.997 1.873 0.842 0.056
-1.176 1.837 1.140 1.079 -0.692 2.511 0.301
-0.694 -0.619 1.194 1.467 -0.061 1.033
0.331 -0.519 -0.721 1.033 1.401 -1.193 2.110 0.872
-1.788 0.671 -0.143 0.391 -0.870 -0.418 -0.233
-0.329 -0.830 0.671 -0.039 1.096 0.100
0.166 -0.691 -1.027 0.053 1.838 -0.175 0.353 -2.283
0.678 0.048 -0.708 -1.780 0.209 0.519 0.701
-0.892 1.534 1.628 2.177 0.778 -0.018
-0.997 0.960 0.605 -0.561 0.511 -0.121 -0.455 -0.259
-0.399 -1.172 -0.091 -0.506 -0.876 0.873 -0.521
0.835 -2.148 0.307 0.854 0.824 1.006
-0.209 0.526 -0.504 0.604 0.370 -1.327 1.021 0.708
-1.042 -0.476 -0.532 0.217 0.933 0.521 -0.255
0.461 1.286 1.077 -0.378 0.852 0.552
0.256 -0.547 2.590 0.332 -0.847 -1.078 -0.589 0.561
-2.185 0.079 1.696 1.669 1.033 0.588 2.427
-0.048 -0.565 0.510 0.154 2.068 0.903
0.723 1.644 1.462 -0.975 -0.804 -0.135 0.421 0.680
-0.317 1.093 0.200 1.384 0.879 1.021 -0.492
0.526 1.009 -1.212 -0.204 0.146 1.525
-0.812 1.464 0.725 -1.023 0.364 0.446 0.566 0.592
-0.432 0.277 -0.211 -0.636 1.233 1.499 0.654

Table36.txt

0.861	-0.743	-0.918	-0.085	0.316	0.096		
0.117	0.824	1.819	2.425	0.313	0.349	-0.138	0.494
-1.041	-0.746	-0.382	0.420	-0.117	0.441	0.133	
0.865	-0.684	-0.017	-0.168	0.490	0.027		
-0.701	-0.886	-0.851	0.109	0.996	0.579	0.109	-1.136
0.913	1.812	-0.275	0.327	-0.240	-1.814	-0.794	
2.281	1.622	-0.937	0.091	-0.598	-1.669		
0.174	-1.395	-1.977	1.277	0.653	3.365	0.066	0.275
-0.570	1.227	-0.053	1.048	0.221	-1.679	-0.771	
-0.721	1.535	-2.362	-1.081	-1.482	-1.871		
-0.723	1.061	-0.943	0.573	1.084	-0.557	-1.305	0.159
-1.360	0.758	0.725	3.572	1.200	0.984	-0.084	
-0.392	-0.696	2.321	-1.068	0.490	0.170		
0.982	0.617	0.152	0.302	-0.558	0.672	1.157	0.775
-0.080	-0.442	-0.078	0.046	-0.526	-0.238	1.006	
-1.380	-0.039	-2.075	-1.179	-0.750	-1.130		
-0.398	0.125	0.496	-0.589	-0.011	0.922	1.019	2.873
-1.364	0.706	0.250	1.058	0.924	0.946	1.403	
0.413	-0.747	0.755	1.657	-0.263	1.145		
-0.817	-0.561	1.318	0.856	-0.658	-1.100	0.831	1.748
0.804	1.581	-1.291	-1.015	0.156	0.176	-0.227	
-0.860	-0.350	1.265	0.208	0.496	-1.077		
0.939	0.968	-0.195	-2.056	0.288	1.222	-1.198	0.603
0.802	-0.592	0.213	0.393	-0.166	-0.284	0.452	
-0.680	0.266	-1.046	0.242	0.273	1.015		
-0.368	1.266	0.928	0.499	-1.063	0.084	0.150	0.504
-0.341	-0.591	0.171	0.798	-0.356	1.405	-0.045	
0.099	1.433	-0.560	-0.150	0.483	2.421		
0.266	-1.905	0.571	0.007	1.589	-0.976	0.416	0.796
-0.467	-0.585	-0.483	-1.216	-0.841	-0.310	1.406	
-0.392	-0.890	1.374	-0.173	0.181	0.046		
-0.203	-0.138	0.864	-0.867	0.267	-0.119	-0.659	-0.081
1.375	0.820	-1.522	-1.261	0.711	-1.209	1.034	
-0.489	-0.871	-0.711	-0.712	1.183	-1.602		
1.318	-2.120	-1.011	-0.490	0.589	0.861	0.093	0.901
2.679	-0.074	-1.921	0.403	0.113	-1.597	-0.037	
-0.136	-0.459	0.468	-0.695	-1.423	-1.923		
1.241	-0.623	-3.386	1.722	0.132	1.150	-1.121	-0.767
0.091	-0.223	1.427	2.243	-0.071	-0.430	-0.305	
1.605	1.666	-2.285	-3.330	-1.824	0.711		
-0.510	1.111	1.008	-0.267	-1.497	-2.402	-0.276	-0.535
0.453	0.728	0.259	-1.577	-1.579	-0.071	-0.210	
0.578	0.247	2.203	0.823	0.361	-0.991		
1.390	-1.490	-0.784	-0.850	1.404	-0.200	0.237	0.181
1.135	-0.852	-1.992	0.271	-2.153	-2.046	-0.560	
-0.755	1.995	-2.424	-1.691	-0.865	-0.901		
1.717	-1.773	0.416	-0.230	0.669	0.224	0.299	0.530
-0.206	1.019	0.451	0.275	0.620	0.439	-0.591	

Table36.txt

1.841	1.291	0.818	-0.525	0.609	0.717		
-1.510	0.771	-0.125	1.720	-1.794	0.909	0.078	0.133
-1.940	0.182	1.701	0.738	0.229	0.286	0.053	
0.231	0.307	-0.844	-0.273	0.421	0.454		
-1.100	2.432	0.502	1.596	1.068	-0.175	1.006	-0.854
-1.887	-0.321	1.647	-0.835	-0.774	1.668	0.249	
0.787	-1.481	-1.270	-0.016	1.401	0.997		
0.136	1.023	-0.873	-0.182	-0.273	0.254	-0.671	-1.052
1.265	0.442	-2.509	-0.177	-0.882	-1.308	-1.001	
0.318	1.735	-0.585	-0.739	0.641	1.376		
0.521	1.311	0.436	0.239	0.386	-0.219	0.730	0.013
0.354	-1.275	0.051	0.305	0.034	0.430	-1.039	
-0.584	-0.681	0.294	2.281	-0.505	0.451		
-0.859	0.629	-0.006	0.089	2.380	1.509	0.334	-0.864
0.678	0.706	-0.571	0.935	-0.085	-0.629	-0.038	
0.425	0.650	0.863	0.435	0.604	-1.363		
-1.551	1.372	0.801	-0.867	-0.815	-0.227	0.629	-0.290
-1.550	-0.411	1.377	1.461	0.294	1.745	1.036	
0.096	-2.593	1.164	0.585	1.612	1.378		
1.245	-0.795	0.016	-0.911	-0.873	-0.419	0.071	0.437
1.357	0.667	-1.268	0.718	0.012	-1.216	-0.678	
0.624	0.882	-1.173	-1.692	-1.164	0.703		
1.830	-1.337	-3.914	-1.191	2.882	0.205	-1.074	0.124
1.334	-0.235	-3.769	-1.659	-1.362	-1.023	0.871	
1.751	2.786	-1.258	-1.384	-0.960	-1.904		
1.129	2.358	1.031	1.479	1.292	-1.231	0.044	0.522
-1.151	-0.148	0.725	2.119	0.310	0.725	1.045	
0.489	-1.106	1.446	1.874	0.212	-1.476		
-0.508	-0.243	0.205	-0.146	-1.524	-0.592	0.741	0.502
0.742	-0.624	1.837	-0.933	-0.006	0.627	-0.234	
-1.307	-0.189	0.592	-1.326	0.753	-1.200		
-0.856	-0.201	1.171	1.259	0.918	0.557	0.866	-0.125
0.016	0.508	-0.093	-1.946	-0.873	-0.159	1.186	
-1.246	-1.182	0.910	-0.031	0.219	0.013		
-0.012	-0.944	-0.820	0.583	1.292	0.934	-0.452	-0.204
0.714	-1.014	-0.893	-0.146	-0.774	-0.435	-0.193	
-0.584	0.812	-0.571	1.952	-2.596	-0.186		
-0.456	1.226	0.563	-1.448	0.961	0.027	-0.029	0.217
0.464	0.130	-1.095	-0.864	-0.681	-0.228	0.353	
-0.061	-2.512	0.383	1.331	-0.806	-0.988		
-0.243	0.053	0.117	-0.701	-0.648	-0.204	0.233	1.957
0.195	0.551	-2.006	-0.559	-1.695	0.035	1.137	
-1.814	0.056	0.795	0.070	-0.458	-0.683		
1.138	1.786	0.601	-0.308	0.634	-0.596	0.308	0.287
-2.158	0.161	-0.417	1.205	0.549	0.474	0.620	
-1.002	-0.474	2.473	1.725	0.161	0.767		
-1.929	-0.179	-0.816	1.527	0.143	-0.195	0.532	-0.412
0.291	1.104	0.071	0.662	-0.496	0.522	-1.429	

Table36.txt

-0.281 -1.611 0.135 -0.062 -0.886 -0.873
0.894 0.000 -0.410 -0.690 0.936 -0.784 0.703 0.330
-0.081 -1.112 0.841 -0.508 0.167 0.216 -0.417
0.367 -0.574 1.144 1.038 -0.555 -0.357
0.265 -1.040 0.352 0.386 -0.646 -1.315 0.773 1.605
0.624 -0.016 -0.614 -1.222 0.260 -0.449 0.696
-0.938 0.000 -1.041 0.927 -0.527 1.342
-1.494 0.640 -0.047 -0.985 0.951 0.331 -0.796 -1.664
0.445 -0.471 0.300 -2.922 -0.636 -0.882 0.320
-0.657 0.508 1.524 0.246 1.469 0.297
0.288 -1.166 1.349 0.042 0.254 -0.689 1.288 -0.381
0.041 0.313 0.016 -2.857 -0.296 0.651 0.114
-0.089 -0.464 2.125 2.129 0.031 -0.144
1.758 -1.154 0.027 -1.704 -0.503 0.259 -0.065 -0.572
0.191 -0.541 -2.286 -0.969 -0.484 -1.083 0.606
0.222 -0.373 2.325 2.360 -0.456 -0.484
-0.286 -0.777 0.008 -1.258 -0.550 1.865 0.397 0.478
-0.005 0.503 -1.909 -0.497 -1.128 -0.491 -0.764
0.005 -0.434 1.573 1.002 -0.281 -0.570
1.948 -1.774 -1.296 -1.602 0.843 0.397 -2.775 1.376
0.162 0.500 -2.486 -0.861 -0.636 -2.815 -3.091
-0.257 1.443 -0.252 0.384 -1.888 -1.452
0.459 -2.503 0.030 -0.379 0.731 -0.418 -0.939 1.276
-0.102 0.979 -0.587 0.079 0.628 -2.978 -0.388
-0.721 -1.343 -1.200 0.196 -2.053 0.307
0.531 -1.670 -1.300 -0.137 -0.936 1.028 -0.607 1.907
0.942 0.032 -0.067 -0.391 -1.165 -1.156 0.752
0.704 -1.172 -0.124 0.319 -1.409 -0.411
-0.130 -0.635 -0.851 0.554 -0.681 1.159 0.858 1.096
0.290 -0.037 -0.103 -0.933 -0.920 -1.347 0.040
1.102 -0.022 0.869 0.370 -1.032 -0.123
0.157 -0.054 -0.312 -0.698 -1.205 -0.105 0.462 0.251
-1.231 -0.202 -2.046 -1.598 -2.070 -0.473 -1.357
0.708 0.652 1.108 0.108 -0.431 -0.297
0.536 -1.706 0.821 -1.201 0.118 1.272 -0.868 0.116
0.661 0.418 -0.965 -0.926 -1.011 -1.654 0.888
-0.402 -0.413 0.948 2.149 -0.440 -1.060
0.236 -0.630 -1.685 1.016 0.106 -0.596 -0.178 0.356
-0.911 2.677 1.697 -0.742 -0.613 -0.655 0.271
0.631 -0.437 0.418 -1.220 -0.905 -1.033
0.172 -1.536 -0.585 0.188 0.250 -1.256 -0.033 0.965
0.336 -0.896 0.552 -2.815 -0.931 -0.320 -1.034
-1.086 -0.247 -0.495 0.323 -0.260 0.228
1.409 -1.461 1.074 -0.143 -0.178 1.347 -1.326 -0.151
0.293 0.204 -1.150 0.624 -0.462 -1.448 -1.329
0.783 2.101 -1.118 0.788 -0.597 0.134
0.811 -1.530 -0.057 -0.216 -1.538 -1.468 2.779 0.056
-0.463 -0.895 -1.627 -1.998 -0.160 -1.128 0.131

Table36.txt

-0.370	1.861	1.046	1.249	-0.238	0.481		
-0.948	-2.536	-0.622	-0.420	0.301	0.605	-0.805	0.380
-1.089	0.938	-2.061	-0.683	-0.106	-0.810	-0.352	
-0.257	-1.025	0.806	1.253	-0.391	0.533		
0.197	-0.689	0.991	-0.097	-1.148	-0.890	1.629	1.488
-1.244	-0.101	-0.377	-0.351	-2.172	1.597	-0.030	
0.766	-0.441	1.500	2.439	0.473	-0.459		
1.511	-2.005	-0.724	-1.246	0.109	-0.410	-0.560	-0.027
-0.038	1.400	-1.456	-1.336	-1.890	-0.926	-1.295	
-0.804	-1.445	0.291	0.457	-0.321	0.096		
0.228	-1.392	-0.514	-1.616	-0.327	1.368	0.381	0.922
0.748	-0.354	-1.840	-2.067	-2.573	-1.544	-1.588	
-0.376	-0.658	1.245	0.833	0.572	-0.209		
0.080	-2.750	-1.810	0.470	-0.676	0.687	-1.630	0.041
0.252	0.406	-0.661	-0.801	-1.233	-2.138	-1.709	
-0.198	0.849	0.729	0.003	-0.480	-1.114		
-0.118	0.167	0.368	-0.255	0.987	0.003	1.757	-0.760
-1.124	-0.470	-0.587	-1.698	-1.465	-0.842	0.733	
-0.283	-2.048	1.812	0.900	-0.271	-0.666		
0.443	-2.670	-0.352	-0.519	-0.683	0.167	-0.240	0.135
0.727	-0.057	-1.926	-0.515	-0.868	-2.018	-0.739	
0.170	1.096	0.694	2.172	-0.669	-0.589		
1.926	-0.702	0.124	0.436	0.002	0.459	0.218	-0.829
-1.014	-0.050	-0.819	0.050	-0.883	-2.588	-2.169	
0.612	-0.792	-0.280	-1.002	-0.412	0.258		
0.826	0.000	-0.153	-1.434	-0.396	-0.076	-0.906	0.251
-0.857	0.129	-0.384	0.030	-0.204	-1.868	-1.861	
-0.549	0.279	0.283	0.542	-1.503	0.103		
0.991	-2.340	0.041	1.195	-2.267	-0.916	-0.080	-0.555
0.355	-0.628	-1.263	-1.747	-1.404	-0.011	-0.305	
-0.633	-0.579	1.904	2.089	0.849	0.100		
1.071	-1.695	-1.996	-1.235	0.188	-0.276	-1.739	0.300
1.201	0.639	-3.133	-0.519	-1.483	-2.822	-1.839	
0.403	1.270	-0.414	-0.575	-2.239	-0.680		
0.681	-1.184	-1.384	-1.525	0.758	0.448	-0.914	0.862
0.088	-0.120	-2.526	-1.001	-1.140	-1.702	-2.488	
-0.057	0.245	-1.358	-0.775	-0.930	-0.029		
0.848	5.452	-2.173	-0.628	-2.343	-1.843	-1.020	-0.479
1.510	-1.331	-1.209	-3.027	-1.632	-0.549	-1.547	
-0.932	-1.860	0.834	0.703	0.612	-1.056		
0.567	-0.369	-0.104	-1.215	0.272	1.385	-0.929	0.824
-0.228	0.853	-1.504	-0.293	0.200	-1.829	-2.489	
1.224	0.312	-1.214	0.172	-0.294	0.242		
1.145	0.034	-1.002	0.221	0.911	0.345	0.864	-0.710
0.194	0.729	-1.047	-2.242	-1.988	-0.873	-0.853	
-0.163	0.502	-0.942	0.028	-0.540	-2.048		
1.737	-1.327	-0.722	-1.870	1.765	1.322	-1.356	-0.402
-0.184	0.130	-1.872	-0.864	-0.791	-2.541	-2.194	

Table36.txt

-0.545	1.102	-0.064	-0.676	-2.073	-0.508		
1.840	-2.095	-0.477	-1.764	-0.782	0.106	-1.641	0.845
-1.157	1.341	-1.834	0.016	-0.811	-1.697	-0.913	
1.826	0.487	-0.695	-0.566	-1.064	-0.002		
1.676	-1.361	-1.176	-0.567	-0.283	0.646	-1.232	-0.225
-0.711	-0.278	-0.983	0.495	-1.016	0.515	-1.536	
0.164	0.343	-0.108	0.075	-1.320	0.711		
1.264	-1.235	-0.242	-0.707	-0.372	0.839	-1.731	-0.103
-0.298	1.123	-0.785	-0.439	-1.137	-1.676	-2.643	
-0.044	0.358	0.403	-0.130	-0.445	-0.783		
-0.786	-0.391	-0.814	0.226	-0.196	0.228	0.577	-0.103
-2.038	1.936	0.751	-0.515	-0.208	0.013	1.090	
-0.656	-0.191	0.818	1.311	-0.708	0.657		
1.956	-0.851	0.099	-2.097	0.239	-0.205	-1.620	0.399
0.272	0.364	-0.479	-1.019	-0.460	-1.466	-2.973	
0.515	0.364	-1.047	-0.851	-0.590	0.528		
0.672	-1.640	-0.107	-2.396	0.543	0.486	-0.175	0.146
0.921	-0.457	-2.055	-0.153	-0.979	-1.986	-2.029	
-1.366	1.530	-0.831	-0.955	-0.817	-1.552		
-0.301	-3.840	-0.408	-1.266	0.656	1.382	-0.774	-0.319
-0.704	0.117	-2.343	0.236	0.229	-2.475	-1.850	
-0.289	0.311	0.046	1.244	-0.076	1.698		
-0.651	-1.456	0.235	-0.620	-0.686	1.259	-0.328	-0.246
-0.799	0.660	-0.435	0.075	-0.790	-0.846	-1.263	
1.620	-0.069	0.929	1.202	-0.652	-0.541		
1.005	-3.108	-1.349	-1.071	-0.218	0.662	0.324	-0.108
2.021	0.471	-2.630	-3.322	-0.971	-2.221	-2.123	
0.609	0.785	1.197	0.029	-1.676	-2.861		
-0.549	0.604	1.238	-0.708	0.947	-0.034	1.417	-0.663
-0.820	-0.271	0.669	1.015	0.050	-1.187	0.011	
0.627	-1.590	2.256	-0.049	-0.858	1.043		
1.274	1.165	0.078	-1.230	-0.645	2.251	-0.483	0.217
-1.662	0.493	-1.249	-1.019	-0.749	-1.536	-0.987	
0.509	-1.133	-0.237	0.099	0.028	0.537		
0.421	0.464	0.170	-1.020	1.617	0.899	-0.293	-1.818
-0.334	0.870	-0.757	0.302	-0.287	-2.989	-1.027	
-0.853	0.680	-0.632	-1.370	0.232	-1.203		
0.992	-1.533	-0.007	-0.598	0.095	-0.111	0.215	-0.534
-0.455	1.694	-2.625	-0.567	-0.895	-2.524	-1.886	
0.684	0.323	-0.319	-1.714	-0.492	0.669		
-0.766	-1.832	-0.054	-1.715	-0.558	-0.245	0.499	0.185
0.242	0.345	-2.182	-1.380	0.283	-1.276	0.017	
0.567	-0.447	1.704	0.437	0.771	0.108		
0.408	-2.405	-0.022	-0.672	-0.100	-0.594	0.343	-0.184
-0.570	2.406	-0.384	-1.688	-0.512	0.033	-0.400	
1.608	-0.877	-0.266	-1.080	-0.712	-0.593		
1.344	0.843	1.839	-1.589	0.275	1.971	-2.193	-0.107
-0.587	0.642	-1.069	-0.188	-0.751	-0.870	-1.939	

Table36.txt

1.078	0.293	0.735	-1.136	-1.362	-0.157		
1.845	-1.306	-0.857	-1.126	-1.443	-0.527	-0.203	0.847
0.901	1.156	0.009	-1.642	-0.803	-0.652	-0.941	
0.208	-0.346	0.622	-1.251	-0.337	-0.614		
-1.294	-1.431	0.607	0.052	-0.683	-2.171	0.897	0.739
0.288	-0.548	1.235	-1.463	-0.741	1.396	1.696	
0.406	-1.403	1.016	0.319	1.493	0.553		
0.424	-1.581	-1.031	-1.016	0.913	0.882	-0.154	-0.851
-0.036	1.081	-1.894	-0.825	-1.187	-1.275	-0.861	
-0.773	-0.782	0.799	-1.397	-1.015	-0.023		
0.406	-2.268	-1.469	-1.448	0.486	0.596	0.284	-0.491
1.054	0.394	-2.719	-1.661	-0.053	-1.954	-1.500	
-0.206	0.016	0.263	-1.033	-0.630	-1.623		
0.270	-2.148	-1.414	-0.513	-0.458	0.566	1.438	1.166
0.491	0.655	-0.986	-1.035	-0.491	-1.854	-1.036	
0.454	0.589	0.164	-1.038	-0.096	0.136		
0.482	-1.422	-0.781	-1.420	-0.639	0.571	0.513	1.117
-0.629	0.982	-0.753	-1.409	-1.203	-1.639	-2.783	
-0.044	0.520	0.452	-0.290	-0.650	0.542		
1.168	-1.768	-1.072	-1.419	-0.005	0.958	0.551	0.360
-0.883	0.357	-0.658	-0.714	-0.668	-1.457	-2.522	
0.328	0.303	0.769	-0.791	0.291	0.621		
1.487	-2.460	-0.807	-1.105	-1.462	-2.898	-1.049	-1.015
1.558	-1.185	-1.523	-0.940	0.016	-0.844	-0.317	
0.858	0.262	1.369	1.454	-1.517	-0.795		
1.273	-0.731	-1.466	-0.365	1.057	1.029	-1.433	-0.245
0.371	-0.684	-1.937	-0.188	-0.074	-1.662	-1.677	
0.589	0.084	-0.010	0.039	-0.210	-0.312		
0.978	-3.274	-0.882	-1.638	-0.579	-0.829	-0.040	-0.365
1.092	0.551	-3.137	-4.501	-1.298	-1.828	-1.861	
0.139	2.094	0.544	-0.840	-3.095	-1.307		
2.389	-2.112	-1.225	-1.499	1.152	0.477	-3.284	0.261
0.354	0.391	-3.333	-0.939	-1.048	-2.057	-3.009	
0.220	1.460	-0.926	-1.613	-1.484	-0.344		
2.763	-1.981	-0.901	-1.636	1.148	0.714	-2.950	0.108
0.614	0.776	-2.513	-1.293	-0.932	-2.507	-3.313	
0.186	1.372	0.251	-1.041	-1.902	-0.355		
1.918	-0.926	-0.604	-0.322	0.982	0.954	-0.147	-0.218
0.544	0.635	-1.645	-1.850	-0.582	-1.330	-2.153	
0.121	0.637	0.608	-1.152	-1.891	-1.514		
1.646	-1.168	-0.181	-0.196	0.954	0.835	-1.413	0.038
-0.094	-0.319	-2.929	-1.552	-0.596	-2.828	-2.156	
-0.563	1.318	1.005	-1.047	-1.101	-0.589		
1.329	-0.776	-0.266	-0.700	1.113	0.619	-1.145	-0.100
0.547	0.032	-2.954	-1.138	-0.671	-2.794	-2.411	
0.543	1.094	0.646	-1.575	-1.000	-0.868		
-0.271	-2.035	-0.698	0.392	0.599	1.547	-0.036	0.351
0.307	0.081	-1.029	-1.299	-1.255	-0.874	-0.724	

Table36.txt

0.427	-0.699	0.409	1.631	-0.779	0.324		
1.590	-2.467	-1.020	-1.091	0.890	1.129	-2.812	0.510
0.693	1.156	-3.042	-0.355	-0.591	-2.220	-3.142	
-0.440	0.899	0.304	-0.404	-1.749	-0.264		
1.943	-2.261	-0.776	-1.947	0.708	0.579	-3.188	0.176
0.656	1.216	-3.039	-0.846	-1.066	-2.770	-3.994	
-0.066	0.615	0.005	-0.570	-1.208	-0.246		
0.451	-1.978	-0.172	-2.039	0.523	-0.437	-0.517	0.152
-0.999	0.787	-0.872	-1.714	-0.262	-0.636	-2.440	
0.030	-0.030	1.105	-0.333	-1.207	-0.849		
0.293	-1.308	0.121	-1.044	0.171	0.429	-0.617	-0.171
0.480	-0.498	-1.066	-1.392	-0.467	-0.933	-1.688	
-0.372	0.207	1.129	0.083	-1.346	0.235		
-0.159	-1.342	-1.004	-1.461	0.519	0.343	-1.008	0.268
0.740	-0.701	-2.021	-0.773	-0.889	-1.648	-1.982	
-1.533	0.472	-0.276	0.179	-1.482	-0.528		
-1.022	-0.753	0.982	1.197	-1.483	-0.816	1.730	0.084
0.438	-0.870	1.426	-1.075	-0.947	-0.570	0.862	
-0.641	-1.115	0.559	-0.214	0.315	0.069		
1.814	-2.448	-1.629	-1.905	0.288	1.603	-3.045	0.652
1.006	1.350	-2.239	-1.473	-0.922	-2.607	-3.473	
-0.235	1.370	-0.344	-1.405	-2.535	-0.626		
2.167	-2.781	-1.116	-1.856	0.548	0.663	-3.223	-0.120
0.836	1.015	-2.564	-0.880	-0.471	-2.526	-3.482	
-0.341	1.329	-0.071	-1.737	-2.443	-0.682		
-0.184	0.252	1.468	-0.001	-0.126	0.120	1.311	-0.130
-0.464	-0.004	0.588	-2.099	-0.894	0.282	0.921	
-1.102	-1.849	-0.391	0.522	-1.560	0.380		
0.062	-1.786	-0.349	-0.973	-1.256	-0.472	0.677	0.060
0.903	-0.551	-2.117	-1.653	-0.608	-0.879	-1.297	
0.394	0.712	1.909	2.695	0.465	-0.102		
1.711	-2.264	-1.840	-1.003	0.550	0.573	-1.530	-0.528
1.590	0.609	-2.626	-1.893	-1.367	-1.598	-2.117	
0.172	1.122	0.760	1.167	-1.044	0.213		
0.864	-2.721	-0.611	-0.688	-0.874	0.110	-0.374	-1.157
0.980	0.007	-2.099	-1.688	-0.387	-1.861	-2.284	
0.267	0.023	1.075	1.678	-0.653	0.111		
-0.040	-1.387	0.876	-1.348	-0.420	0.808	0.148	0.923
-0.986	0.903	0.335	-0.283	-0.019	0.005	-1.405	
-0.234	0.630	1.201	0.534	-0.815	0.746		
0.959	-1.365	-1.511	-2.190	0.394	-0.444	-0.340	1.705
0.529	-0.845	-2.896	-2.540	-0.975	-0.676	-0.019	
-0.954	1.452	2.197	0.624	-1.197	-0.871		
-1.143	-0.586	0.143	0.384	1.546	2.177	-0.289	-0.256
-2.513	-0.936	1.955	0.331	0.180	-0.937	-0.224	
0.093	2.641	2.527	-0.874	-0.426	-0.044		
-0.131	-1.718	0.975	-0.829	-0.523	-0.182	1.801	0.280
0.620	-0.528	-1.158	-2.123	-0.500	-0.321	1.097	

Table36.txt

-0.417	0.055	0.245	-0.460	0.092	-0.156		
0.859	-1.491	-1.015	-1.833	1.117	2.801	-1.650	-0.577
-1.209	1.482	-1.631	-1.284	0.081	-2.113	-2.440	
0.118	1.658	0.858	-1.620	-1.977	0.444		
0.823	-1.498	1.107	-2.116	-2.385	-0.751	0.346	1.370
0.163	-0.104	-2.449	-1.843	-1.150	-0.464	0.959	
-0.419	0.445	1.663	2.371	-0.716	-0.197		
1.245	-0.640	-0.448	0.171	-0.617	-0.945	-0.270	0.909
0.659	0.782	-1.636	0.690	0.656	0.042	-0.405	
0.760	1.301	0.425	1.312	-1.466	-0.755		
2.063	-2.598	-0.775	-0.177	-0.578	-0.336	-0.522	0.266
1.319	0.285	-2.078	-2.837	-1.577	-2.120	-2.232	
-0.140	0.039	-0.451	-1.315	-0.803	0.044		
0.372	-1.797	-0.686	-1.723	-0.014	1.408	-3.092	0.914
0.250	0.266	-3.133	-1.774	-0.338	-2.726	-1.810	
0.850	1.605	0.115	-0.432	-1.789	-0.706		
0.798	-0.946	-0.191	-0.184	0.348	0.919	-1.192	1.750
-0.138	0.782	-1.803	-1.123	-0.915	-1.182	-1.217	
-0.165	-0.926	1.230	0.604	0.116	0.658		
1.263	0.145	0.148	-0.356	-1.292	-0.347	0.817	0.446
0.416	-0.268	-1.246	-0.833	-0.254	0.440	-0.523	
0.585	0.997	0.521	1.275	-0.781	0.092		
1.269	-1.274	-0.743	-0.565	-1.602	-1.173	0.163	0.203
1.419	0.501	-3.016	-3.301	0.669	-0.694	0.326	
0.286	-0.565	2.584	1.773	-0.250	0.251		
1.994	-2.534	-2.663	-0.700	-0.357	0.632	-0.757	-0.664
1.921	0.469	-3.424	-2.158	-2.227	-2.387	-2.979	
-0.371	2.050	-1.356	-1.404	-1.571	-1.477		
1.281	-1.196	-0.709	0.225	-1.025	0.944	0.479	-1.103
0.285	-0.078	-0.702	-2.062	-0.395	-0.804	1.223	
0.892	-0.434	0.253	-0.183	-0.683	-0.655		
1.663	-1.550	0.164	-0.775	-0.412	1.813	0.479	0.270
0.861	-0.100	-1.550	-0.645	-0.561	-1.945	-1.226	
0.308	0.365	-0.049	-1.299	-0.620	-0.344		
1.080	-1.514	-0.533	-0.353	0.144	2.383	-0.029	-0.196
0.644	-0.120	-0.646	-0.516	-0.348	-2.059	-1.584	
0.172	0.458	0.445	-1.115	-0.975	0.426		
1.054	-2.011	-0.514	-0.648	-0.859	0.016	0.869	0.615
0.928	0.408	-1.533	-2.617	0.117	-0.879	-1.507	
0.047	-0.490	1.824	1.012	-0.265	-0.391		
1.439	0.058	-2.508	0.818	-0.317	0.739	1.248	1.202
-1.267	0.402	0.433	-0.207	-0.448	-1.114	-0.070	
0.980	0.480	0.317	0.408	-0.405	0.176		
1.709	-0.281	-1.184	-1.427	0.042	1.452	-1.680	0.291
0.152	-0.039	-1.964	-0.624	-0.017	-1.454	-2.835	
-0.087	1.618	-0.406	-0.783	-1.154	-0.297		
2.513	-0.861	-2.137	-0.337	0.040	1.322	-2.610	-0.080
-0.035	0.644	-1.841	-1.874	-1.472	-2.563	-2.653	

Table36.txt

-0.290	2.599	-0.500	-1.631	-0.096	-0.768		
-0.150	-0.613	-1.009	-0.615	-0.926	1.035	-0.403	0.121
0.125	-0.628	-0.618	-2.305	-0.926	-1.551	-1.796	
-0.979	0.290	-1.225	-0.097	-1.585	-0.251		
1.190	-1.809	-1.078	-1.823	0.146	1.817	-2.852	0.535
1.003	-0.636	-2.524	-1.094	-0.186	-3.455	-3.521	
-0.532	1.263	-0.891	-1.607	-1.341	-0.329		
1.426	-1.873	-0.755	-2.388	0.672	1.362	-2.703	-0.480
0.508	0.809	-3.359	-2.600	-0.924	-2.942	-3.722	
-0.226	1.049	0.892	-0.967	-2.115	-0.261		
1.234	-1.943	-1.074	-2.167	0.482	1.472	-2.417	-0.122
0.629	0.919	-3.433	-2.770	-0.968	-2.973	-3.379	
-0.828	0.805	1.221	-1.140	-2.384	0.107		
0.516	-1.909	-0.313	-0.617	0.711	0.679	0.411	-0.705
0.662	0.444	-0.764	-1.795	-1.358	-0.671	-1.612	
-1.214	0.813	-0.611	-1.067	-0.621	0.287		
1.856	-0.087	1.154	0.122	-0.771	0.068	-1.200	0.471
0.086	0.239	-0.019	-0.812	-1.617	-0.788	-0.970	
-1.318	0.541	-0.096	-1.056	-0.595	0.212		
2.508	-1.085	-1.143	-0.933	-0.593	0.357	-2.688	0.394
0.920	1.082	-2.864	-1.684	-0.768	-2.824	-3.666	
-0.504	0.435	0.627	-0.913	-1.963	0.031		
2.739	-1.581	-0.661	-1.566	-0.587	0.695	-2.274	0.758
0.776	1.288	-2.819	-1.607	-0.092	-3.429	-3.665	
-0.626	0.935	0.742	-0.580	-1.824	-0.087		
1.818	-2.622	-2.347	-1.252	0.117	1.197	-2.404	-0.390
1.015	1.211	-3.082	-0.541	-0.586	-2.923	-3.226	
-0.759	0.809	0.277	0.902	-1.316	-0.126		
-1.441	-1.052	-0.099	-0.481	-0.110	-0.764	1.408	0.863
0.719	-0.500	1.077	-2.247	0.096	0.030	0.569	
0.192	-1.444	1.618	2.471	0.312	-0.008		
0.860	-1.961	-2.059	-0.623	-0.164	1.183	-1.925	0.476
-0.395	0.388	-2.442	-0.894	-0.432	-2.413	-3.212	
0.211	0.073	0.806	-0.453	-1.972	-0.619		
1.636	-0.538	-0.942	-0.765	1.331	0.661	-1.372	0.195
0.369	0.687	-1.794	-0.993	-1.542	-0.816	-2.526	
-0.273	-0.966	-0.732	-1.511	-2.725	-0.806		
2.143	-1.065	-0.758	-0.703	-0.113	1.852	-0.636	-0.095
-0.095	0.121	-1.877	-2.157	-0.493	-2.491	-1.372	
-1.088	1.590	0.401	-0.112	0.488	0.071		
0.316	-0.929	-1.234	-0.738	1.172	0.251	-1.697	0.165
-0.769	0.335	-0.668	0.486	-0.645	-0.809	-1.884	
0.502	-0.183	0.896	-0.160	-0.985	-0.155		
0.812	-0.742	0.269	0.083	-0.448	1.019	-0.660	-0.132
-1.067	-0.059	-1.092	-1.623	-1.309	-1.723	-2.133	
-0.280	0.568	-1.783	-1.948	-1.765	-0.452		
1.007	-1.031	-1.162	-0.827	-0.832	1.451	-1.466	0.348
-0.249	-0.355	-2.401	-0.768	-1.016	-2.206	-3.256	

Table36.txt

-0.801	0.943	-0.752	-1.652	-1.735	-0.510		
1.275	-1.687	-0.585	-1.243	0.002	0.686	-0.322	-0.047
0.222	-0.193	-1.328	-0.482	-0.425	-2.204	-2.525	
-0.007	-0.070	-0.729	-1.074	-1.950	0.051		
0.240	-1.183	0.117	-0.323	1.404	1.432	-1.006	0.020
0.208	-0.639	-1.552	0.053	0.707	-0.642	-2.261	
-1.295	-0.541	-1.305	0.303	-0.754	0.551		
0.996	-1.211	-1.061	0.196	-0.349	0.762	-1.333	0.525
0.832	-0.028	-2.158	-0.643	-0.621	-0.395	-2.551	
0.006	-0.486	1.327	-0.816	-0.628	0.434		
-0.417	0.152	-0.804	-1.826	1.128	-0.537	-0.624	0.225
-0.805	-0.574	-0.312	-0.594	-0.042	-1.509	-1.515	
1.433	0.425	-1.143	-0.035	-1.108	1.085		
0.030	-1.422	0.483	-0.800	-0.022	1.334	0.512	0.971
-0.796	0.543	-0.355	-1.215	0.087	-0.552	1.248	
-0.435	-1.801	1.546	1.135	-0.669	-0.868		
0.236	-0.519	0.757	-0.504	-0.106	0.459	-0.751	0.620
0.477	-0.302	-1.532	-0.015	-0.683	-0.079	-0.421	
-0.400	-0.016	-0.327	0.205	-0.258	-1.464		
0.729	-0.337	-0.057	-0.877	0.481	0.988	-1.209	0.076
0.410	-0.523	-1.797	-0.273	0.333	-0.299	-1.819	
0.206	0.967	0.205	0.401	-0.463	-0.121		
1.233	0.385	1.366	-0.799	-0.183	1.076	-0.657	-0.535
0.786	-0.180	-1.534	-0.971	0.167	-1.341	-1.057	
0.861	0.545	0.494	1.184	0.086	1.091		
1.582	0.074	0.072	0.356	-1.474	0.032	-0.647	0.824
-0.928	-0.160	-0.589	0.544	0.296	-0.151	-0.593	
1.449	0.411	-1.416	0.115	-0.710	0.308		
1.704	-1.398	-0.089	-0.815	0.138	0.295	1.247	0.466
0.600	-0.238	-2.032	0.203	-0.853	-0.398	-0.852	
0.585	-0.741	1.412	0.418	1.003	0.249		
1.569	-1.396	-1.051	-0.924	-0.729	0.218	-0.725	0.075
1.974	0.876	-2.657	0.129	-1.203	-2.613	-2.182	
0.253	1.078	-0.604	0.209	-0.603	-0.059		
1.653	-1.265	-0.345	0.279	-1.209	0.441	-1.512	-0.133
0.163	-0.349	-2.307	-1.175	-0.931	-0.793	-1.061	
-0.665	-0.048	-0.886	1.342	-0.201	0.901		
0.695	-1.964	-0.743	-0.835	-0.452	2.254	-1.937	0.153
0.556	0.178	-1.155	0.570	0.331	-1.635	-2.694	
-0.407	0.236	-0.973	-0.265	0.641	0.739		
1.508	-1.966	-1.688	-2.807	-0.450	1.820	-2.145	0.847
0.406	-0.256	-2.910	-1.496	-0.234	-1.781	-2.987	
-0.383	1.075	-0.166	-1.072	-1.053	0.701		
0.774	-2.625	-1.831	-1.378	-1.426	0.573	-1.391	0.114
1.759	-1.128	-2.581	-2.188	-0.514	-1.117	-2.438	
-0.796	0.564	1.163	0.980	-0.822	-1.066		
-0.197	-0.610	0.201	0.632	-0.732	-0.569	0.764	0.867
1.206	0.535	-0.364	0.270	-0.422	-1.141	1.143	

Table36.txt

0.055	-2.051	0.411	2.211	-0.136	-0.670		
2.010	-1.723	-0.457	-1.187	1.600	2.583	-2.084	-0.159
-0.032	0.060	-1.928	-0.453	-0.992	-2.582	-2.505	
-1.131	1.233	-0.428	-0.394	-0.849	0.098		
1.550	-1.984	0.036	0.360	0.660	0.505	-2.593	-0.113
-0.072	-0.163	-2.237	-1.651	-1.328	-2.179	-1.978	
0.017	0.362	-0.469	-0.036	-0.071	-0.562		
1.507	-1.051	-2.147	-1.298	1.174	1.311	-1.637	1.297
-0.542	0.778	-2.908	-1.927	-0.062	-2.450	-2.854	
-0.899	1.445	0.197	-0.165	-2.395	-0.115		
1.026	-1.151	-0.054	-1.171	0.513	1.380	-0.469	0.035
1.501	-0.285	-3.305	-2.105	-1.112	-2.722	-3.245	
-0.066	1.927	0.703	-0.898	-1.531	-0.802		
-0.070	-1.001	-1.130	-0.321	-0.993	-0.568	-0.372	1.938
-0.715	0.558	-2.258	-0.838	-0.836	-1.771	-0.785	
-0.274	-0.109	-0.376	0.242	-1.683	-1.200		
0.050	-1.810	-1.478	-2.196	-0.283	0.740	-0.356	-0.465
-0.607	-0.205	-1.002	-1.527	-1.041	-2.043	-1.282	
0.157	1.226	1.237	0.405	-0.834	-1.106		
0.757	-1.925	-0.509	0.275	0.402	-0.118	-0.013	0.089
0.319	-0.245	-1.515	0.474	-0.430	0.112	-1.031	
0.711	-1.594	0.747	1.787	0.249	-1.727		
1.995	-1.317	-1.119	-1.422	0.902	1.879	-1.841	1.051
0.000	-0.359	-2.463	0.511	-0.038	-2.389	-2.813	
-0.777	0.505	0.212	-0.332	-1.169	-1.558		
2.216	-1.551	-1.780	-1.149	-0.043	1.817	-2.028	-0.008
0.169	-0.316	-2.641	0.796	-0.674	-2.533	-2.141	
-0.321	0.893	0.128	-0.896	-0.705	-0.641		
2.068	-1.018	-1.672	0.381	-0.971	0.321	-0.429	0.581
0.894	0.253	-2.718	-0.828	-0.851	-1.136	-2.642	
0.152	1.354	1.815	0.419	-1.122	0.194		
1.059	0.003	0.403	-0.945	-0.290	1.183	-1.484	0.299
-1.325	-0.310	11.000	-0.716	-0.603	-1.368	-1.873	
0.065	-0.401	-0.814	-1.395	-2.291	0.372		
1.618	-1.252	-0.365	-1.167	-0.918	0.848	-2.226	0.790
0.709	-1.506	-1.845	-0.027	-0.815	-1.732	-3.236	
-0.503	-0.587	-1.124	-1.570	-2.886	-0.633		
1.314	-1.355	-1.914	-1.714	0.407	1.123	-1.608	0.735
0.257	-0.714	-2.158	-0.501	-1.318	-2.115	-3.538	
0.130	1.500	0.928	0.422	-3.165	-0.586		
1.361	-1.123	-1.581	-1.244	0.100	1.081	-2.016	0.658
0.213	-0.428	-2.532	-0.215	-0.258	-2.490	-2.780	
-0.227	0.076	0.257	-0.563	-2.488	-0.409		
-0.323	-1.201	-0.597	-0.285	-0.605	0.214	-1.132	0.731
-0.380	0.218	-0.511	-0.692	-0.112	-1.642	-0.280	
-0.013	0.454	-0.310	-0.654	-0.473	-0.730		
1.223	0.588	0.166	0.292	-0.140	1.446	-1.097	-0.236
-0.553	-0.423	-1.482	0.883	-1.047	-1.710	-1.204	

Table36.txt

0.556	-0.279	-1.124	0.381	-1.728	-0.454		
1.425	-0.690	-0.989	-1.507	0.794	0.918	-1.700	0.139
-0.272	-1.032	-1.448	-0.691	-0.040	-2.553	-1.776	
-0.406	-0.191	-0.675	-1.357	-2.158	-0.074		
0.110	-2.527	-0.709	-1.280	-1.157	-0.834	0.321	-0.147
0.996	0.606	-1.114	-1.201	-0.682	-2.456	-2.307	
0.377	-0.110	0.245	-0.885	-1.268	-1.304		
-1.062	-1.071	-0.687	1.009	-1.067	0.394	-0.953	-1.280
-0.705	0.407	-0.722	-2.629	-2.925	0.180	-0.625	
0.713	-0.733	0.154	-0.374	-1.934	-0.369		
1.555	-1.579	0.041	0.131	-0.615	0.186	0.035	0.410
0.380	0.726	-1.022	-0.460	-2.210	-1.026	-1.157	
0.233	0.379	1.367	0.685	-1.267	0.705		
0.429	-0.939	-0.181	-0.819	0.712	1.332	-0.013	0.135
0.903	0.591	-1.403	-1.232	-0.543	-0.830	-1.436	
-1.175	-0.355	0.932	1.087	0.756	-0.187		
0.578	-1.112	0.618	-0.315	-0.932	1.144	0.788	0.763
-1.141	0.852	-1.175	-0.640	0.826	-0.866	-1.322	
0.591	-0.510	0.176	0.773	0.006	0.865		
0.965	-1.894	-1.275	-1.203	-0.421	-0.092	-0.400	-0.933
0.294	-0.657	-3.086	-1.906	-0.339	-0.991	0.414	
0.495	-0.103	-0.230	0.045	-0.870	-0.213		
0.537	-1.226	0.640	-0.003	0.503	0.880	-1.190	0.261
-1.186	0.209	-0.328	-1.581	-1.695	-1.271	-1.929	
0.233	-1.031	-1.411	-1.273	-1.698	-0.638		
1.125	-0.492	-1.074	-0.430	0.952	1.250	-0.751	0.247
0.107	0.613	-1.786	-0.614	-0.162	-1.565	-2.603	
-0.444	-0.125	-0.854	-0.988	-1.560	0.215		
0.910	-1.504	-1.407	-0.433	-0.452	1.529	0.162	0.260
0.066	-0.503	-0.917	-2.049	-1.156	-2.011	-2.254	
-0.495	1.294	-0.170	-1.366	-1.741	-0.873		
0.398	-0.892	-0.741	-0.672	-0.752	0.128	-0.051	0.877
-0.939	0.463	-0.096	-0.855	-0.501	-2.534	-1.132	
-0.450	0.676	-0.541	-1.111	-0.742	0.441		
2.437	-1.671	-1.777	-2.131	0.500	1.409	-2.371	0.228
-0.239	1.291	-2.793	-1.774	-0.619	-2.500	-2.658	
-1.139	0.817	1.194	-1.288	-2.648	-0.445		
0.597	-0.168	-2.132	-0.227	-1.223	-0.042	1.513	0.223
0.603	0.611	-2.149	-2.302	-1.334	0.756	0.771	
-0.770	0.325	-0.259	0.701	-1.121	-0.085		
0.807	0.515	-0.666	-0.977	1.410	0.999	-1.353	0.637
0.052	0.794	-1.103	-0.364	-0.971	-2.245	-1.447	
0.476	0.482	0.520	-0.497	-1.872	-1.188		
1.278	-0.069	-0.794	-0.793	0.867	1.288	-1.778	-0.458
-0.567	0.447	-2.022	-0.326	-0.325	-1.982	-1.583	
0.080	0.653	-0.016	-1.647	-1.413	-1.061		
-0.643	-0.259	-0.591	0.671	-0.733	2.102	0.327	-0.104
-0.188	0.481	-0.293	0.473	0.311	-0.074	0.108	

Table36.txt

-1.184	1.079	0.573	-0.246	-0.333	0.158		
-0.699	0.027	2.090	-0.790	0.193	1.652	1.415	0.956
-0.158	-0.157	0.779	-1.811	-0.684	-0.131	0.658	
0.370	-0.935	-0.512	0.284	-0.161	0.943		
0.847	-0.400	-0.335	-0.633	1.292	1.958	-1.381	0.080
-0.609	0.292	-2.100	-0.050	-0.384	-2.097	-1.833	
-0.399	1.127	-0.150	-0.098	-0.386	0.361		
0.630	-0.656	-1.180	-0.200	0.203	0.284	-2.308	0.507
0.383	0.356	-2.358	0.049	-1.760	-2.045	-2.142	
-0.366	0.588	0.430	-1.139	-1.073	-1.220		
-1.400	-3.049	-1.855	-1.909	-0.752	5.541	-2.280	-0.216
0.032	-1.525	-1.439	0.122	-0.066	-1.936	-0.719	
-0.195	-0.953	0.145	0.106	-1.812	0.342		
1.651	-1.370	-1.375	-1.999	-1.600	0.895	0.897	0.473
1.404	-0.300	-1.101	-1.702	0.611	0.056	-0.326	
-0.216	0.536	1.115	0.659	-0.318	-0.054		
0.249	-1.515	-1.081	-1.570	0.082	-1.220	1.527	-0.408
1.388	-0.112	-2.470	-1.950	-0.790	-0.598	-1.212	
1.285	0.500	0.272	0.658	-0.958	-2.782		
0.605	-1.568	-1.080	-0.604	-0.037	0.913	-1.879	0.652
0.601	-0.196	-2.793	-1.036	-2.221	-3.278	-1.693	
-1.231	0.820	-0.409	-1.184	-2.462	-1.010		
1.783	-1.042	-0.978	-1.400	0.324	1.121	-1.247	0.383
0.932	0.359	-1.867	0.144	-0.016	-2.901	-2.142	
0.722	1.528	0.458	-1.013	-0.802	-0.720		
-0.158	-0.655	-1.508	-1.985	-0.368	0.837	0.535	1.000
0.500	0.228	-2.047	-0.378	-0.335	-1.666	-1.965	
-1.375	-0.190	0.189	0.010	-0.928	-1.173		
-0.156	-0.595	-1.716	-0.778	0.250	1.527	-0.629	0.157
-0.571	-0.310	-0.334	-2.049	-0.246	-1.152	-2.072	
-1.364	1.351	-0.096	-1.433	-1.195	-1.235		
0.853	-1.708	-2.239	-0.989	-0.250	0.565	1.260	-1.032
0.503	0.491	-1.030	-1.654	-0.861	0.885	0.259	
0.251	1.046	0.448	0.848	-1.964	-0.285		
2.737	-1.552	-1.854	-1.560	1.297	1.342	-2.348	0.125
0.006	1.009	-2.401	-0.783	-0.507	-2.583	-3.240	
0.243	1.320	0.761	-0.963	-2.143	-0.785		
1.093	-3.171	-1.925	-0.617	0.451	1.416	-1.266	1.065
-0.925	0.096	-1.437	-1.476	-0.556	-1.508	-1.716	
0.361	1.959	0.027	-1.418	-1.639	-0.447		
1.641	-1.920	-2.081	-1.329	0.649	1.226	-2.787	0.235
-0.047	0.195	-3.067	-0.822	-1.294	-2.621	-2.798	
-0.986	2.112	0.212	-0.861	-2.179	-0.149		
1.609	-1.545	-2.037	-0.900	1.145	1.304	-2.360	0.827
-0.826	-0.007	-2.531	-1.307	-0.378	-2.252	-2.767	
-0.644	2.204	0.544	-1.264	-1.639	0.183		
0.604	-1.026	-1.342	-0.024	0.578	1.736	-0.805	-0.409
-0.280	-0.283	-0.587	-1.521	-1.041	-1.917	-1.595	

Table36.txt

0.400	0.082	-0.101	-0.263	-1.234	-0.632		
1.793	-1.449	-0.939	-0.955	0.484	1.937	-2.122	-0.350
-0.437	1.286	-1.934	-2.143	-1.087	-2.941	-3.494	
-0.279	1.178	0.222	-1.119	-1.681	-0.683		
1.733	-1.435	-2.502	-0.531	0.759	1.803	-2.188	0.017
-0.836	1.460	-2.250	-1.902	-1.069	-2.410	-3.326	
-0.273	0.348	-0.167	-0.757	-1.527	-0.390		
-0.038	-0.477	-1.300	-0.245	-1.040	0.290	-1.346	-0.965
0.345	0.534	-1.183	-2.041	0.418	-1.918	-0.179	
-0.507	0.455	0.167	-0.970	-2.113	-0.209		
-1.615	0.594	-0.476	0.950	0.134	0.035	-1.250	-0.376
-0.044	-0.422	0.734	-1.408	-0.074	-0.858	0.416	
-1.164	0.806	-0.519	-2.345	-1.834	-0.956		
-0.193	-1.308	-1.673	-1.813	0.042	-0.733	1.162	0.202
0.652	-0.410	-0.084	-1.929	-0.120	-0.529	0.780	
0.784	-1.042	-0.563	0.447	-1.626	-0.721		
1.490	-0.296	-1.501	-1.633	-0.189	-0.984	0.387	-0.760
1.383	-0.343	-0.179	-3.785	-1.065	0.593	-0.064	
0.802	-1.572	-0.267	1.392	-1.657	-0.831		
0.069	0.253	0.618	-0.456	1.198	0.592	-1.677	0.326
-1.876	0.337	-1.312	-0.813	-0.546	-2.335	-1.470	
0.019	0.362	0.039	-0.547	-0.861	0.317		
-1.759	0.881	2.937	0.317	-0.005	0.350	-0.973	-0.414
-1.807	0.892	1.141	-1.639	0.005	1.167	0.994	
0.396	-1.275	2.253	0.114	-1.009	0.847		
0.111	-0.853	-1.982	-1.097	0.103	-0.328	0.647	-0.009
2.951	0.021	-1.904	-3.356	-0.562	-0.048	-0.824	
0.729	-1.256	-0.471	0.242	-2.784	-2.028		
-0.645	0.791	-2.056	0.918	-0.790	-0.635	-0.381	-1.507
1.579	-0.551	-2.670	-1.766	-0.884	-0.971	-1.952	
-1.524	-0.638	1.012	-0.292	-1.970	-0.856		
0.825	-0.670	-1.710	-0.890	-0.840	1.510	0.963	-0.913
1.187	-0.684	-1.914	-2.285	-0.633	-1.400	-1.009	
-0.421	1.525	-1.350	0.137	-1.481	-0.524		
0.067	-0.894	-0.133	0.982	-0.604	-0.198	-0.847	0.445
-1.041	-0.165	-0.994	-1.413	-1.582	-2.089	-1.054	
-0.244	0.316	0.317	-1.116	-1.834	-0.256		
0.847	-1.380	0.147	-0.644	-0.069	1.339	-0.940	-0.870
0.116	1.036	-0.389	-2.361	-0.986	-0.911	-1.872	
-0.103	1.177	0.385	-0.150	-1.711	-0.838		
0.014	-2.000	-0.146	0.084	-0.356	0.846	0.746	-0.069
0.287	0.696	0.584	-2.303	-0.395	-0.061	-0.239	
0.974	0.586	1.124	1.371	-1.466	-0.645		
0.868	-3.069	-0.558	0.045	-0.663	-0.449	-0.648	-1.455
1.319	1.363	-1.477	-3.525	-0.136	0.228	0.138	
0.499	0.635	0.119	1.496	-1.566	-1.177		
-0.867	-0.491	-0.723	0.539	0.039	0.160	-1.073	-1.613
0.101	2.506	0.094	-3.527	-0.845	0.870	-0.921	

Table36.txt

0.273	0.897	1.311	0.896	-0.922	-0.784		
0.364	-1.340	0.458	0.384	0.331	1.241	-1.023	0.044
-0.526	0.711	-1.669	-1.920	-1.472	-2.650	-1.773	
0.146	0.474	0.785	-1.030	-0.709	-0.500		
0.363	-0.964	-1.317	-1.729	0.168	0.607	-0.611	-0.785
-0.048	0.061	-1.712	-2.507	-1.204	-0.830	-0.266	
-0.090	-0.411	0.385	-0.691	-2.005	-1.703		
1.156	-2.128	-1.361	-0.536	-0.122	0.808	-1.233	-0.157
-0.783	0.613	-1.926	-1.560	-0.682	-2.221	-1.491	
0.011	0.744	0.079	-0.044	-1.314	0.185		
1.310	-1.334	-0.333	0.463	-0.105	0.613	-2.030	-0.139
0.209	0.104	-1.506	-1.292	-1.419	-1.853	-1.484	
-0.242	0.439	0.380	0.838	-1.414	-0.376		
-0.163	-2.479	-0.278	-0.367	-0.415	-0.526	-0.383	-0.769
0.552	0.049	-1.315	-3.195	-1.134	-0.414	-0.634	
0.677	0.601	0.691	0.830	-1.959	-1.138		
-0.429	-1.178	-0.174	0.120	1.341	0.198	-0.881	0.075
0.738	0.588	-0.180	-1.934	-1.423	-1.500	-0.896	
-0.344	-0.243	-1.476	-1.288	-1.966	-0.890		
0.738	-0.998	-0.114	0.223	0.420	-0.637	-1.450	-0.146
0.451	-0.253	-1.204	-1.471	-1.598	-0.316	-0.238	
0.333	0.801	1.048	-0.980	-1.435	-0.021		
-0.423	-0.828	-0.005	0.650	-1.275	0.952	-0.330	-0.028
-1.599	-1.513	-1.551	-2.565	-1.021	-0.505	1.002	
-0.058	0.130	1.306	-0.101	-1.966	-0.873		
-1.696	0.087	0.088	1.311	-0.214	-0.228	-0.219	-0.713
-1.060	-0.237	-0.113	-2.180	0.063	-0.633	0.248	
-1.253	-0.299	0.127	-1.555	-1.317	-1.534		
1.285	-0.935	-0.754	-1.314	0.632	0.370	-0.273	-1.433
1.305	0.486	-2.169	-2.567	-1.488	-0.397	-1.026	
-0.093	0.400	0.490	-1.133	-1.834	-1.382		
1.839	-0.477	-1.360	-0.391	1.328	0.591	-0.877	0.273
-0.499	0.938	-1.222	-2.756	-1.344	-1.932	-1.159	
-0.856	-0.019	0.658	-1.885	-2.184	-0.344		
1.378	-0.714	-0.938	-0.926	0.051	0.274	-1.239	-0.851
1.109	0.669	-2.737	-2.716	-1.136	-1.091	-1.052	
-0.633	0.986	1.016	0.685	-3.252	-2.663		
-0.653	-1.369	-0.232	-1.018	-0.270	1.590	-1.487	0.516
-0.716	0.700	-1.147	0.431	0.701	-1.338	-2.153	
-0.057	1.113	1.165	0.765	0.386	0.712		
-0.020	-2.233	-0.480	-1.240	-0.873	-0.204	-0.004	0.277
0.938	-0.504	-3.395	-2.034	-1.467	-0.533	0.118	
1.041	1.186	1.058	-0.492	-1.210	0.509		
2.400	-0.044	-0.428	-1.007	-1.909	-0.768	1.334	0.767
-0.799	-0.661	-1.041	-0.488	0.040	-0.317	1.687	
-0.557	-0.855	1.579	-0.376	-0.789	-0.921		
-1.150	-1.063	1.618	-0.044	-0.708	-0.434	0.017	-0.337
-0.591	-0.022	-0.488	-2.430	-0.997	-0.658	-0.874	

Table36.txt

-0.764 0.126 -0.047 -1.229 -1.462 0.129
-1.147 -0.482 2.255 1.948 -1.733 -1.446 0.835 -0.051
-1.182 1.140 1.858 3.782 2.183 2.462 2.423
0.929 0.224 0.813 1.529 3.660 1.610
1.427 -2.235 -1.891 -0.852 0.351 0.303 0.635 0.738
0.872 -0.937 -1.999 -1.105 -0.664 -1.802 0.331
-0.724 1.260 0.935 0.662 -1.625 -0.272
-1.889 -0.358 0.051 -0.870 1.028 2.124 -0.304 -1.579
-1.213 -0.791 -0.054 -0.415 -0.279 0.378 1.156
-0.947 -0.788 -0.539 -0.694 0.095 1.032
0.079 -1.302 0.449 -0.641 0.966 1.112 -0.590 0.574
-1.821 -0.515 -1.315 -1.998 -0.809 -0.745 -1.152
-0.357 0.920 0.421 -0.140 -0.374 -0.195
1.423 -1.058 -0.482 -0.683 0.432 0.905 -0.956 0.527
-0.781 0.015 -1.737 0.800 0.876 -2.444 -1.772
0.071 0.676 1.667 0.323 -0.161 1.327
0.455 -0.877 0.368 -0.951 0.641 -0.841 1.033 0.176
-1.058 0.221 -1.645 -1.427 -0.849 -1.111 -0.421
0.278 0.661 1.473 1.068 -0.283 -1.193
1.540 0.469 -1.515 -1.034 0.663 1.205 -1.232 -1.156
1.231 1.187 -2.399 -4.418 -0.848 -0.624 0.659
0.507 0.895 1.405 -0.807 -0.856 -1.406
-0.500 -1.380 -0.993 -1.180 0.285 0.405 0.321 0.149
-0.036 0.867 -1.024 -2.364 -0.758 -0.998 -0.286
0.252 1.687 1.344 -0.916 -1.678 -1.330
-0.418 -0.401 0.773 0.895 0.006 2.052 -0.231 0.785
-3.218 2.139 2.335 1.307 -0.007 0.518 -0.277
-0.346 -0.248 0.750 1.312 0.218 1.314
-1.650 0.277 0.052 0.780 -1.118 1.081 0.741 1.022
-1.533 -0.581 2.303 -1.555 0.036 -0.914 0.628
0.301 -0.433 1.345 1.774 0.368 0.188
1.170 -1.148 -1.238 -1.976 1.299 0.984 1.407 -0.330
0.679 -0.003 -1.385 -0.026 -0.650 0.322 -1.095
-1.193 0.065 1.224 0.677 0.878 -0.623
1.470 -0.372 0.758 -0.506 -0.781 -0.375 -0.812 0.085
0.220 0.757 -1.535 -1.497 -0.469 -1.062 -0.584
-0.115 0.307 0.791 0.053 -1.142 0.274
0.658 -2.853 -1.298 -0.861 0.445 1.551 -1.578 2.017
-0.981 -0.529 -1.238 0.943 0.868 -1.045 -1.318
0.695 1.754 0.584 0.845 1.056 0.879
1.203 -1.730 -0.689 -0.387 0.619 1.665 -2.090 -0.677
-0.241 1.044 -1.966 -0.473 0.345 -1.965 -1.688
-1.431 0.296 -0.119 0.613 0.181 -0.385
-0.218 -2.323 -0.956 -1.500 0.336 1.452 -1.554 0.449
0.936 0.399 -2.094 -0.365 0.053 -0.785 -0.301
-0.535 1.131 0.041 -0.008 -1.524 0.549
-1.142 1.919 1.362 1.402 0.478 2.463 -0.237 1.435
-4.356 0.928 1.889 2.104 2.566 1.508 0.969

Table36.txt

1.990	-1.647	1.101	2.518	3.074	3.082		
-0.356	-0.237	0.623	0.862	1.727	1.224	-1.188	-0.506
-0.554	0.910	0.953	-2.219	-0.112	-1.699	-1.115	
0.293	0.591	-0.921	-1.364	-1.655	0.224		
1.154	-0.511	-1.255	-1.608	-0.348	0.213	-0.029	0.784
-0.701	0.169	-1.596	-1.572	-1.019	-1.547	-1.179	
0.645	1.712	0.555	0.171	-2.110	-0.837		
0.065	-0.550	-0.675	-1.259	-0.198	0.190	1.054	-0.662
0.827	1.467	-1.872	-3.469	-1.333	-1.231	0.057	
1.181	-0.510	0.761	-0.491	-2.056	-1.989		
-0.758	-0.094	-0.840	0.667	0.718	1.416	-0.186	-0.515
-1.078	-0.629	-0.655	-0.291	-0.806	-0.771	0.967	
0.329	-0.678	-0.524	-2.008	-1.802	0.899		
-0.245	-1.250	-1.145	0.045	0.531	-0.429	-0.781	-0.909
0.756	0.096	0.138	-3.955	-1.502	-1.592	-1.447	
-0.384	0.255	-0.719	-2.260	-1.837	-1.445		
0.195	0.168	-0.965	-1.804	-0.824	0.569	1.181	0.211
0.179	0.652	-0.172	-0.407	-1.368	0.015	0.483	
0.815	-0.642	2.694	1.453	0.750	0.865		
-0.794	-1.897	-0.075	-0.501	-1.565	-0.878	-1.235	-3.052
1.676	-1.337	-1.763	-0.117	-0.033	-0.250	-0.473	
0.042	0.579	0.933	0.480	-1.259	-0.996		
-0.656	0.212	0.514	-0.793	0.558	-0.285	-0.156	0.561
-1.345	1.218	0.048	-3.232	-1.558	0.932	0.921	
-0.123	-1.355	0.139	-0.475	-1.154	-1.729		
1.506	-2.411	-1.371	-0.688	-0.266	-0.240	-0.478	-0.501
2.344	0.332	-1.694	-2.337	-0.818	-1.455	1.131	
0.378	-0.618	-0.279	0.663	-1.364	-0.701		
1.060	-1.468	-1.516	-0.445	0.293	0.948	-2.173	-0.617
1.211	0.942	-2.470	-1.746	-0.447	-2.182	-2.710	
0.349	0.738	-0.135	-1.808	-1.976	0.000		
-1.249	-2.028	-0.792	-0.412	0.534	0.806	-0.547	0.296
0.099	0.507	-0.649	-0.257	-0.429	-2.098	-2.084	
0.404	-0.547	0.444	-1.814	-2.524	-0.916		
-0.920	-2.974	-0.942	-1.014	0.399	0.060	-1.197	-0.092
-1.541	0.975	-0.454	-1.110	-1.423	-1.818	-1.039	
-1.135	-1.088	-1.134	-0.516	0.089	-0.951		
1.111	0.316	-1.399	-0.360	0.503	0.922	-2.508	0.439
0.794	-0.116	-2.255	0.742	0.849	-2.994	-1.556	
-0.655	2.398	-5.149	-3.903	-0.590	-1.385		
-1.412	-0.278	-0.563	0.131	-0.036	0.170	-0.576	-0.203
-0.911	0.236	-0.698	0.592	-0.849	-0.897	-0.247	
-0.610	0.341	-2.771	-1.592	0.545	0.465		
0.498	-0.257	-0.334	-0.003	0.839	0.188	0.007	0.946
0.142	1.467	-1.077	-1.356	0.045	-0.136	-2.118	
0.670	2.628	-0.430	-0.337	0.052	-1.351		
-0.220	0.120	1.221	0.465	0.759	-0.017	0.526	0.641
0.636	-0.250	-1.411	-0.831	-0.418	0.311	-0.366	

Table36.txt

0.427	0.084	1.211	0.024	-0.400	-0.808		
-1.318	0.639	0.687	-1.384	-0.198	0.279	1.222	0.339
1.320	0.519	-1.976	-0.709	-1.602	0.561	-0.884	
0.207	0.996	0.001	-1.603	-2.204	-1.511		
-1.013	-0.901	-0.336	0.141	0.570	-1.032	-1.200	-1.084
1.336	-0.422	-0.952	-1.445	-0.429	-2.345	-1.697	
-0.204	0.394	0.016	-1.078	-0.340	-0.836		
0.683	-0.858	-1.035	-1.070	-0.588	1.284	-0.224	1.149
-0.242	1.019	-1.148	-0.173	0.454	1.170	-0.687	
0.475	-0.063	1.020	1.619	-0.132	0.891		
0.193	-1.396	0.324	0.677	0.479	-0.216	0.148	-0.106
-0.155	0.295	0.367	2.049	-0.679	-1.277	1.855	
0.162	0.690	0.456	0.825	-0.301	0.296		
0.965	1.496	-0.381	0.304	1.644	0.136	-2.277	-0.374
-0.284	0.280	0.122	-0.023	-0.265	-1.159	-2.256	
-0.134	1.616	0.028	-2.618	-1.043	-1.286		
-0.852	1.682	0.482	0.749	-0.672	-0.635	0.027	0.318
-0.554	0.757	2.767	0.190	-0.279	-0.792	2.272	
-0.067	-1.107	0.755	-0.587	1.024	0.191		
0.040	0.699	1.137	1.299	1.167	-0.212	1.467	0.247
-1.136	0.191	0.723	0.971	0.982	-0.120	0.565	
0.789	0.249	0.034	0.828	-2.540	0.418		
1.101	-0.608	0.301	-0.420	1.086	-0.673	0.026	-1.291
-0.351	0.189	-1.196	0.399	0.423	-1.011	-0.152	
-0.329	0.686	-1.222	-0.493	0.440	-0.336		
-0.131	-0.925	0.485	0.132	2.024	0.439	-0.552	0.512
-0.719	0.761	0.966	0.401	-0.935	1.008	-0.497	
0.495	0.434	1.584	0.479	0.138	0.743		
0.888	-0.026	-1.344	-1.504	0.289	-0.830	0.917	-0.294
1.136	-0.341	-0.001	-1.318	0.902	-0.609	-0.516	
0.147	-0.880	1.575	0.952	-0.348	-1.343		
0.735	-0.174	-1.117	-0.728	0.819	-0.075	-1.757	0.109
0.171	1.183	-0.556	-1.761	-0.477	0.356	-1.028	
-1.480	0.059	0.075	-0.017	-2.696	-0.642		
0.001	2.769	0.973	-0.135	-0.089	0.519	0.260	0.083
0.809	0.245	0.306	0.326	0.612	2.115	1.780	
-1.869	-1.328	1.359	2.754	0.050	0.673		
1.478	-0.217	-1.294	0.096	0.356	1.292	-0.937	1.007
-1.747	1.056	0.626	0.503	0.461	0.338	-0.981	
-0.831	2.216	-2.509	-2.719	0.483	-0.333		
2.718	0.881	-0.383	-2.356	0.108	0.965	-0.770	0.682
0.537	-1.597	0.716	0.279	0.501	0.232	-1.898	
2.088	0.050	-0.295	-0.816	-0.478	-0.269		
-1.027	0.891	0.581	1.149	-0.116	1.142	0.246	0.885
-1.784	-0.823	1.273	2.625	1.031	1.173	1.185	
-0.940	-2.082	1.129	3.441	2.566	0.809		
-1.136	0.254	-1.343	-0.990	-2.623	-0.657	-0.220	-0.345
1.028	-0.745	0.195	-1.147	-1.662	-1.670	-1.730	

Table36.txt

-0.162 0.771 -1.721 -4.035 -0.089 -0.527
1.597 0.904 -0.671 0.165 0.850 1.295 -1.155 -0.147
-0.915 1.499 -0.993 -0.072 0.614 -1.856 -1.346
0.262 1.738 -2.225 -1.129 0.507 -0.456
-1.274 2.254 1.794 0.875 -1.745 1.400 -0.671 -1.052
-0.296 1.028 1.159 -0.167 -1.105 0.688 1.670
-1.303 -0.590 -0.618 0.193 0.438 0.976
-1.414 2.401 0.273 -0.221 -0.455 -0.042 -0.811 -0.011
0.066 -0.004 0.153 -1.240 0.014 -0.667 -1.158
-0.844 -0.813 0.667 -0.023 -0.376 1.822
0.348 -0.700 -0.761 -0.978 0.705 0.337 -1.165 -0.384
1.223 -0.179 0.376 0.292 1.582 0.088 -2.307
2.417 2.448 -0.303 0.402 -1.211 0.150
0.867 -2.159 0.127 -1.263 0.230 0.317 -1.137 -0.992
1.162 0.308 -0.333 -2.784 -0.367 -0.181 0.448
-0.915 0.222 0.799 -0.580 -0.879 -0.081
-0.873 -0.506 -0.543 -1.237 -0.332 0.937 0.676 1.604
-1.374 -0.145 -1.206 0.922 0.286 0.185 -1.184
-1.478 0.531 2.142 -0.191 -0.433 0.130
1.068 0.319 0.122 1.049 1.587 -0.340 -0.607 -0.448
0.809 -0.751 -0.088 -1.665 0.064 -0.020 -1.426
-0.277 0.402 -0.037 0.747 0.497 -1.175
1.854 0.063 0.188 1.181 0.559 -0.528 -0.160 -0.495
0.673 0.687 -1.137 0.079 0.694 -1.626 -0.901
0.578 1.153 0.190 -1.091 -0.743 0.608
1.566 -1.477 0.088 1.275 -0.747 -1.103 -0.724 0.268
0.708 -0.174 -2.504 1.505 0.493 1.605 0.113
0.628 -0.264 0.214 1.396 -0.676 0.640
-1.683 1.257 2.797 0.739 -1.621 -1.069 1.055 0.008
0.224 -0.983 1.006 0.089 -0.432 1.223 0.575
-0.009 -1.457 0.475 0.063 1.453 0.014
-0.797 -0.292 -0.085 0.227 2.420 1.671 0.477 0.089
0.004 -0.150 -0.414 -0.727 -2.350 0.426 -1.240
-2.131 0.426 1.047 0.883 -0.196 0.890
0.679 -0.123 0.659 -0.275 0.963 -1.824 -0.640 0.295
0.044 -0.156 0.404 -0.466 -0.797 0.298 -0.453
0.113 -1.317 0.032 0.795 -0.186 0.620
0.101 0.656 -0.808 -0.315 0.415 1.083 -0.636 0.103
0.962 -0.927 -0.549 -3.017 0.993 -0.087 0.362
-0.531 0.445 1.286 1.188 -0.076 -0.210
-0.633 0.483 -0.735 -0.676 0.165 0.452 -0.190 -0.491
-0.363 -0.527 -0.148 1.338 0.616 0.529 -1.040
0.077 -1.457 -0.405 -1.180 0.747 0.063
0.837 0.982 -0.476 -1.103 -0.556 -0.893 -0.758 0.732
-0.633 -0.473 0.482 -0.131 -0.512 0.448 -1.497
0.049 1.470 0.532 -0.566 0.669 1.054
-0.105 2.072 1.226 0.834 0.233 -1.575 -0.669 0.361
-1.204 -1.121 2.014 2.020 0.739 1.160 -0.139

Table36.txt

0.697	-0.998	0.433	0.816	0.698	-0.158		
0.349	1.333	1.535	-0.258	0.484	-0.981	-0.265	1.233
-1.634	1.404	0.982	-0.621	-0.619	0.790	-1.654	
0.044	0.410	2.223	0.426	0.344	0.662		
-0.329	2.053	-0.186	1.904	-0.566	0.520	0.095	0.985
0.478	0.741	-0.851	0.013	-0.084	-0.110	0.193	
-0.357	-0.387	-0.848	0.462	2.132	0.764		
1.078	-0.385	1.003	1.138	0.955	-1.450	-0.570	1.429
0.017	-1.597	-1.023	0.508	0.486	0.318	0.392	
0.243	-0.633	0.063	-0.092	-0.154	-0.897		
-1.037	-0.994	-0.287	0.856	0.610	-0.521	-0.864	0.162
0.296	0.190	0.889	-1.198	-1.168	-0.262	-0.804	
0.520	1.021	-0.374	-1.051	-0.025	1.715		
0.638	0.136	-2.429	1.184	1.120	1.161	0.755	0.018
-0.611	0.822	-0.246	1.438	-0.616	-0.752	-0.889	
-0.955	0.047	-3.182	-1.627	-2.050	-1.511		
0.728	-0.610	0.725	1.137	0.928	-0.502	-1.184	-0.286
-0.367	-0.298	1.691	2.219	0.847	-0.789	0.061	
0.421	-1.063	0.995	-1.118	0.705	-0.544		
-1.409	2.174	0.231	-0.298	0.455	0.011	-0.566	1.034
-0.113	-0.696	-0.109	0.658	-0.122	-1.624	0.116	
0.283	0.830	0.705	0.096	-0.359	0.789		
0.441	0.116	0.106	-1.228	0.855	0.623	-0.809	0.463
-1.860	0.744	1.120	1.136	-0.005	0.893	-0.339	
-0.363	-0.530	-0.458	1.156	1.439	0.857		
0.431	0.259	1.457	-0.383	-0.020	-0.773	0.620	0.482
0.910	0.503	-1.456	-0.526	1.338	0.655	-1.262	
-0.766	0.251	-0.835	1.018	0.272	-0.844		
-0.058	1.289	0.252	-0.766	0.683	0.224	-1.144	0.677
0.143	-0.208	0.155	0.592	-0.621	0.714	-1.861	
-0.332	0.673	-0.349	0.162	0.246	1.252		
-1.292	0.640	0.094	1.326	1.358	0.922	1.279	1.079
-1.632	0.896	0.177	-1.804	-0.612	1.289	0.361	
-0.463	0.871	0.153	0.566	0.282	1.663		
0.545	-0.513	-0.985	-0.335	1.658	1.208	-0.801	0.341
-0.235	-0.275	-1.300	-1.162	-0.516	-1.139	0.282	
0.389	-0.067	-0.460	-2.385	0.209	-0.989		
1.213	-0.397	-3.192	-0.732	-0.340	-0.136	-0.766	0.212
1.258	0.249	-2.031	-0.777	-0.978	-2.057	-1.159	
0.121	1.697	-1.190	-2.835	-1.342	0.221		
1.147	0.196	-1.338	-0.728	-0.503	0.513	-0.793	0.041
-0.738	1.547	1.572	0.729	0.124	-0.327	-0.287	
0.343	1.629	-2.291	-2.171	-1.494	-0.148		
-1.349	1.613	1.512	1.006	-0.046	-0.398	0.311	-1.128
0.344	0.570	-0.978	-0.453	-1.335	-1.129	-0.402	
0.697	-0.333	1.223	-0.834	-0.624	-0.710		
-0.607	0.871	1.780	2.167	-0.188	-1.478	2.044	0.676
1.902	1.225	2.367	0.713	-0.604	0.964	0.332	

Table36.txt

0.857	-0.189	-1.256	-0.985	1.529	2.084		
0.647	-0.203	-0.343	0.927	-0.923	1.423	-2.206	0.323
-0.760	1.027	-0.298	1.594	0.722	-0.271	-0.861	
0.153	0.904	0.677	-0.530	-0.239	0.946		
-1.923	1.270	-0.889	0.676	-0.635	-0.089	-0.151	0.586
-0.452	0.040	0.361	0.749	0.686	-0.100	-0.849	
0.374	-0.677	-1.076	0.671	0.551	0.078		
-1.417	2.579	0.417	0.647	0.300	-0.068	0.104	-0.391
-2.789	-0.330	0.683	0.254	0.180	1.491	1.851	
1.070	-1.309	-0.474	-1.373	1.979	-0.059		
0.146	1.072	-0.873	-0.503	-0.272	0.133	-0.793	1.414
0.466	0.896	-1.355	-0.861	-0.579	-1.339	-0.714	
-0.071	2.823	-0.755	0.251	0.305	1.939		
-0.119	-0.058	0.112	-0.148	1.064	-0.126	1.047	-0.349
1.282	-0.763	0.026	-0.389	-0.127	0.177	-0.602	
-1.015	-1.052	-0.187	1.992	0.033	-0.661		
0.174	-0.732	0.706	0.493	0.929	0.945	1.962	-0.776
-0.109	0.340	-1.246	0.834	-0.671	-0.636	-1.264	
1.683	-0.297	0.812	0.160	0.981	-1.182		
-1.204	1.859	1.520	0.565	0.475	0.610	0.236	-0.490
-0.979	-0.431	1.646	1.494	0.717	1.013	-0.028	
0.976	-1.629	2.696	0.739	1.942	0.878		
-0.580	-1.056	-0.886	0.228	0.024	1.138	0.555	0.869
1.115	0.984	-1.809	-1.506	-0.702	0.418	-1.559	
-0.238	2.422	-1.041	-1.310	-1.500	0.279		
2.841	-1.537	-2.493	-1.930	1.528	1.491	-1.437	0.755
1.186	0.519	-3.585	-2.183	-0.565	-0.325	-0.548	
0.416	2.147	-0.001	-1.770	-1.855	-0.992		
0.298	-1.131	0.293	-0.717	-0.576	-0.855	0.853	-0.194
0.761	0.118	-0.295	0.863	0.079	0.399	2.363	
-0.405	-1.655	0.200	1.454	-0.696	0.331		
-0.365	-0.357	1.542	-0.084	1.304	0.241	0.881	-0.465
-1.512	0.654	0.581	-1.889	-1.067	-0.458	-0.449	
-1.122	0.901	1.573	-0.225	-1.249	0.950		
-0.512	0.260	-0.245	0.940	0.465	0.823	-0.430	-0.608
0.230	0.114	-0.395	-0.189	-0.269	1.358	0.210	
-0.225	-2.301	1.078	0.639	0.645	0.293		
0.787	-0.794	0.526	-1.573	0.894	-0.429	0.593	0.067
0.448	-0.054	-1.651	-0.764	0.377	-0.699	-0.809	
-0.979	-1.636	0.451	1.482	-0.565	-1.065		
-0.838	2.270	1.355	-0.294	1.385	0.527	1.262	0.517
-1.410	-0.618	0.038	0.216	-0.345	0.090	-0.288	
-0.150	-0.291	1.366	1.420	0.755	0.059		
0.153	-1.232	0.400	1.514	-0.558	0.360	-0.397	-0.031
0.774	-0.279	0.961	0.179	-0.846	0.436	-1.646	
-0.754	1.012	-0.180	0.002	-2.033	-0.249		
0.757	0.282	1.772	-0.696	0.722	-0.855	0.542	-1.162
-0.241	-1.052	0.361	0.486	0.441	-0.538	0.202	

Table36.txt

-0.113 -1.134 -0.967 0.057 -0.163 0.514
-0.187 -1.197 0.511 -1.067 -0.175 0.205 0.357 1.069
0.876 0.140 -1.111 -1.141 -1.209 -0.201 0.182
0.216 0.591 -0.231 0.068 -0.682 -0.490
-1.898 0.059 0.217 -0.727 -0.423 -1.224 -0.194 0.032
1.366 0.421 0.622 -1.088 1.193 -0.433 0.088
-1.700 -1.234 0.319 0.587 1.068 -0.197
-0.349 0.249 0.992 1.756 0.390 -0.272 -0.180 0.373
-0.534 -0.866 -1.503 0.398 -0.567 -1.608 0.569
-0.750 0.234 -0.434 -1.216 0.956 -0.852
0.902 -1.074 0.054 1.149 -1.091 0.632 0.514 -0.266
0.286 1.092 -0.780 -0.005 -0.943 0.360 0.165
-1.506 0.280 1.655 1.076 -0.153 -0.758
0.057 -0.181 1.090 0.918 1.010 -0.448 0.197 0.391
-2.787 -0.663 -0.506 1.374 -1.431 0.918 -0.052
-1.829 -0.367 0.515 2.050 1.001 0.295
0.288 -1.488 -1.139 0.759 -0.050 0.269 0.437 0.106
1.026 0.883 -0.204 -0.058 -0.473 0.283 1.892
-0.116 -1.212 2.564 2.043 0.150 -0.351
-0.558 -0.857 -0.148 0.943 -0.619 -1.393 1.416 0.556
0.257 -0.469 -0.083 1.056 0.384 -0.033 1.841
0.923 -0.903 1.109 1.979 0.760 -0.049
-0.362 -0.715 1.087 -1.373 1.118 0.792 0.940 1.213
0.388 0.089 -0.805 -0.927 -0.462 0.303 1.149
-0.815 -1.796 1.223 -0.068 -0.670 -0.099
-1.393 0.301 1.501 1.288 -0.397 -0.382 2.219 0.942
-0.676 0.709 1.494 -0.687 -0.876 1.430 1.812
-0.762 -1.315 0.636 -0.745 0.782 0.495
-0.580 -2.275 0.690 1.091 -0.315 -0.200 0.651 -0.730
0.759 -1.962 1.813 -0.644 0.557 -0.083 1.289
-0.920 0.265 0.655 1.554 -0.538 -1.226
-1.031 1.472 0.861 -0.715 -0.571 1.002 0.657 0.557
-0.062 1.019 -0.715 -1.782 0.085 0.148 0.266
-1.260 -0.870 0.842 1.083 -0.156 0.323
1.692 -1.059 -2.800 -1.015 -0.163 0.138 0.643 1.171
1.805 1.040 -2.688 -1.720 -0.670 -0.749 0.904
0.062 1.091 1.790 0.729 -1.265 -0.669
0.034 0.351 -0.583 -0.280 0.064 -0.888 0.743 0.753
0.285 0.566 -0.509 -0.154 0.744 0.763 1.306
0.166 -1.158 2.264 2.128 -0.399 -0.293
0.495 0.204 0.905 -0.455 -0.350 0.547 1.145 0.301
0.994 -0.458 -0.833 -1.196 -0.202 0.152 0.013
-0.142 1.026 -0.283 1.492 0.196 -0.309
-0.843 0.511 1.776 -0.500 0.439 0.490 -0.414 -0.066
0.545 -1.047 0.421 0.462 -0.581 0.181 0.792
-0.223 -0.494 0.677 0.646 0.513 1.049
-1.543 -1.281 -0.246 0.688 1.223 0.593 0.249 1.039
0.910 -1.014 -1.129 0.811 -0.437 0.802 1.839

Table36.txt

-0.632 -1.258 2.108 1.483 0.688 -0.095
0.220 0.246 -0.174 -0.971 -1.323 -0.997 1.905 -0.303
0.987 -1.885 -0.376 -1.157 -0.294 -0.204 2.104
-0.356 0.894 1.108 -0.702 0.265 -1.142
1.389 -0.821 0.310 1.475 0.542 -0.986 0.020 -0.279
0.453 -0.461 -0.912 -0.612 0.575 -0.756 -0.456
-0.211 0.848 1.202 1.698 0.164 -0.630
1.811 -1.692 -1.565 -1.132 0.253 -0.426 -1.071 1.180
0.954 -0.420 -3.449 -1.327 -1.339 -1.951 -2.387
-0.284 0.677 -0.514 -1.371 0.302 -0.543
1.322 -1.429 -0.696 -1.070 0.413 -0.459 -0.985 1.067
0.258 -0.763 -2.406 -1.256 -0.582 -2.148 -2.077
0.002 0.849 -0.343 -1.982 -0.754 -0.175
0.104 -0.213 -1.622 -0.456 2.186 1.272 -1.035 0.028
0.943 -1.163 -1.988 -0.842 0.018 -0.904 -2.145
0.044 0.846 -0.332 -1.114 -1.323 -1.747
0.538 -1.771 -1.062 -1.521 0.445 0.739 0.809 -0.332
0.835 -0.232 -1.449 -1.682 -0.118 -1.188 -1.057
-0.791 -0.053 -0.221 -0.421 -2.667 -0.284
0.880 -2.077 -0.961 -1.738 1.027 -0.143 -0.931 0.505
0.898 -0.325 -1.153 -0.546 -0.194 -1.511 -1.362
0.340 1.492 0.361 -0.326 -0.050 -1.541
1.271 -1.123 -0.887 -0.232 0.338 0.864 -1.076 0.178
0.605 0.423 -1.494 -0.757 0.347 -0.887 -1.295
0.059 -0.037 0.795 1.065 -1.363 -0.750
-5.384 -4.196 -4.474 3.470 -0.810 5.419 11.000 3.293
-5.529 0.082 -5.890 -6.068 -5.351 -0.491 1.155
-0.741 -2.036 3.175 -0.046 2.009 1.539
-1.179 -1.211 -2.235 -1.784 -0.059 -0.235 0.420 0.303
0.549 1.110 -1.897 -2.331 -1.646 -0.933 -0.486
-0.572 -0.120 1.198 0.176 -1.144 -0.614
0.412 -1.781 -2.023 -1.919 0.827 -0.875 -0.561 0.612
0.296 0.679 -1.949 -1.234 0.201 -0.364 0.081
0.502 -0.234 0.578 -0.689 -0.767 -0.172
-1.112 -0.171 1.391 0.480 0.120 0.722 2.443 2.091
-0.062 0.427 0.775 -1.823 -2.648 1.229 -0.090
-1.819 -2.777 -0.790 0.209 -0.099 -1.185
1.130 -0.301 -1.375 -1.425 -0.444 0.707 -0.532 0.984
0.743 -1.513 -1.930 -0.506 -0.606 -0.223 -0.674
0.172 -0.995 0.361 0.616 0.243 -0.984
-0.345 -1.548 -0.828 -1.196 -0.226 0.111 0.088 0.100
0.669 0.293 -2.080 -3.073 -1.179 0.120 -0.383
0.167 -1.251 0.572 0.541 -2.711 -2.161
1.874 -1.315 -1.985 -0.062 0.920 1.094 -2.013 -0.437
-0.973 0.104 -1.164 -2.821 0.038 -4.198 -1.450
0.247 -0.416 -0.914 -2.168 -1.793 -1.107
1.352 -1.741 -1.218 -0.035 0.963 0.792 -1.381 0.577
-0.144 0.223 -1.291 -1.907 -0.907 -2.319 -2.396

Table36.txt

0.563	1.159	1.724	-0.717	-2.282	-0.648		
-0.131	-1.831	-1.551	-1.706	0.364	-0.175	1.272	1.401
1.122	0.593	-0.813	-3.336	-1.894	-0.679	0.149	
0.749	-1.140	-1.866	-0.464	-0.126	-0.696		
0.377	-1.320	-0.416	-0.328	0.593	-1.349	-1.092	1.390
0.798	0.872	0.710	-1.874	0.132	-0.846	-0.606	
-1.340	-0.760	1.338	-0.200	-2.274	-1.442		
-0.373	-0.324	-0.562	0.015	2.618	0.647	-1.331	1.277
0.541	0.120	-1.305	-0.406	-0.578	-0.932	-1.660	
0.477	-0.528	-1.508	-1.759	-2.045	-0.435		
-0.520	0.323	-0.398	0.150	0.806	0.683	-0.094	-1.294
-1.740	-0.192	1.735	0.904	0.874	2.237	0.683	
0.975	-0.390	-0.898	-1.284	0.646	0.980		
0.404	0.231	0.137	0.738	0.781	0.543	-0.750	1.104
-0.855	0.141	-0.438	-0.365	0.059	0.472	-0.814	
1.440	-0.727	-1.220	-0.953	-1.645	-0.510		
-0.889	-0.964	-0.975	-0.564	0.947	0.896	-0.777	-0.084
-0.699	0.154	-1.158	-0.179	0.584	-1.847	-1.190	
-0.177	-0.989	0.562	0.089	-1.128	0.116		
-0.016	1.150	0.735	0.350	-0.874	-0.121	-0.304	-0.138
-0.380	-0.617	0.075	-0.394	-1.367	-0.940	-0.535	
0.931	-0.295	-0.412	-1.303	-2.212	-0.424		
0.863	-1.365	-1.191	0.142	1.381	0.174	-1.395	-0.158
0.317	0.010	-0.532	-0.324	-0.933	-2.893	-2.719	
0.647	0.745	0.071	-1.736	-0.115	-0.186		
0.287	-2.725	-0.712	-1.119	-0.134	-0.997	0.854	0.788
0.423	0.313	-1.740	-1.587	0.506	-0.594	0.128	
-0.882	-0.521	1.121	0.054	-1.224	-0.739		
1.624	-1.115	-1.480	-0.586	0.748	0.133	-1.601	0.474
0.451	0.778	-1.893	-2.003	-0.479	-2.997	-2.594	
-0.629	0.027	-0.002	-0.664	-2.212	-0.194		
-0.540	-1.738	0.166	1.652	0.891	-1.412	-2.305	0.879
-0.686	-0.372	-0.612	-1.336	-0.497	-0.253	-0.177	
0.115	-1.273	0.316	-0.768	-0.820	0.307		
-0.033	-1.742	-1.239	-1.296	-0.451	0.784	-0.338	1.728
0.939	-1.631	-2.106	-0.791	0.252	-1.181	-0.237	
-0.754	0.210	-0.275	0.947	-1.081	0.351		
-0.302	-0.124	0.503	-0.640	-0.092	0.195	-1.237	0.007
-1.766	0.707	-1.320	-1.590	-0.257	-1.596	-1.264	
-0.538	0.338	-0.238	0.460	-1.626	-0.795		
-1.064	-1.327	0.458	-0.030	-0.742	0.042	1.384	0.447
0.313	-0.429	0.067	-2.296	-0.135	-0.980	-0.122	
0.495	0.789	1.183	0.670	-0.161	0.516		
0.223	0.110	0.867	0.576	0.136	-0.381	1.536	0.908
-3.478	0.250	0.039	1.121	1.942	0.513	2.773	
0.948	-2.061	1.393	4.151	2.060	1.479		
-1.033	-1.190	-1.216	-1.302	0.187	0.593	1.217	1.752
-2.211	-1.004	-1.294	-2.176	-0.487	-0.029	1.320	

Table36.txt

0.303 -1.081 -0.426 -1.430 0.575 1.213
-1.945 0.974 2.776 -0.935 0.229 -0.064 1.547 0.627
-2.753 -1.108 1.181 -1.666 -1.027 1.636 2.238
-0.456 -3.115 1.136 0.418 1.560 2.205
-0.256 -1.445 -0.057 -0.897 0.557 1.129 -0.810 -0.705
-0.585 0.400 -1.319 -1.704 -0.080 -2.733 -1.769
0.287 0.970 0.170 -1.606 -1.415 -0.611
-0.113 -1.698 -1.393 -0.044 -0.460 0.055 -0.659 -0.301
0.570 0.161 -1.432 -0.824 0.539 -0.383 -1.372
-0.120 1.205 -0.959 -0.635 -1.783 -0.689
-1.007 -0.003 0.714 0.787 -0.103 -0.349 1.120 -1.650
-1.088 -0.184 1.209 -3.215 -2.458 -0.295 0.179
-0.775 -1.092 0.490 -1.889 -0.957 -0.580
1.039 -0.528 -2.129 -0.856 0.194 1.601 -2.061 1.410
-1.152 -0.553 -1.962 -0.032 -0.718 -3.012 -2.362
-0.685 0.604 0.273 -1.290 -0.357 -0.250
-2.114 -0.679 1.241 -0.672 -0.054 -1.450 0.937 -0.371
-0.145 -0.494 -1.163 -2.436 -1.587 0.461 1.277
0.742 -2.039 1.363 1.168 -0.305 1.398
-1.223 -0.612 0.463 -1.045 -0.607 -0.946 -0.764 -0.461
0.988 -0.593 -0.648 -3.323 -0.853 -0.592 -1.084
0.019 -1.120 1.003 -1.110 -1.346 -1.547
-0.405 -1.668 -0.741 0.655 1.170 0.290 -0.496 1.359
0.021 -0.417 -1.412 -1.375 0.781 -2.254 -0.505
0.996 0.134 -0.778 -0.981 -1.760 -1.022
-1.281 -0.448 0.040 1.061 -0.863 0.359 1.175 -1.607
0.147 -0.116 0.172 -2.948 -2.183 -0.390 0.563
1.338 -0.850 -0.503 -0.641 -1.439 -0.799
0.666 -0.495 1.225 0.780 0.987 0.041 -0.779 0.877
-0.050 -0.252 -0.476 -1.254 0.411 -1.415 -0.935
0.535 1.190 0.166 -0.098 -1.817 -0.077
0.880 -0.234 -1.190 -0.172 1.906 0.988 -1.290 -0.004
0.168 0.107 -1.696 -0.012 0.127 -2.274 -1.577
-0.286 -0.583 -1.003 -0.490 -0.786 0.090
1.363 -0.867 -0.653 -1.044 0.792 0.066 -1.130 0.157
-0.331 0.351 -1.583 -0.841 0.242 -1.835 -1.581
0.384 -0.696 0.317 -0.433 -1.235 -0.294
-1.751 0.570 0.603 0.469 1.738 0.928 -0.549 -0.313
-0.879 0.362 0.639 0.107 -0.402 -1.323 -1.064
-0.573 -0.777 -1.781 -0.448 -1.237 0.823
1.498 -1.452 -0.254 -1.956 -0.120 0.379 1.163 -1.075
-0.860 0.316 -0.108 -2.968 -0.127 0.454 0.035
0.346 0.103 0.549 1.532 -0.919 -0.011
-0.220 -1.384 -0.120 0.984 -0.183 1.023 -0.122 1.004
0.182 0.248 -0.951 -1.090 0.167 -0.506 -1.349
-0.820 -1.686 0.713 -1.075 -1.575 0.461
-0.027 -0.337 -0.145 0.222 -0.064 -0.418 0.422 1.498
-1.685 0.351 -0.161 -0.860 -0.246 -0.256 -0.339

Table36.txt

-0.452 0.453 0.941 0.751 -0.983 -1.043
0.744 -0.928 -1.882 -1.185 0.804 0.784 0.496 0.381
-0.591 -1.177 -0.044 -1.697 -0.007 -2.232 -1.291
-0.073 1.058 0.136 -0.990 -1.215 0.084
1.747 0.444 -0.428 -0.244 0.733 0.217 -0.202 0.603
0.021 0.252 -0.235 -0.381 0.083 -2.145 -1.725
0.384 -0.867 0.205 0.447 -1.416 -0.022
1.018 -1.812 -0.156 0.049 1.313 -0.765 -0.004 0.173
-0.490 -0.193 -1.343 -2.081 0.950 -0.769 -0.224
-0.995 -1.669 0.960 0.335 -0.098 -1.449
-0.293 -0.240 -0.138 -0.392 0.376 0.924 -0.974 0.000
-0.005 -0.220 -0.485 -1.035 0.150 -1.441 -0.027
-0.395 -0.097 -0.475 -0.163 -0.633 -0.320
0.327 -2.259 -0.101 -1.312 0.674 -1.053 1.660 2.169
0.238 -0.046 -0.086 -3.560 0.328 -0.877 1.075
-0.350 -0.887 0.554 -0.347 -2.587 -1.397
-0.402 -0.361 0.328 0.007 1.300 0.171 -0.996 -0.780
0.462 1.080 -1.192 -1.993 0.240 0.327 -0.024
0.487 0.122 0.446 -0.598 -1.539 -1.235
-1.084 -1.013 0.987 0.178 -0.062 -0.831 0.333 -0.008
1.053 -0.120 -0.459 -1.044 0.705 -1.142 -1.078
-0.333 -0.652 -0.765 -0.107 0.372 0.818
0.388 -1.352 0.831 -0.031 -1.968 -0.821 1.833 -0.801
-0.030 -0.295 -0.175 -3.009 -0.449 1.530 1.745
0.280 -1.318 0.345 -0.972 -0.911 0.419
1.448 -0.388 -0.950 -0.653 1.576 1.218 -2.147 0.705
-0.205 -0.327 -1.993 -0.045 0.389 -2.345 -1.508
-0.388 0.034 0.148 -0.826 -1.315 -0.253
-1.300 -1.072 -0.637 0.074 1.048 0.213 -0.325 -0.331
-0.679 -0.117 -0.401 -1.829 0.359 -0.956 0.639
0.264 -0.570 0.763 -0.469 0.546 0.267
-0.515 0.197 1.121 -0.241 1.653 0.431 0.730 -0.579
-0.443 1.725 0.856 -0.837 -1.853 -0.145 -0.741
-0.210 0.149 0.956 0.142 -2.775 -0.838
-1.964 1.004 -0.209 0.048 -0.684 -1.088 -0.001 0.951
-1.513 -2.286 1.475 -2.221 -0.782 0.623 0.823
-0.867 -1.218 -0.743 -0.704 0.184 2.049
0.622 -1.017 -0.641 -0.057 -0.183 1.596 -1.817 -0.125
-0.898 -0.278 -1.189 -0.707 0.281 -1.371 -1.581
0.758 0.635 -1.321 -1.215 -1.084 0.092
0.190 -0.669 -0.747 -1.683 1.471 0.981 -1.351 -0.098
0.648 0.552 -0.733 -2.852 -0.436 -0.822 -0.187
0.011 -0.367 0.294 0.393 0.056 -0.515
-0.386 -0.268 -0.734 -0.058 0.699 0.927 -0.888 0.321
-0.406 0.311 -1.408 -1.995 -1.082 -1.785 -2.406
-0.014 0.011 -0.770 -1.708 -1.722 -1.149
-0.818 -0.540 -0.211 1.155 -0.142 0.859 0.245 -0.111
-0.605 -0.263 -1.651 -0.597 -0.635 -1.253 -1.473

Table36.txt

0.437	0.281	-0.230	0.082	0.340	0.255		
-0.686	-2.945	-1.302	0.439	-0.219	0.210	2.090	-1.138
0.540	-0.888	0.340	-3.285	-1.311	0.188	0.711	
-0.522	-0.669	-1.021	-0.788	-1.552	-1.277		
1.085	-1.317	-2.126	-1.553	1.178	1.284	-0.983	-0.243
-0.175	0.959	-2.195	-2.743	-0.949	-2.133	-2.081	
0.787	-0.145	-0.690	-2.015	-2.464	-0.312		
1.257	-2.813	-1.846	-0.994	1.248	1.026	-1.194	0.272
0.435	0.432	-1.576	-0.766	-0.132	-1.859	-1.762	
0.640	-0.191	-0.051	0.151	-2.180	-0.101		
0.770	-1.173	-1.823	-1.104	0.975	1.436	-1.612	0.522
-0.034	0.640	-1.389	0.094	0.649	-1.973	-1.936	
-0.608	-0.762	0.045	0.282	-1.287	-0.078		
-0.145	-1.822	-0.063	-1.033	-0.512	0.089	0.493	0.797
0.433	-0.458	-2.336	-2.151	-1.309	-0.998	-1.842	
1.160	0.630	0.774	-1.884	-1.296	-1.267		
2.202	-1.545	-0.531	-1.005	0.256	0.173	-2.132	-0.223
0.904	-0.126	-2.534	-1.859	-1.180	-3.883	-3.003	
0.565	1.973	0.822	-0.382	-1.085	-0.206		
-0.267	-0.661	-1.008	-0.550	1.705	1.696	-0.186	0.813
-0.498	-0.085	-2.527	-0.761	-1.027	-1.897	-1.911	
0.514	0.649	0.072	-1.008	-0.530	-0.556		
-1.102	-1.346	0.674	0.264	0.959	0.003	1.123	0.248
-0.217	-0.941	0.271	-1.540	-1.367	-1.186	1.324	
0.577	-1.585	1.165	1.328	-0.167	-0.283		
-0.532	-1.082	0.320	-1.014	-1.177	-0.790	0.840	-0.825
-0.291	0.463	-0.628	-1.100	0.558	-1.086	0.371	
-0.686	0.343	1.414	1.069	-1.216	0.129		
0.265	-0.386	0.135	0.613	-1.767	-0.479	0.352	-1.903
-0.953	-0.039	-0.994	-1.125	-1.420	-0.183	1.065	
-0.317	0.295	1.396	-0.631	-1.379	-0.826		
0.847	-3.367	-0.645	-2.091	-0.973	0.085	0.059	0.366
1.456	0.386	-2.822	-2.432	-0.984	-2.022	-1.923	
0.044	-0.112	0.597	0.414	-0.873	-0.843		
-1.166	0.208	1.127	-0.357	-0.331	0.459	1.411	-0.541
0.463	0.105	0.916	-3.141	-0.712	0.797	1.227	
-1.694	-1.038	0.297	1.385	0.181	0.944		
1.221	-1.699	-0.940	-0.253	1.585	2.039	-1.485	-0.302
-0.027	-0.631	-1.347	-1.272	-1.102	-1.877	-1.441	
0.142	0.942	0.708	-0.038	-1.543	0.673		
-0.871	-0.101	0.804	-0.322	0.135	-0.022	-1.234	0.003
0.031	0.837	-0.114	-1.625	-1.444	-1.168	-1.903	
0.030	0.169	0.458	-0.110	-0.142	-0.970		
-0.053	-1.198	-1.574	-0.941	-0.240	2.068	0.046	0.165
0.484	-0.326	-0.737	-1.209	0.078	-1.556	-0.411	
0.075	0.375	0.808	0.987	-0.590	-0.054		
0.533	-0.037	-0.001	-1.177	-0.532	0.703	0.316	0.303
1.259	-0.496	-0.450	-3.158	-1.061	0.241	0.172	

Table36.txt

-0.882 0.901 1.632 -0.327 -1.662 -0.474
0.672 -0.836 -1.341 -0.219 -0.320 -0.425 1.161 0.838
0.741 -0.009 -1.421 -1.585 -1.292 -1.207 0.059
1.721 0.013 0.859 0.903 -0.473 -0.370
-1.538 0.649 1.412 0.003 -2.248 -0.158 2.278 -0.447
-0.862 -0.649 0.778 -2.589 -1.176 -1.654 -0.114
-0.463 -0.757 -0.287 -0.503 -0.010 -0.739
2.332 -2.423 -1.518 -0.590 1.005 0.007 -1.523 0.862
0.415 -0.287 -3.176 -0.885 -0.568 -0.770 -2.126
0.333 1.189 -0.146 -0.574 -0.335 -0.323
-1.267 -1.249 -0.349 -0.779 -0.082 1.029 -0.474 0.084
0.967 0.365 -0.643 -0.915 0.274 -1.743 -1.559
-0.132 0.289 1.191 0.376 -1.073 -0.837
0.289 -0.708 -0.390 -0.857 -0.698 1.454 -0.094 0.448
1.443 -0.239 -1.051 0.392 -0.091 -0.185 -1.449
0.652 0.546 -1.156 -0.266 0.316 -0.523
0.373 -0.331 -0.515 -0.337 -0.481 0.748 -1.234 1.384
-0.692 -0.009 -0.534 -1.402 1.210 -2.244 -1.178
-0.076 0.234 -0.283 0.944 -1.439 1.104
-0.416 -1.558 0.705 -2.817 -0.722 0.479 -1.564 0.936
0.554 -1.483 -0.402 0.797 0.135 -0.718 -1.547
-1.413 0.562 -0.637 1.251 -1.055 -0.035
-0.116 0.287 0.093 -1.356 0.889 -0.767 1.876 0.488
-1.400 -0.824 0.525 -1.679 0.361 -1.164 -0.069
-0.442 -1.656 0.445 0.893 0.356 0.758
1.423 -0.704 -1.818 -1.818 -3.644 3.625 -0.918 0.092
-1.221 -3.027 -3.477 1.158 -2.015 -1.429 -0.374
1.764 2.949 0.831 0.496 0.015 1.033
1.019 -0.323 0.454 -1.615 -1.255 1.666 -0.103 0.495
-0.361 -0.526 0.155 0.210 0.724 -0.906 0.215
0.384 -1.414 -0.567 0.444 0.825 0.142
-1.873 1.143 0.607 -0.114 -0.640 0.482 1.127 -0.406
-2.206 0.280 0.763 0.464 -1.050 0.338 0.769
0.601 -0.564 0.273 1.107 0.410 0.464
-1.490 0.711 0.001 -0.171 -1.301 -0.089 2.155 0.359
-0.144 -0.101 -0.694 0.230 -0.087 0.085 0.046
-0.007 0.586 0.145 0.260 0.322 0.000
-0.988 -0.590 1.112 -1.198 0.730 0.967 -1.309 1.150
-0.875 0.654 -0.465 -1.185 1.098 -2.518 -1.003
0.231 -0.320 0.079 0.709 -1.910 0.211
-0.934 -1.042 1.054 0.989 -0.656 0.382 0.507 -0.628
0.531 -0.141 -1.232 -2.076 -0.042 -0.730 -0.454
1.460 0.302 1.591 1.665 0.424 -1.531
0.627 -0.390 -0.463 -0.796 -0.060 -0.113 -0.233 -0.233
-0.169 -0.415 -0.941 0.459 -0.177 -2.703 -1.547
-0.224 0.965 -0.120 1.066 -1.778 -0.189
-0.979 1.252 -0.634 1.085 -0.015 -0.373 0.476 0.472
-1.320 -1.017 -0.688 -1.015 -0.573 -0.276 -1.421

Table36.txt

0.713	-0.326	0.891	-0.084	-0.327	0.893		
0.512	-1.637	0.246	0.005	0.038	1.467	1.007	0.898
0.958	-0.003	-2.184	-1.195	1.472	-1.860	-1.796	
0.954	1.419	0.011	0.368	0.175	1.648		
1.910	0.145	1.601	-0.466	0.437	1.478	0.694	-1.216
-0.656	-0.780	-2.173	-1.378	0.601	-1.036	-1.591	
1.457	0.169	-1.451	1.193	-0.739	0.379		
-1.028	0.832	1.275	0.767	-0.700	-0.487	-0.665	-0.220
-0.180	-1.001	1.531	0.546	0.723	0.398	1.111	
-0.439	0.967	-0.465	1.365	0.049	-0.438		
1.114	-2.285	-0.238	-0.288	-0.093	0.210	0.165	-1.162
-1.402	-0.805	-0.583	-0.735	-0.388	-1.044	-0.545	
0.862	1.512	1.483	0.302	-1.283	0.035		
-0.270	-0.459	0.532	1.650	-1.797	-0.614	0.594	-0.825
-1.295	-0.945	1.132	1.112	-0.208	-1.170	-0.117	
2.886	-0.050	0.070	0.749	-0.095	-0.205		
-0.017	-1.421	-0.778	-1.507	0.278	2.014	-0.488	1.131
-1.196	0.388	-1.847	-0.787	-1.045	-3.002	-0.783	
1.564	1.622	-0.015	0.470	-1.472	1.179		
-0.462	1.948	0.801	0.630	-1.304	-0.770	0.943	-0.775
-2.779	-0.967	0.576	-0.136	1.250	0.452	0.019	
-0.444	-0.481	-0.182	2.075	0.355	0.602		
-1.335	-1.988	-0.472	-0.919	-0.736	1.634	0.196	-0.260
-2.543	0.938	-2.339	0.268	-0.103	-2.514	-0.324	
-1.237	-2.543	1.930	2.504	-1.588	2.094		
-0.389	-2.028	0.565	-2.028	-2.415	2.120	0.767	0.832
-3.865	1.503	-2.105	-0.641	-1.197	-2.118	-1.096	
-0.314	-0.425	0.062	1.414	0.815	3.560		
0.900	-3.630	-1.039	-0.164	-1.478	-1.998	2.127	-0.859
-0.130	0.404	-2.099	0.110	0.429	-2.027	1.845	
1.922	0.601	0.230	1.489	0.692	0.675		
-0.068	-0.113	-1.443	-2.859	0.259	1.886	-0.419	-0.779
0.489	1.109	-2.024	-1.103	-0.950	-1.632	-2.902	
0.099	0.093	0.096	-0.906	-0.774	0.663		
-0.509	1.311	-1.113	-0.644	1.043	0.104	-0.783	-0.044
-0.424	-0.100	-0.537	-1.411	-0.751	-0.785	-1.625	
-1.194	0.945	0.601	-0.830	-2.737	-0.233		
-0.539	1.007	-0.470	0.998	-0.357	1.453	0.089	0.137
-1.136	-0.709	-0.925	-0.355	0.047	0.160	-0.739	
-1.305	-1.087	-0.820	-0.221	-0.021	0.176		
-0.271	0.653	0.470	0.485	1.437	0.205	0.437	-0.191
-0.816	0.611	0.386	-0.901	0.103	-0.306	0.202	
0.880	-0.710	-1.106	-0.067	0.552	1.579		
0.371	-0.886	-1.115	-0.638	0.004	-0.492	-0.753	-0.869
0.985	-0.457	-2.967	-1.852	0.136	-1.998	-0.621	
0.885	0.511	-1.126	0.141	-0.747	-1.213		
-0.461	0.210	0.445	-0.315	-0.426	1.594	-0.321	-0.172
-1.275	-0.291	0.466	0.790	0.835	-0.307	-0.425	

Table36.txt

0.405 -0.251 2.425 1.238 0.584 1.053
-4.148 0.114 -0.969 -0.468 0.442 2.912 1.212 4.337
-4.725 5.766 -3.627 0.298 0.655 0.387 -0.107
1.750 -0.999 -0.691 2.470 0.750 1.629
-0.171 0.113 -0.150 -0.499 0.789 0.796 1.108 -0.964
-0.095 0.373 -0.219 -2.188 -0.696 -1.442 -1.735
0.246 0.115 -0.401 -0.977 -1.116 -0.530
0.108 -0.782 -0.473 -2.247 -0.052 0.419 -1.510 -0.137
0.794 0.904 -1.403 -0.508 -0.326 -1.454 -2.722
-0.549 0.170 0.593 -1.331 -0.928 -0.467
0.724 -1.089 0.443 0.142 -0.461 0.557 0.116 0.066
-0.465 -1.542 -0.823 -0.343 0.434 0.103 -0.101
-0.384 -2.094 0.224 1.321 -0.453 0.502
1.309 -1.019 0.141 0.242 -0.796 1.021 -1.055 -0.235
0.670 -0.511 -0.373 -1.286 -0.708 -0.996 -1.907
0.819 0.683 -1.115 0.678 -1.118 -0.083
0.116 1.505 -1.416 0.832 0.217 0.399 0.624 -1.135
-2.249 -0.652 -0.343 -0.651 0.697 0.746 -1.025
1.860 -1.604 0.001 1.251 0.659 0.906
0.144 0.380 -0.118 -0.127 -0.372 -0.114 -0.620 -1.260
-1.248 -1.102 -1.334 0.502 1.124 -0.438 0.662
1.743 1.727 -0.447 1.140 0.341 -0.235
0.001 0.867 -0.513 -0.461 0.595 0.611 -0.145 -0.145
-0.016 -0.044 0.038 -0.922 0.900 -0.335 -0.223
0.928 -1.415 -0.165 0.375 -0.941 0.057
-1.980 1.841 0.720 1.224 -0.739 -0.370 0.569 -1.019
-0.196 -1.356 0.302 -0.857 -0.495 1.609 1.472
-0.238 0.218 -0.078 0.392 -1.071 2.166
0.175 -0.515 0.363 -1.118 0.388 0.600 -1.681 1.233
-1.088 -0.678 -1.453 -0.299 1.283 -1.276 -1.678
-0.274 1.532 0.009 1.828 -0.260 1.407
-0.134 -0.938 -0.239 0.192 0.422 1.638 -1.183 0.392
-0.235 -1.363 -1.917 0.489 0.038 -1.537 -1.169
-1.648 0.470 -0.522 1.752 -0.711 1.088
0.532 0.392 0.098 -0.072 0.382 0.881 -2.387 -0.848
-0.411 0.226 -2.064 -0.960 0.626 -1.597 -1.419
-0.418 -0.590 0.005 0.144 -0.696 -0.188
1.478 0.870 -0.104 -0.349 0.677 1.051 1.107 -1.253
0.111 -0.099 -0.671 -1.530 0.859 -1.169 -0.182
-0.236 0.019 0.876 1.437 1.134 1.221
-0.404 0.029 0.864 -0.211 -0.454 1.393 1.216 0.227
-0.122 -0.702 -0.830 -1.687 0.054 -1.566 -1.795
3.945 -0.499 0.088 1.828 0.777 0.669
-5.604 -2.914 1.293 3.067 -1.532 -2.296 -1.083 1.879
-5.789 5.955 0.072 -2.505 -2.275 -2.284 -2.832
0.069 -1.730 -0.016 3.989 1.983 2.179
0.137 0.506 -0.700 -0.406 0.334 0.113 -0.890 0.884
0.628 -0.371 -0.002 -1.907 1.052 -1.967 -1.744

Table36.txt

0.737 1.265 -1.544 -2.094 -1.515 0.987
0.002 1.014 0.135 -1.094 -0.129 -0.087 -0.791 0.338
-0.145 -1.024 0.606 -0.085 0.768 -0.445 -0.827
0.612 -0.108 0.010 0.098 -1.073 0.837
-0.339 -1.128 -0.730 -0.556 1.287 0.398 -1.389 0.569
0.067 -0.026 -1.648 -2.010 -0.712 -0.242 -1.598
0.056 -0.303 -0.918 -0.687 -0.893 -0.280
-1.414 -0.673 0.106 0.724 -0.009 1.171 1.018 0.676
-0.031 -1.609 -1.141 -1.700 -0.522 -0.058 -0.640
-0.496 0.624 0.128 -0.176 -0.683 0.001
0.719 -2.168 0.587 -1.282 -0.444 0.819 -1.235 1.405
0.454 -0.214 -1.412 0.494 0.505 -0.652 -2.149
0.352 0.327 0.393 1.184 -1.119 -0.460
-1.159 1.212 0.370 -0.230 -1.609 -0.131 2.612 0.332
-0.141 -0.274 0.201 0.382 -0.268 0.421 0.096
1.310 0.374 0.675 0.696 0.537 -1.184
0.378 -1.521 0.356 -1.151 -0.954 0.423 -0.703 1.468
1.484 -0.419 0.818 0.037 -0.958 -2.188 -0.294
0.319 -1.415 -0.175 1.762 -0.690 0.733
-1.730 0.721 0.462 -0.448 -1.107 -0.113 0.757 -0.764
-2.227 -0.176 2.047 0.899 0.948 0.059 0.842
0.972 0.405 -0.336 1.146 1.168 1.271
-1.628 1.702 1.196 0.966 -1.005 -0.033 0.340 -0.524
-2.579 -0.900 0.956 -0.920 1.230 -0.171 -0.301
1.199 -0.254 -0.520 1.498 1.166 1.710
0.504 1.177 1.635 0.070 -0.759 -0.406 -0.874 0.616
-0.253 -1.056 1.127 -0.382 -0.012 -1.493 -0.207
0.450 -0.464 1.037 1.166 1.055 0.019
-1.059 0.971 -0.287 -0.137 -0.968 0.013 -1.995 0.334
-0.243 -0.757 -0.169 1.441 -0.344 -0.624 1.243
0.240 0.477 -0.342 2.814 0.306 -0.051
-0.791 -0.507 0.809 -1.412 -1.210 -0.112 0.197 1.401
-1.051 -1.133 -0.004 -0.693 -0.024 -1.180 -0.120
0.984 1.003 -0.396 0.543 -0.092 0.325
-0.153 -0.845 -0.253 -0.469 0.662 1.002 -0.335 0.383
-0.282 1.102 0.387 0.671 -0.655 -1.914 -0.541
-0.084 -0.750 0.364 1.084 0.376 0.319
1.051 -0.858 -1.157 -0.935 -0.738 0.421 -0.818 0.771
0.508 1.004 -1.608 -0.729 -0.684 -1.274 -1.591
1.295 1.381 0.138 -0.656 -0.483 -0.137
-0.122 1.091 -0.007 1.442 -0.642 0.175 -0.254 0.390
-0.908 -0.740 0.599 -1.756 0.420 -0.738 0.810
0.984 1.178 -0.739 1.864 0.302 0.644
1.343 -1.642 0.284 -0.504 -0.998 0.121 0.455 -0.497
0.316 1.284 -1.228 -1.276 -0.923 -1.748 -2.674
0.450 -0.857 0.715 0.920 -0.624 0.374
0.925 1.038 -0.420 -1.759 0.380 -0.902 -0.566 0.580
-0.631 -0.183 0.043 -0.192 0.972 -0.615 -0.127

Table36.txt

0.447 0.277 1.859 1.608 0.975 -0.280
0.539 -0.336 -1.348 -1.558 -0.452 0.508 -0.320 0.138
0.203 -0.632 -2.692 0.375 -1.010 -0.539 -1.338
0.002 0.135 -0.910 -1.443 -0.208 -0.302
0.216 -0.032 1.126 -1.780 -0.882 -0.225 0.208 -0.128
-1.353 -0.446 -0.258 -1.010 -0.414 -0.969 -1.299
0.617 -0.573 0.414 1.443 -0.298 -0.834
0.881 -2.359 0.363 -0.251 1.232 0.924 -0.464 1.025
0.765 -0.307 -0.357 -0.163 0.546 -2.072 -0.981
-0.002 2.753 -1.412 -1.547 1.016 -1.713
0.629 0.220 -0.296 -0.995 -0.962 -1.217 -0.732 -0.156
0.979 -1.014 0.501 -0.573 -0.250 0.606 -0.280
-0.493 0.432 0.160 -0.783 -1.657 0.555
1.114 -0.878 0.857 -0.042 -0.132 0.040 -0.622 -0.371
-0.856 1.041 -1.461 0.093 0.564 -0.716 -1.610
-0.544 -0.188 0.219 0.734 1.546 1.017
1.431 -2.308 -1.905 -1.427 -0.476 -0.654 -1.849 0.496
0.332 -0.674 -1.865 -1.838 -1.525 -1.497 -2.490
0.534 0.035 -0.560 -0.250 -1.082 0.175
0.695 -1.604 -0.211 -1.851 -0.773 -0.491 -0.505 0.298
1.289 -0.217 -0.941 -0.828 -0.854 -2.207 -1.683
0.357 0.497 0.574 0.054 -1.523 -0.480
0.960 -1.616 -2.265 -1.761 0.461 0.531 -1.662 0.654
0.597 0.206 -1.864 -0.931 -0.969 -1.856 -2.902
0.346 1.220 0.147 -0.246 -1.732 0.388
0.464 0.107 0.116 0.503 -0.200 0.870 -1.368 -0.396
-0.719 0.579 -0.497 0.922 -0.772 0.492 -0.299
-0.627 -1.266 -0.851 -0.726 -1.207 1.282
2.094 -1.302 -1.623 -0.155 0.859 -0.269 -1.208 0.052
-1.271 -0.320 -1.564 0.226 -0.277 -0.861 -1.278
0.588 1.367 0.509 0.262 0.002 0.129
1.497 -0.725 -1.081 -0.895 0.383 0.385 -0.823 -0.107
0.204 0.320 -1.411 -1.811 -0.502 -1.906 -2.205
1.239 -0.489 -0.222 0.282 -0.967 0.405
0.903 -1.293 0.971 -1.893 0.066 1.178 -1.986 1.070
0.064 -0.826 -2.480 0.802 1.002 -1.035 -2.125
0.263 0.530 1.036 0.500 -0.558 0.372
0.506 -2.449 0.633 -0.638 0.364 0.351 -0.321 0.782
-0.473 -0.468 -2.964 0.860 1.500 -0.817 -1.548
0.424 1.097 1.079 -0.407 0.034 -0.569
1.638 -2.189 -1.546 -2.163 0.264 2.031 -1.041 1.538
0.063 0.040 -3.243 -1.027 0.779 -2.623 -2.919
-0.708 0.333 0.668 -1.586 -0.975 -0.154
0.844 -2.280 -1.580 -0.514 -0.123 1.495 0.107 1.003
-0.132 -1.148 -2.333 -0.859 0.477 -2.366 -1.893
-0.480 1.958 0.490 0.188 -0.137 0.437
-1.035 -1.604 1.228 -5.424 -0.998 -0.468 -1.609 -1.464
11.000 -11.000 -11.000 1.240 -5.231 -4.037 1.863

Table36.txt

-2.359	-6.590	0.291	1.577	6.934	11.000		
1.636	-1.762	0.609	-1.215	0.791	0.493	-1.516	1.122
-0.409	-0.784	-1.842	0.323	1.385	-2.446	-2.554	
0.553	0.687	1.503	0.281	-0.622	0.444		
1.643	-1.705	-0.389	-1.203	-0.358	1.336	-1.334	0.905
-0.958	-0.226	-2.498	1.897	1.097	-1.157	-1.870	
1.087	0.475	0.867	1.325	0.243	0.660		
-0.085	-1.817	1.262	0.499	-2.182	-1.143	-0.159	-0.265
1.368	-0.790	-0.623	1.467	1.469	1.272	-0.628	
1.007	0.648	0.750	0.385	0.875	0.813		
1.650	-0.725	-1.243	-1.434	-0.009	0.877	-0.540	-0.814
0.450	-0.995	-1.670	-0.884	-0.205	-2.627	-2.796	
1.303	0.195	0.819	0.245	-0.326	-0.139		
1.317	-2.200	-0.169	-1.080	-0.393	1.103	-1.377	0.001
-0.254	0.355	-2.123	-0.087	0.756	-1.990	-1.880	
0.797	0.333	1.777	0.480	-1.184	0.259		
0.823	-1.469	0.423	-1.823	-0.028	0.230	-0.981	0.401
0.863	-1.459	-2.979	-0.550	0.779	-2.224	-2.548	
0.558	0.432	0.306	-0.845	-0.814	0.241		
1.631	-0.398	-1.463	-0.292	1.225	0.639	-1.009	-0.885
1.627	0.939	-1.987	-2.664	-0.521	-2.730	-3.974	
0.345	0.541	-0.055	-0.725	-1.677	-0.403		
0.879	0.099	-0.960	-0.189	-0.173	-0.173	0.595	-0.755
1.118	-0.196	-0.551	-3.494	-1.690	-1.312	-2.333	
1.028	0.071	-0.252	-1.183	-1.879	-1.268		
0.496	-1.775	-0.076	-0.023	-1.465	-0.631	-1.327	-0.452
0.559	-0.256	-2.162	0.051	1.207	-0.930	-1.984	
1.013	0.751	0.897	0.927	0.137	0.573		
0.443	-0.570	-1.407	-1.940	0.307	0.687	-0.652	-0.443
0.296	0.631	-1.534	-2.820	-0.746	-2.081	-2.922	
0.539	0.403	0.023	-0.603	-2.182	-0.371		
0.791	-0.799	-1.309	-0.453	-0.657	-0.297	-0.292	-1.066
-0.007	-0.141	-1.584	-3.420	-2.208	-3.450	-2.622	
0.485	0.306	-0.972	-0.855	-1.951	-1.212		
1.419	-1.167	-1.603	-1.012	-0.465	-0.299	-0.544	-0.824
1.641	0.280	-1.413	-0.922	-1.520	-1.808	-1.919	
0.602	0.299	0.117	-0.418	-0.999	-0.243		
1.899	-1.045	0.515	-1.985	-0.132	0.920	-0.706	0.416
-0.251	0.045	-2.375	-0.236	-0.123	-2.511	-3.531	
-0.715	0.792	-0.399	-0.538	-1.792	0.564		
0.775	-1.744	-0.635	-1.833	0.046	0.428	-1.846	0.743
0.247	-0.154	-2.125	-1.641	0.085	-1.884	-2.484	
-1.103	1.948	-0.970	-1.291	-1.107	1.129		
-0.310	-0.406	-1.204	-1.064	-0.485	0.940	-0.271	0.032
-1.579	-0.911	-0.948	-0.697	1.033	-1.405	-1.023	
-0.206	-0.047	0.217	-0.172	-0.899	1.330		
-0.321	-0.328	-1.456	-0.410	1.609	1.856	-2.420	0.851
-1.693	0.033	-1.412	0.187	1.679	-0.879	-1.795	

Table36.txt

0.971	1.006	-2.565	-2.583	0.649	1.836		
-0.917	-0.055	-1.346	0.450	-0.045	-0.124	0.291	-2.348
0.867	-5.475	-0.771	-1.123	0.819	-1.243	-0.239	
1.229	0.450	0.013	-0.021	-1.848	-0.050		
-0.610	-0.603	-0.458	-0.664	0.931	0.757	0.309	0.021
-1.145	0.175	-0.367	-0.820	-0.364	-0.758	-0.747	
0.716	-0.503	-0.234	0.049	-0.604	0.158		
-0.801	-0.552	-1.646	-0.080	0.105	0.940	1.044	-0.744
-1.149	-0.043	-2.562	0.654	-0.872	-0.115	-0.453	
0.117	-0.779	1.001	-0.295	-1.318	-0.595		
-1.999	1.239	0.060	-0.359	-0.840	-0.392	1.005	-0.215
0.088	0.799	0.858	-0.776	0.134	-1.241	0.802	
1.315	-0.108	-0.234	0.731	-0.942	-0.496		
1.247	-1.153	-3.107	-1.299	0.068	0.254	-1.936	1.333
-0.560	-1.495	-3.483	-1.833	0.810	-2.952	-2.168	
0.659	-0.271	0.318	-0.049	-1.519	0.209		
0.019	-1.839	-1.926	-1.491	-1.878	0.323	0.603	0.861
0.519	0.602	-0.852	-0.995	0.741	-1.302	-2.281	
0.265	0.168	1.173	0.683	-1.287	-0.264		
1.201	-1.437	-2.249	-0.931	0.127	0.593	0.007	1.496
0.098	-0.326	-1.539	-1.147	-0.022	-0.413	-0.860	
0.677	-0.020	0.875	-0.144	-0.183	-0.683		
1.297	-2.512	0.188	-2.502	0.851	1.885	-2.574	1.639
1.494	-0.003	-2.757	-0.771	0.725	-2.538	-2.620	
0.482	1.778	0.138	-0.469	-1.834	-0.112		
3.459	0.201	3.109	-1.832	-0.435	0.948	-4.929	-4.846
11.000	-4.322	-4.897	-1.542	0.220	-1.168	-0.336	
-0.737	-3.520	1.492	-1.501	6.701	6.099		
-4.421	-0.010	2.402	-2.714	-4.307	5.104	-2.208	-2.641
-3.170	0.930	-4.460	-1.580	-0.994	-6.059	1.737	
-4.036	-11.000	2.049	0.125	7.661	11.000		
0.306	0.007	-2.892	-0.591	-0.236	0.973	-0.633	0.832
0.317	0.340	-2.905	-1.402	0.970	-2.916	-2.199	
0.551	-0.633	1.039	-0.446	-0.633	-0.663		
1.034	-1.461	0.439	-0.806	-0.231	0.584	-1.749	0.206
1.706	0.373	-2.430	-0.907	0.723	-1.707	-2.655	
0.318	0.527	0.692	-1.233	-2.093	-0.812		
0.833	-2.324	0.607	-1.986	0.742	1.125	-1.561	0.868
0.529	0.086	-2.268	-0.083	1.646	-1.675	-2.370	
0.709	0.800	1.323	-0.481	-1.467	0.449		
1.139	-0.475	-0.230	-2.708	0.914	1.471	-2.398	0.473
0.049	-1.189	-3.168	-0.877	1.294	-2.072	-3.055	
0.080	1.134	0.219	0.323	-1.539	-0.262		
1.652	-0.497	-1.120	-2.045	0.487	0.771	-1.989	0.604
0.444	-0.454	-2.744	-0.551	0.565	-2.709	-3.220	
0.228	0.039	0.626	-0.818	-1.384	-0.009		
2.642	-2.164	-2.012	-2.476	-0.522	0.850	-2.006	-0.294
1.109	-0.295	-2.346	-0.223	0.636	-1.138	-3.056	

Table36.txt

-0.062 1.446 0.028 -0.861 -0.673 0.550
-5.239 -7.034 2.283 0.495 -4.328 1.348 -1.869 -3.529
-11.000 -2.958 -0.578 0.353 -3.463 -3.389 1.426
0.455 1.266 2.070 1.885 0.071 0.087
-0.189 0.565 0.142 0.248 -0.975 -0.939 1.640 0.271
-0.020 0.515 0.998 -2.318 -1.241 0.381 -0.584
0.813 -1.260 0.265 0.433 -1.043 -1.690
-0.287 -0.691 -0.103 -0.154 1.023 0.465 -0.028 0.486
-0.050 0.086 -1.085 -0.399 0.641 -2.753 -1.100
1.225 1.307 0.199 -0.808 0.005 -0.665
0.900 -0.902 -0.062 -0.951 -0.887 -0.508 -0.961 0.597
-1.323 -0.579 0.552 0.626 -0.143 0.491 0.446
0.664 -0.757 1.178 1.582 -0.429 0.111
-1.804 -4.388 -1.200 0.121 -2.806 -1.380 5.778 5.024
-6.476 -5.232 -3.110 -1.566 -1.545 -1.720 3.174
5.502 -5.733 2.625 2.505 -0.803 -0.933
-11.000 -2.893 2.219 1.307 -0.376 7.992 1.374 3.927
-3.189 -3.299 -11.000 -2.062 -4.722 -3.999 -1.191
1.777 -4.386 -1.109 -0.573 1.582 2.716
0.137 -3.107 -0.924 -0.956 -0.113 3.431 -0.655 0.510
1.641 0.378 -2.178 -1.097 -0.558 -1.954 -1.555
1.539 1.234 -0.588 1.463 -0.879 1.011
0.428 -1.569 -2.304 -0.999 1.472 0.874 -1.547 0.725
-0.390 -0.056 -2.450 -0.532 0.243 -2.158 -1.418
0.017 0.667 0.645 -0.238 -0.802 0.214
0.557 -1.042 -1.880 -0.568 0.381 0.353 -0.471 1.164
-0.087 0.184 -3.036 0.823 -0.581 -1.814 -1.587
0.193 0.364 -0.035 -0.242 -1.628 0.284
1.806 -0.050 -1.540 0.944 1.099 0.900 -1.415 -0.436
-0.308 0.402 -1.107 -0.483 1.461 -3.057 -2.241
0.559 0.586 1.193 -0.114 -1.365 -0.825
0.882 -1.402 -0.844 -0.505 -0.088 1.501 -4.136 -0.227
0.888 -0.297 -2.513 0.052 0.418 -1.241 -1.824
0.026 0.366 0.188 -0.232 -1.339 -1.163
0.472 -1.064 -1.594 0.069 -1.541 0.640 0.448 -0.481
1.268 0.057 -1.195 -1.777 0.014 -2.105 -1.114
0.996 -1.647 -0.593 -0.868 -1.832 -0.526
1.191 -1.550 -2.312 -1.744 1.002 0.559 -1.740 0.332
-0.279 0.769 -3.076 -0.586 -1.020 -2.304 -1.005
0.058 -0.457 -1.599 -0.324 -1.344 0.422
1.154 -0.526 -1.278 -1.361 0.138 -0.011 -1.705 0.222
0.623 0.180 -1.944 -1.072 -0.266 -2.001 -1.378
0.979 -0.146 0.530 1.381 -1.336 -0.203
0.675 -0.007 -2.026 -0.561 -0.638 0.449 0.004 0.375
0.449 0.393 -2.198 -1.291 -0.304 -1.825 -1.387
0.703 -1.259 0.647 -1.782 -1.445 0.078
-0.425 -0.773 -0.582 -1.015 -0.153 0.733 -1.700 0.297
0.149 -0.330 -0.426 -1.640 1.463 -1.263 -0.776

Table36.txt

-0.546 0.639 0.208 -0.335 -1.697 0.633
0.838 -1.052 -1.598 -2.001 1.200 0.281 -0.810 0.548
-0.083 0.489 -2.500 -1.382 -1.389 -2.387 -2.496
0.534 0.911 0.679 -0.301 -1.242 -0.471
0.842 -0.435 -1.867 -2.031 0.390 0.574 -0.805 0.641
-0.070 0.439 -1.746 -1.777 0.189 -1.619 -1.789
1.193 -0.233 -0.015 -1.541 -0.855 -0.454
1.539 -1.794 -1.870 -1.348 0.598 1.458 -1.378 1.243
-1.142 -1.117 -2.878 0.370 0.464 -2.744 -1.384
-0.162 -0.993 1.602 -0.240 -1.269 -0.358
0.638 0.026 -0.158 -1.682 1.590 0.895 -1.618 0.298
0.951 -0.326 -1.370 -0.168 0.613 -1.202 -1.391
-0.513 -0.547 1.845 0.305 0.165 0.548
0.816 1.066 0.471 -1.545 1.000 1.466 -1.635 -0.272
-0.205 -0.462 -0.792 0.730 1.235 -1.074 -1.958
-0.169 -0.169 0.035 0.078 0.022 0.094
0.000 0.022 -1.478 0.601 -1.261 0.396 -0.654 -0.625
-0.361 -1.777 -0.120 0.070 0.448 -1.468 -0.717
-0.014 0.908 -1.129 0.271 -0.916 -0.066
0.340 0.850 -0.239 -0.074 1.267 -0.098 -0.276 -0.965
0.485 -0.740 -1.310 -1.885 -0.278 -1.709 -0.613
2.829 -0.547 0.090 0.560 -1.073 -0.017
1.027 -1.238 -1.242 -0.620 -0.903 -0.312 0.401 0.956
0.955 0.583 -2.419 -0.441 -1.042 -2.115 -2.518
0.063 -0.445 0.144 0.190 -0.641 -0.279
0.186 -0.227 -1.179 -0.680 -0.335 -0.129 -0.295 -0.276
-0.455 0.242 -1.533 -1.410 0.363 -2.115 -1.507
1.549 0.662 -0.343 0.630 0.208 -1.229
2.282 -0.948 -1.351 -1.090 0.998 0.967 -1.330 -0.753
0.261 0.260 -2.427 -1.311 0.654 -2.667 -1.613
0.910 -0.514 0.627 0.102 -1.113 -0.783
-0.541 -1.084 -0.764 -2.125 0.340 1.007 -1.728 0.180
1.491 -0.491 -1.937 -0.229 0.663 -1.449 -1.271
0.680 -0.738 0.380 -1.049 -1.762 -0.198
1.005 -0.937 0.251 -1.636 0.031 1.732 -1.490 0.971
-0.297 -1.843 -2.802 0.939 1.640 -0.870 -2.021
0.901 0.251 1.404 2.042 -0.906 0.389
0.491 -1.729 0.814 -1.635 1.795 1.740 -1.861 1.011
-0.097 -0.471 -1.937 -0.352 1.914 -2.514 -2.184
0.499 0.941 0.950 -0.299 -1.400 0.460
1.879 -1.769 -1.883 -2.182 -0.264 0.630 -1.156 1.481
1.220 0.312 -1.445 -1.434 -0.121 -2.253 -2.242
-1.015 1.019 0.747 -0.599 -1.312 0.157
1.608 1.184 -1.637 -1.596 -0.990 -0.790 -0.459 -0.866
0.816 -0.886 -2.129 -0.786 -0.149 -1.241 -2.727
0.812 1.110 0.367 -0.110 -0.420 -0.224
1.779 -1.073 -1.581 0.282 -1.125 -0.587 -0.862 0.352
1.045 -0.830 -1.420 -0.109 -0.258 -1.624 -0.665

Table36.txt

0.909	0.066	-1.320	-0.753	-1.449	-0.929		
0.582	-0.524	-0.051	-1.526	0.862	1.073	-0.974	-1.188
-0.134	-1.048	-0.650	-0.723	0.370	-1.628	-1.137	
0.764	-0.600	0.363	-1.691	-0.125	-0.354		
0.639	-0.836	0.172	-1.882	1.653	0.357	-1.936	0.391
0.928	-0.684	-0.731	-0.104	-0.344	-1.143	-1.720	
0.124	0.435	0.123	-0.476	-2.043	0.535		
0.639	-1.071	-1.664	-1.638	0.149	1.053	1.068	0.242
4.339	-2.077	-3.159	-0.534	0.474	-1.438	0.012	
0.139	-3.591	0.169	-0.701	0.551	2.854		
1.600	-1.457	-1.168	-1.900	0.772	0.773	-1.058	-0.617
0.151	0.129	-2.027	-2.122	-0.908	-2.774	-3.311	
0.755	1.250	0.331	-0.293	-1.252	0.124		
-0.787	0.443	-0.754	-0.128	0.535	0.552	-1.061	0.495
-1.024	-0.233	-1.766	-1.532	1.585	-1.553	-1.067	
0.700	-0.470	0.063	-1.604	-0.904	1.075		
0.019	0.453	-0.519	-0.080	1.429	0.099	-0.055	-0.477
0.860	-0.075	-0.076	-1.986	0.527	-1.395	-1.808	
1.046	-0.145	0.672	-1.160	-0.792	0.920		
0.611	-0.584	-0.035	-1.841	1.029	1.250	-1.725	1.392
0.208	-0.848	-2.653	-0.973	1.711	-1.236	-2.055	
-0.027	-0.060	0.335	-1.029	-1.235	-0.148		
0.703	-1.598	-0.708	-1.292	1.136	1.071	-1.010	1.960
0.050	-1.342	-2.716	-1.398	0.362	-2.540	-2.082	
-0.161	-0.292	-0.613	-2.910	-2.446	-0.546		
0.176	0.207	0.141	-0.285	0.755	1.346	-0.197	1.088
-0.205	-1.262	-0.590	0.391	-0.297	-1.395	-0.729	
-0.788	0.198	0.865	-0.151	-0.798	1.178		
0.356	-1.276	-1.873	-2.693	0.611	0.900	-0.984	0.636
-0.178	0.308	-1.426	-2.602	-0.693	-0.575	-2.681	
1.100	-0.794	-0.963	-0.577	-2.257	0.150		
0.000	-0.293	-0.655	0.095	-1.154	-0.307	0.051	-0.248
-0.729	-0.973	0.448	0.739	0.228	-0.909	0.020	
0.381	-0.041	1.185	-0.188	-0.286	0.750		
0.594	-1.613	-1.712	-0.972	-0.048	0.473	-1.191	-0.118
0.517	0.662	-1.368	-3.166	-1.565	-1.316	-2.298	
1.400	-0.526	0.714	-1.016	-1.654	0.187		
1.837	-2.002	-2.169	-1.150	-0.013	-0.021	-1.453	-0.650
0.892	1.675	-2.493	-2.121	-2.286	-1.640	-2.681	
-0.557	-0.461	0.125	-1.015	-2.177	-1.648		
-0.298	-0.851	-1.081	-0.225	-0.555	0.093	1.222	1.066
0.449	-0.663	-1.414	-1.157	0.600	-0.645	-0.814	
-0.040	0.413	1.500	1.081	-0.726	-1.974		
0.556	0.823	-2.315	-1.088	-0.276	0.897	0.294	0.598
0.938	-0.654	0.453	-1.725	-0.142	-0.677	-1.330	
-0.035	-0.906	1.243	1.166	-1.106	0.339		
3.935	-1.129	-1.318	-0.855	-0.420	-1.698	-1.699	1.981
-3.538	4.235	-1.590	-1.472	-1.438	-1.041	-1.302	

Table36.txt

-0.523	0.003	0.196	1.778	2.775	2.568		
0.000	2.026	-0.847	-0.515	-0.827	-0.124	-0.400	0.156
-0.148	-0.443	-0.122	-1.301	-0.574	-1.062	0.301	
0.424	0.943	0.372	-0.268	-1.538	0.789		
0.111	-1.703	-0.361	-0.913	-0.429	-0.861	0.935	1.574
0.035	-0.556	-0.578	0.135	-0.949	-0.003	0.190	
0.285	-0.447	0.908	1.196	-0.593	0.008		
0.387	0.054	-1.917	-0.040	-1.024	-0.806	0.400	1.145
1.218	-0.471	-0.664	0.332	-0.587	0.164	-0.917	
0.655	1.366	-0.393	1.889	-0.355	-0.133		
2.087	-1.756	-1.972	0.308	0.392	-0.047	0.887	0.677
0.884	-0.397	0.221	-0.188	-0.854	-0.792	-1.065	
-0.091	-0.089	-1.350	0.007	-1.190	-0.483		
0.329	-0.104	1.027	-0.916	-0.251	-1.735	1.024	2.113
-2.414	0.298	-2.058	-1.368	-0.710	-1.682	-1.977	
2.140	-1.847	0.763	1.389	0.150	1.368		
-1.286	-1.420	0.952	-0.040	-0.678	0.164	0.231	0.840
-1.091	-0.445	-0.018	0.052	-1.238	-0.943	0.535	
-0.405	-1.348	-1.230	-0.295	0.093	0.489		
0.932	-0.400	-1.149	-0.637	1.514	1.187	-0.142	-0.588
-0.171	-0.296	-2.660	-1.449	0.191	-1.059	-2.172	
-0.173	0.719	1.314	-0.510	-2.544	-0.100		
0.221	-0.583	-3.019	-0.713	0.389	0.613	-0.626	-0.762
1.418	-0.849	-2.533	-0.183	-0.179	-0.036	-0.636	
-1.579	-1.871	-0.453	-2.207	-1.025	-0.692		
1.712	-1.586	-0.744	-1.291	-0.216	0.687	-1.619	-1.193
-0.537	0.149	-1.968	-0.319	0.209	-2.236	-1.297	
1.882	1.036	0.832	1.205	0.502	0.644		
1.351	-2.319	-1.257	-1.006	0.612	1.345	-0.926	-0.241
-0.330	-0.182	-1.964	-0.782	-0.392	-1.570	-2.753	
0.443	-0.333	1.389	0.253	-1.616	-0.356		
-0.914	0.053	0.142	-0.665	-0.267	0.773	-0.300	0.511
0.439	-0.721	-1.633	-0.655	-0.908	-1.537	-0.226	
0.052	-0.134	0.690	-0.012	-0.365	-1.106		
0.215	-2.127	-1.798	0.831	-1.425	-1.419	-1.133	0.226
1.205	-0.575	-3.575	-0.256	0.142	-2.680	-1.576	
0.255	-1.358	1.712	0.859	0.937	1.406		
-0.950	-0.260	-2.562	-0.208	-0.160	0.567	-0.989	0.009
0.461	1.185	-0.497	0.049	-1.394	-2.023	-1.277	
1.100	-0.575	0.653	-0.624	-0.217	-0.776		
1.593	-0.256	-1.050	0.618	-0.154	-0.538	-0.942	-0.831
-0.430	1.140	-0.888	-0.828	-0.526	-2.698	-0.804	
-0.110	-0.779	-0.257	-0.337	-1.829	-0.282		
1.059	-1.722	-1.234	-0.333	0.305	-0.696	-0.621	1.075
-0.566	0.812	-0.512	-2.098	-0.825	-1.789	-0.267	
-0.375	0.721	-0.246	0.296	-0.428	-0.462		
-1.155	-0.942	-1.554	-0.971	1.544	1.257	-1.120	0.687
-0.197	-0.055	-1.982	1.141	0.868	-0.975	-1.134	

Table36.txt

-1.015 0.180 -0.728 -0.703 -1.455 0.386
-0.190 -2.307 -2.401 -0.422 -0.243 1.078 -1.975 0.760
1.053 0.939 -1.748 -1.282 -0.404 -1.458 -1.129
-0.600 -0.729 0.021 -0.460 -2.174 -1.437
-0.356 -1.795 -1.178 -2.726 -0.325 0.149 11.000 1.493
11.000 -0.620 -3.797 -0.251 -0.112 -7.034 -2.993
-5.852 -11.000 -0.273 -0.588 -11.000 11.000
-1.307 -1.845 -1.257 0.163 0.298 1.007 0.764 0.509
2.868 -0.004 -2.380 0.483 0.625 -2.354 -2.607
-0.537 -0.292 0.732 -2.473 -1.932 1.749
0.582 -1.741 -0.613 -2.027 1.444 0.794 -1.085 0.150
0.472 -0.848 -2.156 -0.421 0.814 -1.189 -1.958
-0.317 0.906 0.282 1.520 -0.620 0.197
0.283 -1.180 -1.060 -0.920 1.831 1.219 -0.798 0.471
0.177 -0.354 -2.442 0.281 0.216 -2.113 -2.338
-0.940 1.084 0.884 -1.545 -1.343 0.772
0.044 -0.448 -2.197 -0.489 0.215 0.551 -0.537 1.479
0.282 0.328 -1.333 -1.659 0.550 -0.719 -1.156
1.071 -1.189 0.552 -0.128 -0.639 -0.668
1.108 0.195 -0.871 -0.746 0.527 0.319 -1.305 0.491
-0.401 0.497 -1.023 0.283 0.904 -1.842 -1.654
-0.116 0.484 0.977 0.433 0.175 -0.705
1.329 -0.406 -2.204 -0.568 0.766 0.565 -0.756 0.676
1.069 0.198 -2.268 -1.541 -1.755 -2.312 -1.436
1.212 0.425 -0.711 -1.544 -1.463 -0.892
0.034 -2.103 -1.566 -2.087 0.736 0.213 -1.395 0.806
0.959 -1.481 -3.247 -1.656 -0.725 -2.645 -2.833
0.608 -0.239 -0.917 -1.602 -1.435 -0.622
1.982 -1.200 -3.993 -2.084 0.242 0.008 -1.956 1.278
0.665 0.728 -4.399 -0.845 -1.153 -2.975 -2.380
0.139 0.526 0.955 -2.066 -1.422 0.136
1.565 -1.357 -0.369 -1.786 1.137 1.655 -1.462 1.655
0.355 -0.630 -1.675 -0.985 0.114 -1.197 -1.721
-0.059 1.041 1.782 0.405 -0.216 -1.124
-1.237 0.119 0.254 -0.476 1.013 0.365 -0.539 0.731
-1.118 -0.163 -0.336 -1.099 -1.040 -1.812 -0.358
-0.488 -0.669 -0.375 -1.982 -0.412 -0.261
0.825 -2.655 -0.920 -2.658 1.020 0.678 -2.163 0.655
1.835 -1.044 -2.757 -2.459 0.361 -2.166 -3.777
0.798 2.155 -0.705 -1.529 -1.549 -1.294
0.532 -1.766 -1.681 -1.375 0.217 1.861 -0.947 0.297
0.472 -0.422 -2.864 -0.619 0.742 -2.038 -2.789
-0.994 0.282 0.457 -0.148 -0.864 -1.122
-0.417 0.891 -0.433 0.384 -0.950 -0.086 -0.785 1.456
-0.506 0.006 -2.065 -0.237 -0.248 -1.850 -1.158
0.427 0.347 0.278 -0.016 -0.457 0.524
1.120 0.094 -1.819 -2.038 0.777 0.151 -1.396 0.766
0.200 0.107 -0.709 0.354 0.294 -2.126 -2.764

Table36.txt

-0.104 0.587 0.722 -0.837 -0.840 -0.599
1.226 -1.599 -1.123 -0.145 0.248 0.673 -0.339 0.360
-0.241 -1.256 -1.292 0.316 -0.931 -0.150 -3.354
0.215 1.124 -0.130 -1.141 -0.725 0.473
0.965 -2.256 -0.508 -0.365 -1.309 0.634 0.617 0.535
1.473 -2.134 -2.177 -1.939 -1.402 -1.956 -1.228
0.831 0.741 -0.104 -0.753 -0.958 -1.393
1.095 -1.688 -0.805 -1.032 0.135 1.157 0.059 -0.121
1.883 0.384 -1.258 -1.295 -0.630 -1.358 -1.343
-0.640 -0.113 -0.359 0.138 -0.033 0.326
0.537 -0.796 -0.026 -0.386 1.181 0.552 -0.498 0.279
0.567 0.074 -1.304 0.520 -0.366 -1.095 -1.643
-1.178 0.564 0.820 -0.262 -1.135 -1.395
1.549 -1.242 -0.079 -2.052 2.267 1.681 -0.387 -0.204
-0.193 -1.120 -0.591 -0.852 0.765 -2.345 -1.585
-1.119 0.630 0.466 0.224 -0.104 0.921
1.408 -2.483 -1.362 -1.495 0.827 1.363 -1.267 1.486
0.613 -0.440 -2.173 -0.407 -0.124 -2.669 -2.582
-0.181 0.545 -0.312 -2.076 -1.897 -1.142
2.013 -1.459 -1.300 -0.932 0.391 -0.710 -0.402 -0.322
1.624 -1.304 -1.027 -1.306 -0.649 -0.774 -0.417
-0.149 1.203 -1.157 -1.577 -0.307 -0.383
1.192 -1.145 -0.354 -2.770 0.723 0.471 -2.706 0.993
0.868 -0.917 -1.540 -0.892 -0.477 -1.940 -2.558
-0.179 1.017 -0.070 -1.543 -1.753 0.881
0.277 -0.751 -1.373 -1.451 0.818 1.144 -0.343 0.866
0.908 -0.559 -3.046 -0.857 1.511 -2.400 -2.145
-0.328 0.079 2.219 -0.294 -1.269 0.341
0.718 -1.552 -1.553 -0.695 -0.503 -0.294 -1.786 1.113
0.168 -1.318 -1.732 -0.073 -0.367 -1.670 -0.275
1.600 -0.833 0.862 0.373 -0.886 -1.067
1.007 -0.963 -1.332 -0.751 -0.846 -0.814 -0.851 -0.813
0.302 0.231 -1.633 -2.468 -1.394 -1.898 -1.898
1.333 -0.124 0.434 -0.692 -1.036 -0.301
1.335 -0.693 -0.201 -1.258 -0.007 0.502 -2.352 0.470
-0.254 -1.210 -2.330 -2.659 -1.020 -2.788 -2.579
-0.546 1.005 0.181 -1.662 -1.392 -0.198
1.804 -0.079 -0.763 -0.681 -0.849 0.586 -0.997 0.755
-0.882 -0.156 -0.585 -0.275 -0.168 -1.745 -2.632
0.205 -0.182 -0.037 -0.811 -0.124 1.252
-0.996 0.113 -0.386 -0.982 -0.462 0.622 -0.816 2.281
-4.388 -5.460 -3.273 -2.179 -1.650 -3.392 -2.122
0.948 1.262 -0.989 2.659 -0.328 1.936
1.161 -2.971 -0.192 -1.042 -0.396 0.634 -0.875 0.977
0.297 -1.125 -3.419 -0.705 -0.061 -2.806 -2.825
-0.266 2.135 -0.418 -2.986 -1.144 -1.305
0.274 -0.728 0.567 -0.980 -0.337 -0.033 0.167 1.215
1.208 -0.045 -0.743 -1.202 -0.516 -0.672 -1.864

Table36.txt

0.676	-0.353	-1.515	-0.502	-1.241	-1.325		
0.835	-0.611	-0.848	-0.308	-0.401	0.013	-0.727	-1.015
0.656	0.080	-1.526	-2.441	-0.887	-1.084	-2.412	
0.010	0.165	-0.178	-0.587	-1.582	0.589		
0.469	-0.668	-1.313	-0.246	-0.635	0.565	-1.285	0.377
0.899	-0.222	-1.533	-3.405	-1.904	-2.806	-2.974	
0.409	0.432	0.061	-0.879	-1.972	-0.006		
0.989	-1.355	-1.202	-0.912	-1.602	1.752	0.839	1.668
-0.390	-0.417	-0.997	-0.317	-1.234	-0.992	-0.001	
0.794	0.580	0.570	-0.427	-0.844	-0.072		
-0.437	0.147	0.982	0.272	-0.181	-0.749	2.828	0.258
-0.788	0.000	-0.467	0.366	-0.866	-0.371	0.173	
-0.809	-0.302	-0.346	0.071	-0.399	0.413		
-1.279	1.113	0.201	1.851	-0.502	0.815	1.437	0.182
-0.217	0.136	0.567	-1.147	-0.954	1.578	-0.619	
0.548	-1.575	-0.635	-1.423	-0.385	-0.315		
-1.027	1.777	0.628	1.938	-0.752	-0.802	1.639	-0.420
-1.972	-0.232	0.853	-1.886	-1.349	1.386	0.362	
1.523	-2.053	0.308	0.410	0.196	1.278		
0.062	1.147	0.641	-0.321	0.941	0.076	1.383	1.533
-2.390	-0.794	-0.210	0.839	0.554	-0.562	-0.437	
0.058	-1.427	0.962	-0.150	-0.883	-0.227		
0.538	-0.197	-0.005	-1.014	-1.364	-0.547	0.214	0.452
0.222	0.257	-2.179	-0.193	-0.186	-1.428	-1.051	
-0.507	0.299	0.393	1.517	0.044	-0.605		
0.358	-1.622	-1.240	-0.178	-1.019	-0.477	1.804	0.169
-0.783	-0.784	-1.726	-1.624	-0.013	-0.774	1.350	
1.488	-0.238	1.089	0.866	0.556	0.042		
0.848	-2.198	-0.565	0.928	-0.809	-0.561	0.176	1.380
0.526	-2.190	-0.901	0.942	-0.198	-1.138	-0.258	
0.008	-0.651	0.008	0.041	-0.477	0.203		
-5.657	0.720	1.397	-6.679	-1.342	4.375	2.400	3.525
-11.000	-11.000	-3.406	-5.472	-7.034	-4.079	0.848	
1.882	11.000	1.199	-3.973	0.911	2.655		
0.864	0.406	-0.010	-0.208	-1.384	-2.348	2.103	-0.103
-0.488	0.107	-0.236	-1.823	-0.079	-0.969	-1.277	
0.862	-1.422	0.106	-0.372	0.493	-0.796		
0.862	-0.588	0.013	1.399	-0.871	-0.610	0.506	-0.913
0.653	0.891	0.721	0.235	0.358	0.426	0.694	
-1.122	-0.439	2.630	0.281	0.398	-1.151		
-1.397	-0.579	-0.208	1.081	0.006	1.074	-0.035	0.665
0.110	-0.490	-0.245	-0.813	-0.743	-1.134	-1.188	
-0.641	1.374	0.522	1.474	0.088	1.006		
-1.397	-3.752	-0.302	1.690	-1.397	0.043	-1.037	0.417
-3.432	-2.028	-1.272	0.068	0.046	0.258	-0.838	
0.742	0.555	0.885	0.981	0.652	-0.155		
0.882	-1.137	-1.320	0.839	-0.440	-3.362	-5.223	5.738
-5.673	-3.719	-2.419	-3.154	-1.369	-2.437	0.213	

Table36.txt

-2.166	-0.250	1.135	1.912	-2.161	-0.172		
-0.139	-0.792	-0.141	-3.096	0.035	0.170	0.689	0.600
2.015	-0.528	-0.780	-1.599	-1.061	-0.704	-1.572	
0.540	0.079	-0.936	-1.587	-0.622	-0.131		
0.601	-0.974	0.501	-0.020	-0.816	-0.048	-0.318	-0.415
0.580	-0.465	-0.922	0.228	0.783	-0.953	-1.497	
0.804	0.937	1.120	0.202	0.122	1.288		
1.810	-0.152	0.385	-1.011	0.617	1.181	-0.860	0.444
0.430	-1.172	-0.671	-1.478	0.629	-1.781	-2.954	
0.298	-0.272	-0.214	-1.035	-1.220	1.100		
1.636	-1.878	-1.270	-1.927	0.187	0.503	-1.159	1.347
-0.528	-0.818	-0.843	0.043	0.940	-1.094	-1.683	
0.598	1.055	0.393	-1.061	-0.879	-0.369		
0.845	-1.158	-1.889	-2.346	-0.794	0.379	-1.788	-0.370
0.279	0.178	-2.120	-1.490	-0.823	-1.955	-2.918	
0.346	0.537	0.016	-0.665	-1.085	-0.603		
-0.229	-0.228	-0.655	-0.774	0.689	0.256	-0.687	1.329
0.792	-0.616	-1.235	0.060	-0.430	-0.259	-2.475	
0.443	0.434	0.841	0.981	-0.645	0.937		
1.341	-1.248	-0.481	0.312	-2.023	0.206	-0.860	1.130
0.231	-1.975	-0.116	0.127	0.352	-0.697	-0.736	
-0.421	0.389	1.103	-1.429	0.077	0.925		
0.261	1.326	-1.829	-0.470	1.017	1.480	-0.345	1.816
-0.804	0.284	-0.967	0.800	-0.190	-0.405	-1.182	
0.461	0.024	0.091	-0.453	0.678	-0.135		
1.307	0.007	0.005	-0.326	-1.617	-0.463	-0.632	0.254
0.815	0.326	-1.709	-0.182	-2.368	-1.485	-1.756	
0.597	0.571	1.010	-0.821	-0.296	-0.509		
0.929	-2.161	-1.616	-2.357	0.358	1.308	-1.886	0.607
0.402	0.581	-2.390	-2.196	-0.647	-2.209	-3.783	
0.391	0.445	0.696	-0.003	-1.729	-0.356		
0.530	-1.544	-0.979	-1.306	-0.390	-1.033	-1.130	-0.365
1.729	0.206	-1.250	-2.338	-1.124	-1.556	-2.311	
1.297	-0.714	0.296	-0.385	-1.719	-0.121		
1.551	-0.292	-0.997	-0.405	0.763	0.672	-0.260	-0.517
2.209	0.915	-1.055	-3.069	-1.236	-1.817	-2.848	
0.379	0.132	0.259	-1.045	-1.529	-1.304		
1.174	-1.411	0.138	0.001	-1.198	-0.950	1.380	-0.980
1.327	-0.231	-1.280	-0.165	0.350	0.208	-0.156	
1.250	0.107	0.616	1.212	-0.555	-1.011		
1.725	0.770	-1.007	-0.172	0.247	0.349	-0.996	0.180
-0.419	0.206	-2.016	-1.933	0.260	-1.783	-1.452	
0.177	-0.745	0.841	1.246	-1.205	0.326		
2.370	-1.077	0.045	-3.332	-0.051	0.989	0.063	7.896
-2.155	-3.886	0.155	-1.836	-2.266	-3.324	-1.259	
0.439	-2.336	2.031	4.211	3.885	3.319		
-1.044	-0.797	-0.873	-0.460	0.800	0.287	0.575	-0.188
0.688	-1.292	0.359	1.715	-0.266	-0.720	0.545	

Table36.txt

1.345	-0.219	-0.141	0.904	1.070	0.705			
0.091	0.978	0.451	-1.165	-0.372	3.722	-0.032	-1.396	
-1.025	0.299	1.397	-1.047	2.259	-0.938	0.195		
0.952	-0.659	-1.608	0.651	-0.360	-0.521			
-0.202	1.244	-0.933	0.240	-0.688	0.007	-0.309	1.300	
-0.944	-0.519	0.397	0.136	0.692	0.889	1.384		
0.781	-1.670	-0.236	-0.646	0.675	-0.188			
-0.132	-0.403	-0.621	-0.876	-1.367	-0.486	1.166	1.107	
1.121	-1.830	-0.232	-1.292	-0.874	-0.960	1.175		
0.162	-0.349	0.310	-0.068	-0.072	-0.194			
-0.414	1.081	1.026	-0.032	0.671	-0.642	0.779	-0.799	
-2.026	-0.920	-0.002	0.372	-0.027	-0.040	1.445		
-0.744	-1.640	1.219	-0.385	0.297	0.206			
0.966	1.443	-0.138	1.488	1.536	0.256	-0.854	0.068	
-0.714	-0.165	0.291	-0.197	-0.539	-1.004	0.762		
1.690	-0.267	0.827	0.989	1.170	-1.305			
4.998	4.863	3.500	4.914	0.911	1.190	-1.743	-4.558	
11.000	-11.000	-3.775	-0.631	0.144	-1.728	-2.065		
-0.494	-1.825	-1.087	-2.670	5.438	5.611			
0.501	-0.326	-1.013	0.170	0.498	0.091	0.698	0.763	
1.446	0.119	-1.808	-1.654	-1.694	-0.678	-0.115		
-0.301	-0.273	0.884	-0.098	0.895	-1.077			
1.321	-2.014	2.489	1.557	-1.795	3.624	-0.383	2.490	
2.504	2.710	-6.839	-5.198	-3.639	-2.927	2.780		
3.902	-4.748	0.441	-0.308	0.599	2.530			
-1.920	2.011	1.127	1.120	-0.582	-0.426	0.346	0.300	
-1.737	1.268	1.848	-1.219	-0.963	0.899	2.739		
-0.650	-1.480	0.266	-1.210	0.855	-0.827			
-0.228	-0.415	-1.808	-0.106	0.476	-0.067	-1.277	-0.166	
0.033	-0.579	-1.445	-1.705	0.309	0.180	-0.880		
0.188	0.484	-1.161	-1.275	0.087	0.698			
-0.137	0.754	-1.155	-0.646	0.089	-0.012	1.927	2.232	
-0.310	-0.187	0.770	-0.840	-1.014	0.062	1.346		
-0.804	-1.438	0.831	0.134	0.434	-0.925			
1.132	-0.244	-1.053	-0.200	-0.499	0.149	0.000	0.068	
0.015	-0.156	-0.492	-0.520	-1.663	-0.903	-1.028		
-0.322	0.236	-0.575	-1.087	0.115	0.398			
-5.616	-2.750	0.527	-4.957	-5.236	1.380	11.000	2.562	
-6.937	1.919	4.730	1.260	-4.779	0.419	1.424		
0.472	1.045	-0.746	-0.637	1.929	1.763			
0.003	-0.571	0.842	-0.137	-0.036	0.020	0.185	0.210	
0.074	-1.140	-0.577	-0.867	0.605	-0.332	0.509		
0.513	-1.011	-0.222	0.978	-1.894	0.742			
-1.096	0.705	-0.354	1.360	-0.608	-0.659	0.763	0.818	
-2.122	-0.010	0.492	-1.386	-1.107	1.024	1.235		
-0.048	-1.774	-1.240	0.803	0.674	0.214			
1.248	-1.688	-0.889	-0.638	1.018	0.236	-1.583	0.327	
1.537	-0.921	-1.247	-0.387	-0.073	-1.662	-1.155		

Table36.txt

1.494	0.442	1.903	0.989	0.062	0.550		
0.241	0.947	-0.839	-1.381	-1.229	-1.324	-0.896	0.310
1.177	-0.153	-1.134	-0.473	-0.651	-0.938	-0.352	
-0.403	-0.739	-0.085	-1.284	-0.578	0.294		
2.138	-0.527	1.450	-1.909	0.794	-0.189	-0.611	-1.488
0.738	0.090	0.161	-1.044	-0.731	-0.218	-0.255	
-1.237	1.864	0.678	0.417	1.138	-0.793		
1.618	-1.260	-0.852	0.080	-0.524	1.059	-1.207	-0.513
0.552	-0.126	-0.270	-0.755	-0.311	-0.600	-0.584	
0.938	-0.173	-2.160	-1.275	0.203	-1.051		
0.052	-2.363	0.514	0.042	-1.279	2.847	0.943	0.717
-0.474	0.631	-2.595	-1.939	-0.526	-2.071	-0.497	
2.472	-0.470	-0.641	0.109	-0.172	1.437		
2.115	-0.909	-0.241	0.861	-1.485	-1.096	-0.295	0.039
0.855	0.923	-0.724	0.286	-1.108	-0.438	0.189	
-0.350	0.086	-1.180	-1.871	-1.574	-0.439		
-0.633	0.936	-1.609	0.165	0.280	-0.424	0.148	-0.881
1.100	0.265	-1.102	-1.406	1.018	-1.531	0.818	
0.369	-0.185	-0.231	0.967	1.747	0.570		
0.223	-1.434	0.010	-0.189	-0.321	0.615	-0.979	0.103
-0.896	0.412	0.668	-1.219	0.446	-1.819	0.398	
-0.584	-1.044	1.379	0.462	-0.546	1.252		
-1.180	-0.496	0.254	1.214	-1.129	-0.325	0.748	-0.382
-0.758	-0.229	-1.019	-1.987	-0.988	0.448	1.480	
-0.353	-1.638	-0.097	0.689	-0.056	-0.726		
1.084	1.271	-0.394	-0.099	0.006	1.436	0.624	-0.436
0.257	-0.940	0.614	0.877	0.213	0.195	-0.289	
-0.046	0.253	0.438	-0.765	1.319	0.684		
0.504	0.544	-0.129	-1.020	-0.278	0.560	0.499	-0.956
-1.158	-2.273	-1.999	-0.094	1.751	-0.777	-1.312	
-0.769	-0.751	1.801	0.443	0.052	0.245		
-1.493	-0.087	-0.178	0.072	-1.082	-0.925	0.042	1.115
-1.235	0.345	1.098	0.261	-0.484	-0.363	0.818	
-0.399	-0.706	-0.819	1.435	0.932	1.084		
1.648	0.538	-0.881	0.256	-2.362	0.645	1.048	1.006
-0.476	-0.695	0.518	1.962	0.443	0.733	0.365	
0.782	-0.978	-0.027	1.545	0.560	0.806		
-0.227	-0.025	0.561	-0.505	-0.616	-0.562	-0.194	-0.626
0.689	-0.142	-1.178	0.340	-0.245	0.088	-1.580	
0.448	0.699	-1.169	-0.784	-0.632	0.440		
-0.122	-1.468	-0.862	-0.716	-0.599	1.903	0.131	0.346
-0.245	0.173	-0.200	0.039	0.026	0.541	-0.011	
-0.810	-0.425	-1.611	1.821	1.619	0.372		
0.353	-0.916	-0.041	0.168	-0.295	-0.742	-0.324	0.796
-0.972	-0.048	1.018	0.192	-0.233	-0.690	0.784	
0.730	-0.037	0.358	0.253	-0.057	-0.601		
1.333	-0.311	1.014	-1.036	0.144	-0.040	-0.590	1.687
-0.263	1.580	0.090	0.590	-0.620	0.726	-0.150	

Table36.txt

0.221	1.537	-0.782	-1.286	-1.283	0.659		
-0.096	-0.295	0.228	0.591	0.721	0.508	-1.129	-0.014
-0.306	-0.154	-0.183	0.721	0.012	-0.886	-1.524	
-1.268	0.528	1.123	1.483	0.746	0.337		
1.040	-1.375	-1.091	0.345	0.492	0.715	0.650	0.396
-0.485	-0.647	-1.778	-0.245	0.426	-1.158	-1.206	
0.508	-1.022	0.134	0.500	-0.226	-0.301		
1.010	1.292	-0.331	0.750	-1.207	0.384	0.637	0.162
-1.225	-0.780	-0.306	-1.868	-0.689	-0.710	-0.776	
-0.752	0.589	2.139	-1.664	0.691	0.176		
-1.039	-0.131	-0.725	2.582	0.452	-1.562	-1.149	-1.708
-0.397	0.374	0.347	-0.623	-0.908	-1.839	0.576	
-0.177	-0.361	-0.285	0.741	-1.671	0.022		
2.180	-0.863	-1.293	0.252	0.371	0.905	0.967	0.030
-0.793	2.299	-0.257	-0.134	0.970	-0.284	-0.223	
0.189	1.189	1.424	0.203	0.925	-2.588		
0.261	0.579	0.183	-1.838	-0.622	1.248	1.879	0.317
1.437	0.527	0.635	-0.892	-0.415	-0.691	0.392	
-0.449	-0.761	0.250	0.163	0.727	-0.502		
-0.953	-1.881	-1.636	-0.321	-0.365	0.490	0.343	0.419
1.044	1.146	-0.182	0.022	0.305	-0.669	-0.902	
-0.345	-0.028	0.109	-1.323	-1.699	-0.067		
-1.334	0.391	0.658	0.699	-0.494	-0.792	-1.356	0.184
0.030	-0.585	0.388	0.976	0.046	0.805	0.284	
-1.689	2.072	-2.015	0.062	0.473	-0.280		
1.572	0.288	0.535	-0.400	1.067	-1.055	-0.121	0.666
-0.378	1.007	-1.231	0.884	-1.098	1.596	-0.104	
-0.253	-0.545	-0.984	0.695	-0.572	-0.846		
0.313	1.949	1.177	0.058	0.747	-0.369	1.515	1.529
-0.252	-0.056	2.148	0.422	0.753	-0.728	0.477	
0.077	-0.947	0.345	-0.259	1.818	-0.332		
0.792	-0.666	-0.553	-0.389	0.086	0.831	-0.958	0.643
1.819	1.391	-1.117	-0.609	-1.172	0.109	-2.354	
1.832	0.733	0.883	0.045	-1.019	0.133		
0.224	-0.207	0.999	-0.495	1.456	0.560	-0.180	0.637
0.540	-0.024	-0.658	0.516	-0.104	-0.300	-0.936	
0.159	0.783	0.898	0.604	0.185	-0.644		
-0.103	1.582	0.254	1.245	-0.510	0.894	1.131	-0.918
-0.608	0.466	-0.097	-2.264	0.009	0.455	1.444	
-1.152	-0.881	1.976	0.235	1.234	0.795		
0.648	-0.317	-2.066	-0.560	0.041	-0.730	-1.140	-0.312
-0.487	0.855	-0.333	0.097	-0.344	-1.016	-1.302	
1.636	1.161	-1.271	-3.156	-0.573	-0.868		
-0.464	-0.390	2.942	-1.976	-1.163	0.808	1.412	-1.202
1.802	0.168	-0.110	-0.028	-1.492	-0.464	0.777	
-1.362	1.311	0.071	-0.331	0.167	-0.076		
-1.098	0.692	-0.906	0.344	-0.832	-0.854	-0.786	0.058
0.580	-0.618	-0.439	0.897	-0.019	0.206	0.283	

Table36.txt

-0.583 -0.015 -0.044 -1.123 0.028 -0.316
-0.577 -2.042 -1.640 -0.288 -0.316 0.016 0.001 0.283
0.768 0.111 -1.347 -1.496 -0.317 -2.949 -1.519
-0.671 1.192 -0.274 0.176 0.000 -0.983
0.963 -0.664 -1.338 -0.848 0.772 0.606 0.497 0.792
1.380 0.379 -1.519 0.495 1.506 -0.494 -0.032
1.143 -2.712 0.192 1.607 -1.263 -0.405
-0.649 -0.409 -0.584 0.141 -0.142 0.301 0.971 0.264
0.433 0.171 -2.150 1.009 -1.029 -0.006 -0.731
0.408 1.420 -1.579 1.174 0.532 -0.719
0.929 0.652 0.075 -0.264 0.930 -0.893 0.707 0.230
-0.692 1.236 0.681 -0.078 0.373 -1.457 2.158
-0.395 0.622 1.226 -1.286 0.154 -0.278
-0.874 0.063 1.360 -2.310 -1.636 -0.624 1.578 -0.003
1.378 -0.466 -0.280 -0.296 -0.603 2.752 0.465
-1.092 0.353 -0.280 0.969 0.677 0.967
0.600 -0.365 -0.303 0.669 -0.550 -0.144 -0.396 -0.932
1.433 0.807 -0.782 -1.375 0.643 -0.253 -1.587
-0.210 0.340 0.921 1.342 0.660 -1.590
-1.934 0.045 -0.744 0.848 0.423 -0.620 0.191 1.943
-0.392 0.566 0.455 -0.457 1.781 0.722 0.918
0.397 0.332 -1.273 -0.383 1.046 1.257
0.603 -0.099 0.022 -0.415 1.522 0.850 -0.003 0.108
0.287 0.164 -1.075 -0.868 0.310 0.594 0.265
-0.064 -1.385 0.109 -0.012 -1.342 1.009
0.096 -0.269 1.927 0.550 0.700 -0.007 -1.210 0.108
-1.335 -0.789 -0.034 0.788 -0.771 -0.051 0.774
0.280 1.162 0.484 1.418 -0.128 0.738
0.024 0.522 -1.174 0.817 0.020 1.548 -0.141 0.798
1.107 -0.654 -0.511 -0.821 0.380 0.623 2.205
-0.200 -0.262 0.790 -0.438 0.089 0.853
0.309 0.606 1.913 -0.495 -0.453 0.576 0.156 0.258
-0.163 -0.183 -0.221 -0.426 0.068 -0.862 -0.030
-0.378 1.020 0.236 -1.489 -2.112 0.040
-0.029 -1.169 1.040 0.838 1.197 0.074 1.001 -0.176
1.478 -0.876 0.056 -1.658 0.087 -0.315 -0.503
0.061 -0.101 0.895 -0.266 -0.984 0.060
-0.757 0.886 0.203 0.450 0.444 0.700 -1.247 0.092
0.153 0.469 -0.388 0.170 1.011 0.418 -0.008
1.482 1.292 -1.969 -1.267 1.219 2.118
1.642 1.520 0.355 0.201 -0.045 1.669 -0.192 -1.076
0.527 0.132 -1.592 -0.010 -1.536 0.920 -1.318
-0.188 -0.822 -0.078 0.486 -0.810 0.602
0.866 1.404 0.055 -0.532 0.479 -0.919 0.302 1.692
-0.380 -0.777 -0.835 0.237 1.339 -1.331 -0.656
-1.121 0.713 -1.416 -1.129 -0.670 -0.358
-1.277 -0.875 0.417 0.294 -0.193 -1.129 -0.410 1.018
2.099 -0.538 1.499 0.102 -1.045 -0.248 -1.285

Table36.txt

-0.135 0.146 -0.505 -0.832 -0.002 -0.394
-0.871 -0.899 0.018 -1.394 1.301 0.451 -1.966 0.202
0.046 -0.573 -0.379 -0.473 -0.580 -0.582 -0.498
0.636 0.029 -1.753 -0.675 -0.537 0.563
-0.681 0.200 0.386 0.124 1.809 -1.108 -0.214 -0.167
1.296 0.280 0.773 0.928 0.051 -0.316 0.840
-0.908 0.173 0.630 0.466 1.304 0.394
-0.722 -0.058 1.457 -0.677 2.715 -1.162 0.379 1.312
0.687 -0.771 1.311 1.236 0.291 0.085 1.008
-0.949 -0.144 -1.244 -0.970 -0.036 0.047
1.222 -0.179 -0.355 -0.514 -0.563 0.236 0.318 1.412
0.760 0.580 -0.699 0.929 -0.779 -1.425 -1.801
-0.690 -0.909 -0.388 0.239 -0.995 0.275
0.749 1.736 1.970 -0.363 -0.258 -1.007 -0.346 0.878
-0.797 -0.417 0.101 0.041 -0.817 -0.140 -1.698
-0.865 -0.485 -0.588 -2.872 0.478 0.649
-0.172 0.529 0.400 1.716 -0.766 0.388 0.788 -0.356
-0.297 -0.145 -0.532 0.281 -0.822 0.538 1.375
2.513 0.278 -0.717 -0.349 1.451 -0.259
0.244 0.413 -0.680 -1.946 -0.649 0.694 0.483 0.799
0.129 1.446 -1.201 1.735 1.900 0.970 -0.263
0.532 0.179 -0.186 1.551 -1.274 2.457
0.488 0.452 0.559 1.851 0.192 -0.574 -1.418 -0.451
-0.034 0.638 0.930 -1.491 -0.489 -1.156 -0.136
-0.682 -0.783 -1.208 -1.026 0.875 -1.383
-0.230 0.515 1.642 0.706 0.265 0.753 0.973 -0.766
0.198 -0.280 0.309 1.097 -0.295 -0.163 -0.070
-1.680 1.151 -1.450 -1.572 1.827 -0.141
-0.539 -1.332 0.108 0.653 -0.532 0.633 1.257 0.080
0.474 0.755 -0.395 1.071 -0.024 1.134 -0.492
-0.366 0.265 -0.255 -0.554 -0.293 -0.488
-1.038 0.408 0.924 0.722 -0.021 1.160 0.257 -0.358
0.239 -0.757 -2.554 0.472 -2.831 -0.221 0.128
1.547 -0.068 -1.724 -0.176 1.889 1.571
1.699 -0.155 -2.474 0.576 -0.100 -0.832 -0.889 -1.235
0.207 0.442 -0.371 0.632 0.522 -1.684 -1.580
0.089 1.300 1.459 -0.582 0.315 -1.078
0.329 -3.045 0.355 0.351 -0.958 -0.699 -0.836 -1.029
0.275 0.676 1.188 0.614 -0.633 0.862 -0.372
0.856 -1.282 1.056 1.018 -0.047 -1.185
-1.335 1.116 0.939 0.757 -0.559 0.096 0.676 -0.195
-0.161 -0.902 -1.453 -0.553 -0.190 1.780 0.864
0.223 -0.355 -0.236 1.330 0.873 1.322
-0.922 1.782 0.010 0.421 0.358 0.445 -0.050 0.348
-0.294 1.739 0.165 -0.618 -0.954 0.684 -0.395
-1.053 -1.622 0.068 0.436 -0.026 0.982
0.529 -2.300 0.293 1.863 1.845 -0.638 1.790 0.093
0.107 0.121 -0.329 0.332 0.313 -0.662 0.114

Table36.txt

0.048	0.723	0.962	-0.547	0.269	-1.200		
1.435	0.306	0.417	0.828	-0.995	-0.144	1.049	0.250
0.065	0.359	0.411	-2.267	-0.704	-0.461	-0.322	
0.962	-1.164	-1.110	-0.568	0.258	0.040		
-0.558	-1.167	-0.865	0.345	-0.740	1.815	-0.466	0.888
0.490	-1.712	-0.809	-0.896	-1.335	-1.044	-0.272	
0.080	2.008	0.608	-2.491	-0.667	-0.165		
1.256	-0.143	-0.142	0.426	0.993	0.796	-0.308	0.210
-1.550	0.459	2.362	-0.614	1.734	-0.245	-1.376	
0.924	1.406	0.778	0.955	0.203	0.102		
-1.487	2.107	1.681	0.005	-0.516	1.029	-0.234	1.195
-1.097	0.399	1.549	0.133	-1.036	-0.140	0.418	
-1.656	0.020	-0.259	1.565	0.112	-0.605		
1.229	-0.566	0.253	-0.819	0.148	0.693	-0.380	-0.081
-0.038	0.041	-1.625	-0.655	0.320	-1.104	-0.660	
-0.051	2.369	-1.270	-0.973	0.985	0.256		
1.457	-1.879	-0.237	-0.216	1.862	0.105	-1.420	0.917
0.505	-0.725	0.090	-0.426	-1.131	-1.806	0.008	
0.305	0.654	0.595	-0.572	-2.449	-2.470		
0.339	-1.446	-1.617	-0.692	0.125	-0.195	-0.336	-1.133
-0.677	-0.823	-1.602	0.773	-1.435	-1.723	-0.418	
-2.154	-0.022	-1.564	-2.600	0.462	-0.257		
-0.491	2.659	0.431	-0.377	-1.633	-0.276	0.250	0.082
-0.458	-2.186	1.179	1.646	0.268	1.273	0.284	
0.926	-1.986	0.001	0.761	0.549	1.597		
-0.476	0.030	0.351	0.365	0.077	0.597	0.776	0.536
0.148	0.527	0.280	0.394	-0.097	1.088	1.778	
1.104	-1.423	0.937	-0.203	0.917	0.165		
-0.936	1.604	0.316	0.217	0.126	-0.779	1.913	0.795
-0.659	0.426	1.188	1.503	-0.172	0.849	1.598	
-1.390	-0.698	1.295	0.100	0.483	-0.119		
0.805	1.038	0.789	-0.058	0.275	0.493	-1.208	0.475
-0.096	0.273	-0.543	-0.329	-0.782	-1.121	-0.091	
-0.315	0.250	-0.071	-0.748	1.410	2.023		
0.343	-0.639	1.465	-0.197	0.417	0.881	-0.113	-0.949
0.390	0.508	0.667	-0.452	1.831	-0.711	0.535	
0.754	-0.078	1.955	1.496	-2.027	-0.677		
0.518	-1.409	0.140	0.250	0.340	0.693	-0.142	-0.624
1.616	-1.185	-0.869	-0.102	-0.034	-0.868	-0.210	
-0.908	2.121	-2.074	0.613	-0.706	-2.043		
0.170	-0.086	-0.840	1.047	0.199	1.007	0.571	0.993
1.133	0.250	-1.400	-1.548	-1.401	-0.102	-0.870	
1.016	-2.303	1.202	-0.392	-0.846	0.577		
1.016	-0.145	0.735	-0.414	0.268	0.987	-0.071	0.298
-0.213	0.053	-0.595	-0.522	0.243	-0.081	0.977	
0.138	-1.410	1.194	0.091	-1.184	0.559		
0.338	2.346	0.973	1.957	0.261	-1.469	0.484	0.237
-0.095	-1.505	1.300	-0.799	-1.154	0.700	1.415	

Table36.txt

-0.340 -1.304 -1.101 1.766 1.148 -0.348
0.150 -2.450 0.120 -0.393 0.620 -0.006 0.519 -0.065
-0.526 0.509 -1.853 0.309 -0.070 0.765 1.216
1.065 -1.262 1.232 1.124 -0.490 -1.018
-0.266 -0.653 -1.347 -0.054 -0.223 0.691 -0.761 0.131
0.012 0.554 0.388 0.554 1.401 0.509 0.720
-0.154 0.449 0.664 -0.282 -0.385 -0.074
-1.535 0.789 -0.355 0.481 0.260 -0.679 0.166 -0.443
-0.892 -0.225 -0.705 -0.313 0.071 -1.638 0.299
0.011 -1.909 -0.807 0.626 0.282 -1.261
-0.003 -0.215 -0.604 -0.975 1.998 0.305 0.017 0.833
1.084 -2.104 0.304 -1.162 -0.869 -0.161 0.464
-1.804 0.970 1.823 0.917 -0.878 -1.872
0.646 2.605 2.212 1.287 0.302 1.020 -0.196 -1.419
-1.195 0.073 2.589 -0.169 0.552 -0.250 1.822
1.553 -0.991 0.285 -0.077 1.182 0.107
-0.178 -0.609 0.361 0.635 1.234 -0.366 0.038 -0.169
0.371 -0.021 -0.731 -1.025 -1.319 -0.713 -0.668
1.169 -0.919 -0.976 -2.053 0.320 -1.006
-0.545 -0.129 -0.218 1.270 -0.154 0.000 0.576 0.186
0.915 1.402 -0.678 0.938 -0.987 0.779 -0.098
-1.102 -0.734 -1.409 -1.237 1.478 -1.390
-1.707 0.036 -0.005 0.465 -0.846 -0.504 0.275 -0.129
0.220 -0.609 -0.511 0.689 -0.390 1.390 -0.868
-0.563 -0.142 -0.033 -0.536 1.019 0.378
0.414 -0.317 -1.036 -0.240 -1.464 -0.036 -0.689 0.961
0.805 1.275 -2.123 -0.484 -0.559 -0.771 -0.703
0.118 0.230 -0.167 0.854 -0.619 -1.209
0.086 -0.032 0.121 -0.175 1.034 1.257 0.582 -0.695
0.027 1.019 1.198 -0.805 0.458 1.092 0.239
-1.165 0.270 0.075 1.125 -0.745 0.992
1.077 1.604 -0.222 -0.874 0.331 0.972 2.094 -0.279
0.037 0.889 0.294 1.854 1.755 0.203 -0.552
-0.962 -0.536 -1.491 -1.238 -0.047 -0.175
-1.065 0.262 -1.299 -0.877 -1.359 -0.062 0.770 -0.838
-0.938 0.898 -1.549 -0.142 -0.443 -1.255 -0.675
0.735 0.518 0.407 -0.653 -0.589 -1.723
-0.719 0.618 -0.609 -0.123 -2.526 -0.451 0.354 0.585
0.649 0.746 -0.709 0.786 -0.239 0.847 0.108
-0.398 0.557 1.225 0.278 1.416 -0.250
-0.665 0.392 1.261 0.465 -0.132 0.597 0.890 0.974
-2.101 -0.044 2.667 1.151 -0.490 -0.995 -0.489
-0.093 0.653 0.602 0.655 0.102 -0.611
-0.844 0.226 0.744 -0.043 0.132 0.842 0.069 -0.494
0.195 0.779 -1.023 -2.405 0.777 0.619 0.881
0.323 -0.518 -1.143 -2.228 -0.997 -0.505
0.372 -0.435 -2.166 -1.339 1.402 0.815 0.432 -0.786
2.532 -0.024 -1.708 0.613 -0.205 1.479 -0.777

Table36.txt

-0.337 1.250 1.144 1.708 -0.546 0.007
-0.249 -0.072 1.488 -0.190 1.596 -0.049 0.502 0.596
-0.847 0.114 0.397 -0.130 1.460 1.096 -0.123
0.161 -0.560 0.901 -0.453 0.782 0.567
-1.565 0.675 -0.488 -0.709 0.263 -0.159 0.662 1.659
0.518 0.929 -0.239 -2.793 -0.287 0.606 -1.431
-0.076 0.654 -0.320 -1.241 -0.926 -0.657
0.799 1.895 -1.298 0.856 -0.545 0.862 -0.784 -0.021
-0.540 0.423 -0.493 -0.799 -0.588 1.137 0.134
1.246 -0.463 -0.083 -0.013 -1.227 0.413
-0.561 -0.326 1.300 0.413 0.514 0.135 -1.028 0.458
-1.438 0.953 0.894 1.070 -0.753 -0.327 -1.663
-1.381 -0.769 -0.923 -0.427 0.557 0.593
2.212 1.617 -0.150 0.677 0.276 -1.352 1.113 0.645
0.299 -0.043 -0.008 -0.549 -0.293 -0.552 1.256
0.097 -0.844 -1.126 0.690 1.776 -0.733
0.778 0.668 -0.122 0.554 0.021 1.152 1.553 -1.311
1.091 -0.726 -0.691 1.047 -0.781 -0.355 0.250
-0.979 -0.664 -0.119 -0.480 -0.419 1.085
0.294 0.237 -0.658 -1.342 1.048 1.411 -0.760 0.476
-0.355 -0.896 -0.962 -0.803 0.957 -1.713 -1.967
-0.176 0.766 1.056 -1.186 -0.421 0.145
0.840 -0.656 0.008 -2.183 1.542 0.972 -0.074 0.315
-0.050 0.155 -0.255 0.573 0.741 -1.225 -1.024
-0.534 -1.320 0.959 -0.398 -0.236 0.847
-2.864 -2.322 -0.644 0.527 3.261 3.104 -0.989 0.991
-3.329 2.171 -4.039 -1.769 -2.228 -1.262 1.061
-0.815 -2.037 -0.253 1.487 -0.290 -1.443
0.549 0.014 -1.076 -0.976 -0.784 1.305 0.681 0.936
-1.471 0.040 -0.858 0.149 0.015 -2.130 0.359
1.431 -1.919 0.195 0.384 0.235 1.172
-0.058 -1.372 -1.024 -1.114 0.837 -1.680 -0.221 -0.367
-0.080 0.477 -1.633 -0.281 0.706 0.071 -0.906
-0.248 -0.759 -0.882 -0.502 -0.789 -0.161
-0.155 1.941 -0.577 0.957 0.790 1.347 0.977 -0.405
-0.827 -0.445 1.867 0.066 -0.685 0.187 0.618
0.064 -0.212 -1.849 0.755 0.511 1.257
0.502 -0.804 0.313 -0.557 0.887 1.288 -0.972 0.907
0.868 -0.713 0.234 -1.179 -0.925 -0.044 -0.257
1.620 -0.346 -0.068 -1.853 -1.152 0.215
-0.246 -0.038 0.049 0.105 0.345 -0.903 0.661 -0.346
-1.351 -0.212 -0.282 -1.378 0.069 0.433 -0.687
0.322 1.086 0.846 0.038 -1.177 -0.099
-0.170 -1.272 -1.506 -0.478 0.704 2.744 -2.624 0.121
0.836 -0.995 -2.613 -2.595 -2.286 -1.749 -1.609
-1.416 -0.035 0.616 -0.678 -1.072 -0.881
-1.036 1.293 -0.135 0.243 1.542 0.418 -1.542 -0.201
-0.143 -0.395 -0.841 0.081 -0.401 -1.121 -1.583

Table36.txt

0.263 1.938 0.269 -0.010 -0.417 0.447
0.514 -1.770 -0.770 0.149 -1.381 2.182 -1.201 -0.512
0.768 0.245 -1.361 -2.688 -1.398 -1.841 -1.409
0.308 2.660 -0.316 1.827 -0.068 0.586
0.306 -0.336 0.079 -0.836 0.639 0.489 0.056 -0.832
-0.760 -0.550 -0.894 -0.061 0.058 -1.770 -0.810
0.571 -0.690 -1.391 0.767 -0.211 0.166
-0.156 1.981 1.024 -0.676 1.253 0.867 -0.572 0.328
-1.777 -1.217 0.083 -0.867 0.716 -0.822 -0.159
-0.075 0.348 0.153 -0.268 -1.252 0.474
0.386 -0.716 0.105 0.466 0.675 2.418 -0.797 -0.284
0.456 -0.747 -0.927 -2.608 -0.974 -1.721 -1.825
1.051 -0.334 0.366 1.322 0.359 -0.154
1.615 0.047 -0.682 -0.365 0.849 2.045 0.901 0.022
-0.346 -0.915 -1.051 -0.251 0.100 0.061 -1.659
-0.285 0.995 0.429 0.826 -1.000 -0.486
-0.989 0.577 -1.526 0.576 -0.335 0.048 0.183 -0.907
-0.430 0.785 -1.178 -0.396 -1.930 -0.570 0.198
0.292 0.696 -0.322 0.853 -1.653 0.010
1.433 -0.252 -0.798 -1.670 0.642 0.933 -1.575 -1.206
-0.286 -0.430 -1.178 0.570 0.020 -0.910 -2.096
0.695 0.870 -0.910 0.855 -0.053 0.431
-0.002 -0.288 -0.095 -0.314 1.655 1.191 -1.539 -0.215
-0.147 0.689 -1.261 -1.047 0.196 -0.912 -0.830
0.046 0.675 0.070 -0.195 -0.404 1.170
0.288 -2.903 -1.138 0.445 -0.128 -0.625 0.492 0.519
-0.370 0.757 -1.467 0.070 0.432 -0.826 -1.686
0.465 -0.309 0.716 -0.938 -1.136 -0.742
0.968 0.591 1.902 -0.966 1.564 0.235 0.035 -0.298
0.205 -0.534 -0.751 -0.863 0.460 -0.838 -1.311
-0.350 -0.196 -0.641 0.194 -0.382 1.027
0.047 0.267 0.040 0.004 1.006 0.391 0.748 -1.729
-0.598 -0.004 -0.446 -2.414 0.311 0.240 0.609
0.490 0.352 -0.103 1.162 -0.362 -0.195
0.379 -0.318 -0.012 0.555 0.790 -0.067 0.671 0.112
1.297 0.420 -0.961 0.792 -0.033 -1.009 -0.917
-0.368 -0.156 -0.132 -0.409 0.112 -0.712
1.684 0.149 -0.578 0.039 0.743 1.625 -0.669 -1.079
-0.887 -0.188 0.012 -0.923 -0.001 -2.197 -1.397
0.127 -0.206 0.734 1.480 -0.150 -0.882
0.503 -2.160 0.069 -0.251 -0.013 -0.245 -0.180 0.375
1.206 -2.937 -2.345 -0.169 -1.385 -1.221 -0.133
0.039 -1.117 -0.600 0.538 -0.302 1.028
-1.458 0.728 0.371 0.389 0.077 0.671 -0.816 -0.088
-0.486 0.334 0.806 -0.921 0.371 0.337 0.732
-0.237 -0.897 -0.252 0.004 0.317 1.296
0.041 -0.661 -1.464 -0.772 0.418 0.973 -1.428 0.292
0.396 -0.068 -1.206 -0.341 0.575 -0.321 -1.028

Table36.txt

-0.508 0.929 0.005 0.228 -0.936 -0.202
1.204 -1.919 -0.347 -0.616 0.224 1.428 -1.363 0.812
0.903 -1.261 -2.343 -1.647 0.764 -1.825 -2.250
0.212 1.574 1.107 -0.935 -0.351 -0.038
1.614 -1.231 -0.538 -0.610 -1.191 -0.137 0.471 -0.099
-0.918 -1.540 0.983 0.636 0.986 -1.387 -1.626
0.842 2.863 -0.098 0.971 0.121 -0.656
1.507 -0.351 -1.513 -0.530 -1.029 0.413 0.778 -0.711
1.803 -1.317 0.165 0.677 -0.149 -1.056 -0.644
-0.135 -0.366 1.558 1.498 0.175 1.595
1.875 0.074 -0.815 -1.378 -1.157 1.025 -0.187 -0.049
1.262 0.432 -1.218 -0.433 -0.252 -2.550 -1.214
0.610 0.882 0.132 0.449 -1.259 -0.212
0.894 -2.187 -1.241 -0.409 0.969 1.552 -1.599 0.637
0.326 0.707 -1.257 -0.589 0.364 -2.457 -2.443
0.891 1.007 -0.554 -1.879 -0.640 0.224
2.175 -0.970 -0.609 -1.091 -0.949 1.584 1.992 -0.624
4.984 -2.664 -2.845 -0.383 -2.117 -2.988 -2.246
-0.154 -0.735 0.350 -1.393 -0.946 -0.048
-1.742 -3.624 -0.954 11.000 2.757 3.571 -3.998 -0.329
11.000 -11.000 -0.710 0.381 1.339 -5.814 -0.172
6.075 -11.000 0.281 11.000 -6.358 11.000
2.349 -1.099 0.595 -0.420 0.080 1.237 -0.500 -1.599
0.738 0.227 -0.751 0.725 1.131 -1.408 -1.814
1.375 0.704 0.308 -0.060 -0.735 -0.744
2.542 -1.891 -1.809 -0.019 0.154 1.323 -0.665 -0.227
0.248 -0.943 -1.088 -0.043 -0.046 -1.721 -2.074
0.416 0.417 0.132 -0.204 -1.134 -0.987
1.603 -0.936 0.124 -1.742 -0.293 -0.756 -0.671 0.951
0.478 0.385 -1.514 -0.801 -0.305 -1.877 -1.432
-0.135 1.221 0.103 -0.710 -0.142 0.147
1.197 -1.160 -1.243 -0.835 -0.372 1.499 -0.283 0.165
0.533 -1.365 -1.832 -1.016 0.283 -3.531 -1.609
1.350 1.918 -0.581 -0.803 -0.945 -0.853
1.927 -2.112 -2.226 -0.675 -1.513 3.020 -0.462 -0.862
0.309 -2.019 -2.712 0.395 0.270 -0.649 -1.691
0.523 0.274 1.027 0.051 -0.518 0.388
0.688 -1.446 -1.426 -1.368 -1.530 0.678 -0.637 -0.051
5.259 0.133 -2.734 -1.896 -0.579 -2.196 -2.654
0.321 0.034 -0.570 0.109 -0.834 0.538
1.596 -1.107 -1.682 -0.062 -0.519 1.140 0.224 0.141
1.170 -0.014 -1.066 -0.738 -0.717 -0.453 -0.456
1.586 0.660 -0.726 -0.275 -0.090 -0.516
1.510 -1.288 -2.242 0.307 -0.666 0.345 -1.364 1.012
0.307 -0.667 -1.233 1.361 0.820 -1.454 -1.070
-0.498 0.652 0.478 1.416 0.368 -0.589
0.531 0.820 -0.387 0.125 -1.212 -0.632 1.592 4.452
-0.599 -0.780 -1.911 0.470 -0.320 -1.386 -1.970

Table36.txt

0.148	0.875	0.321	-1.042	-1.639	-0.329		
1.666	-1.080	0.547	0.101	-0.645	1.308	-0.456	0.008
0.663	0.933	-0.083	-1.535	-0.225	-0.061	-1.413	
-1.582	-0.661	0.267	-0.374	-0.381	-0.364		
0.151	-0.999	0.550	-0.308	-0.142	0.987	0.157	1.339
-0.431	-0.583	-1.457	-0.630	-0.158	-0.820	-0.998	
1.362	0.065	1.104	0.845	-1.305	0.299		
0.809	0.585	-1.037	0.134	-0.089	1.914	-0.672	0.732
-1.429	-0.726	0.213	-0.233	0.863	-1.044	-0.323	
0.137	0.011	-0.912	0.630	-0.261	-1.045		
1.373	-2.046	-2.291	-1.234	0.821	0.110	0.858	0.837
-0.806	-0.697	-1.383	1.190	-0.069	-1.517	-1.508	
0.428	1.112	1.546	1.016	0.231	0.263		
0.368	-1.509	-2.737	-0.788	0.352	1.323	-1.471	0.239
-1.209	-0.037	0.141	0.356	-1.118	-0.839	-0.726	
1.428	0.988	-1.207	-0.065	-1.430	-1.518		
0.082	0.958	-0.148	0.260	0.274	-1.525	0.411	-0.390
-0.578	-0.164	0.456	1.578	-1.619	-0.675	0.509	
1.401	-0.935	0.204	0.417	-0.128	1.713		
-0.787	0.175	0.468	-0.846	0.262	-0.099	-1.057	0.136
-0.039	-0.797	-0.596	1.098	-0.356	-2.266	-0.648	
-0.501	0.348	0.396	-0.069	-1.212	0.692		
0.930	-1.768	-0.595	-0.494	0.741	1.229	-0.574	0.692
-0.590	-1.292	-1.670	-0.723	0.244	-2.036	-1.316	
0.441	1.569	1.477	0.199	0.078	1.292		
5.704	4.670	-5.030	-11.000	1.177	-5.749	0.528	6.293
11.000	-6.880	-6.807	2.598	3.485	1.666	2.413	
-2.943	-11.000	-1.941	-3.242	11.000	11.000		
-0.022	0.864	2.019	0.315	-0.544	-0.212	-0.018	0.279
-0.640	1.155	-0.314	0.117	-0.196	-0.683	0.337	
-1.377	-1.245	0.965	1.336	-0.511	1.153		
0.145	-1.359	0.703	-0.467	0.309	2.233	-0.753	0.575
-1.646	-0.373	-0.182	-0.359	0.803	-0.256	-0.962	
1.036	-0.662	-0.313	-1.622	-1.135	-0.029		
0.025	-1.225	0.861	-1.559	0.782	2.104	-1.118	0.656
0.216	-1.076	-1.801	0.285	0.806	-1.501	-1.784	
0.002	1.261	0.381	0.839	-0.198	0.344		
2.370	-1.058	-1.969	-0.420	-0.267	1.212	-0.759	1.589
-2.497	0.271	-1.695	-0.560	-0.025	-0.605	-1.249	
0.958	1.082	0.863	1.363	-1.238	-0.110		
0.852	-0.067	-1.566	-0.985	-0.026	2.149	-1.758	1.153
-0.406	-1.169	-2.754	-0.837	0.038	-2.352	-2.020	
1.028	0.867	0.392	-0.102	-0.071	0.442		
1.715	-0.570	-0.239	-0.203	-0.298	0.330	0.158	1.171
0.875	-0.958	-1.174	-1.510	-1.674	-1.449	-1.834	
-0.150	0.745	-2.147	-1.350	-0.610	-1.445		
0.699	-2.311	-2.397	-2.090	-0.507	-0.134	-1.658	0.483
2.284	-1.055	-4.104	-1.711	-1.926	-3.819	-4.337	

Table36.txt

-0.106	2.667	-1.546	-3.915	-1.719	-1.447		
-0.145	-1.141	-1.536	-1.401	-0.758	1.972	0.529	-0.125
1.153	0.263	-1.698	-0.530	0.229	-1.342	-3.033	
0.515	1.655	-1.297	1.605	0.714	0.033		
1.399	-1.642	-0.462	-0.084	-1.336	-2.488	0.075	-0.363
2.006	-0.102	0.640	0.000	-0.805	-0.598	-0.377	
0.529	0.430	1.237	1.012	0.601	0.656		
1.098	-0.832	-1.570	-1.440	-1.160	-0.586	-0.529	0.046
1.106	0.037	-1.019	-1.141	-1.306	-0.771	-1.660	
-0.187	0.684	-1.692	-0.365	-0.453	0.304		
0.970	-0.317	-0.888	0.051	1.811	1.907	-1.185	-0.053
0.180	-0.332	-1.914	0.194	-0.465	-1.343	-1.640	
0.056	0.526	-0.229	-0.378	0.167	-0.236		
0.295	-0.844	0.238	-0.472	0.223	1.027	-1.001	0.378
0.325	0.519	-0.484	-0.236	-0.176	-0.888	-2.722	
0.256	-0.891	-0.625	0.140	-0.841	0.857		
1.488	-1.919	-1.903	-1.327	-1.690	-0.370	-0.077	0.476
0.967	-0.508	-1.506	1.225	0.130	-0.656	-1.000	
1.339	0.815	0.912	1.429	-0.054	-0.915		
1.116	-1.409	-0.690	0.838	-0.720	-0.240	-0.278	-0.417
1.145	-0.204	-0.273	-0.784	-0.570	-0.704	0.172	
0.183	0.106	0.820	0.755	0.801	-0.195		
1.869	-0.810	0.105	0.107	-0.299	-0.066	-0.076	-0.180
1.891	0.224	0.281	0.244	-1.144	-0.776	-1.251	
0.226	0.548	0.729	0.334	1.173	-0.143		
1.534	0.047	-0.802	-1.364	-0.878	0.467	-1.192	-0.043
0.949	-0.618	-3.347	-1.599	-0.351	-1.658	-3.427	
1.068	0.844	0.522	0.463	-1.725	-0.315		
2.333	-0.819	-1.634	-0.993	-1.693	-0.087	0.160	-0.829
0.126	0.511	0.068	-0.269	-0.561	-1.916	-1.731	
1.744	0.908	-0.517	-0.754	-0.608	-0.878		
0.280	-0.985	-0.049	0.489	-1.716	-1.328	-0.318	-0.155
1.525	-0.695	-1.901	-1.400	-1.144	-0.576	-1.593	
0.459	0.584	-0.683	-2.732	-0.544	-0.599		
0.336	-0.988	0.930	0.374	-1.222	0.028	-0.930	0.332
0.344	0.097	-0.582	0.030	0.280	1.676	-1.423	
1.148	0.083	-0.048	-2.479	-0.256	-0.487		
1.487	-0.894	0.518	-0.079	-0.751	1.113	-0.090	0.253
1.009	0.171	-0.583	0.763	-0.227	-0.430	-1.569	
0.417	0.010	0.517	-0.590	-0.113	0.091		
3.213	-1.855	-0.505	-0.855	-0.823	1.813	-0.549	0.940
-0.609	-0.663	-1.008	0.219	-0.471	-0.720	-1.703	
2.676	1.267	0.060	-0.681	0.266	0.641		
1.630	-2.536	0.266	0.835	-1.337	-0.700	-0.633	1.265
1.701	-0.285	-0.854	-0.216	-0.012	-0.476	-1.248	
1.579	0.438	0.223	-1.368	-1.100	0.698		
-0.643	-0.253	0.680	1.423	-2.090	-2.375	1.466	-0.078
2.156	-0.367	0.453	2.318	-0.077	2.085	-0.064	

Table36.txt

1.427	-0.216	-0.349	-1.055	1.063	0.277		
1.583	-1.070	1.214	-0.713	-0.042	1.454	-0.500	-0.518
1.216	-0.767	-1.726	-1.055	0.743	-1.466	-1.540	
0.772	0.741	0.199	0.053	-0.692	0.546		
-0.294	-0.919	0.063	-0.330	-2.249	0.761	0.499	0.189
1.552	-0.095	0.498	-1.927	-0.665	-0.659	-0.033	
0.526	1.011	0.475	0.540	-0.670	0.336		
-0.031	-0.755	0.529	0.863	0.409	-0.224	1.190	0.002
0.679	-0.746	0.332	0.415	-0.463	0.664	-1.427	
1.671	0.826	0.662	-0.975	-0.815	0.604		
0.767	-1.011	0.457	0.884	-2.018	-0.620	1.650	0.204
0.869	0.659	0.578	1.073	0.988	0.760	-0.575	
0.812	1.336	-0.103	-0.517	1.495	0.219		
0.029	0.879	-0.859	-0.159	-0.592	2.023	3.180	1.206
-1.145	-0.444	-1.200	0.141	-0.555	-1.208	-2.171	
1.028	-0.202	-0.393	0.402	-0.405	0.851		
-0.639	0.501	0.868	0.372	-1.467	1.195	1.775	0.322
-1.177	-0.802	1.044	0.464	-0.156	0.291	0.312	
-0.403	0.342	-0.597	1.359	0.232	1.548		
-0.359	-1.432	-0.420	-1.060	-0.861	1.065	-0.907	-0.431
0.954	-1.502	-0.220	-0.227	-0.185	-0.321	-0.175	
-0.752	1.506	0.725	-1.434	-0.036	0.306		
0.276	-2.448	-0.961	-0.507	1.078	1.871	-0.436	-0.223
0.516	0.017	-0.146	-0.657	0.237	-1.242	-1.421	
-0.598	-0.663	0.133	-0.117	-1.795	-0.773		
-0.076	-0.281	-1.227	-0.868	1.702	0.252	-0.922	0.695
0.356	1.031	-1.216	-0.353	-0.806	-1.526	-0.882	
-0.073	0.827	0.603	0.464	-0.738	0.307		
-0.801	0.840	-0.770	-1.352	0.301	0.397	-0.018	0.039
0.396	-1.082	0.730	0.610	-0.247	-0.915	-1.787	
0.093	-0.916	0.698	0.373	0.717	0.359		
-0.120	-1.297	-1.354	0.602	-0.514	-0.156	-1.412	0.612
-0.196	1.683	0.099	-1.819	0.657	1.072	1.355	
0.993	0.068	0.267	-0.604	0.103	0.592		
0.575	-1.296	-0.576	0.211	-0.595	-0.798	0.404	-0.316
0.041	-0.352	-0.115	-0.782	0.217	-0.556	0.768	
0.164	0.057	0.434	-1.634	0.062	0.727		
0.956	-1.015	-0.614	-2.117	1.230	1.219	-1.705	0.195
0.613	-1.087	-2.131	-1.263	0.395	-1.682	-1.738	
0.524	0.953	0.309	-0.571	-0.028	-0.052		
0.265	-0.762	-0.502	-1.500	0.747	0.695	-2.443	0.568
0.274	-0.049	-1.017	0.001	0.539	-1.882	-0.851	
0.588	1.782	0.149	-0.491	-1.409	-0.346		
1.442	-0.152	-0.409	-1.969	-0.387	0.563	-2.500	0.216
-0.550	0.704	-0.671	-1.748	0.046	-1.036	-0.672	
1.367	0.772	-0.074	0.427	-0.404	0.854		
11.000	-0.034	-0.814	-3.122	1.179	-1.401	1.738	2.053
-6.390	-0.299	-1.814	-0.823	-1.061	-4.220	-0.377	

Table36.txt

-0.730	-3.381	0.991	0.974	3.346	2.039		
0.513	-0.238	-1.927	-0.961	0.239	0.999	-0.340	0.310
-0.602	-0.653	-2.074	-0.706	0.785	-1.279	-1.300	
1.137	1.151	0.480	-0.977	-0.990	0.168		
-1.626	-2.498	-11.000	-3.997	-3.305	-3.881	3.114	5.185
11.000	2.468	-4.416	1.179	-0.678	-5.444	2.150	
-4.330	-11.000	-0.788	-0.154	-7.034	11.000		
1.024	-1.971	0.180	0.988	-0.688	0.638	0.571	-1.182
2.097	-1.841	-0.925	-0.784	-1.142	-0.270	-1.213	
0.598	-0.455	0.887	1.375	-0.674	-0.246		
-0.475	-0.807	-0.016	0.487	-0.385	1.477	-0.754	-1.602
0.083	0.747	-0.783	-1.104	0.421	-0.241	-1.700	
0.366	1.073	0.513	0.021	-0.184	-0.173		
0.246	-0.844	-1.952	-0.921	-1.088	1.091	0.628	0.031
1.339	0.425	-1.031	-0.009	0.666	-3.172	-1.406	
0.527	-0.348	0.407	2.702	-0.682	0.547		
1.937	-0.500	-1.352	-0.846	1.833	0.658	-1.200	-0.211
-1.351	-0.359	0.329	-1.749	0.803	-1.494	-0.112	
-0.129	-0.015	-1.220	0.113	0.967	0.375		
-0.001	3.839	-0.418	-0.406	1.290	1.093	0.067	1.337
-1.534	-0.998	-0.570	-0.950	-0.251	-0.480	-1.465	
-0.436	0.725	-1.259	-2.553	-1.188	-0.039		
-0.465	-0.076	-0.385	0.149	-0.132	-0.569	-0.294	0.210
-0.938	-0.446	-1.788	0.012	-0.683	-0.064	-1.399	
-0.427	-0.482	-1.201	0.339	-0.634	0.426		
2.060	-0.038	-1.241	-0.954	-0.592	-0.861	0.481	1.645
0.131	-0.667	-1.014	-1.968	0.139	-2.934	-2.881	
0.353	0.263	-1.122	-0.858	-0.330	-1.377		
0.189	-1.114	-0.512	-0.078	0.728	1.767	-0.742	1.602
-0.443	-0.447	-0.713	-1.325	-0.488	-1.203	-1.281	
-1.521	0.200	0.267	0.583	-0.590	-0.655		
-0.747	-0.178	-0.078	-0.801	0.555	2.263	-0.830	0.177
0.252	0.260	-1.342	-1.425	0.934	-1.256	-1.332	
0.297	-0.258	-0.464	-1.409	-0.476	-0.284		
-0.817	-2.493	0.184	-0.782	0.752	0.803	0.211	0.081
-3.452	-0.632	-0.048	-0.252	-0.672	-2.320	-3.229	
-1.260	0.587	1.063	-0.294	-1.153	1.224		
-0.842	-1.681	-0.183	1.152	-1.414	2.113	-2.063	1.054
-1.140	0.795	-0.952	-2.330	-0.983	-1.927	-2.128	
-1.502	-3.894	0.708	1.839	-0.668	0.537		
1.436	0.642	-0.432	-1.743	1.137	0.578	0.067	0.748
11.000	-5.803	-5.096	-1.116	0.547	-4.523	-1.479	
-5.571	-11.000	-0.875	7.406	11.000	7.505		
0.747	-3.769	-0.181	1.230	0.204	0.181	-0.997	0.710
1.010	1.134	-0.685	-0.872	-1.392	-1.106	-0.425	
-0.406	0.276	-0.782	1.036	-0.755	-0.268		
-0.282	-1.128	1.544	1.252	0.805	1.520	0.560	-0.648
-1.480	-1.362	-0.618	-1.661	-1.072	-0.371	0.169	

Table36.txt

0.350 -1.405 0.511 -0.697 0.445 1.310
-0.823 0.533 -0.375 0.477 0.227 1.089 -0.247 -0.696
-0.168 -0.664 0.848 -0.908 0.751 0.360 -0.319
-1.837 -2.223 0.034 -0.390 -1.262 1.163
-0.040 -1.492 0.159 -0.014 0.937 1.043 -1.604 -0.332
1.357 0.695 -1.498 -1.484 0.443 -1.453 -0.621
-0.785 0.357 0.106 0.236 -0.112 -0.796
0.694 0.506 0.515 1.754 0.147 1.306 -0.447 -0.679
0.306 -1.057 -0.294 -0.287 -0.768 -1.297 -0.008
-0.013 -0.168 -0.434 0.868 -1.993 0.616
-0.315 -0.207 0.716 0.406 -0.102 -0.270 0.511 -0.188
-0.096 -0.686 0.317 -0.805 -0.846 -0.747 -1.152
2.544 0.512 -0.503 -0.509 -0.843 -0.574
0.268 1.208 0.409 -0.104 1.427 0.679 -0.334 -0.444
0.417 0.019 -0.432 0.621 2.063 -0.527 -0.923
-0.855 -0.170 0.332 0.682 -0.802 0.737
-0.133 -0.659 -0.649 -1.364 0.743 1.834 -1.862 -0.217
0.408 0.343 -1.538 -0.115 -0.027 -1.736 -1.606
-0.039 0.904 0.160 -0.933 -2.390 0.855
0.819 -0.148 -1.072 -1.397 0.294 0.984 -0.592 0.287
-0.272 -0.468 -1.720 -1.476 1.890 -1.385 -1.629
-0.735 -0.638 0.952 0.138 -2.537 0.073
0.563 0.328 0.408 -0.956 0.202 1.810 -0.702 -0.704
0.402 -0.839 -0.684 -0.586 -0.352 -1.900 -1.750
-0.688 -0.878 -0.575 0.857 -1.366 0.104
1.042 -0.680 -0.946 -1.132 0.229 0.333 -0.675 2.264
-0.744 -0.304 -1.871 0.118 1.250 0.348 -1.077
1.701 -0.121 0.340 0.659 -0.359 -0.363
-1.055 0.047 -0.159 1.187 1.156 0.366 -1.063 -0.056
-2.620 -1.034 0.225 -0.185 0.926 0.099 0.379
0.049 -0.007 0.546 0.687 -0.808 1.307
2.389 -0.688 -0.847 0.213 0.593 0.574 -0.679 2.009
0.674 0.933 -1.255 -0.816 -0.093 -0.600 0.313
-0.518 0.406 0.271 -0.277 -1.608 -1.278
-1.167 1.466 0.384 1.790 0.247 0.109 0.244 0.127
-0.988 -0.326 -0.460 -0.133 0.736 -1.000 0.792
0.649 -2.502 0.423 -0.706 0.401 1.136
-0.936 0.270 0.679 -0.419 -0.255 2.038 0.014 0.759
-1.411 -0.761 0.156 -1.088 1.077 -1.224 -0.119
0.405 -1.492 -0.185 1.290 -1.392 1.611
-1.213 2.146 0.509 0.835 0.406 1.604 -0.776 -1.486
-1.610 -0.594 0.176 1.048 -0.424 0.044 0.282
0.327 -1.905 -1.178 0.322 0.994 1.615
0.286 -1.132 -1.835 -0.514 0.806 1.354 -0.822 -0.905
-0.946 0.466 -0.684 -1.228 0.751 -1.739 -1.161
-0.475 0.779 -0.587 0.377 -1.673 -1.040
-0.123 0.362 -0.195 0.946 0.217 1.082 0.526 -0.958
-0.264 -0.737 -1.091 -0.740 0.923 -1.338 -1.501

Table36.txt

-0.223 -1.441 -0.066 0.577 -1.206 1.418
0.523 -1.214 -0.055 -1.124 1.047 1.180 0.282 -0.362
-1.111 -0.314 -0.330 0.666 0.526 -0.749 -0.069
-1.705 -0.072 -0.343 -0.254 -1.036 1.123
-0.831 -0.963 -1.086 -0.997 -0.094 0.384 -1.692 -0.120
0.375 -0.503 -1.012 0.275 0.301 -0.865 -0.019
0.918 0.105 -0.094 -0.384 -0.165 0.171
0.640 -2.131 0.511 -1.727 1.510 1.370 -0.882 0.635
-0.012 -0.946 -0.612 0.022 0.767 -2.245 -0.803
0.482 -0.019 1.763 1.710 -1.556 -0.868
2.649 -1.211 -1.653 0.084 1.378 0.270 -0.986 -0.611
1.183 -1.675 -2.555 0.075 -0.522 -2.652 -2.431
0.407 0.869 0.072 -0.491 -2.090 -1.084
2.066 -0.061 -1.397 -1.749 0.186 1.939 -0.640 0.437
0.559 -0.631 -1.867 -0.756 0.792 -1.808 -2.464
0.199 0.932 1.295 -0.290 -0.863 0.221
1.802 -1.046 -2.208 -1.976 0.560 0.711 -2.161 0.175
1.182 -1.521 -2.532 -0.348 -1.148 -2.618 -1.835
1.263 1.097 -0.109 -0.381 -0.740 -0.914
1.037 -0.982 -1.046 -1.034 1.299 1.476 -1.610 0.295
0.090 -0.155 -2.683 0.282 -0.144 -2.785 -3.382
-0.126 1.134 0.578 -1.310 -1.329 -0.692
2.529 -0.398 -1.282 -2.146 1.743 2.217 -1.463 0.185
-0.136 -0.683 -2.212 -0.615 -0.141 -1.534 -2.184
-0.360 0.025 0.600 -0.571 -0.647 -0.554
1.982 -1.397 -0.363 -1.633 0.685 2.107 -1.921 0.304
0.828 0.436 -1.846 -0.550 0.079 -1.767 -2.338
-0.693 0.003 1.143 1.658 -0.475 -0.368
1.303 -2.528 -1.655 -1.105 1.309 1.153 -1.654 0.012
0.207 -0.965 -1.540 -0.191 0.597 -1.933 -1.682
0.251 0.504 0.303 -0.460 -1.303 -0.256
1.290 -2.410 -1.994 -0.766 0.400 0.888 -1.190 0.194
-0.095 -0.152 -3.207 -0.100 -0.209 -3.049 -1.780
-0.189 1.203 0.833 0.276 -1.328 -0.586
3.189 -1.216 -0.900 -1.562 1.038 0.754 -0.879 0.445
-0.376 -0.646 -1.735 -1.414 0.055 -2.368 -1.937
0.370 0.798 0.261 0.280 -0.291 0.333
1.278 -1.701 -1.359 -0.616 -0.240 1.106 -0.754 1.209
0.104 -0.148 -3.835 -0.033 -0.213 -2.047 -1.506
1.114 0.314 0.465 0.637 -0.920 -0.680
0.507 -0.045 -1.699 -3.010 0.052 0.417 -1.364 0.025
-1.233 -1.506 -2.779 -0.957 -0.137 -1.596 -1.835
0.185 0.254 1.144 1.283 0.019 -0.137
0.113 0.449 -0.189 -0.775 -0.004 -0.364 0.350 -0.177
0.931 -1.880 -0.743 1.447 -0.476 0.215 1.449
-1.712 0.383 -0.395 -0.397 -0.174 -1.649
0.251 0.947 1.463 -1.749 -1.868 -0.433 0.621 1.637
0.193 -0.372 0.296 -0.305 0.474 -0.221 -0.462

Table36.txt

-0.541 1.611 0.140 -0.816 -1.119 0.236
0.748 -1.934 -1.362 0.576 0.073 0.778 -1.381 0.694
0.031 0.871 -2.940 1.745 0.182 -0.521 -1.671
-0.041 -0.060 0.505 0.585 0.208 0.654
1.327 -0.280 -1.486 2.234 -0.549 0.351 -1.533 0.393
0.952 -0.129 -1.513 0.134 -0.260 0.180 -1.380
-1.042 -0.876 1.505 0.574 0.832 0.731
0.390 -0.971 -0.189 -0.532 0.261 0.349 0.655 1.212
1.548 0.487 -0.112 1.658 0.550 1.393 0.294
1.697 0.182 0.149 1.417 -1.325 0.374
-0.083 -0.599 0.164 0.182 0.834 -0.369 1.223 1.452
-0.216 0.265 -1.110 0.547 -0.029 1.780 1.024
-0.322 0.889 -1.724 1.194 0.052 1.362
0.583 -1.037 -0.176 -0.821 -0.065 0.135 0.455 0.723
1.735 0.178 -0.605 0.507 -0.265 -0.270 -1.168
-0.274 -0.801 1.080 0.112 -0.483 0.570
0.545 0.691 -0.118 -0.517 -0.086 -0.083 1.056 -0.092
1.108 -0.025 -0.339 0.133 0.796 0.311 0.934
-0.130 -1.002 -0.044 0.504 -0.501 0.768
0.891 1.184 -0.285 1.479 -0.819 -1.425 0.554 -0.029
-2.362 1.988 1.536 0.206 0.373 1.144 0.654
0.111 -1.046 0.624 0.214 1.051 0.086
-0.475 2.103 0.957 0.465 -0.669 -1.707 1.437 0.202
-0.785 1.038 1.920 1.696 0.885 1.643 2.086
-0.526 -0.763 -0.779 -0.641 1.971 1.227
0.453 1.086 0.319 2.239 -1.703 0.177 1.065 -0.959
1.523 -0.764 0.991 -0.090 -2.273 -0.265 -0.432
-1.544 -0.606 1.006 1.472 0.055 -0.432
0.071 1.531 -0.185 0.394 0.230 0.961 -0.681 -0.008
0.030 -0.203 0.049 -0.650 0.581 -0.729 -0.739
0.301 -0.806 0.457 0.843 -0.491 0.496
-1.781 1.263 1.004 2.128 0.336 2.013 1.090 1.249
-0.640 0.194 0.359 2.937 -0.208 0.819 0.617
-0.095 -0.499 -0.263 0.801 0.510 0.695
0.699 -0.965 -0.237 0.370 -0.319 0.542 0.571 1.780
-0.124 0.127 -0.859 -0.593 -0.944 -0.025 0.457
-0.059 0.206 1.746 -0.138 -1.496 -1.069
0.468 1.097 -0.362 -1.198 1.070 0.392 -0.842 1.390
0.107 0.809 -1.653 0.402 0.424 0.475 -0.511
-0.944 0.645 -0.402 -0.251 -0.950 -1.213
-0.267 0.944 0.257 -0.799 1.953 -0.531 -0.919 0.204
0.246 -0.837 -0.506 -0.600 0.236 -1.433 -0.763
-0.326 -0.216 1.317 -0.530 -0.172 -1.516
-0.538 -0.324 0.344 -1.492 0.168 0.158 -0.950 -1.425
0.041 0.453 -0.240 0.535 1.174 -1.049 -1.399
-0.565 0.119 -1.284 1.792 -0.787 1.125
0.652 -0.002 0.613 0.387 -0.354 -1.792 -0.230 -2.500
1.521 -0.321 -0.308 -0.206 0.865 -0.474 0.455

Table36.txt

-0.070 0.608 0.136 -0.842 -0.529 0.430
-0.023 -1.233 -0.722 -0.108 0.644 -0.934 0.866 -0.586
1.749 -0.438 -1.236 0.072 -2.195 -0.368 -1.890
0.770 -0.313 -0.258 1.054 0.868 -0.013
0.582 0.465 0.574 0.787 0.820 -0.533 -0.050 -1.240
1.594 -1.592 -1.891 0.073 -1.936 -0.980 0.470
0.580 1.538 -0.361 0.445 0.270 0.397
0.632 -0.220 1.165 -1.701 1.276 0.977 -0.115 0.416
0.746 -0.080 -1.497 -1.021 0.489 -1.567 -2.072
-0.424 1.236 0.710 0.417 -1.777 -0.849
-0.116 -0.030 0.201 -1.353 0.263 0.794 -0.843 0.033
0.818 -0.593 -1.398 -1.574 0.548 -1.209 -1.190
-0.140 0.544 0.590 0.097 -1.584 -1.168
2.657 -1.077 -1.508 -1.781 -0.388 0.014 -0.816 -0.050
1.531 1.139 -1.480 0.699 0.021 -0.822 -1.893
0.407 0.795 -0.350 1.003 0.874 -1.358
1.831 -0.499 -1.296 -1.323 -0.797 0.837 0.173 -0.679
0.433 0.649 -0.026 1.310 0.146 -1.044 -0.562
0.277 0.431 -0.087 0.115 0.538 -0.418
-0.732 0.058 -0.763 0.409 0.353 1.251 -0.584 0.529
-0.576 -1.262 -0.534 1.084 0.510 -0.693 -0.199
-1.129 -0.213 -0.482 1.965 0.481 0.080
0.396 0.041 0.925 -2.097 0.467 1.344 -1.449 -0.146
-0.842 -0.222 -2.114 0.118 0.822 -0.149 -1.744
-0.459 1.127 0.317 -0.561 0.165 0.283
-0.071 -0.186 -0.596 0.302 -0.272 -0.432 0.679 0.202
0.493 0.141 -1.453 -0.068 0.371 -0.416 -1.123
1.119 0.078 0.550 0.536 1.070 -2.072
-0.110 -0.489 0.520 0.443 0.257 -0.888 0.213 0.714
-0.197 0.737 -0.493 -0.075 0.550 0.448 -0.002
-0.291 -0.478 -0.299 0.519 1.287 -0.423
0.481 -1.325 -1.564 -1.832 0.383 -0.220 0.726 0.371
2.479 -0.138 0.474 -1.623 -0.638 0.132 0.237
-0.328 0.080 0.712 0.508 -0.940 -0.454
0.877 -1.634 0.251 -0.010 0.754 0.296 -1.964 0.795
-0.067 0.324 -2.608 -0.520 -0.612 -1.169 -1.353
1.199 0.169 -0.432 0.374 -0.395 0.030
0.580 -1.618 -0.004 0.019 1.348 0.627 -0.616 0.502
0.039 -1.614 -2.735 -0.038 -0.301 -1.738 -1.185
0.840 -0.642 -0.580 -0.027 -0.423 -11.000
1.026 -0.619 -0.189 -0.690 0.324 0.843 0.531 0.922
1.099 -0.769 -0.835 -1.278 -0.343 -0.567 -0.328
-1.037 -0.590 0.484 -0.056 -1.085 -0.014
-0.374 -1.679 0.213 -0.548 -0.785 0.824 0.784 0.002
0.306 1.207 -0.517 -1.988 -1.361 -0.899 0.225
-0.143 1.039 -1.744 -0.025 -1.386 -0.978
-0.651 0.030 0.167 -1.780 0.619 1.013 -1.329 0.027
0.067 0.710 -0.820 -0.542 -1.186 0.946 -0.583

Table36.txt

0.935	-1.888	-0.457	-0.660	0.006	-0.896		
0.314	-1.902	-0.708	0.404	0.603	1.265	-1.030	1.218
-0.462	0.754	-2.060	-1.406	-0.277	-1.247	-1.473	
-0.237	0.323	0.777	-0.110	0.531	-0.977		
-0.304	-0.528	-1.798	-0.288	-1.596	0.486	-0.187	0.709
0.584	-0.300	-1.936	-1.482	-0.679	-1.628	-1.976	
0.833	-0.581	1.656	-1.542	-0.319	0.053		
-0.073	-1.390	-0.855	-1.517	0.008	-0.160	1.366	-0.084
0.920	-0.087	-2.035	-1.869	-0.957	-1.165	-0.194	
-1.364	0.190	-0.617	-0.953	-0.158	-1.320		
-0.020	1.862	0.313	-0.706	-0.160	1.045	-1.321	1.283
-1.742	-0.890	-1.468	-1.593	-0.142	-1.010	-1.285	
-0.882	0.057	-0.399	-0.009	-1.055	0.397		
0.580	0.320	-1.250	-0.412	0.973	-0.912	-1.041	-0.618
-0.535	0.276	-1.809	-1.122	-0.255	-1.910	-1.796	
-0.625	0.671	-0.690	-0.429	-0.702	0.647		
-1.420	-0.137	0.884	-1.303	0.856	0.379	0.417	0.772
-0.956	-0.142	0.206	0.444	0.142	-0.623	0.007	
1.697	-0.945	0.702	1.756	0.381	0.792		
0.665	-1.011	-1.624	0.175	-0.435	-1.251	-0.398	0.733
0.987	-0.304	-2.496	-1.140	-1.069	-0.905	-0.259	
0.726	-0.448	0.650	-1.054	-0.485	-1.146		
0.096	-1.055	-2.058	-1.402	-0.992	-1.619	1.010	-0.530
0.736	0.816	-1.334	-2.574	-0.138	-0.186	-0.354	
0.110	0.127	0.561	1.707	-1.070	-1.487		
-1.248	-1.357	-0.552	-1.343	1.954	-0.615	0.063	-0.190
-1.216	0.686	-2.266	-1.288	-0.246	-0.599	0.408	
-0.855	0.006	-1.006	-0.410	0.074	-0.600		
1.707	-1.483	-1.456	0.032	-0.568	0.879	-0.370	2.217
-0.689	0.371	-0.473	0.454	-1.006	-0.494	-0.466	
-0.611	-0.257	0.021	0.592	0.412	0.340		
0.004	0.968	0.237	0.814	0.014	1.286	0.882	1.661
-0.344	0.118	0.380	-0.111	-1.101	1.530	0.901	
0.990	-2.424	-0.699	0.071	-1.397	0.158		
-0.797	-1.928	-0.942	-0.730	0.460	-0.410	2.715	-0.273
1.065	-0.171	-0.808	-3.055	-0.230	0.326	-0.586	
0.380	-1.247	2.148	0.637	-1.830	-1.048		
0.798	0.132	0.741	-0.747	-1.823	-2.222	-1.066	0.662
1.412	-0.212	-1.895	-0.556	-0.345	-0.781	-0.819	
0.904	0.132	1.146	-1.475	-0.284	-0.465		
1.862	-0.758	-0.351	-1.012	1.204	1.924	-0.400	0.925
-0.829	-0.492	-1.406	-1.552	-1.792	-0.308	-2.012	
-0.055	-0.180	1.216	-1.094	-0.540	-0.826		
0.191	-0.300	-0.062	-1.753	0.960	-0.510	0.278	1.418
0.638	-0.216	-0.512	-0.429	-1.743	0.643	-0.121	
-0.184	-0.073	1.551	0.944	-1.224	0.653		
1.170	-0.681	0.503	-1.009	-0.333	0.769	-1.460	-0.049
-1.429	0.118	-1.422	-1.140	-0.271	0.194	-0.856	

Table36.txt

0.975	-1.337	0.881	0.931	-1.780	0.084		
0.985	-0.047	-0.059	-0.222	0.279	-1.375	0.244	0.940
0.474	0.850	-1.687	-3.168	-0.223	1.104	-0.285	
-0.444	0.641	0.264	-0.616	0.523	-0.043		
0.383	0.577	-1.309	-0.167	0.275	-1.479	-0.702	0.475
-0.526	-0.547	0.053	-1.897	-0.108	-0.559	-0.562	
0.622	-0.640	-2.287	-0.462	-0.238	-0.018		
1.246	-1.527	-0.991	-0.655	0.679	0.292	-1.823	0.862
0.256	0.659	-2.608	-1.029	-1.202	-1.676	-2.205	
0.448	0.552	0.130	-0.742	-1.664	0.266		
0.557	-0.903	-0.843	-0.795	1.014	0.681	-2.166	0.653
-0.726	0.099	-2.854	-0.881	-0.357	-2.005	-2.152	
-0.583	0.252	-0.267	-1.616	-0.488	0.321		
0.778	0.352	-0.416	-1.888	0.151	0.638	-0.960	0.963
0.432	-0.611	-2.207	-0.647	-0.695	-0.889	-2.773	
-0.290	-0.052	0.385	-2.063	-1.413	0.291		
-0.011	0.764	-1.795	-1.648	1.283	-0.702	-1.638	1.745
1.264	0.024	-1.368	-2.471	-0.012	-1.240	-1.639	
0.067	0.236	-0.485	-0.009	-0.862	-2.006		
0.637	-0.216	-0.752	-0.357	1.886	2.123	-1.885	0.815
-1.943	-0.255	-1.335	1.052	1.203	-2.024	-1.427	
0.197	1.574	0.437	0.175	-0.707	-0.264		
-0.127	-1.589	-0.375	0.479	0.417	-1.728	-0.472	0.665
0.071	0.611	-0.430	-1.115	-0.252	-1.148	0.731	
-0.146	-0.020	0.497	0.172	-0.007	1.534		
1.170	-2.086	-1.051	-1.591	2.146	1.244	-1.739	0.153
-0.280	-0.467	-2.594	-1.448	-0.575	-1.918	-1.605	
-0.430	-0.164	-0.170	-0.517	-0.288	-0.568		
-0.947	-0.254	-1.392	-0.217	2.118	0.009	0.151	-1.390
0.206	0.354	-1.618	-0.945	-0.240	-0.829	1.428	
1.168	0.457	-0.926	-2.556	0.446	-0.178		
2.706	0.366	0.334	-1.126	-0.688	-0.596	0.296	1.150
0.301	0.145	-2.476	-1.143	-0.615	-0.634	-0.331	
-0.855	1.106	0.308	-0.906	0.364	-1.405		
-1.242	1.395	-0.784	0.571	-0.095	1.214	-0.850	-0.450
0.209	0.627	0.448	0.710	-0.298	-0.447	-0.155	
0.494	0.588	-0.896	-1.958	0.311	-0.738		
1.652	-1.142	0.058	0.221	0.239	1.127	-1.238	-0.309
0.062	-0.666	-0.796	-1.546	-0.555	-1.457	-0.187	
0.177	1.681	-0.377	-0.362	-0.005	-0.238		
2.824	-3.073	-1.983	-2.394	0.108	0.998	-1.993	-0.295
0.374	0.574	-2.785	-1.615	-0.609	-2.419	-3.222	
1.195	1.444	0.840	-0.410	-1.318	-0.590		
2.418	-3.280	-1.647	-2.033	0.353	0.189	-3.006	-0.129
0.559	0.958	-3.173	-1.058	-0.459	-2.101	-2.957	
1.369	0.963	-0.284	-0.674	-0.938	-0.464		
2.852	-1.339	-0.848	-2.294	0.114	1.260	-2.029	1.414
0.456	0.296	-2.319	-0.914	-1.620	-0.876	-2.458	

Table36.txt

-0.026 0.261 0.261 -1.855 -1.913 -0.594
3.052 -1.419 -0.783 -2.769 -0.360 1.085 -2.216 1.234
1.469 0.865 -2.892 -1.677 -1.444 -1.404 -2.882
0.043 1.607 -0.438 -1.830 -1.511 0.019
1.821 -0.065 0.004 -1.157 1.206 2.361 -0.663 -0.441
0.932 -0.394 -1.007 -1.833 -0.689 -1.784 -1.573
0.736 0.559 -1.375 -1.634 -0.499 1.243
-0.648 0.431 1.052 1.297 -0.619 -0.122 0.309 0.459
-0.676 -1.471 -1.974 -1.789 -0.817 -2.402 -0.187
0.424 -1.418 2.090 -0.609 -0.320 -0.855
0.019 0.427 0.577 -0.079 0.260 -0.367 -0.476 0.996
0.219 0.074 -1.594 -0.655 -0.293 -1.641 -0.355
0.002 1.178 -0.742 -0.283 0.207 -0.975
0.695 -1.065 0.903 0.325 -0.582 0.309 -0.302 1.139
0.297 0.442 -1.052 -1.656 0.090 -1.421 0.591
-0.029 0.265 0.675 0.425 -0.093 -0.802
1.380 -1.427 -0.749 -2.991 0.708 1.504 -1.369 -0.244
0.917 0.929 -2.887 -1.716 0.173 -1.606 -3.351
-0.559 0.766 -0.664 -0.494 -1.822 -0.099
1.802 -1.781 -1.412 -2.235 0.699 0.467 -1.760 0.582
1.349 1.501 -3.909 -0.912 0.208 -1.733 -3.228
-1.005 0.827 -1.361 -1.433 -2.211 -0.148
-0.013 0.611 -0.492 -1.321 -0.139 -0.273 -1.034 2.408
0.037 0.694 -0.696 -0.754 -1.558 -0.452 -2.015
-0.022 0.289 -0.509 -0.935 -1.210 1.077
0.673 -0.465 -1.527 -1.790 -1.110 -0.819 1.936 0.984
0.703 0.030 -2.529 -1.229 0.613 0.400 0.515
-0.223 -0.496 0.560 0.882 -1.204 -1.608
1.343 -0.618 -0.245 -1.202 0.481 0.743 -2.481 0.608
-0.292 0.057 -2.798 0.347 -0.023 -2.683 -1.502
-0.511 0.914 0.010 -0.920 -1.906 0.007
0.783 -1.513 -0.052 -0.715 -1.346 -1.052 0.426 1.590
0.929 -0.025 -0.357 -2.169 -0.276 -0.702 -1.021
0.499 0.268 1.152 0.464 -0.199 -1.390
-0.562 -0.583 -0.115 0.029 -0.005 -0.873 -0.218 0.734
-0.094 -0.073 -1.823 -0.874 -0.189 -1.903 -0.853
0.199 0.360 0.991 0.446 -0.348 -1.337
1.195 -1.517 -1.036 -0.851 -1.021 1.214 -0.106 -0.690
1.934 0.165 -0.841 -1.015 -0.205 -0.530 0.131
-0.384 0.837 -0.130 -0.896 -1.177 -0.031
1.622 -2.050 -0.676 -1.459 -0.146 1.205 -1.551 0.427
1.023 0.274 -2.906 -1.523 -0.625 -1.395 -2.459
-0.129 1.595 -0.849 -0.942 -1.848 -0.743
0.024 -0.766 -0.358 -0.236 -0.765 0.689 -1.739 0.626
-0.902 1.363 -1.206 -0.809 -0.543 -0.590 -1.012
0.285 0.016 -0.926 -0.541 -0.425 0.206
1.248 -1.406 -1.431 -2.810 -0.303 0.242 -2.335 0.440
0.226 1.577 -2.423 -1.672 -1.040 -1.209 -2.966

Table36.txt

-0.302	0.557	-0.124	0.076	-1.154	-0.246		
-0.137	-1.460	-1.448	-1.019	0.512	-1.107	-1.827	1.448
0.776	2.131	-3.274	-2.021	-1.961	-1.809	-1.816	
-0.790	1.770	1.085	0.395	-1.602	-0.135		
1.021	-0.743	-0.710	-1.754	0.828	0.967	-2.720	2.597
0.578	-0.082	-2.649	-0.030	-0.894	-2.201	-2.303	
-0.274	0.371	-0.065	-0.094	-1.504	1.021		
-0.943	-1.067	-0.584	0.428	0.398	-0.047	-0.571	-0.285
-0.048	0.656	-1.176	-0.880	-1.829	-1.476	1.462	
-0.402	0.442	-0.159	-0.104	0.355	-0.474		
0.960	-3.573	-0.541	-0.759	0.122	-0.902	-0.442	0.378
-1.035	-0.249	-0.204	-1.584	-1.487	0.221	1.170	
2.150	1.637	-0.426	0.657	0.588	-1.435		
1.966	-0.806	-0.493	-1.112	-0.462	0.136	-1.679	0.042
0.231	-0.446	-2.594	-0.318	-0.054	-0.794	-1.321	
-0.407	1.205	-1.047	-0.865	-0.849	-1.013		
0.880	-1.257	-0.432	1.968	-1.458	-0.114	-0.478	0.050
0.176	-1.101	-1.568	-0.239	-0.346	-2.134	-1.063	
0.814	0.247	-0.267	0.689	-0.030	-1.503		
-0.349	-0.800	-1.089	-0.373	-0.405	-1.255	0.704	1.630
-0.839	1.598	-1.092	-1.792	-0.849	0.314	0.743	
-0.048	0.483	0.868	-0.049	1.147	-0.299		
2.139	-1.495	-0.641	-1.966	1.780	1.363	-3.168	0.912
0.177	-0.115	-1.678	-0.253	-0.252	-1.159	-2.719	
0.277	1.280	0.085	-0.026	-1.323	-0.549		
1.042	-2.275	-0.031	0.216	-1.153	-1.128	0.039	1.110
0.430	1.050	-0.776	-1.628	-1.205	-1.322	-1.126	
-0.098	1.018	-0.388	-1.058	-0.471	-0.037		
1.205	-1.513	0.773	1.707	0.185	-0.687	-0.100	1.413
2.173	-1.482	-0.304	-1.492	-0.261	-1.506	-0.358	
-1.137	0.085	-1.600	-3.834	-0.235	0.172		
1.194	-0.073	-0.284	-1.189	2.004	1.645	-1.957	1.443
-1.101	-0.622	-1.091	-1.916	-0.032	-2.250	-2.201	
-0.934	-0.418	0.141	-1.012	-2.212	-0.079		
-0.680	-0.531	0.061	-0.908	0.803	1.419	0.128	-0.346
0.726	0.141	-1.357	-1.067	-0.255	-0.671	-1.524	
-0.433	-0.427	-0.012	-1.284	-0.522	0.306		
-0.107	-0.019	-1.166	-1.310	-0.486	0.049	0.346	-0.052
0.292	1.509	-2.714	-1.163	-1.598	-0.904	-0.463	
1.350	-0.967	-0.146	-0.032	-0.590	-1.532		
1.264	-0.523	-0.836	-0.673	-0.725	0.641	-0.768	-0.179
0.689	0.866	-0.911	2.077	-0.608	-1.706	-0.652	
-0.546	-0.495	-1.370	0.435	0.508	0.176		
2.596	-2.197	-0.600	-1.385	0.236	1.547	-0.932	0.951
0.098	-0.159	-4.496	-0.783	-0.673	-1.349	-3.429	
-0.562	0.061	1.431	0.418	-0.879	-0.573		
-0.162	-2.003	-1.360	-1.129	-0.643	0.031	-1.409	-0.907
1.190	0.507	-1.127	0.050	-0.328	-1.302	-1.217	

Table36.txt

0.631	1.065	-0.529	0.877	-0.361	-1.020		
1.101	-1.810	-2.297	0.050	0.638	0.353	-0.095	0.303
0.199	1.710	-3.307	-1.992	-0.673	-1.010	-1.182	
0.736	-0.174	-0.326	0.139	-0.920	-0.605		
1.635	-0.827	-0.962	-0.193	0.131	0.897	-2.090	0.660
-0.454	-0.655	-2.414	0.720	-1.162	-1.699	-1.169	
0.031	0.910	-0.870	-0.389	-1.346	-0.788		
-0.554	0.381	-1.677	-0.164	0.848	1.093	-1.835	1.079
0.357	-0.929	-3.189	-1.163	-0.448	-1.262	-0.865	
-1.646	0.366	0.073	-0.151	-1.044	-0.504		
-0.926	-1.882	-0.012	-2.034	0.284	-1.357	0.361	1.198
1.067	-0.823	-1.308	-0.646	-1.257	-0.893	-0.253	
0.171	0.669	1.509	1.599	-1.195	-0.317		
0.939	-0.529	-0.571	-2.288	0.720	0.641	-2.481	0.834
0.918	0.269	-3.700	-1.912	-0.370	-2.016	-2.959	
-0.249	1.268	-0.004	-1.333	-1.963	-0.194		
0.310	-1.130	0.507	1.306	0.496	-0.606	-1.402	1.024
-1.284	1.120	-1.518	-0.840	-1.136	-1.581	-0.508	
0.441	0.202	0.538	0.134	-1.011	0.170		
0.257	-1.291	-0.797	-0.851	0.110	0.139	0.257	1.091
-0.871	-0.120	-0.809	-0.817	-1.661	-0.206	0.093	
-0.696	0.914	0.236	0.759	0.081	1.095		
-0.545	-0.287	0.783	0.654	-0.969	-0.362	2.101	-0.123
-0.075	-0.025	0.003	-0.473	-0.919	-0.084	0.908	
-0.337	-0.757	0.191	-0.290	0.380	-1.397		
1.431	-1.294	-2.343	-0.873	0.593	-0.407	-0.703	-0.904
0.183	0.672	-1.450	-1.304	-0.686	-0.616	1.073	
0.029	0.355	0.520	0.465	-1.039	-0.548		
1.775	-1.327	-1.749	-1.434	-0.712	0.843	-1.656	0.314
1.042	-0.341	-2.223	0.339	0.333	-1.294	-1.717	
-0.496	0.904	0.043	-0.124	-0.942	0.210		
1.994	-1.641	-2.682	-2.201	1.436	-0.634	-2.456	2.304
-0.552	0.091	-3.058	-0.350	-0.699	-1.648	-2.996	
-0.788	0.028	0.204	-1.855	-1.296	-0.271		
-1.134	-0.220	-0.251	-1.084	0.821	0.652	-0.417	0.708
0.648	-0.074	-1.827	0.301	-0.158	-0.127	-0.511	
1.569	0.908	-1.064	-1.359	-1.181	-1.822		
0.660	-1.035	-0.429	-2.255	1.000	0.143	-1.790	0.974
0.266	0.344	-2.816	-1.220	-0.466	-2.692	-3.183	
-0.029	1.879	0.052	-1.209	-0.983	0.064		
1.188	-1.686	-1.062	-1.650	-0.464	-1.109	-1.629	0.918
-0.798	-0.779	-2.371	-0.929	-1.485	-2.229	-0.572	
0.401	0.723	-0.015	-0.209	-0.134	-0.183		
1.738	-1.373	-1.121	-1.221	-0.244	-0.751	1.403	1.123
1.417	-1.295	-0.760	-1.110	0.022	-0.581	-0.211	
0.319	0.258	0.421	-0.150	-1.541	-0.040		
0.408	-0.916	-1.145	-1.390	0.522	0.199	-1.153	1.195
0.405	0.592	-2.993	-1.716	-1.984	-1.942	-1.924	

Table36.txt

-0.969	0.092	-0.597	-1.765	-1.534	-1.440		
0.458	-1.796	-1.234	-0.259	-0.527	-0.840	0.060	1.564
0.539	-0.137	-2.557	-2.849	-1.584	-1.487	0.913	
0.114	-0.369	0.471	1.671	-0.962	-1.266		
0.995	-1.378	-1.047	-2.298	0.238	0.691	-1.017	0.283
-0.170	-0.006	-3.440	-0.258	-0.083	-1.526	-1.198	
-1.218	1.089	-1.209	1.448	-0.959	0.583		
0.371	-1.821	-0.026	-0.199	-0.075	-2.240	0.818	0.460
0.684	-0.018	-0.135	-2.053	-1.819	-0.682	-0.788	
0.862	1.437	0.870	0.829	-0.525	-2.405		
1.826	-1.624	-1.555	-1.926	-0.349	-0.344	-1.764	0.259
0.210	0.475	-2.877	-2.745	-1.009	-1.679	-2.349	
0.143	-0.554	0.431	-0.857	-1.212	-0.105		
0.899	-1.578	-1.602	-1.220	1.438	0.404	-2.367	0.423
1.560	0.376	-3.469	-1.637	-0.931	-0.899	-2.268	
-0.895	0.415	-0.790	-0.893	-1.271	-1.082		
2.890	-2.662	-0.734	0.821	-0.477	1.334	0.665	0.325
0.775	0.461	-1.479	-3.169	-1.491	-1.941	-1.633	
-0.250	0.535	0.073	-0.876	-1.723	-2.238		
2.231	-1.891	-1.615	-1.469	1.522	1.417	-2.113	-0.306
0.428	-0.911	-3.283	-1.483	-0.625	-1.810	-2.530	
0.233	0.264	-0.568	-0.745	-1.757	-0.234		
0.060	-1.561	-2.104	-0.141	0.544	-0.619	1.597	1.629
2.701	0.565	-2.790	1.348	-1.429	0.273	-0.929	
0.767	-0.771	1.456	1.304	-0.799	-0.584		
-0.030	-1.126	-0.726	-1.006	1.172	-1.200	0.083	1.154
-0.043	0.145	-1.806	-0.939	-1.020	-0.737	-0.009	
-0.658	0.875	1.313	-0.361	-1.120	-0.671		
0.139	-2.985	0.942	-1.086	-1.254	-1.011	0.803	0.014
1.329	0.065	-2.230	-0.070	0.084	0.361	-0.075	
-0.248	-0.210	1.993	3.061	1.270	-1.106		
2.237	-2.012	-1.842	-2.447	0.174	1.039	-1.709	0.300
0.435	1.719	-3.492	-1.450	-0.983	-1.981	-2.025	
-0.653	-0.289	-0.056	-1.066	-2.709	-0.587		
1.027	-0.900	-0.577	-2.670	1.373	0.964	-1.209	-0.287
1.175	-0.179	-2.763	-0.271	0.489	-0.692	-2.982	
-0.753	0.805	1.383	-0.626	-2.428	-1.071		
0.975	-0.570	-0.320	-0.608	-0.115	-0.096	-0.641	1.222
2.126	0.565	-1.338	-1.879	-1.706	0.326	-0.088	
0.845	-0.770	1.758	1.631	-0.456	-0.992		
1.858	-1.617	-0.103	-1.578	0.653	1.278	-1.631	1.362
1.282	-0.962	-2.859	0.403	0.939	-1.376	-2.414	
0.886	1.506	0.687	-0.145	-1.273	0.067		
0.708	-1.666	-2.751	-0.952	-0.070	1.327	0.389	1.742
-0.548	0.893	-1.804	-1.062	-1.097	-0.928	-1.185	
1.706	0.144	0.008	0.299	-1.852	-1.217		
0.868	-1.300	-1.372	-0.801	0.064	1.164	-1.148	-0.426
0.224	0.047	-2.056	0.156	0.212	-1.577	-0.985	

Table36.txt

-0.217 0.844 -0.832 0.142 -0.647 0.044
-0.509 -0.486 0.513 -2.263 1.292 1.256 -1.629 1.994
-1.160 -1.901 -1.145 -0.254 0.754 -0.749 -1.310
-0.222 0.718 -0.741 -1.141 0.087 0.382
0.780 -0.455 -0.991 -0.084 -0.623 0.155 -0.766 0.435
-0.656 -1.429 -1.172 0.539 0.879 -0.735 -0.783
0.085 -0.648 0.776 2.065 -1.878 -1.414
0.794 -1.626 -1.172 -0.434 0.394 -0.713 -0.210 -1.196
-0.208 1.093 0.072 -0.802 -0.680 -0.844 0.758
-0.590 0.138 0.354 -1.422 -0.489 -0.111
1.536 -0.884 -0.712 -0.472 0.580 -0.461 -0.313 1.069
1.051 0.092 -1.358 -0.730 -0.083 0.297 -0.477
0.154 -0.520 0.813 -0.185 -0.463 -0.615
0.807 -1.311 -0.523 -1.327 0.313 -0.668 -1.864 0.139
0.333 0.250 -1.849 -0.878 -0.486 -1.319 -0.003
0.572 2.072 0.564 -0.830 -0.817 -0.194
1.866 -1.025 0.249 -1.292 0.145 1.307 0.081 0.705
1.294 0.157 -2.437 -1.824 -0.122 -1.623 -2.289
-0.934 -1.069 -1.511 -0.510 -1.231 -0.371
1.615 -0.130 -1.533 -0.844 1.237 0.757 -0.224 0.018
-0.434 -0.729 -0.594 0.294 -0.069 -1.309 -0.299
0.175 -0.590 -0.774 -0.196 0.321 1.007
0.835 -0.432 -0.530 -0.961 -1.714 -1.736 3.191 0.088
-0.660 -0.193 -0.552 -1.680 0.776 -0.716 -0.794
-0.014 -0.533 -0.249 -0.968 0.329 -0.733
0.244 -0.011 0.364 -1.753 0.225 -0.800 -1.140 1.949
0.552 -0.519 -0.960 -0.356 -0.538 -1.155 0.409
-0.481 -0.753 0.736 -0.264 -0.294 -0.517
-0.471 0.194 0.701 -0.711 0.186 0.789 -0.669 1.484
-1.386 -0.150 -2.678 -0.433 -0.218 -1.299 -1.558
-0.571 0.615 -1.000 -0.539 -0.512 -0.330
0.809 -2.190 1.181 0.614 -0.389 0.446 1.025 0.671
-0.752 0.555 -0.326 0.950 0.754 0.241 -0.387
0.784 1.470 0.161 -0.091 -0.182 0.412
1.943 -2.402 -1.752 -2.192 0.247 0.722 -1.731 0.926
1.517 0.155 -3.762 -1.916 -2.528 -2.819 -3.876
-0.132 1.620 -1.422 -2.921 -1.817 -1.316
1.977 -1.684 0.560 -0.038 0.712 0.007 -0.520 0.101
2.337 1.312 -1.450 -0.001 -0.326 -1.856 -0.686
-0.939 -0.516 -1.388 0.574 -0.544 -0.737
1.190 -1.806 0.029 -0.134 -0.685 1.876 0.152 -0.007
-0.128 -0.494 -1.789 -1.166 0.761 -0.311 -0.091
-0.333 0.382 0.925 -0.558 -0.232 -1.507
-0.864 0.741 -0.069 -1.337 1.643 0.817 -1.136 0.522
0.778 -0.888 -2.014 -1.200 -0.413 -0.218 -1.300
-0.082 0.506 -0.909 -0.232 -0.410 -1.229
-0.090 -1.289 0.017 -1.655 -0.487 -1.797 0.254 1.353
0.379 0.287 0.734 -0.886 -1.473 0.004 1.716

Table36.txt

-1.080 -0.527 0.637 0.231 0.497 -0.864
2.337 0.091 -0.657 0.037 -2.304 0.904 -1.348 0.735
0.821 -0.834 -0.458 -0.144 -0.362 -1.409 -0.717
0.922 -0.003 0.956 -0.288 -0.471 0.109
-0.059 -1.006 0.406 -1.027 -0.661 1.268 0.836 -0.304
-1.215 0.450 -0.498 0.455 -0.867 -0.777 -0.152
0.738 -1.282 0.190 0.941 1.358 0.753
0.032 0.321 1.028 -1.111 -1.584 -0.713 -0.534 -0.246
0.335 11.000 -1.394 0.391 -0.374 -0.156 -0.907
0.611 -0.024 -1.572 -1.222 -1.484 -1.048
-0.984 -0.521 0.426 -1.397 -0.132 0.847 -0.442 -0.521
0.907 -0.680 -0.382 -0.732 0.165 -0.658 -0.282
0.987 -0.789 -0.164 -0.201 0.351 -0.865
0.073 -1.589 0.288 0.921 -0.197 -0.774 -0.168 0.436
0.415 0.837 -0.925 -1.427 -1.256 -1.315 -0.871
0.415 -0.124 0.390 -0.196 -0.362 0.076
2.155 -1.626 -0.502 -1.515 0.939 0.852 -1.304 1.080
1.221 0.064 -2.213 -1.870 -0.086 -2.021 -1.887
-2.189 0.898 0.174 -0.839 -1.575 -0.665
1.444 -1.189 0.199 -1.944 0.632 1.044 -1.162 0.964
0.443 0.062 -0.905 0.753 -0.568 -1.672 -2.202
1.074 -0.041 0.946 0.577 0.469 -0.450
1.172 -1.294 -0.624 -1.773 0.641 0.636 -1.328 1.152
0.233 -0.923 -2.363 -0.814 0.024 -0.448 -2.408
0.692 1.064 0.253 -1.004 -0.813 -0.639
1.808 -2.103 -0.504 -0.105 0.328 -1.193 -0.116 0.422
-0.005 0.056 -1.798 -1.703 -0.262 -1.548 1.135
0.145 0.756 1.065 2.728 -0.267 -0.074
-1.588 0.582 0.475 0.304 0.956 0.252 -1.791 1.644
-0.369 -1.272 0.149 0.226 -0.365 0.200 -0.859
0.073 0.215 0.980 0.498 -0.030 -0.295
0.571 -0.785 -0.534 -1.596 1.582 1.163 -1.711 0.512
1.343 -0.610 -2.381 -2.021 -0.727 -1.232 -2.124
0.592 0.649 -0.586 -1.148 -2.030 -0.404
0.505 -2.004 -1.349 -0.521 1.187 0.415 -1.793 0.840
-0.408 0.660 -4.049 -1.904 -0.915 -1.342 -2.042
0.185 1.156 -0.295 -0.652 -1.151 -0.982
0.774 -0.580 -2.398 -0.544 0.287 -0.114 -1.261 0.881
0.693 0.655 -3.215 0.264 -2.294 -1.355 -0.391
-1.725 0.078 -1.245 0.126 -1.768 -0.672
2.921 -0.524 -1.576 -2.839 0.097 0.611 0.364 1.621
-0.591 -0.964 -2.710 -0.161 -1.570 -2.511 -1.021
0.715 0.142 -0.795 -0.567 -1.192 -0.959
2.082 0.404 -0.685 -0.829 -2.436 -1.398 0.714 -0.836
-0.812 1.011 -1.131 -0.107 0.087 0.755 1.260
0.434 -0.024 -0.543 0.560 0.001 0.313
0.669 -0.524 0.123 -0.235 0.556 0.832 -1.528 1.018
0.686 0.491 -2.016 0.308 -0.528 -1.752 -0.468

Table36.txt

0.328 -0.323 -1.107 -1.683 0.142 -1.160
-0.312 0.204 0.880 1.208 0.423 -1.518 1.205 0.094
-0.958 0.175 1.663 -0.617 -1.876 -0.318 0.250
-1.418 0.013 -0.788 -0.488 -0.025 0.403
-0.514 0.043 -1.425 -0.056 -0.147 1.005 -1.063 0.340
-0.442 1.072 -1.267 -1.498 -1.022 -1.543 -2.947
-0.793 -0.222 -0.437 -1.522 -0.735 -0.971
1.349 -0.392 -0.244 -2.251 2.571 2.058 -1.823 1.716
-0.610 -1.203 -2.347 -0.415 0.111 -0.519 -1.273
-0.048 0.411 0.439 -0.293 -1.173 0.940
-0.359 -1.418 1.316 -0.622 -0.850 0.643 1.057 2.147
0.558 0.604 -1.984 -1.993 -0.375 -1.386 -1.528
0.499 0.467 -0.263 0.294 -0.782 -1.364
-0.090 1.181 0.552 -0.341 -0.122 0.924 1.003 0.391
1.071 -1.130 -0.954 -0.629 -1.104 -0.557 0.370
0.206 0.364 -0.915 1.359 -0.317 0.501
-0.101 -0.672 -0.934 -0.818 0.845 0.256 -1.591 -0.305
0.548 0.508 -2.542 1.489 0.309 -0.363 -0.516
-0.140 0.229 0.382 1.547 -1.259 0.278
0.968 -0.707 -0.559 -0.475 0.431 1.392 -1.032 0.627
0.906 -0.105 -1.966 -1.408 -1.177 -1.156 -1.304
-1.776 -0.159 -1.373 -0.179 0.129 -0.853
0.662 -0.328 0.103 0.253 1.046 0.721 0.003 0.010
-0.182 -0.016 -0.123 -0.510 -0.855 -0.176 -0.452
-0.023 -0.615 0.269 -0.294 -1.808 -1.649
1.343 1.641 -0.022 0.871 -0.546 0.140 0.270 0.278
-1.666 -0.223 0.234 -1.704 -0.515 -2.917 1.851
-0.401 0.021 0.886 0.899 1.589 -0.508
-1.302 1.628 2.117 -0.175 -0.449 0.891 1.179 0.114
-1.375 0.093 2.277 1.439 0.163 1.005 -0.105
1.054 -0.835 -0.028 1.893 -0.781 0.676
1.387 1.545 0.810 -0.236 2.059 0.990 -0.184 -0.130
-2.081 -0.409 -0.924 -0.087 -0.067 -0.561 -0.278
-0.898 1.169 -0.283 0.543 -0.009 1.390
0.772 -2.229 -0.144 -1.890 0.561 0.297 -11.000 0.454
3.114 -0.562 -1.751 -0.941 -11.000 -6.075 5.790
0.692 -0.256 1.245 0.723 -0.698 0.605
0.881 -0.908 -0.122 -1.674 1.364 1.640 -0.176 1.692
0.465 -0.372 -0.909 -0.963 -0.637 -0.895 -1.214
-0.510 0.013 1.777 0.554 -0.204 0.582
-1.282 -0.201 1.413 -1.550 -0.994 1.145 0.557 0.662
-1.103 -0.140 0.688 1.874 1.390 0.564 -0.320
0.324 1.046 0.115 2.584 0.349 1.107
0.779 0.463 -1.902 -1.314 -1.284 0.565 -1.795 0.113
0.630 -0.813 -2.619 0.846 1.057 -1.386 -1.423
-0.627 0.755 0.623 -0.624 1.365 -1.234
-1.680 0.767 2.453 -0.041 -0.066 0.652 -0.119 -0.632
-0.257 0.698 0.037 -0.752 0.452 -0.038 0.393

Table36.txt

-0.454 -0.797 0.537 0.079 0.355 0.269
-0.422 0.568 0.101 -0.901 0.462 0.535 -0.346 0.073
-0.919 -1.647 -0.544 -0.345 0.128 0.365 0.144
-0.068 -0.312 -1.500 -0.486 1.017 1.715
-1.469 0.342 2.041 0.697 0.019 0.512 0.655 -0.192
-1.380 0.185 0.291 0.472 0.779 0.933 1.448
-0.192 -0.282 0.249 1.934 1.170 2.593
-0.519 1.560 0.494 1.237 0.692 0.522 -1.002 0.711
-1.372 -0.770 1.738 -1.907 0.269 0.325 0.130
0.841 -1.548 -1.116 1.193 0.364 0.225
-4.717 -5.587 -6.668 0.100 11.000 1.011 -3.021 -0.440
-1.198 -4.212 -2.000 2.277 2.129 -3.292 -0.210
0.258 -0.443 -0.663 8.041 1.795 4.485
-0.513 -1.002 -1.337 -0.596 0.613 0.465 0.058 0.645
-0.075 1.110 -0.628 -0.775 0.444 -0.695 0.128
-0.290 -0.123 0.093 1.031 -0.910 0.499
-1.476 1.030 0.041 0.289 0.104 -0.014 -0.490 -0.400
-1.481 -0.116 1.849 0.077 -0.556 2.755 1.148
-0.152 -0.986 -0.995 1.046 0.579 0.095
-0.060 -0.969 -1.371 1.659 -0.122 1.800 -2.064 -0.279
-0.116 -1.611 -1.164 0.502 0.586 -0.301 -0.370
-0.455 0.031 0.569 -1.084 -0.682 -0.175
-0.075 1.451 1.038 -2.154 1.878 0.186 0.095 -0.186
-0.778 -0.805 -0.416 -1.264 0.226 -0.819 0.675
-0.183 0.487 -0.662 -0.272 0.882 0.418
0.533 -0.136 -0.547 -0.756 0.065 1.305 -1.536 0.343
-0.880 -0.109 -0.258 -1.499 -0.386 -1.461 -1.643
-0.149 -0.157 1.477 0.803 -0.238 0.738
0.179 -1.290 0.665 -0.996 0.352 0.540 -0.525 1.316
-0.593 -0.049 -1.176 -0.452 -0.449 0.488 -0.542
-1.078 -0.028 0.943 -0.005 -0.972 0.826
-1.986 4.455 1.370 -2.445 2.596 -1.354 5.468 3.313
-11.000 -0.267 -6.442 5.102 0.440 -2.892 -0.782
0.704 -1.293 1.030 11.000 1.268 6.624
-0.365 0.674 1.243 0.231 0.335 0.309 0.519 -0.941
-0.276 -1.862 0.536 -0.629 -0.244 -1.339 -0.108
0.611 -0.005 -0.089 -0.500 -0.034 0.770
-0.612 -0.414 -0.423 1.166 0.039 -0.896 1.067 0.006
-0.030 0.564 -1.303 -0.703 0.379 -0.083 -0.741
-0.715 -0.962 1.152 0.151 -1.004 0.131
1.639 -0.237 0.265 -2.191 1.831 0.933 -2.029 -0.028
-0.454 0.069 -1.383 0.154 0.815 -1.585 -1.538
-0.424 1.821 0.611 -0.048 -0.488 -0.507
0.625 0.560 1.283 -0.754 2.365 0.637 -0.962 0.333
-1.640 -1.018 1.049 2.113 0.040 -0.644 0.026
-0.866 -0.576 0.016 0.985 0.779 0.035
-0.174 0.414 0.192 -1.856 1.216 1.557 -1.285 -0.217
-0.965 -0.750 -0.989 -0.011 1.892 -1.662 -1.407

Table36.txt

-1.072	-0.111	-0.068	0.538	-0.691	-0.812		
0.079	0.499	0.451	-0.181	0.861	1.332	-1.243	2.269
-1.320	0.502	-1.628	-0.610	0.088	-0.277	-0.755	
-1.955	0.266	-0.462	0.048	-0.725	-0.259		
0.782	0.399	-1.757	-2.143	1.240	0.446	-1.760	0.622
0.069	-1.016	0.046	-0.648	-0.405	-0.886	-1.347	
-0.630	1.217	-0.976	-1.423	0.215	0.243		
1.288	-2.162	-1.321	-0.778	0.754	1.225	-3.158	-0.222
-0.422	0.135	-0.909	-1.355	0.531	-1.076	-1.856	
-0.390	1.736	-0.878	-1.262	-0.908	-0.976		
-0.568	-0.934	-0.061	-0.914	-0.229	-0.566	0.692	0.135
-1.155	0.222	-1.223	0.363	0.766	-0.413	-1.482	
-0.040	0.699	-0.458	0.013	1.150	0.064		
0.547	0.878	-0.165	0.289	-1.627	1.023	-1.240	-0.937
-0.790	0.791	1.448	0.373	0.643	0.988	-0.664	
0.844	-0.754	0.400	0.752	0.310	1.158		
0.497	0.701	0.039	0.279	-0.366	1.235	0.394	0.428
-0.890	0.881	0.630	0.032	-1.881	2.310	0.677	
0.185	0.286	-0.889	0.611	-0.412	-0.184		
0.655	0.671	1.006	1.215	0.241	0.165	-0.649	1.803
-0.964	0.013	0.859	1.084	0.195	0.741	1.025	
0.354	0.380	-0.510	0.298	-0.843	-0.220		
0.376	-0.097	-1.063	0.595	1.177	-0.604	-0.390	-0.383
-0.382	0.739	-0.681	-0.472	-0.628	-0.660	-0.523	
-0.747	0.352	0.458	-2.040	-1.166	-1.044		
0.688	-0.215	-0.443	-0.543	0.992	2.084	-1.447	1.014
0.131	0.407	-2.133	-0.534	0.217	-0.929	-2.606	
-0.208	0.990	-2.511	-2.437	-0.605	-0.503		
-1.167	-0.719	-0.891	-1.988	1.022	0.763	-1.050	0.769
0.974	1.017	-1.265	-0.131	1.623	-1.910	-0.237	
-0.898	-1.357	0.852	-1.419	-0.157	-0.851		
-0.637	-0.265	-0.946	-0.897	1.416	2.177	-1.113	-0.298
0.401	0.511	1.237	0.231	0.422	-1.068	-2.158	
-0.123	-0.396	-0.741	-1.051	-0.808	0.729		
-0.742	-0.769	0.685	1.284	1.317	1.515	-1.509	-0.890
1.922	0.237	0.507	-1.159	-0.436	0.601	-1.715	
0.868	1.971	-0.450	-0.393	0.257	0.462		
1.305	0.263	-0.104	0.160	0.132	0.277	1.219	-0.807
0.407	0.189	0.420	-0.100	-0.436	0.610	0.278	
-0.634	-0.608	-1.579	-1.252	-0.638	0.844		
0.991	0.534	-0.994	1.789	0.313	0.117	-2.291	-1.026
0.587	0.415	-1.113	0.497	0.102	-1.568	-1.850	
0.450	3.757	-3.447	-2.697	-0.204	-1.419		
0.526	1.029	-1.465	1.066	0.107	1.855	-2.443	0.158
-0.238	-0.551	-1.938	0.787	-0.859	-1.720	-3.271	
0.017	1.459	-3.529	-2.863	-0.949	-0.700		
0.062	-1.398	-0.558	0.402	0.044	0.314	-1.675	-0.778
-0.818	-0.743	-1.833	0.418	0.180	0.528	-0.788	

Table36.txt

-0.186	1.780	-2.447	-0.966	-1.444	1.484		
1.184	-0.410	-0.810	-0.616	0.350	0.493	-1.007	1.626
0.713	1.183	-0.937	-1.630	-0.410	-1.316	-1.000	
-0.098	1.389	-1.449	-1.203	-0.383	-0.306		
1.869	-1.147	1.635	-1.148	0.939	1.914	-2.010	-0.716
0.300	-0.893	-0.365	1.140	0.104	-0.471	-1.512	
-0.362	1.421	-0.529	-2.136	0.257	-1.020		
-0.900	0.605	0.164	-0.373	-0.897	2.033	-1.019	1.361
-0.233	0.932	-0.665	-0.753	0.301	0.394	-1.509	
-0.170	1.599	-2.217	-1.067	-3.074	-1.525		
-0.581	0.595	-0.048	-0.662	0.934	1.660	-0.249	-0.429
-0.578	-0.248	-0.056	-1.213	1.596	0.160	-1.917	
-0.740	-0.299	-0.764	-0.903	-1.328	-0.091		
0.352	0.616	-0.430	-0.863	1.591	2.339	0.298	0.985
-0.893	0.994	-1.197	0.540	-0.287	-1.831	-1.804	
0.949	-0.365	0.685	-0.970	-0.800	-0.147		
0.020	-0.906	1.122	-0.148	-0.375	0.412	1.982	0.433
0.077	0.790	0.823	0.531	-1.483	0.836	0.340	
-1.356	-0.692	-0.251	0.210	1.514	0.967		
-0.551	0.778	-1.781	0.269	0.993	1.018	-1.008	0.328
0.248	0.633	0.588	-0.870	-0.346	-2.147	-0.995	
0.105	0.291	-1.044	-3.500	0.027	0.626		
-1.038	2.637	0.200	1.425	-1.703	-1.197	-1.337	-1.872
-1.111	-0.835	2.322	0.259	-1.327	0.916	0.598	
0.195	-2.128	-0.503	0.448	1.707	-0.697		
0.535	1.265	0.142	2.427	0.303	-1.261	1.041	0.301
0.836	-0.612	-0.149	0.916	-0.043	0.572	-0.635	
0.476	1.001	-0.615	0.276	-1.068	-1.303		
0.626	-0.329	0.165	-0.006	3.298	-0.073	-0.717	0.228
-0.923	-1.015	-0.260	-0.723	-2.772	0.097	1.844	
0.401	2.486	-0.923	-0.729	-0.064	-2.407		
2.697	-0.973	0.063	-2.378	-0.100	0.493	-1.474	-2.075
-0.272	-0.887	-0.502	-0.071	0.896	0.343	-0.871	
-1.134	0.308	1.238	0.111	0.047	-0.763		
0.800	-1.754	-1.079	-1.806	1.037	0.160	-1.347	-0.372
-0.509	0.565	-0.413	-0.594	-0.751	-0.855	-0.486	
0.735	0.300	0.014	0.798	-0.637	-0.070		
-0.422	0.345	-0.341	0.331	0.377	1.879	-0.525	1.064
-1.031	0.882	0.504	-0.546	-0.131	0.933	0.284	
-1.013	-0.159	1.225	1.382	-0.014	-1.434		
0.495	0.977	-0.564	0.300	0.039	2.304	-2.449	1.727
0.536	1.412	-0.676	-0.212	-0.265	-0.737	-1.332	
-0.173	2.615	-2.877	-3.864	-0.387	-1.262		
-0.130	-0.053	0.181	-1.807	-1.372	0.361	0.083	0.629
0.717	-0.867	0.216	-0.789	-0.333	0.552	-0.100	
1.115	0.571	-0.929	-2.830	1.169	-0.920		
1.117	-0.525	0.143	1.363	0.392	-0.203	0.367	-1.933
0.261	1.546	0.891	-0.054	-0.309	0.694	-1.861	

Table36.txt

-0.013 0.563 0.595 1.199 0.052 -0.624
0.321 -0.780 0.199 -0.574 -1.469 -0.477 -0.639 0.404
0.324 1.809 -1.708 -1.154 -1.465 0.719 -1.765
0.215 1.248 -0.375 -2.162 -0.147 -0.932
0.997 -1.049 -2.190 -0.636 0.281 1.033 -1.219 -1.587
-0.251 0.363 -1.418 0.367 1.109 -1.384 -1.552
-0.263 1.263 -0.476 -2.073 -1.114 -1.069
0.433 2.317 0.936 -0.220 -0.058 0.914 -1.237 -0.147
-0.650 1.099 0.869 -0.405 -1.024 0.459 1.327
-1.402 -1.338 -0.088 -0.723 0.357 1.751
0.690 0.874 -0.749 -0.656 -0.347 1.133 -1.209 -0.984
1.843 0.799 0.254 -0.926 0.206 -1.097 -0.714
-0.174 1.296 -1.105 -1.984 -0.231 0.378
2.310 1.454 -0.666 -0.015 0.104 0.717 -2.426 -1.782
-1.124 -0.884 -1.941 0.118 1.309 -0.528 -1.620
1.818 1.510 -3.298 -2.146 -0.665 -1.828
0.696 -0.477 -1.601 0.001 -0.358 0.384 -1.255 -0.572
0.574 0.348 -0.232 -0.202 1.921 -0.157 -0.989
0.415 -0.252 -0.872 -1.825 -0.478 0.169
0.465 0.703 0.035 -0.022 1.201 -0.061 0.023 -0.382
-0.780 0.717 1.002 2.497 1.384 2.252 -0.002
-1.784 -0.214 -0.143 2.556 1.241 1.249
1.300 0.257 2.162 0.986 1.328 0.308 -2.219 0.136
0.303 0.554 -1.093 1.192 -1.041 0.186 0.118
-1.255 0.087 -0.720 -1.381 0.483 -0.997
1.862 0.566 0.535 2.143 0.580 0.202 -0.093 -0.349
-1.363 -0.062 0.138 0.015 -0.598 -0.333 -1.221
-0.516 1.892 -1.040 1.356 -0.883 0.746
1.564 1.467 -0.106 0.124 0.595 0.302 -0.566 0.095
0.600 0.287 -0.391 2.398 0.076 0.559 -1.038
0.957 -0.040 -0.407 0.782 0.763 -0.180
0.490 -0.562 -1.628 1.116 1.333 1.595 -1.407 -0.942
0.746 -0.348 -1.286 -0.184 1.667 -0.388 -0.485
-1.216 1.456 -0.371 0.544 0.263 -0.267
-0.739 0.854 -0.682 2.424 0.458 -0.679 0.068 -0.063
1.468 1.085 0.849 0.750 0.658 0.450 -0.042
-2.002 -1.545 -0.321 -0.525 0.523 1.123
-0.247 2.024 -0.501 -1.297 1.025 0.237 0.483 0.627
-1.985 -1.278 1.509 -0.276 -0.539 -0.503 -0.552
-0.690 -0.261 -1.117 -1.146 1.109 -1.078
-0.492 -0.782 -0.380 0.407 -0.990 1.295 -0.909 0.665
1.247 1.401 -0.968 -0.960 -0.434 1.180 0.899
-0.203 -1.001 -1.614 -1.043 0.522 -0.640
-0.276 0.933 0.308 -0.569 0.010 -3.197 0.295 1.611
0.049 0.497 1.862 -0.277 0.011 0.315 -0.431
-0.967 -0.362 -0.460 -1.409 1.400 0.158
0.236 0.726 0.707 -1.164 -0.843 -0.037 0.130 0.800
-0.722 0.094 1.489 2.235 0.443 -0.262 -1.446

Table36.txt

0.132 -0.658 -0.142 -0.775 0.969 0.178
-0.356 1.100 1.897 0.733 1.148 -1.329 0.022 -0.137
1.258 0.335 1.569 0.270 -0.276 1.983 0.185
-0.152 -0.695 0.070 0.911 1.344 -0.192
1.131 0.512 -0.073 -1.842 -0.167 -1.332 1.051 -0.353
1.574 1.045 -1.729 1.812 -0.618 -2.014 -0.414
-1.655 1.175 -1.623 -1.873 0.661 0.114
0.365 -2.514 0.938 1.419 -1.317 -0.589 0.459 -0.713
-1.020 -0.083 -0.126 -1.555 -2.245 -0.798 -1.416
1.743 1.157 -0.663 -1.090 -0.870 -0.861
0.940 -0.643 0.362 0.186 0.554 0.242 -0.072 2.053
-1.333 -1.395 -1.741 1.033 -0.581 -0.299 0.430
-0.685 0.978 -1.900 -0.604 1.410 -1.633
-0.454 0.226 -0.035 0.930 0.748 -0.004 0.537 -1.034
0.338 0.276 1.702 0.921 -0.137 0.215 -1.323
-0.048 0.468 -0.540 0.427 0.174 -0.551
-0.885 1.726 -1.093 -0.347 -0.321 1.162 -0.442 0.195
-1.510 -0.172 0.166 -1.745 0.875 1.510 1.320
-0.058 0.311 1.116 0.869 1.599 -1.473
-0.124 -0.623 -0.637 -1.592 0.465 -0.826 -0.428 -0.664
0.560 0.660 1.615 0.568 0.027 -0.447 -0.927
0.062 0.463 -2.033 -2.979 0.105 -0.550
-0.154 -0.861 0.572 1.027 1.337 -0.866 -0.339 0.515
0.950 -0.722 -0.380 -1.425 -0.766 -0.832 0.189
1.789 0.308 -1.145 -0.816 -0.699 -0.574
0.551 1.372 -0.712 0.765 -0.007 0.858 -0.325 0.415
-1.108 -0.616 0.670 0.029 -1.242 -0.184 2.404
-1.125 0.374 1.819 1.284 -0.880 -0.150
0.643 -1.587 -1.697 0.462 -0.351 -0.512 -0.531 0.541
-0.354 -0.069 0.058 0.614 -0.344 0.870 -0.851
0.213 2.011 -0.689 -0.090 -0.432 -0.127
0.095 -0.651 1.569 -1.189 1.055 -0.305 1.078 2.240
-0.634 -0.456 -0.212 0.360 -0.981 -0.143 2.757
1.116 0.937 -2.468 0.592 -1.189 -1.178
1.125 -0.107 -0.558 -1.252 1.086 0.869 0.852 -0.197
0.849 0.510 0.599 0.374 1.392 -1.618 -0.684
0.126 3.190 -2.048 -2.114 -0.930 0.585
-0.191 0.579 0.701 -0.397 0.457 -0.715 -0.817 -0.860
-0.325 -0.536 0.939 -0.295 1.663 -0.353 -0.497
-0.390 1.451 -2.787 -2.055 -0.703 -1.050
-0.010 -0.334 -0.038 0.109 1.718 0.773 0.961 0.792
0.752 -1.597 -0.845 0.057 1.835 -1.524 0.173
-1.431 -2.052 0.360 -1.451 1.412 -1.514
-0.344 0.006 1.435 0.125 -1.170 2.376 -1.886 -1.114
-0.586 0.776 0.524 0.075 -0.477 -0.088 -0.594
0.109 -0.901 -0.601 -0.157 0.902 1.092
1.543 -1.034 -0.240 0.586 0.768 1.157 0.851 0.783
2.142 0.553 0.198 -0.299 0.595 -2.279 -0.181

Table36.txt

0.068 -1.164 -0.460 -0.396 -1.860 -1.030
0.054 1.479 -0.021 2.144 0.990 0.384 0.101 -0.025
0.378 1.622 0.599 -1.070 0.504 -0.442 1.899
-2.241 -2.002 1.164 -1.011 -0.349 -0.586
0.185 2.716 -0.415 1.102 0.423 -0.230 -0.868 0.252
-1.188 0.632 -0.599 -1.259 1.529 0.225 1.987
-2.233 -0.057 0.020 0.433 -0.183 -1.493
1.377 0.449 -0.268 0.349 -1.033 0.335 -0.323 -0.266
1.437 0.560 1.102 -0.268 -0.981 -0.104 0.211
1.223 0.482 -1.070 -1.815 0.818 -0.167
0.868 -1.249 0.094 -0.445 -0.106 1.171 -0.463 0.046
0.572 0.658 0.129 0.701 -0.149 -1.465 -0.545
-0.118 -0.103 -0.794 -1.258 1.381 0.492
-0.314 -0.499 0.959 -0.041 -0.055 -0.818 -0.005 1.530
-0.814 -0.365 0.662 -0.814 0.467 -0.251 1.811
-0.195 0.066 1.114 2.082 -0.278 -0.628
0.233 0.578 0.380 -0.605 1.307 -1.072 -0.590 0.085
0.228 0.258 -0.250 0.378 0.565 1.190 1.741
-0.039 -0.438 -0.613 1.299 -0.861 -1.232
0.325 -0.942 0.999 1.578 0.792 -0.643 1.025 1.380
0.818 -1.551 1.067 2.126 0.536 -0.027 0.268
0.181 -1.062 1.493 2.167 -0.050 -0.604
-0.916 -0.024 0.490 -0.970 0.419 -1.008 -0.247 -0.056
0.505 0.790 0.716 -0.914 2.551 1.018 0.233
1.860 0.236 2.482 -1.044 -1.625 -1.127
-1.219 1.369 0.759 0.222 0.096 2.085 -0.679 0.307
-0.320 -0.397 0.988 0.413 -0.703 -0.326 2.010
-0.820 -0.798 -1.456 0.154 0.313 -2.373
-0.572 0.730 -0.057 2.065 0.532 0.897 -0.695 0.214
-0.943 1.546 0.625 0.307 -0.223 -0.435 0.510
1.001 0.524 0.753 -0.732 0.947 -0.095
-0.782 -0.567 0.444 -0.070 2.270 0.482 -0.118 0.327
-0.533 1.790 -1.118 0.118 0.057 1.367 1.642
-1.769 -0.058 0.080 -0.566 -0.418 0.290
0.228 -1.185 1.000 0.545 0.394 1.853 -0.608 -1.925
-1.506 1.632 1.455 -1.251 -0.689 -0.469 -0.070
1.245 -0.088 -0.244 -0.290 -0.125 -1.088
-0.360 -0.513 -0.561 -0.475 1.047 0.115 0.399 0.435
1.125 -0.301 -2.423 -0.325 -0.683 1.110 0.399
0.800 -0.989 0.783 1.111 0.407 -1.886
0.145 -0.698 0.015 -0.994 -0.159 -0.740 -0.584 1.730
0.851 0.742 0.603 0.089 -0.821 0.058 1.243
-0.228 0.409 1.030 0.494 -0.596 -0.771
1.481 0.634 0.722 1.236 -0.660 1.178 0.661 2.254
-0.116 0.323 0.937 0.614 -0.781 1.511 0.064
-0.941 0.485 -1.149 -2.217 0.811 0.996
1.495 0.150 0.272 1.510 -0.583 0.883 0.775 -0.476
1.097 -0.821 2.201 0.516 -0.773 0.864 0.483

Table36.txt

-0.240 -0.564 0.117 -0.469 0.638 -0.068
0.686 0.816 -0.828 1.356 -1.071 -0.002 0.620 -0.459
0.427 1.330 0.240 -0.448 0.194 -0.111 1.422
0.048 0.071 0.539 -0.448 2.391 -0.905
-1.174 1.245 0.503 1.093 -0.642 -0.184 2.012 0.267
-1.366 -0.020 1.544 0.926 0.405 1.156 1.067
-0.631 -0.070 -1.140 -0.128 0.610 0.939
1.174 -2.972 -0.042 -1.312 -0.774 -0.663 1.518 0.379
-0.227 -1.347 0.740 -0.432 0.548 1.757 1.353
0.501 0.809 0.508 0.103 0.140 -0.909
-0.176 0.467 -1.898 -0.556 0.129 0.713 0.051 0.738
0.883 1.303 -2.345 0.705 1.521 0.250 -0.262
-1.456 -0.042 0.162 -0.308 -0.164 -2.583
0.579 0.566 0.716 0.809 1.029 -0.939 0.935 -1.786
-0.897 -1.093 0.819 0.169 1.483 -0.285 1.931
-1.871 0.178 0.423 -0.974 0.768 0.529
-1.354 -1.181 0.159 -1.180 0.533 -1.116 0.095 0.832
-0.674 -0.143 0.297 -0.028 0.862 0.410 -0.197
-2.239 -0.294 0.274 0.380 0.026 -0.210
0.130 -1.410 -1.161 -0.225 -0.028 -1.066 -0.742 1.009
0.237 0.361 -0.579 1.254 0.810 0.025 1.930
-1.125 -0.389 -0.291 1.622 0.475 0.943
0.838 -0.328 0.225 1.233 -0.230 -0.301 1.628 -0.176
0.091 -0.663 -0.561 -1.958 -0.981 0.663 0.374
1.298 0.491 -0.795 -0.038 1.777 -0.956
-0.305 -0.705 -0.777 -0.548 -1.182 -0.228 0.521 0.044
-0.782 0.667 1.004 -0.407 -0.886 1.284 -0.351
0.209 -0.221 1.131 -0.924 -0.710 0.516
-1.253 0.059 0.682 0.170 0.692 -0.862 1.342 0.412
0.097 -0.338 0.070 -0.982 -0.029 -0.451 1.594
-0.146 0.540 -1.211 -0.239 1.448 -0.333
-0.042 -0.060 -0.299 -0.008 0.877 0.928 0.517 0.394
-0.689 0.395 -0.849 0.052 -0.916 -0.576 2.400
0.414 -0.278 0.735 0.743 2.663 1.960
1.527 -0.145 -2.301 -0.682 -0.751 -0.821 0.741 -0.051
0.424 0.344 0.130 -0.016 -0.538 0.601 0.624
0.127 -0.131 0.388 -1.129 -0.819 -1.002
-0.656 0.510 2.141 1.380 -1.606 -0.511 1.287 -1.037
0.187 -0.406 -0.865 0.814 0.853 0.436 -0.076
1.738 -0.298 0.132 -1.041 1.507 -0.657
0.911 0.180 0.618 0.368 0.780 2.149 0.613 0.404
1.503 -1.390 -1.468 -2.481 1.068 -0.365 -0.738
1.511 0.253 0.134 -0.743 0.867 -1.019
0.447 0.315 0.850 -0.964 -1.004 -0.399 1.943 -0.085
-1.548 -1.174 1.067 0.960 0.557 0.444 -0.177
-0.694 -0.219 1.460 0.943 1.861 1.085
-1.435 -1.416 0.691 0.445 -0.664 0.829 -0.096 0.851
0.984 -0.309 0.855 0.419 0.537 0.971 0.557

Table36.txt

-0.427 0.914 0.470 -0.367 -0.475 -0.883
1.133 1.278 0.310 -1.606 -0.407 -1.021 0.521 -1.253
0.396 -0.555 0.746 0.923 -0.075 0.393 1.536
-0.795 0.593 0.194 1.655 0.238 0.325
0.265 -2.423 -0.084 0.473 -1.330 -1.059 1.550 1.367
-0.384 1.103 -0.613 -0.318 -1.197 0.592 -0.189
1.270 1.451 1.090 1.006 1.319 -0.147
0.409 -0.328 2.483 0.926 -0.164 -0.395 2.087 1.157
0.212 -0.113 1.682 0.578 -1.876 1.020 1.792
0.418 -0.589 2.056 1.146 0.131 -0.168
0.437 0.050 0.871 0.240 0.078 -1.055 0.369 1.320
-0.053 1.193 0.968 -0.057 0.011 -0.580 -0.874
-0.862 -0.566 0.781 -0.453 1.729 -0.043
-0.503 -0.904 -0.589 -0.106 1.417 0.672 -0.958 -0.756
0.833 -1.017 -0.205 -0.960 -1.019 1.862 0.612
-0.191 -0.327 1.128 1.876 0.393 0.394
-0.519 -0.453 0.246 -0.245 1.058 -0.457 -0.003 -0.613
0.566 -1.095 0.704 -0.274 0.696 1.814 -0.276
1.539 1.278 0.368 0.474 0.595 -0.402
-0.646 -0.814 1.438 -1.518 -0.144 -0.625 1.761 0.377
0.124 -0.106 0.151 -0.269 0.851 1.955 0.696
1.069 0.264 0.291 1.103 0.019 0.447
1.551 0.414 -0.590 -0.916 0.325 -0.689 -0.700 -0.059
0.750 0.527 0.642 -1.098 -0.449 -0.110 0.512
0.506 1.382 1.304 0.079 0.913 -1.092
-1.133 0.519 -0.065 0.230 0.544 2.148 -1.966 0.924
0.111 -0.890 0.692 -0.628 0.204 -1.685 0.014
1.151 -1.788 -0.944 -1.609 -1.527 0.330
-0.045 1.421 -0.085 -0.132 -0.175 -0.201 2.365 -2.007
-1.652 0.373 1.091 -0.886 0.077 0.801 1.695
-1.619 0.049 0.746 2.123 2.486 0.109
-0.211 0.270 0.312 0.526 -0.652 0.647 1.533 0.721
0.552 1.105 0.681 -1.570 0.419 1.818 1.563
-1.387 -1.479 0.957 -0.051 1.638 -0.933
0.727 0.149 -1.060 -1.322 2.079 0.807 -1.043 -0.577
0.419 0.260 1.811 -0.185 0.626 -1.370 -1.309
1.310 1.007 -1.561 1.361 -1.002 0.205
0.368 -1.429 0.407 1.255 0.890 0.507 -0.101 0.675
-0.776 -0.128 0.593 0.079 0.254 -0.754 -0.390
-0.942 0.948 -0.480 0.629 -1.300 0.432
-0.540 -1.372 -1.406 -0.155 -1.873 0.946 0.229 -0.527
0.415 2.341 1.262 -1.260 -0.259 0.246 1.384
0.340 2.113 -0.191 1.673 -1.547 0.426
0.392 -1.542 -1.110 -0.254 1.032 -1.261 1.231 -1.023
1.119 0.895 -1.451 -0.173 0.653 -0.330 0.946
-0.086 1.189 1.591 -0.271 0.795 -2.123
0.864 -2.035 -1.601 0.226 -1.430 -0.697 1.238 0.749
-0.268 1.022 0.088 -0.452 -0.086 -0.735 0.494

Table36.txt

-0.414 1.012 -1.790 0.489 -1.525 -1.663
1.183 -1.490 0.748 -2.591 -0.820 -1.378 0.558 -0.836
0.886 0.269 -0.026 0.125 -0.202 -0.654 0.044
-0.746 -0.716 -0.069 -0.466 1.466 -1.370
0.731 0.120 -1.300 -0.791 -0.265 0.982 -1.052 0.249
-0.485 -1.070 -1.060 -0.471 -1.013 -0.385 -0.705
-0.062 0.251 1.085 1.064 -1.032 0.405
1.266 -1.158 0.571 -0.061 -0.285 0.931 1.144 -0.032
-0.946 0.066 -0.523 -0.569 0.427 0.853 0.602
0.644 -0.720 0.443 0.145 0.077 -0.162
0.270 -0.018 2.523 -0.161 0.003 -0.292 0.257 0.025
0.633 0.114 -0.732 -0.918 1.191 0.455 -0.277
0.993 -0.461 0.263 -0.901 -0.847 0.433
-0.114 0.657 1.171 -0.732 1.016 0.793 0.208 0.076
0.092 -0.050 -0.501 -0.193 0.196 -0.879 -0.122
-1.259 1.165 0.268 -1.768 -2.376 -1.844
0.932 -0.433 0.960 0.043 -0.872 -0.817 -0.344 -0.073
-0.011 -0.998 -2.311 -0.823 0.686 -0.885 -0.218
1.319 0.350 0.101 -0.107 -0.187 -1.186
-0.096 -1.644 -0.743 -2.494 3.532 1.270 -1.687 0.717
0.961 0.452 -0.052 -1.087 0.959 0.880 -1.683
-0.582 1.427 0.953 -0.617 -0.590 -0.194
1.112 -1.505 0.796 -1.851 0.352 1.933 -1.379 0.425
0.612 0.455 -1.739 -1.474 0.494 -1.284 -1.339
0.019 -0.777 -0.956 0.565 -0.206 1.244
0.827 -2.265 -0.283 -0.013 0.164 0.610 2.410 0.878
0.068 -0.566 -0.736 -0.398 0.115 2.113 1.300
0.237 -0.799 0.270 -0.267 0.002 0.332
1.618 -0.399 0.209 0.255 -0.101 0.809 -0.300 -1.220
0.262 -0.294 0.234 -0.150 0.568 -0.398 -0.402
-0.892 0.457 0.162 -0.015 0.157 -0.320
-0.072 0.284 0.570 1.137 0.572 0.564 -0.760 -0.247
-0.840 -0.398 0.535 0.087 -0.261 0.922 1.178
-2.634 0.152 -1.056 -0.854 0.239 -0.444
0.389 -0.857 0.187 0.076 0.357 0.579 2.033 -0.559
0.693 0.654 0.425 -0.507 0.384 0.427 -0.283
-0.163 0.642 -0.141 0.583 1.028 0.049
-1.141 0.212 -1.184 0.737 0.724 0.363 0.181 -0.175
-0.227 0.057 1.948 -1.123 0.573 -0.722 1.804
-1.437 -0.559 -0.279 -0.914 -0.402 0.022
0.897 -0.652 -0.554 -0.122 -0.465 0.404 0.142 -0.639
0.196 0.600 -1.356 -0.102 0.815 1.140 0.262
-1.295 -0.681 -0.278 0.524 -0.526 0.198
-1.656 1.064 1.150 1.235 -0.867 0.647 1.163 -1.362
0.419 0.216 1.510 -0.078 -0.379 1.031 1.589
-1.267 -0.819 0.352 0.621 -0.118 0.004
-0.936 0.337 1.188 1.750 -1.216 -3.026 1.504 -0.907
1.246 0.271 2.185 1.439 0.559 2.970 0.967

Table36.txt

0.801 -0.591 -0.686 0.243 1.745 1.237
-0.099 0.809 -0.779 -0.442 0.504 1.457 -0.608 0.765
0.326 -0.891 0.206 1.088 -1.112 0.216 -0.380
0.262 -1.417 1.113 -1.009 0.559 -1.648
-0.559 0.897 -1.113 -0.062 0.006 -1.304 1.290 -0.160
0.191 -0.526 0.423 -1.657 0.021 -0.312 1.532
0.231 -0.499 -0.296 1.313 0.909 -1.854
-0.181 0.733 0.293 0.427 1.336 0.460 -0.071 -0.077
-0.652 -0.123 -0.435 -1.671 -0.188 0.246 -0.440
0.748 -0.127 -0.732 0.013 -0.849 -0.951
-0.241 0.610 1.538 -0.363 -0.922 -0.189 1.103 0.889
0.163 0.347 -2.097 -0.220 -0.145 0.745 -0.704
-0.457 0.102 0.001 0.158 0.068 -1.732
0.614 0.976 0.612 -1.010 1.297 -0.244 0.362 0.677
1.393 -0.404 -0.871 1.327 0.505 0.331 1.284
-0.354 -0.789 -0.306 -0.594 0.326 0.896
0.081 0.915 -0.195 -0.803 0.668 0.787 0.947 -0.722
1.133 1.089 -0.692 -0.647 -0.363 -0.667 -0.726
0.174 -0.886 0.526 -0.105 -1.299 1.078
0.541 -0.349 0.020 -0.891 1.834 -0.448 -0.237 -0.036
-0.589 0.806 -0.833 -0.487 0.847 0.711 -1.601
-0.184 0.190 0.699 -1.079 -0.430 -0.264
-1.934 -0.843 -0.030 -0.918 0.273 1.079 0.437 0.547
-0.584 2.050 0.870 0.710 1.233 1.087 1.446
1.175 -0.956 0.773 2.072 0.849 -0.179
0.809 0.410 0.628 1.179 -0.871 -1.429 0.643 1.224
-0.999 -0.211 0.978 0.089 0.755 -0.904 0.604
-0.047 -0.133 -0.223 -0.426 -0.718 -0.316
-0.145 -0.275 -0.653 0.681 -1.444 -0.155 -0.182 0.587
-1.002 0.122 -0.657 0.150 1.543 0.331 -0.528
0.254 2.741 -1.898 0.143 -1.510 0.312
-0.476 -1.415 0.730 0.555 -0.172 0.967 0.781 -0.518
0.150 0.077 -0.954 1.040 -0.016 -0.477 0.828
-0.117 0.103 0.520 -0.852 0.469 0.327
1.277 -0.042 0.383 0.890 -0.770 -1.142 0.766 0.168
-0.059 0.469 -0.103 0.163 -0.985 1.001 0.990
-0.262 -0.590 1.405 0.231 0.157 -0.820
0.639 -1.387 0.158 1.170 -1.145 -0.460 0.352 -1.228
-0.274 0.057 0.028 -1.088 -0.115 0.502 0.385
0.759 0.725 -0.860 -1.126 -1.215 0.752
0.619 -1.328 -1.933 0.819 1.127 0.178 -0.177 -0.363
0.323 0.353 -1.290 -0.748 -1.018 0.706 0.267
-0.254 0.052 0.073 -0.381 0.485 -0.630
-0.823 -0.732 -0.314 0.557 0.975 0.109 0.246 -0.816
-0.553 0.332 1.952 -0.663 0.421 -0.447 1.529
0.145 -0.205 1.747 0.996 1.996 0.626
-1.610 0.406 -0.050 0.210 -0.728 0.079 1.721 0.549
0.265 -0.477 0.555 -1.384 0.413 0.567 1.841

Table36.txt

-0.432 -0.085 1.326 1.490 -0.399 -0.174
0.137 -0.521 -1.124 0.627 -0.667 -0.828 -0.339 0.510
0.405 -0.153 -0.088 0.000 -0.516 -0.597 0.622
-0.746 1.876 -1.457 2.069 -0.215 -0.600
0.095 -0.690 1.775 1.004 0.400 0.669 1.788 0.720
0.640 0.068 -0.246 -1.653 -0.288 -0.395 1.160
-1.153 -0.807 0.902 2.294 -0.133 -0.356
-0.360 0.126 -0.572 -0.823 0.205 2.348 0.083 0.517
-0.491 0.697 0.282 -1.152 -0.859 0.350 -2.088
-0.341 1.022 0.684 1.498 0.686 -0.077
1.069 0.009 0.688 -0.625 1.249 -0.714 -0.767 0.402
-0.713 1.211 -0.393 -0.399 -0.115 1.396 0.550
-0.066 1.643 -0.676 -0.722 -0.241 -1.117
1.511 0.678 0.386 -0.623 0.004 0.265 -1.186 -0.879
0.288 0.668 -0.742 -1.402 0.431 0.411 -1.384
-0.362 0.607 2.056 1.435 0.240 0.675
1.951 -0.923 -1.835 -1.638 0.650 0.295 -0.129 0.483
0.643 -0.892 0.558 -0.166 -0.234 -0.173 -2.309
-0.712 -0.133 -0.720 -0.619 -0.777 -1.341
0.824 -1.512 -0.039 -1.091 0.871 0.942 0.214 0.818
0.996 0.692 -1.267 0.812 0.152 -0.140 0.152
0.795 0.509 -0.213 0.667 0.175 -0.868
-0.403 0.402 -0.050 -0.295 1.701 2.156 -0.172 -0.215
0.310 1.243 -1.907 -0.467 0.731 -0.480 -2.374
-0.123 1.492 0.087 -0.200 -0.496 0.421
1.203 -0.503 0.361 -0.133 1.572 0.877 1.329 0.669
0.556 0.269 -0.367 -1.493 -0.543 2.051 -1.207
0.434 0.840 -0.330 -0.899 1.070 0.140
-0.917 -0.320 0.220 -0.105 2.063 -1.003 -0.547 0.270
0.050 -0.094 -0.900 0.626 -0.365 0.808 1.051
0.347 0.752 0.039 0.404 -0.471 -1.079
-0.489 0.553 0.692 0.591 0.020 -0.994 -0.097 -0.335
-0.584 -2.083 0.596 0.822 -0.227 0.962 1.408
0.908 2.071 1.558 -0.251 -0.503 1.083
0.067 -0.726 0.769 -1.283 0.930 0.802 -0.624 -0.345
-0.389 0.299 -0.567 0.290 0.760 -0.708 -1.613
0.005 0.235 -0.556 -0.497 0.194 0.299
0.808 -0.681 -0.176 -1.258 0.927 1.369 -1.375 0.106
0.275 -0.322 -0.179 -1.869 0.719 -1.397 -2.302
-0.354 1.133 0.133 -1.732 -1.219 0.322
-1.207 0.773 0.354 0.226 0.370 0.472 0.651 -0.605
-0.621 -0.167 1.745 -1.303 -0.519 -0.334 0.949
-0.372 -1.148 -1.292 0.611 0.683 1.701
-0.180 -1.168 0.517 -0.679 0.498 0.994 -1.324 0.107
1.658 -0.043 -0.943 -0.327 0.111 -0.930 -1.476
-2.510 1.476 0.321 -0.129 -1.437 -1.104
1.247 -0.883 -0.737 0.299 -0.596 0.192 0.341 -0.864
-0.952 0.568 0.782 -0.867 0.237 -0.059 -0.294

Table36.txt

0.656 -0.019 -0.711 0.108 0.804 -1.595
-0.708 0.096 1.453 -0.182 0.067 -1.012 1.024 -1.279
-0.342 1.239 2.299 -1.844 0.334 0.775 0.493
0.519 -0.801 1.189 0.450 -1.045 0.687
0.246 0.184 0.051 -1.557 -0.250 0.239 -0.309 -0.170
0.156 -0.487 0.198 -1.348 0.372 -0.332 -0.927
-1.292 1.085 0.086 0.993 -1.321 0.286
-0.665 1.653 0.304 -0.587 2.638 0.608 -0.872 -0.152
-0.008 0.648 -0.057 -0.712 1.845 -0.731 -1.537
-0.184 0.364 0.439 -1.189 -0.748 1.312
0.196 0.419 0.105 -0.419 2.152 0.459 0.995 -1.079
0.813 0.938 -0.853 -1.727 1.316 -1.508 -1.643
-0.422 0.777 0.161 -0.416 -2.066 -1.082
1.347 -0.678 -1.730 -1.686 0.958 -0.817 -0.330 0.656
1.790 1.217 -2.243 -0.667 -0.860 -1.288 0.045
0.864 1.007 -1.753 0.741 -0.365 -0.193
0.378 0.885 2.183 -0.917 -0.867 -0.427 1.551 -0.132
-0.805 -0.305 -0.357 -0.918 0.683 0.827 2.127
-1.915 -0.113 1.201 -0.758 -0.112 0.120
0.143 1.563 0.497 1.243 0.269 -1.225 -0.032 -0.620
0.368 -0.694 0.398 1.676 2.400 0.529 0.805
-0.912 -0.923 1.148 1.407 0.533 0.070
0.550 -0.347 0.207 0.726 0.386 -1.780 -1.037 0.101
-0.361 0.763 -1.505 -0.292 1.484 -0.068 -0.149
1.960 1.276 0.591 -0.648 -0.399 0.887
0.847 -0.980 0.516 -1.072 -0.218 1.053 0.760 0.768
0.652 0.244 -0.180 0.881 -0.877 -0.132 -0.336
0.146 1.772 0.623 -0.882 -0.105 -0.931
-0.671 0.332 0.084 -0.373 -1.536 0.815 -0.220 0.940
-0.009 0.779 -0.071 -1.737 0.694 0.661 0.357
0.298 -1.102 2.130 -0.377 0.252 -1.941
1.434 -0.649 -0.255 -0.585 -0.019 0.954 -0.680 -0.151
0.128 0.221 -0.606 -0.815 0.639 0.472 -0.443
-0.564 0.705 0.206 -0.519 -0.109 -0.508
0.751 -1.567 -1.678 -0.026 -1.284 0.424 0.086 1.338
-1.723 0.323 -2.308 1.869 0.650 -2.572 0.905
-0.657 -1.185 -0.190 -0.530 0.931 0.281
-0.996 0.837 0.820 1.921 0.473 -0.572 -0.561 0.147
-0.756 1.481 0.892 -0.095 0.096 -0.486 2.156
0.371 -0.324 -0.098 0.842 1.086 0.381
1.100 -0.319 -0.754 0.413 -0.395 -0.087 -1.316 -0.177
-0.328 0.051 -1.920 0.159 0.546 -0.350 -0.599
1.220 0.959 1.051 -0.546 -0.684 0.143
-0.876 1.017 1.755 -0.939 0.206 0.568 1.194 0.760
-0.587 0.715 0.206 -0.501 0.610 -0.124 0.205
0.007 -0.553 -0.223 0.273 1.085 -0.612
-0.393 -0.022 0.808 -1.483 1.382 -0.269 -0.714 -1.302
0.207 0.311 -0.175 -1.668 1.818 -0.315 -1.092

Table36.txt

-0.358 -0.262 -0.230 -0.245 0.171 -1.105
0.774 1.413 -0.721 -0.454 1.762 1.501 -2.107 1.165
1.757 -0.067 0.002 -0.095 0.323 -0.252 -2.518
-1.812 1.296 -0.806 0.462 0.487 0.034
0.100 0.912 -1.570 -0.155 1.290 0.969 -0.970 -1.371
0.136 0.677 -0.649 0.212 -0.822 -0.659 -0.991
-0.378 -0.161 0.753 0.076 -0.187 -0.627
-0.665 0.629 -0.085 -1.591 2.066 2.303 -0.841 0.009
0.752 -0.661 -0.153 -0.749 0.550 -0.524 -2.515
-2.606 0.574 1.086 0.672 -0.607 0.239
0.414 -0.514 0.873 0.143 -0.083 2.439 -1.384 0.380
-0.580 0.095 -0.032 -1.379 0.592 0.152 -1.950
1.452 0.749 0.354 1.042 -0.109 -0.605
-1.093 1.384 -2.007 0.108 0.089 -0.114 -0.146 -0.709
-0.778 0.258 0.006 -0.498 -0.275 -1.104 -1.106
-0.485 1.177 -0.637 1.222 -0.011 1.855
0.763 -1.182 -0.492 -0.013 1.248 1.005 -2.075 0.527
0.487 0.797 -1.557 -1.213 -1.207 0.146 -1.807
-0.774 0.925 -0.480 1.061 0.233 0.003
1.621 -0.298 1.220 -0.942 0.024 1.995 -1.354 1.139
0.266 1.848 -2.086 -1.824 1.087 -1.137 -2.253
-1.478 -0.220 2.321 -0.258 -0.503 -0.095
-0.272 -0.175 -0.257 -0.546 1.645 1.063 0.239 0.203
-0.683 -0.634 -1.055 -0.860 -0.138 -1.953 -1.715
0.370 0.077 0.341 0.907 -0.392 0.078
0.293 -0.161 -0.533 0.669 0.509 1.961 -0.336 2.504
-1.182 0.650 0.619 1.876 1.366 0.983 1.793
0.532 0.472 1.903 1.034 -0.580 -0.172
0.107 -0.797 0.611 0.593 0.783 2.043 1.322 0.147
-0.485 0.069 -0.572 0.584 1.351 1.244 -0.945
-1.503 -0.014 -0.340 1.594 -0.181 0.726
0.520 -0.378 -1.062 -0.641 -0.999 -0.566 0.388 -0.153
0.938 0.234 0.095 -1.800 0.175 -0.237 0.392
-0.032 1.522 -2.149 0.337 -0.413 -1.768
-1.216 -1.020 -0.522 0.974 1.203 -0.555 0.252 0.142
0.764 -1.122 0.943 -0.360 -1.286 1.942 1.045
-0.795 1.352 -0.107 1.469 -0.513 -1.645
0.049 -0.786 -0.527 -0.542 -0.060 0.573 -0.439 0.022
0.144 0.769 -1.107 0.548 -0.545 -1.600 0.502
0.828 -0.707 -0.560 -0.353 0.342 -0.255
0.024 -1.122 0.965 1.354 -2.803 -2.364 0.668 -0.980
0.362 0.337 1.576 0.260 0.141 3.017 0.896
1.014 0.158 -0.508 1.631 1.711 0.327
-0.072 -1.307 0.383 1.743 -0.152 -0.177 1.130 0.764
0.168 0.572 0.714 -0.514 0.232 0.161 0.753
-1.102 -1.498 0.122 0.658 0.185 -1.888
-0.030 0.113 0.433 3.013 -0.651 -1.522 0.101 0.605
-1.612 -0.919 -0.039 -0.393 0.789 1.234 1.854

Table36.txt

-1.201 1.304 0.310 0.639 1.403 -1.070
-2.032 -0.583 0.456 0.965 -2.394 -0.660 0.868 1.213
0.015 -0.327 0.622 0.024 -0.527 -0.964 2.259
-0.024 0.846 -1.180 1.550 0.925 -0.335
-0.140 -0.469 0.013 -0.813 1.045 0.122 -0.438 -0.209
0.001 -1.039 1.027 0.847 0.201 1.331 0.709
-1.322 1.667 0.713 2.021 -0.299 -0.736
-0.540 0.770 0.909 1.616 0.192 0.124 1.841 0.543
-0.802 -0.286 -0.179 0.067 -1.001 0.647 0.557
0.308 1.611 0.391 1.087 0.085 -0.323
-0.907 0.511 0.709 1.245 -0.170 -0.711 1.878 2.036
-1.856 0.338 1.379 1.305 0.433 2.044 1.608
-0.376 0.031 1.710 1.438 0.859 -0.411
-0.541 0.646 -0.233 -1.962 0.667 0.539 -1.235 0.625
0.646 0.572 -1.113 0.029 0.089 0.374 0.561
1.362 0.722 -0.587 0.330 0.620 -0.245
-0.543 -0.100 -2.114 -1.661 1.370 0.511 1.100 1.646
-0.338 -0.444 -0.753 -1.339 -0.807 -0.454 -2.573
-0.430 -1.071 -1.148 0.644 0.194 -0.493
3.141 0.039 0.477 0.695 0.865 -0.752 -0.096 -0.826
-2.889 -1.080 -0.115 0.150 1.279 -1.555 -0.881
0.213 1.088 0.321 -0.595 1.073 -0.143
-1.345 1.414 -0.213 2.005 -0.426 0.091 0.950 -0.221
0.006 0.860 0.074 -0.104 -0.720 0.016 -0.147
-1.652 -0.405 1.484 0.376 0.534 -1.496
-1.711 0.324 0.608 0.605 -2.241 -1.373 0.477 0.478
-0.617 0.953 2.704 1.226 1.038 3.241 4.268
0.620 1.009 0.413 0.181 2.279 0.419
0.523 -0.629 -0.289 -0.325 -0.270 0.029 1.222 1.403
0.398 0.525 -2.364 0.900 -0.349 0.894 0.247
-0.773 0.182 0.560 -0.166 -0.572 0.005
0.661 -0.654 1.231 -0.267 -0.032 -1.066 0.406 -0.821
-0.054 0.276 -0.330 0.840 -1.127 0.815 -0.331
0.753 -0.344 -0.037 -0.405 0.872 0.031
-0.505 -0.537 2.189 0.499 -0.133 0.272 1.425 0.037
-0.665 -0.459 0.334 -2.259 -0.229 1.119 -0.401
-1.273 -0.273 0.082 -0.162 1.643 -0.349
0.734 -1.022 -0.628 -0.185 0.466 -1.534 0.482 1.019
1.065 0.155 1.591 0.765 -0.795 2.222 0.964
-0.250 -0.413 0.568 1.279 0.593 -1.796
1.090 0.471 0.631 -0.566 0.499 -0.633 0.106 -0.538
-0.338 -0.405 -0.005 2.186 -0.302 1.449 -0.328
0.453 0.887 -0.936 -0.406 -0.500 -0.851
-1.233 -0.996 0.151 0.765 -1.296 -0.616 0.821 0.096
0.796 -1.043 0.029 -1.137 0.284 0.333 0.507
1.476 0.800 -0.729 -0.552 0.129 0.406
-0.051 -0.426 0.917 0.484 -0.183 -0.959 -0.261 0.355
0.796 0.650 0.317 0.050 -0.814 0.679 -0.349

Table36.txt

-0.149 1.125 -0.164 1.838 0.868 0.011
0.714 -1.371 -0.051 1.295 -1.479 0.206 0.357 1.587
-0.098 0.665 0.566 -0.475 -1.470 1.799 -0.473
-0.572 0.747 0.920 -1.571 0.271 -0.721
-1.622 -1.180 1.118 2.727 -0.863 -1.778 1.510 -0.276
-0.785 1.674 1.305 0.990 -0.729 0.732 1.577
0.968 0.919 0.904 -0.214 1.467 0.644
0.116 -1.261 0.839 0.317 -0.902 -0.325 -0.457 0.701
-0.879 -0.060 0.960 -0.272 -0.073 0.449 0.284
-0.695 -0.369 -0.027 -0.228 1.289 -1.843
0.789 -1.079 0.343 0.105 -1.354 -1.397 1.004 -0.035
-0.185 0.943 0.037 0.231 0.363 1.187 0.954
-0.918 -1.667 -0.359 0.567 -1.320 1.390
-0.100 -0.756 -0.979 0.534 -0.706 -0.937 1.239 0.679
1.983 -1.069 -0.144 0.379 -1.194 0.914 -0.008
0.307 -0.631 -0.407 -0.423 3.086 0.168
0.661 -0.699 -0.353 1.906 0.774 0.564 1.123 -1.275
-0.331 -0.373 1.587 -0.087 -0.211 0.900 2.203
0.202 -0.338 0.079 0.263 0.510 1.341
-0.573 1.821 1.888 2.411 -1.326 -0.121 -1.498 -1.542
-1.386 -0.382 1.874 0.413 1.569 0.626 1.148
-0.394 -1.294 1.485 0.929 -0.715 0.252
-1.251 1.335 1.475 1.573 0.623 0.545 -0.582 -0.138
0.521 -1.319 0.813 -1.867 1.255 -0.440 0.230
-0.540 -0.311 -0.370 -0.725 -0.382 -0.233
1.053 0.018 -1.231 1.432 1.416 0.298 -0.389 -1.053
0.875 0.685 -0.026 1.025 -0.148 0.131 0.334
0.037 -1.176 -0.678 -0.154 -0.283 -0.432
-1.135 -0.962 -1.553 -0.447 0.751 0.381 0.236 0.488
-1.132 0.756 0.561 1.538 0.739 -1.064 0.603
0.763 0.097 1.248 -0.081 -2.437 0.923
-0.258 0.936 -0.584 0.822 -0.060 0.051 1.025 -0.910
0.393 0.963 0.458 -0.630 0.395 0.637 -0.725
0.922 -0.823 -0.145 -0.141 1.607 0.984
-1.087 0.045 0.165 1.380 0.140 0.770 0.841 -0.893
-0.528 -1.268 0.536 0.770 0.141 1.302 1.135
-1.202 0.508 1.179 -0.836 0.177 1.925
-0.009 0.014 -0.730 -0.506 0.340 1.007 1.017 0.484
0.473 1.104 -1.115 -0.237 -0.509 0.553 1.620
0.014 1.436 -1.790 -0.588 0.448 0.955
1.208 0.661 -0.707 0.289 1.332 1.394 -0.839 0.300
0.028 -0.287 -1.007 0.307 -0.014 -0.451 -1.510
-0.923 0.804 -0.135 0.302 -0.714 1.121
0.285 0.604 0.034 -1.976 -0.007 2.583 -1.004 -1.731
-2.542 1.508 -1.578 0.140 1.997 0.782 -0.935
0.435 0.404 1.881 -0.694 -0.134 0.755
0.268 0.171 -0.766 1.162 0.088 0.219 0.475 -1.135
1.128 1.294 -1.104 -1.088 -0.028 0.224 -0.052

Table36.txt

0.497 -0.437 -0.431 -0.573 0.515 1.672
2.097 -0.240 -1.194 -0.835 1.092 0.275 1.104 -0.295
0.606 -0.176 0.886 -0.513 0.078 -0.942 -1.406
-2.407 0.752 1.485 1.272 -1.150 -0.079
-0.755 -0.086 -1.674 -0.841 1.301 0.611 -1.244 -0.267
0.275 -0.251 0.671 -1.636 -0.783 -1.171 -2.117
0.398 1.113 -0.833 -0.199 -1.380 -0.456
-2.109 1.510 0.505 0.786 1.760 0.965 -0.717 0.309
0.457 0.083 0.886 -1.994 -0.027 0.253 1.420
-1.005 -0.466 0.008 0.080 0.797 0.794
-0.664 -0.924 0.109 0.256 0.626 -2.144 1.215 -0.296
-0.018 0.059 -0.691 1.497 -0.854 0.139 -0.426
-0.651 -0.938 1.747 0.355 -0.350 -0.805
-0.132 0.985 -0.145 -0.399 1.367 1.664 -0.739 0.015
0.309 1.932 1.040 -0.103 0.347 0.159 -1.721
-0.572 -0.070 1.085 1.762 -1.131 0.189
-1.024 2.439 1.040 -0.150 -0.598 0.257 0.752 -0.902
-1.271 -0.253 1.374 0.409 -0.263 0.943 0.008
-0.827 0.038 0.451 1.494 1.383 0.862
0.092 1.087 -0.338 -1.071 0.350 2.596 -0.754 -0.367
-0.573 -0.721 1.137 -0.245 -0.592 -0.702 -1.344
-0.349 0.210 1.067 0.501 0.149 -0.753
-1.844 0.053 0.222 -1.892 1.270 -0.416 -1.560 0.277
-0.115 -0.924 0.915 0.295 -0.017 0.419 -0.485
0.369 0.147 1.227 0.345 0.933 -2.031
-1.104 0.658 0.059 -2.138 -0.018 1.891 -1.015 -2.095
0.349 0.334 -1.120 0.410 -0.374 -0.930 -0.693
-0.203 0.136 1.517 0.346 0.805 0.575
-0.101 -1.296 -0.517 -0.458 -0.066 -0.033 1.117 1.681
1.148 -0.253 -1.200 0.676 0.907 -1.321 -0.236
0.639 -1.971 1.567 1.276 0.347 -0.349
-2.421 2.564 1.657 0.701 1.227 -0.192 1.267 0.546
0.844 0.763 -0.796 0.733 0.429 1.033 0.401
-1.263 -0.778 -0.263 -1.155 0.985 0.707
-0.047 0.428 -0.479 -1.761 1.475 1.705 0.997 0.539
-0.612 -0.246 0.279 1.374 0.291 0.051 -0.011
0.175 -0.498 0.494 0.716 1.538 0.678
-0.493 0.784 -0.854 0.489 0.053 0.480 -0.684 0.387
-1.128 -0.869 -1.062 0.284 0.676 0.106 0.344
-0.019 0.384 0.847 0.178 0.210 0.798
0.143 -0.333 -0.861 -0.088 0.078 -1.063 0.123 -0.434
-0.463 1.554 0.732 1.396 0.655 0.051 -0.157
-1.002 -1.588 1.049 -0.604 -0.730 2.025
-2.661 -0.780 0.121 -0.644 2.033 1.245 1.488 -0.370
0.013 -0.011 1.303 -1.269 1.414 -0.917 -0.317
1.120 0.322 1.093 3.089 -1.125 0.092
-0.139 0.234 0.377 -2.221 1.161 1.258 -1.139 -0.044
-0.142 0.477 -1.532 -1.183 -0.509 -1.828 -2.124

Table36.txt

0.794	0.245	-1.741	-1.690	-2.046	-0.307		
-1.194	0.602	-0.769	-0.895	0.052	1.474	0.675	1.866
-1.090	-0.559	-2.123	-0.135	-0.761	-0.037	-0.167	
1.136	0.992	2.516	-1.126	-0.918	0.573		
0.541	1.754	0.402	-1.350	0.549	1.140	-0.317	0.855
-0.615	-0.713	-0.912	-0.681	1.399	-1.220	-0.557	
-0.185	0.384	0.506	-0.196	-0.469	0.219		
-0.170	-0.374	-0.950	-1.207	-0.536	1.708	-0.083	-0.882
-0.394	-0.576	-0.604	-1.205	1.376	-0.627	-0.329	
0.405	0.588	0.265	-0.773	0.532	-0.466		
0.028	-0.739	-0.091	-1.630	0.377	1.813	0.499	-0.449
-0.867	-0.121	-1.745	-0.350	1.167	0.242	-0.684	
1.220	1.861	-1.176	0.779	0.355	0.534		
-0.726	-0.844	-0.032	-1.908	0.160	0.987	-1.021	0.827
1.354	-0.393	-0.720	-1.116	-0.220	0.197	-1.044	
-0.338	0.151	-0.557	0.149	0.913	0.019		
0.536	-1.294	-0.837	0.212	-0.209	0.786	-1.181	0.064
0.037	0.076	0.050	1.016	0.903	0.603	1.373	
-0.968	0.398	0.885	-0.144	-0.662	0.704		
-1.347	2.400	2.112	0.057	0.283	0.496	1.186	1.202
-1.244	-1.029	1.532	0.735	0.242	1.799	3.028	
-1.934	-1.798	0.125	-1.599	0.386	-0.418		
0.613	-0.547	-0.251	-0.776	-0.208	0.032	2.041	1.050
0.195	-0.432	-0.821	0.719	-1.622	0.649	-0.488	
-0.033	-0.272	0.128	-0.341	-1.029	0.568		
-0.305	-0.498	-1.101	-0.719	-0.352	2.097	0.157	-0.070
-0.791	1.244	1.157	-0.722	0.254	1.693	2.372	
-0.857	-0.840	1.245	0.700	0.987	0.925		
0.527	-0.502	2.092	-1.340	1.809	0.911	-0.964	1.116
0.787	-1.824	-0.413	0.524	-0.218	-0.069	-1.567	
-0.166	0.910	1.839	-0.170	-0.888	1.175		
-0.294	0.996	-1.438	-0.333	-0.822	-0.430	0.154	0.326
0.893	0.469	-1.245	-0.099	1.468	-0.562	1.223	
-0.531	-0.702	-1.206	0.061	1.116	-0.317		
-0.130	1.808	0.295	-2.543	2.277	0.779	-0.550	-1.169
-0.311	-0.684	1.090	-1.167	0.651	-0.075	-2.255	
-0.749	0.136	-0.971	0.306	-0.194	0.962		
-1.752	-0.408	-0.424	0.679	0.369	0.443	0.798	-0.021
-1.892	-0.407	1.166	0.031	-0.699	0.049	-0.537	
-0.218	-0.717	0.893	1.421	1.659	-0.266		
-0.798	1.342	0.499	0.675	0.799	0.115	0.350	1.130
-0.990	0.513	1.109	0.445	1.364	1.651	0.920	
0.763	-0.220	0.304	1.519	0.394	0.586		
0.146	0.234	0.408	0.181	0.918	0.362	0.082	1.458
-0.073	-0.188	0.583	-0.705	-2.013	0.861	-0.105	
-0.139	-0.854	0.626	-1.118	0.628	-0.487		
-1.435	-1.248	-0.565	0.212	-0.422	0.336	0.443	0.093
1.158	0.301	-0.702	-0.801	-1.085	-0.259	-1.027	

Table36.txt

-1.137 -0.635 1.732 1.823 0.347 -0.230
-1.800 -0.531 0.559 -0.986 2.035 1.428 0.002 -0.733
-0.227 0.891 0.894 -0.023 -0.764 -0.272 -0.115
0.639 -1.079 0.617 0.753 1.027 1.605
1.967 -1.470 -0.335 1.225 0.148 1.267 -1.203 0.054
-0.771 0.258 -0.870 -0.066 0.742 -0.453 -2.138
0.546 0.245 0.884 -0.747 -0.727 -1.268
-0.534 -0.297 1.092 0.382 1.089 2.371 -0.264 0.254
-1.007 0.054 0.648 -0.189 0.225 -0.705 0.225
-0.915 0.654 2.048 -0.642 0.029 0.801
-0.591 -0.832 0.106 0.364 1.725 -0.215 -1.151 -0.146
-1.140 1.268 -0.368 -1.059 0.456 -0.640 -0.726
-1.469 0.294 -0.039 0.659 1.013 0.640
0.070 0.642 -0.567 -1.698 0.309 0.806 -2.227 -1.469
-0.883 1.640 -2.229 0.027 -1.041 -0.604 -0.443
-0.581 -0.458 0.567 0.308 -0.794 -0.335
-0.822 1.226 0.198 0.659 -1.076 -0.454 -0.204 0.049
-0.018 -0.017 0.079 0.842 -0.716 0.637 0.668
-1.255 0.660 -0.364 -0.789 0.425 1.034
-1.225 -0.388 0.937 -0.492 -0.682 1.430 0.246 1.261
-0.772 0.930 -1.401 -0.028 -0.166 0.580 0.700
-0.647 0.317 -0.220 0.538 -0.320 0.706
1.068 -1.816 -0.775 -1.466 -0.691 0.877 0.156 0.659
2.803 -0.222 -0.407 -1.001 -1.091 -1.139 -0.522
-1.237 1.277 0.403 0.231 -0.014 -0.475
-0.779 0.303 1.226 -1.863 -0.920 -0.397 0.690 -1.700
-0.009 -1.324 0.432 -0.736 -1.625 -0.310 1.118
-1.201 0.749 0.115 0.067 1.212 -0.431
1.746 0.371 0.721 -0.494 1.180 -0.135 -0.139 -0.188
0.282 2.076 -0.624 -1.161 -0.024 -1.426 -0.496
-1.817 0.148 -1.184 -1.159 0.059 1.022
0.211 0.101 -0.025 -1.922 1.212 1.998 -0.586 0.973
-1.180 0.415 -0.253 -0.288 1.093 -1.224 0.060
1.170 0.307 0.757 -0.992 -0.136 0.246
1.983 -0.425 -1.694 0.052 0.050 1.465 -1.048 -1.253
0.372 -1.453 -1.852 0.314 0.697 0.254 -2.475
-1.152 1.581 0.874 1.424 1.051 0.771
0.054 0.272 0.529 0.000 -0.509 -0.847 0.032 0.422
1.712 0.098 -0.974 -0.338 0.101 -1.589 -0.222
0.316 0.327 1.223 -1.143 0.308 -0.908
0.847 0.188 0.262 -2.213 -1.523 -0.546 -1.603 1.427
-0.226 1.346 -1.229 -0.864 -0.252 0.687 0.071
-0.826 0.724 -0.330 -1.376 0.028 -0.989
1.315 0.157 -0.153 -0.835 1.960 -0.181 -0.133 -0.235
-0.757 -0.171 0.024 -0.215 0.548 0.543 0.653
-1.296 -0.413 -0.752 -0.583 0.243 0.096
0.368 -0.107 -1.419 -1.058 0.281 1.076 -0.268 0.890
0.370 0.084 -0.307 0.663 -1.540 0.822 1.176

Table36.txt

0.338 0.876 -0.067 1.302 -0.268 0.993
1.038 -1.898 -0.276 -1.378 0.236 -0.894 0.424 2.000
-0.093 1.566 -0.638 -1.800 -0.004 -0.418 1.448
-0.594 0.844 0.407 1.462 -0.877 -1.239
0.904 -0.270 0.103 1.055 -1.217 -0.294 1.234 1.256
0.204 0.784 -1.041 -0.595 -0.370 -0.166 -0.359
-0.075 2.791 -0.526 0.356 -0.268 -0.496
0.798 -0.628 0.375 -0.491 0.088 -0.606 -0.470 -0.251
-0.190 0.483 0.032 -0.675 -0.022 -0.042 -0.798
-0.346 -1.238 -1.099 -1.370 -0.478 -0.600
-0.425 -0.501 -1.357 0.219 -1.612 -0.380 0.109 0.905
-0.499 0.809 -1.681 -0.662 0.057 -0.122 -1.219
0.097 -0.239 -1.624 -0.865 -0.982 0.157
0.038 -1.755 0.189 0.250 0.081 -1.131 0.918 0.804
0.590 0.049 0.032 -0.782 -1.191 -0.677 1.373
-0.665 -0.123 0.019 1.385 0.949 -0.378
-0.184 -1.933 -1.000 -0.591 -0.996 0.399 0.486 0.118
1.168 0.846 -0.284 -0.362 -0.283 -0.184 0.082
-0.711 1.605 1.002 0.797 -0.901 -0.409
-0.784 -1.807 0.467 -1.410 0.820 0.439 0.150 1.632
1.216 0.485 -1.270 -1.189 -0.446 -0.618 0.998
-0.887 -1.751 -0.445 1.155 0.124 0.880
-1.085 -1.600 -0.232 -0.131 -0.260 1.126 0.051 1.682
-0.751 2.037 -1.192 -0.246 0.418 -0.333 -0.368
-1.185 -0.083 0.212 0.284 -0.300 -0.690
-3.044 -4.156 -0.056 -1.066 -0.469 0.000 0.474 1.081
-2.587 -4.376 -0.226 -2.659 1.198 -0.720 -0.235
0.372 -2.249 -0.143 -0.092 1.173 1.587

chr21q chr22q chr1p_AI chr1q_AI chr2p_AI chr2q_AI chr3p_AI
chr3q_AI chr4p_AI chr4q_AI chr5p_AI chr5q_AI chr6p_AI chr6q_AI
chr7p_AI chr7q_AI chr8p_AI chr8q_AI chr9p_AI chr9q_AI chr10p_AI
-0.043 -2.842 -0.667 -1.122 -0.923 0.089 0.155 -0.502
1.500 -0.814 -1.569 -1.702 -1.333 -0.255 -2.332
-0.276 -1.097 -0.833 -0.440 -0.128 0.439
0.071 -1.237 -1.464 -0.932 -1.810 -2.382 -1.186 -1.405
-0.136 -1.650 0.645 -3.005 -0.800 -0.996 -1.344
-2.468 -0.822 -2.846 -0.936 0.356 -0.555
1.061 -2.182 1.622 -0.561 2.134 -0.193 0.154 1.333
0.452 0.077 -0.618 -1.541 0.231 0.389 0.750
-0.118 -0.869 -1.550 -0.222 2.274 -0.397
0.361 -1.591 -0.656 0.583 -0.361 -1.026 0.072 -0.206
-2.012 -3.007 0.349 -2.075 -1.217 -0.826 -0.798
0.032 0.422 0.590 -1.690 -0.779 -1.752

Table36.txt

0.369 -1.630 -1.551 1.195 0.083 -0.853 -1.722 -0.131
-1.599 -1.230 -0.254 -0.719 -0.967 -0.351 -2.095
0.185 0.377 -3.581 -0.628 -0.653 0.601
0.852 -0.854 -1.487 -1.235 -1.697 -2.149 -0.687 -0.677
0.210 -0.629 0.940 0.584 -1.373 -1.523 0.529
-1.862 0.164 0.219 -2.546 -0.194 -0.676
1.917 -1.502 -0.832 -1.797 -2.247 -1.913 -0.612 -0.189
1.527 -0.740 -0.205 -1.463 -0.146 -0.148 0.396
-1.127 -1.267 -1.754 -0.372 -1.518 -0.848
0.948 0.152 0.324 -0.931 0.894 -0.605 -1.076 -0.650
-0.670 -0.849 -1.977 -0.479 -1.728 1.077 -0.365
-0.670 -2.034 -0.787 -0.868 0.868 0.707
1.561 -1.917 1.311 -0.524 -0.928 -1.348 -1.254 0.508
-1.374 -3.330 -1.576 -2.579 -0.340 -2.704 2.254
-2.355 -0.445 -2.839 -0.260 -0.180 -0.082
-0.320 -2.472 0.546 0.350 0.526 -0.555 1.462 0.423
0.911 -1.262 -0.147 0.041 0.346 1.326 0.489
1.051 -1.874 0.817 2.247 0.867 0.831
1.292 -2.728 0.850 0.477 1.790 -1.719 -0.479 -2.600
-2.634 -0.311 0.239 0.236 0.062 -0.300 -0.848
-0.087 0.727 -0.613 -1.406 -1.830 -2.478
-0.401 -0.778 -0.515 0.509 -0.409 -0.808 -1.993 -1.015
0.088 -1.658 -1.716 1.225 1.048 -1.436 -0.918
-1.242 0.239 -1.069 0.476 0.627 -1.932
-0.160 -2.182 0.102 0.464 -0.001 1.995 -1.788 -2.143
-0.893 -0.815 -1.053 -0.184 -0.296 -0.789 0.412
0.305 -0.596 1.722 1.817 -0.954 0.389
1.442 -0.273 -0.646 -1.671 -0.069 -0.669 -1.344 -0.255
-1.281 -0.709 -1.188 -1.662 -0.537 -1.499 -1.932
-1.282 0.434 -1.160 -0.884 -1.865 0.006
0.871 -1.456 -1.236 0.800 -1.080 -2.264 -0.714 -0.686
-1.801 -1.096 -0.003 -1.399 0.175 -1.506 -0.635
-1.031 -1.097 0.216 1.235 0.612 0.304
0.092 -0.118 -1.858 0.294 0.790 -0.066 -0.802 -3.297
-2.184 -0.050 0.482 -0.485 -1.289 -1.124 -0.922
-1.432 0.204 0.594 -0.849 -0.147 -0.848
-0.120 -1.019 -1.452 -0.994 -0.917 -0.584 0.059 -1.214
-2.331 -3.230 -3.120 -2.495 -0.696 -1.324 -2.265
-3.083 -0.297 -1.667 -0.857 -0.991 -2.209
0.235 -2.572 0.409 -0.003 0.009 -0.804 0.020 -1.299
-0.252 -0.764 -1.065 -2.534 0.423 -1.054 0.500
-0.433 -0.939 -0.478 0.049 0.417 -0.895
0.527 0.453 0.061 0.504 -0.143 -1.004 -1.157 0.495
-1.416 -0.314 -1.816 -1.307 -0.090 -0.890 -1.290
0.997 -1.285 1.481 -0.401 0.322 -1.040
1.071 0.566 -2.041 -1.815 0.223 0.190 -0.821 -1.659
-0.737 -0.057 -0.678 -2.060 -0.871 -1.323 -2.966
-0.002 1.699 -1.383 -3.850 0.407 -0.156

Table36.txt

0.070	-1.483	-0.767	-0.188	-0.849	0.014	-0.091	-0.181
-1.418	-1.546	-1.463	-0.890	-0.846	-0.563	-2.689	
-1.557	-0.560	-0.840	0.178	-0.178	-0.540		
-0.193	0.821	-0.762	-0.229	0.152	-3.090	-0.847	-0.346
-2.687	-0.844	-1.773	-0.828	0.123	-1.441	0.712	
-1.946	-0.690	0.032	-0.756	-1.363	-1.101		
0.170	-1.369	0.893	0.816	-1.091	-1.480	0.618	-1.403
-1.601	-1.042	0.740	-0.535	-0.537	-0.725	-1.701	
0.832	-1.849	-1.286	-0.873	0.297	-0.697		
0.758	-1.623	13.193	15.324	13.523	18.119	15.935	21.921
13.738	21.504	11.711	21.135	12.219	19.187	12.321	
17.913	8.206	15.963	13.123	9.291	12.645		
0.100	-0.596	-3.315	0.120	-3.360	-0.390	-0.818	-0.987
-0.654	-1.067	-0.030	1.036	-0.536	-1.801	-1.481	
-2.235	0.884	-2.124	-0.281	-0.260	-0.814		
0.184	-1.817	0.369	0.103	-1.842	-0.603	0.472	-1.350
0.062	-1.088	-0.228	-3.489	-1.181	-1.555	-1.688	
-1.916	0.356	-2.603	-0.730	1.242	-1.403		
0.878	-1.629	-0.811	0.261	-1.483	-3.106	-0.945	-0.743
-1.520	-3.424	1.061	-2.771	-0.666	0.617	-0.845	
-2.683	-1.523	-0.869	-1.811	-1.120	-0.248		
1.756	-0.607	-1.162	0.573	-1.966	-2.153	-2.151	-0.996
-0.276	-2.877	-0.082	-0.724	0.124	-1.754	-0.751	
0.302	-0.344	-0.790	-1.500	-2.280	0.221		
0.758	-1.944	-0.226	0.698	0.150	0.957	1.894	-0.799
-1.041	-0.330	-0.950	-1.105	1.383	-1.145	-0.321	
1.256	0.496	0.833	-1.136	-0.958	-0.797		
-4.889	-1.189	-0.072	1.349	2.520	-0.490	-0.229	-0.018
-0.053	0.996	-0.022	1.473	0.693	-2.374	0.308	
1.076	3.205	2.228	0.261	-0.667	-1.250		
0.340	-0.876	-1.121	0.399	0.351	-0.571	0.203	-1.247
-0.188	-1.037	-1.291	0.000	-0.006	-1.281	-0.682	
-1.469	-0.701	-0.690	0.733	-1.954	-1.224		
1.487	-2.695	-0.828	-0.902	0.757	-2.624	0.091	-1.607
-0.616	-1.953	0.140	-2.449	0.259	-0.360	-1.329	
-1.211	0.850	-0.313	0.180	-1.199	-1.085		
0.589	-1.137	-0.296	-2.158	0.761	-2.052	0.432	-3.058
-0.725	-1.880	-1.492	-1.277	0.756	-0.626	-1.686	
-0.913	0.512	-1.583	-0.579	-0.039	-1.759		
0.840	0.126	-0.068	-1.825	-0.562	-0.526	-2.504	-0.972
0.957	-1.976	-2.610	-1.995	-1.392	-1.071	-3.022	
-1.385	-0.116	-0.736	-0.382	-1.136	-0.569		
2.165	-2.775	3.030	1.186	1.049	0.243	1.708	-0.937
-1.170	-0.674	-1.378	0.684	-0.152	-0.587	2.373	
0.652	2.941	-2.383	1.111	-0.227	-0.210		
0.751	-2.862	-1.075	-1.994	0.723	-1.178	-3.139	-1.141
-1.265	1.205	-1.311	-0.922	-1.805	-0.263	-1.332	
-2.417	-1.158	-1.078	-1.610	-2.961	-1.153		

Table36.txt

0.986	-1.508	0.634	-1.143	0.985	0.548	-0.583	-0.532
-0.056	-2.068	0.089	-0.540	-1.368	-1.993	-2.271	
-1.330	-0.171	-0.851	-0.251	0.927	-1.338		
-0.611	-0.712	-3.043	-0.233	-1.003	-1.427	-1.283	0.052
-1.825	-1.727	-0.965	-1.297	0.574	-1.752	0.324	
-2.044	0.413	-1.408	-1.186	0.200	-1.428		
-1.048	-0.579	-0.696	-0.215	-2.450	-1.023	-0.529	-1.040
-0.377	-1.885	-1.608	0.025	0.485	-0.653	-1.972	
-0.339	-3.052	-1.529	1.258	-0.651	-1.077		
0.618	-2.299	-0.321	0.394	-0.941	0.430	0.978	1.118
0.476	0.107	-1.247	-0.254	0.208	-2.264	-0.066	
-1.451	0.195	-0.881	0.836	-0.861	-0.589		
0.397	-1.701	2.362	0.874	0.043	-0.169	-1.545	0.285
0.136	-1.310	0.149	2.016	0.317	-0.176	-0.466	
3.179	-0.016	2.039	0.386	1.128	-0.651		
0.142	-1.216	-0.244	-0.291	-1.436	-1.463	-0.432	-3.409
0.036	-0.910	-1.168	-1.781	-0.868	-0.021	-0.749	
-0.420	-0.024	0.996	-0.844	0.854	-1.337		
0.413	-2.875	-1.274	0.609	-0.774	-2.279	0.018	-0.273
-0.131	-1.557	-0.768	-1.119	0.593	0.044	-0.791	
-1.146	-0.776	-0.663	0.591	-0.878	-2.923		
1.319	-1.743	0.305	0.474	-0.420	0.285	0.354	-2.506
-0.727	-0.063	-0.592	-1.074	0.210	0.425	0.474	
-1.466	0.977	-0.446	-2.086	1.575	0.212		
0.697	-1.308	-3.009	0.646	-0.921	-1.014	-2.891	-0.979
-1.415	-1.908	-3.481	-0.626	-0.367	-2.135	0.227	
-1.959	-2.556	-1.544	-1.963	1.025	-0.288		
0.926	-0.743	-0.923	-1.286	-1.021	-3.220	0.125	-0.717
-0.866	-0.034	-1.861	-1.911	-0.719	-1.439	-1.233	
0.303	-0.199	-1.836	-1.830	-0.688	-1.451		
0.390	-1.141	-1.598	-1.441	2.906	-1.423	1.555	0.279
-0.777	-1.410	-1.116	-3.146	0.210	-2.562	-1.791	
-0.030	-1.914	0.221	-0.246	-0.963	-0.695		
0.633	0.065	-0.773	0.586	-0.086	-1.896	-0.334	-0.881
-0.993	-1.226	-3.252	-1.285	-0.095	-0.539	-0.752	
0.312	0.546	-2.167	-0.460	0.406	1.523		
-0.844	-2.465	-1.053	-0.488	-1.035	-1.941	-0.077	-1.405
-1.797	-0.704	-1.219	-0.110	1.883	-1.027	0.586	
0.995	-1.504	-0.143	-0.246	-0.087	-1.177		
0.836	-1.423	-0.561	2.544	-0.326	-0.004	-0.054	-0.734
-1.156	-0.862	-1.088	-1.357	1.114	-0.303	-1.206	
0.032	-0.178	0.988	0.099	-1.019	-0.127		
-1.925	-0.283	0.459	-2.121	-0.457	-2.830	-0.593	-1.655
-1.338	-1.312	-1.064	-1.672	-1.435	-3.097	-0.903	
-1.960	0.605	-1.154	1.123	-0.532	-1.537		
0.808	-2.071	-1.058	-0.282	0.011	-1.370	0.049	-2.141
-1.624	-1.451	0.866	-0.085	-0.349	-1.789	-1.465	
1.330	-0.506	-1.367	-1.083	-0.496	-2.071		

Table36.txt

1.385	-0.280	-0.890	0.924	-3.176	-0.245	-1.375	-1.915
-1.151	-2.570	-1.900	-0.102	0.642	-1.055	0.108	
-0.149	0.070	-0.449	-1.204	-1.611	0.273		
1.698	-1.650	0.530	-3.160	-2.259	-2.919	1.691	-2.680
-0.911	-0.874	-2.307	-1.693	0.735	-0.278	0.099	
-0.338	0.293	-1.545	0.734	-0.092	-1.676		
0.388	-3.725	1.560	0.321	0.235	-0.003	-0.440	0.499
-0.032	0.601	-2.416	0.065	-1.674	-1.338	0.982	
-1.190	-0.464	-0.419	1.638	1.728	1.158		
1.226	-1.423	-0.100	-0.220	-0.288	0.823	1.014	-1.378
-1.783	1.040	-1.646	-1.382	0.477	-0.505	-0.667	
-1.118	1.205	-0.398	-1.799	-1.039	-1.075		
0.454	-0.461	-0.263	-0.288	2.115	-0.468	1.118	-0.445
1.398	-0.505	-0.434	-1.465	0.358	1.019	0.269	
1.589	-0.750	0.836	1.299	0.650	1.749		
0.200	-1.421	-1.512	-0.327	0.177	0.203	-1.106	-1.679
2.640	1.231	-0.923	-1.186	0.754	0.953	-1.510	
2.490	0.464	1.110	0.292	0.040	-0.120		
-0.890	-0.544	-2.059	-0.672	-0.269	-1.725	-1.366	-2.672
-1.164	-0.691	1.942	-1.850	0.782	-2.212	0.856	
-0.091	1.033	-1.760	-1.805	-1.264	0.052		
0.309	-1.512	1.923	-0.924	-2.235	-1.579	-0.888	-0.744
-0.879	0.381	-1.422	0.416	-0.693	-0.533	0.957	
-1.371	-0.503	-1.883	-1.870	-1.052	-0.915		
0.181	-1.338	-0.702	1.711	-0.869	-0.883	-1.208	-1.701
-0.132	0.170	-3.338	-2.188	-1.434	-1.657	-1.715	
-1.266	-1.021	-0.944	-1.424	-2.707	1.079		
0.551	0.057	-0.755	-1.442	-2.930	-1.618	-0.419	-0.719
-2.846	-1.975	-0.427	-1.349	-0.568	-2.411	-0.097	
0.405	-0.036	-0.445	-0.650	-1.432	-0.421		
0.115	-1.575	0.048	1.362	0.595	-0.818	-2.815	-0.375
-0.938	0.731	0.577	-0.573	-1.201	0.230	-2.323	
0.418	-1.392	0.514	0.514	-0.328	-1.148		
-0.465	-1.895	-1.093	0.775	-0.186	-1.344	-0.901	-1.117
0.287	-1.218	-0.482	0.206	-1.366	-2.627	0.385	
-1.152	-0.642	-0.003	-0.870	-0.868	-0.962		
1.096	-1.610	-2.076	0.333	2.060	-0.347	-1.417	1.013
-1.451	0.143	-0.593	-2.429	-1.177	-1.836	-0.144	
-1.422	0.134	-2.035	-1.169	-0.416	-1.448		
-0.524	-2.098	-0.340	-2.207	-2.122	-0.339	0.255	-1.205
0.349	-0.494	0.438	0.241	-0.589	-0.497	-0.926	
1.373	0.667	-0.594	-2.431	0.661	-0.606		
-1.194	0.345	-0.143	-0.787	0.366	-1.873	-1.877	-0.986
-0.810	-1.322	-0.331	-0.536	-0.230	-2.361	-2.215	
-2.227	-1.023	-2.114	-0.833	-2.304	-2.020		
-0.358	-0.384	-1.352	-1.093	-0.836	-1.591	0.801	-0.736
0.761	0.584	-2.343	-0.137	-1.290	-1.472	-0.698	
0.124	0.904	-1.167	0.088	-0.068	-0.772		

Table36.txt

-0.105	-2.492	2.358	-1.532	-1.791	-1.953	1.124	0.245
-1.293	-2.105	-2.409	-0.821	0.955	-2.356	0.140	
-2.331	-0.300	-0.648	-1.880	0.019	-2.096		
0.459	-0.396	-0.101	-2.534	-1.816	1.054	-1.723	-0.566
0.231	-1.571	-1.099	-2.413	-0.491	-1.099	-0.093	
-2.727	2.206	-1.087	-0.783	-0.019	0.286		
-0.164	-2.016	0.596	-0.206	-1.202	-1.503	-2.556	-0.619
-1.386	0.008	-0.514	-1.405	0.207	-0.246	-1.530	
-1.282	-0.408	0.002	-0.075	-0.235	0.570		
-0.212	-1.152	-2.502	0.401	-0.442	-1.828	-1.156	-0.648
-1.499	-2.993	-0.508	-0.747	0.466	-0.672	-0.966	
-1.441	-1.085	-1.328	0.040	-0.076	0.829		
0.409	-1.821	-0.618	0.692	-0.759	-1.889	-1.212	-0.572
0.345	-1.826	-2.149	-0.914	-0.752	-1.106	-1.277	
-1.019	-2.142	-1.074	-1.078	-0.754	0.696		
0.030	-2.191	-0.643	1.737	0.846	-0.225	-0.760	-0.485
-0.313	-1.502	0.703	-1.022	0.398	-0.425	-0.926	
-1.957	1.235	-1.247	-0.193	-1.747	-1.264		
0.701	0.440	-0.726	-1.183	0.452	-0.524	-0.620	-1.987
-0.145	1.270	-0.133	-1.201	-1.638	-1.726	-0.572	
0.573	-0.554	-0.991	-0.614	0.171	0.472		
1.306	-0.889	0.936	-0.787	-0.631	-2.974	-0.316	-0.700
-2.173	-1.807	-0.259	-2.447	0.712	-0.739	-1.019	
-2.635	-0.675	-0.586	0.304	-1.442	-0.818		
0.080	-1.826	-2.081	-1.752	-0.282	-2.754	-1.712	-0.909
-0.401	0.157	-0.845	-1.921	-1.192	-1.353	0.186	
-2.077	0.614	-2.119	-1.115	-3.020	1.339		
-1.276	0.310	-1.796	-0.311	-1.659	-2.256	-0.794	-2.769
-2.228	-0.674	-3.230	-0.657	-0.564	-2.380	-0.102	
-0.110	-1.184	-0.718	-1.154	-2.775	-1.158		
-0.101	0.204	0.633	-0.910	0.178	-0.717	-0.594	-2.624
-0.458	-1.002	-0.527	0.143	1.529	-0.101	-0.912	
0.017	-1.057	0.316	0.104	-1.522	0.366		
-0.373	-0.037	-2.800	0.267	0.660	-1.705	-2.176	-2.817
-0.513	-2.263	0.995	-1.482	-0.162	-1.786	-0.819	
-0.471	0.503	-0.141	-0.198	-2.439	-2.964		
0.088	0.306	-0.947	-0.506	-1.321	-2.068	-0.348	-0.497
-2.067	-1.755	-0.457	-0.719	0.551	-1.965	-2.507	
-2.899	-1.806	-0.037	-0.326	0.744	-1.987		
-0.962	-0.903	-0.375	-0.618	0.744	-0.754	-0.495	-1.300
-0.300	-0.186	-1.597	-1.428	0.134	0.201	-0.049	
-0.312	-2.062	-2.329	-1.255	-1.397	-2.207		
-0.080	0.909	-2.020	-0.054	-1.930	-1.694	-2.225	-1.784
-1.307	-1.415	-2.291	-1.817	-0.819	-0.277	-0.962	
-1.069	-0.875	1.865	-1.037	-1.414	-0.161		
-0.629	0.984	-0.382	-1.130	-1.805	-1.334	-3.546	0.695
-0.564	-0.713	-0.134	-0.945	-1.928	-0.596	-2.667	
-0.368	-0.922	-2.531	-1.767	0.233	-0.545		

Table36.txt

0.588	0.139	-0.404	0.060	-0.726	-0.444	0.509	-1.254
-0.735	0.248	-0.989	-2.531	0.190	-0.823	0.070	
-0.061	-2.239	-0.121	-1.553	0.175	-1.389		
-0.077	-0.023	-1.411	-0.979	-1.264	-2.470	-1.347	-2.433
-1.076	-2.153	-2.404	0.020	-2.291	-0.754	0.199	
-2.155	-0.568	-1.103	-1.665	-0.240	-1.558		
0.710	-0.146	-0.164	-1.105	-1.377	-1.255	-1.218	-0.774
-1.705	0.314	-2.294	0.005	0.633	-2.816	-1.850	
-1.443	-0.315	-2.470	-1.902	-0.303	-0.146		
1.251	0.665	0.023	0.658	1.991	-1.913	-1.064	-0.216
-0.636	-1.719	-0.118	-1.462	-2.476	-1.107	-0.456	
-0.753	0.139	-0.298	0.138	0.075	-0.998		
1.972	-2.307	-0.977	-0.380	-1.604	-1.823	-0.299	-2.347
-0.447	-1.084	0.655	-1.241	-0.375	-1.563	-2.054	
-0.596	-1.414	-1.698	-1.800	-0.789	-1.095		
1.328	0.430	1.061	-1.335	-1.089	-2.030	-1.177	-1.152
-0.577	-2.252	-0.125	-1.676	-0.205	-1.170	0.081	
-1.623	0.839	-2.011	-2.417	-1.288	-0.591		
0.420	-0.311	0.757	-0.705	-0.598	-1.225	-0.390	-2.030
0.314	-0.893	-1.114	-1.535	-0.433	-1.949	-0.751	
-1.288	1.556	1.051	-1.228	0.523	-0.134		
-1.023	0.062	-1.167	-0.710	-1.198	-1.127	-2.580	-1.242
-2.142	-0.850	-1.703	-1.289	0.817	-3.210	0.683	
-0.678	0.443	-1.010	-0.460	-1.075	-1.000		
0.792	0.464	-2.021	-1.724	0.564	0.391	0.405	-1.764
-1.947	-0.905	-0.408	0.194	0.111	-0.831	1.522	
-2.023	-1.106	-1.250	-0.702	-1.184	0.396		
0.639	0.259	-1.674	-0.100	-0.142	-0.469	-1.924	-2.066
-1.667	-1.116	0.019	-0.545	0.009	-2.619	-0.780	
0.818	0.053	-1.024	-0.304	-1.134	-1.116		
-1.161	0.366	-1.718	-2.710	-0.104	-1.360	0.006	-0.892
-0.833	-1.564	0.011	-0.904	-1.000	-1.471	-0.362	
-1.385	0.348	-1.062	0.764	0.119	-1.387		
0.310	-0.223	-1.768	-0.293	-2.076	-1.705	0.881	-1.190
0.512	-0.933	-1.212	-2.052	-0.199	0.053	-2.060	
-1.421	-0.520	-0.011	-1.427	-0.838	-1.010		
-0.338	-2.298	-1.887	-1.253	0.069	-2.901	-1.939	-1.229
-1.635	-1.047	-0.553	-2.496	0.321	-0.305	-0.301	
-0.396	-3.225	0.660	-1.245	-0.769	-0.381		
1.061	-0.847	1.455	-0.339	0.911	-1.068	-0.067	-1.732
0.313	-0.854	-0.968	-1.099	0.053	0.175	0.376	
-1.180	-0.335	0.000	1.690	0.763	-1.464		
-1.140	-1.266	-0.975	-1.121	-0.489	-1.661	-1.319	-0.503
0.238	-0.753	0.664	-2.207	-0.420	-1.945	0.110	
-0.505	-0.920	-1.678	0.247	1.254	-2.442		
0.689	0.869	-2.542	-1.362	-1.854	-1.909	-1.056	-0.833
0.088	-0.979	0.787	-2.512	0.488	0.343	-0.749	
0.094	-0.276	-1.045	-1.197	-0.277	-1.986		

Table36.txt

-1.601	0.831	-1.130	-0.288	0.462	-1.055	0.532	-1.764
-1.222	-0.903	-1.147	-4.255	-0.684	-1.178	-0.999	
-2.330	0.880	-2.020	-1.004	-0.867	-0.427		
0.802	1.070	0.222	-0.828	-1.597	-0.043	-1.368	-1.616
-0.739	-2.607	0.282	0.113	-0.613	-1.477	-0.106	
1.571	-0.274	-2.388	-1.347	0.566	0.538		
-0.997	0.921	-0.631	-2.501	-1.093	-0.864	-0.080	0.081
-0.842	-2.830	-0.480	-0.693	-0.854	-0.394	-0.963	
-1.905	0.087	-1.153	-0.915	-0.267	-2.312		
0.877	0.410	1.561	-0.841	1.436	0.146	-0.284	-1.991
-0.266	-1.103	-0.992	-1.958	0.620	1.124	-0.428	
-1.845	-2.139	-0.820	-0.593	-1.002	-2.037		
0.583	0.754	-1.826	-0.800	-0.586	-2.011	-0.658	0.333
1.532	-0.258	-0.987	0.924	-0.142	-1.987	-1.561	
0.179	-1.985	-0.419	-0.815	-2.785	0.165		
1.079	0.604	-1.963	-0.928	-0.878	-0.688	-0.196	-1.508
0.124	-1.009	-2.957	-2.852	0.106	-2.449	-0.796	
-0.400	-2.039	-1.260	-1.097	0.411	-1.517		
-1.624	1.056	-1.305	-1.705	-0.604	-0.549	0.609	-1.469
-0.769	-1.290	0.949	-0.550	-1.492	0.256	-0.001	
-1.529	-1.244	0.510	0.195	0.980	-1.542		
1.457	-1.165	-0.851	-0.004	-2.029	-0.368	-2.016	-0.091
1.074	-2.704	-0.059	-0.574	-1.107	-2.553	-0.262	
-0.335	-0.841	1.873	-0.373	-2.221	-0.138		
-0.083	1.055	-0.190	-0.455	-0.660	0.436	-0.604	-1.599
-0.891	-0.850	-0.795	-0.384	-0.344	-1.359	-2.605	
-1.304	-0.408	-3.015	-2.297	0.675	-2.311		
-0.346	-0.696	-1.118	-0.182	0.383	-1.340	-0.981	-1.777
0.017	-0.369	0.493	-0.513	-1.536	-0.267	0.202	
0.255	-0.409	0.101	-1.448	-0.914	0.141		
-1.437	-1.828	-1.057	-1.410	0.739	-2.088	0.135	-0.461
-1.449	-3.242	-0.661	-1.139	-1.777	-1.937	0.992	
0.047	-0.868	-1.295	-2.360	-1.446	0.053		
1.318	0.216	0.202	-0.300	0.054	-0.638	-1.115	-0.094
-0.618	-3.177	1.487	-2.410	-1.088	-2.513	-0.345	
-2.506	-2.476	-1.427	0.588	0.247	-1.267		
0.823	-0.545	-1.802	-2.742	-0.951	-0.219	-2.829	-1.363
-0.417	-1.240	-0.092	-1.991	1.265	-0.629	0.168	
-0.539	-1.905	-2.504	-1.140	-0.796	-1.018		
0.253	1.213	-0.460	-0.493	0.867	-0.425	-1.432	-2.223
-1.418	-3.150	-0.790	-1.179	-1.590	-0.815	-1.535	
-1.268	0.233	-1.681	-2.404	-0.373	-2.223		
0.848	-0.260	-1.212	-0.924	-2.062	-0.767	-4.200	-1.988
-1.623	-2.905	-0.677	-2.094	1.100	0.661	-1.777	
-2.069	0.040	-0.783	-0.733	0.635	-0.585		
-0.107	-0.827	-2.218	-1.323	-1.431	-1.189	-1.507	-2.119
-0.281	-1.026	-1.958	-1.349	0.400	-2.476	-1.590	
-0.063	-1.292	-2.207	-0.922	-2.026	-1.800		

Table36.txt

2.160 0.404 -0.324 -0.844 -0.970 -2.665 -0.174 -0.862
-1.453 -2.196 -0.327 -1.524 -0.467 -0.814 -0.679
-0.053 -0.130 -1.833 1.571 -0.088 -0.207
0.642 -0.886 -1.122 0.879 -0.945 -1.982 0.926 -0.709
-1.513 -0.623 -1.708 -0.084 0.979 -2.315 -0.509
-1.547 -0.021 -0.625 -0.709 -1.544 -2.138
-0.472 0.759 -1.588 -0.337 -0.871 -1.534 -0.026 -0.670
-3.459 -0.463 -0.258 -1.975 -1.646 -0.394 -0.861
-0.934 -0.097 -0.508 -0.462 -0.684 -0.308
0.642 0.150 0.048 -0.965 0.141 -0.136 -0.212 -2.031
0.106 -0.986 -1.587 -1.386 -0.762 -1.076 -0.034
-0.440 -0.852 -0.521 -0.218 1.849 -1.678
-0.248 -0.475 -1.550 -0.076 0.025 -2.461 0.720 -0.379
-0.488 -0.093 -1.916 -1.181 -1.308 -2.292 -1.337
-1.197 -1.234 0.434 -2.312 -0.800 -1.656
0.420 -0.825 1.012 0.624 -1.097 -1.064 -2.301 -1.289
0.138 -1.327 -0.688 0.174 1.474 -0.316 -0.183
-2.671 -0.666 -0.346 -2.297 -1.841 -1.141
-0.296 -1.054 -1.550 -1.324 0.550 -0.278 -0.918 -1.943
-0.760 0.938 -0.502 -1.086 -1.684 -3.017 -2.740
-0.117 1.590 -1.243 -2.543 -0.400 0.086
-0.051 0.179 -2.282 -0.176 -1.700 -1.423 -2.368 -2.023
-0.154 -0.307 -2.633 0.211 -0.251 -0.164 -0.591
-1.420 -0.534 -1.199 -1.760 -0.208 0.057
0.514 0.901 0.451 -0.035 -2.155 0.138 -0.794 -2.715
0.200 -0.564 0.136 -1.595 0.450 -3.262 -0.745
0.200 -1.498 -0.924 0.021 -2.309 -0.643
0.638 0.571 -3.087 0.870 -0.422 -1.050 -1.258 -0.811
-1.300 -1.086 -2.329 -2.707 -0.125 -0.979 0.330
-1.065 -0.315 -0.938 -2.115 -1.183 -3.615
0.508 -1.028 -2.312 -2.054 -0.514 -2.098 -3.811 -1.834
-1.132 -1.650 -2.766 -1.828 -1.690 -2.796 -1.767
0.432 -0.633 -0.101 0.998 0.174 -1.518
-0.507 -1.234 -0.817 0.846 -0.967 -1.539 -0.838 -2.591
-0.565 -1.341 -1.143 -0.692 0.192 -0.393 -0.035
-2.189 -2.453 -1.276 -1.498 -0.786 -0.428
1.596 0.013 0.586 -0.159 -2.303 -2.017 -0.781 -1.134
-2.991 -0.197 -2.214 -2.185 -2.030 -0.730 1.052
-1.646 0.170 -1.054 0.494 0.803 0.396
-0.549 0.310 -3.090 -0.855 -0.694 -3.090 0.000 0.000
0.000 -0.144 0.000 -0.736 0.000 -3.090 0.000
0.309 0.000 0.366 0.000 0.000 -0.736
0.141 -1.376 -2.803 1.007 -1.220 -0.710 0.168 -1.859
-1.172 -1.364 0.576 -1.950 -2.056 0.128 0.902
-2.124 -0.452 -0.573 -1.119 -0.254 -1.118
-1.474 -2.587 0.013 -1.145 -1.275 -1.430 -0.267 -0.864
-1.071 -0.208 -0.928 -1.104 -0.810 -0.237 1.402
0.300 -2.571 -1.257 -0.974 -0.291 -1.006

Table36.txt

-0.764 -1.579 -1.868 -1.061 -0.963 -1.473 -2.401 -1.251
0.706 -1.263 -1.091 0.067 0.265 -1.762 0.227
-1.307 1.271 -2.686 -3.248 -1.828 0.825
-0.092 2.219 -2.463 -0.830 -2.598 -2.385 -0.902 -1.256
0.429 -2.265 -0.016 -1.102 -0.767 -1.663 0.531
-0.658 -0.854 -1.227 0.581 0.246 -0.385
0.653 -2.577 -1.097 1.218 0.208 -2.235 -1.391 -1.716
-0.314 -0.910 1.108 -2.197 -1.324 0.444 0.950
-2.393 -0.009 -0.826 -1.703 0.034 0.010
-0.347 -1.310 -1.171 -0.456 -1.717 -0.584 -2.556 -1.389
-3.250 -1.854 0.007 -2.181 -0.843 -1.924 -0.676
-1.141 -0.684 -1.846 -2.033 0.827 -1.758
-0.587 0.341 -1.569 -1.018 -0.155 -3.101 -0.506 -0.217
-0.442 -0.888 -0.761 -1.608 -0.499 -1.305 0.701
-1.743 -0.547 -1.478 -0.981 -0.099 1.196
-1.551 2.338 -0.815 -0.853 -0.211 -0.799 -1.371 -0.157
-2.496 -0.756 0.224 -3.573 -0.894 -0.229 -0.359
-1.986 -1.291 -1.374 -2.309 -0.443 -1.072
0.825 2.135 -2.408 1.609 -0.870 -1.328 -1.414 -1.713
0.834 -1.797 0.658 -1.567 0.525 -1.453 0.684
-4.258 0.059 0.493 -2.473 -0.515 -0.699
-0.892 0.599 -2.119 -0.953 0.105 -2.109 -0.456 0.450
-1.281 -1.143 -1.637 -1.336 -0.988 1.293 -1.524
-0.846 -0.387 -0.357 -2.096 -0.627 -0.821
1.042 -1.168 -2.214 -0.338 -0.130 -2.100 -0.878 -3.827
-1.331 0.782 -0.629 0.047 -0.948 -0.418 -2.584
-2.525 0.030 -2.684 -1.433 0.076 0.584
-0.704 -0.602 0.647 0.831 0.940 0.171 2.042 -0.849
-0.261 0.766 -2.773 0.229 0.986 -0.378 -1.653
-0.329 2.145 -0.437 1.374 1.116 -0.638
1.318 1.214 -1.176 -1.193 -1.414 -1.698 -1.840 -1.364
-2.440 -0.340 -1.826 -1.819 0.986 -1.212 -0.099
-0.565 -0.704 -2.332 -1.033 -0.419 -2.984
-1.199 -1.537 -0.009 -0.514 -1.689 -0.992 -0.730 -1.875
-0.441 -1.844 -0.175 1.316 -2.075 -1.495 -1.979
0.206 -0.950 -1.282 0.393 -1.311 -0.612
0.027 -0.062 0.357 -0.284 -1.494 -0.138 -1.182 -1.765
-2.587 -1.385 1.322 -2.217 -0.446 -2.447 0.588
-1.690 -0.851 -0.315 -3.288 -0.719 -0.410
0.186 0.035 -0.514 -0.290 -0.422 -0.689 -0.163 -0.478
-2.349 -1.754 -0.183 -1.276 -0.367 -2.498 -1.291
-0.845 0.255 -3.164 1.160 -0.693 0.229
0.723 -0.955 -2.541 -2.743 -0.959 -0.825 -0.370 -2.963
1.937 -2.253 0.281 -1.915 -2.794 -0.228 -1.974
-0.703 -2.551 -1.348 -2.873 -0.607 -1.519
-0.770 -0.305 -1.119 -1.538 -0.830 -2.255 0.053 -0.646
-1.167 -1.299 -1.041 -0.700 -0.676 -0.655 -0.007
-0.998 -1.260 0.884 1.060 -2.975 -2.380

Table36.txt

0.001	-1.478	-0.906	-2.794	0.164	0.070	-1.901	-2.106
-1.491	-2.622	-1.499	-2.317	-3.336	-1.109	-0.568	
-2.453	0.324	-2.074	-0.207	-1.882	-0.104		
0.482	-0.879	-1.447	-1.608	-1.757	-1.165	-2.751	-0.852
0.074	-0.750	-1.809	-1.436	-1.856	-0.808	-0.626	
-0.444	1.555	-1.213	-0.837	-1.516	-2.971		
-0.235	-0.707	-0.296	-0.396	-1.206	-2.131	-1.452	-1.854
-0.179	-1.013	-0.127	0.068	-0.026	-1.890	-0.672	
-0.858	-2.494	-2.671	-0.421	-0.036	1.367		
0.076	0.972	-0.187	-1.226	-2.619	-2.583	-0.002	0.536
-0.431	-2.168	0.392	-2.792	-0.985	-1.489	-0.443	
-2.598	-0.116	-2.074	-1.105	-1.234	-0.079		
0.257	-0.190	-2.018	-3.575	-0.374	-1.015	-0.912	-1.575
0.713	-2.050	-1.601	-2.752	-2.338	-1.326	-0.351	
-0.715	-0.529	-0.093	-0.798	-0.895	-1.517		
0.639	-0.868	-0.825	-0.224	-1.114	-2.304	-1.013	-0.502
-0.639	-2.976	-2.999	-3.709	-0.618	-2.338	-1.221	
-2.463	-1.317	-2.307	-0.615	-0.569	-1.866		
-0.668	0.105	2.411	-0.356	1.050	-2.686	-1.292	-1.400
-1.102	-0.474	-2.547	-2.627	-1.799	-0.263	-0.702	
0.650	0.082	-0.706	-0.217	0.805	-1.418		
0.338	0.274	-0.552	-0.764	-1.654	-0.339	-3.416	-1.613
-1.600	-1.111	-1.026	-0.911	-0.257	-0.934	0.867	
-0.166	-2.629	-3.180	0.030	-0.880	-0.262		
1.652	-0.640	-1.817	-0.416	0.340	-2.189	-2.410	-1.453
0.139	0.612	-2.672	-1.627	0.217	0.312	-0.579	
-1.173	2.480	-0.658	-0.495	-0.278	-0.216		
1.530	-2.516	0.451	-0.156	-0.854	-1.136	-1.422	0.941
-0.723	0.351	-0.121	-1.545	0.167	0.549	-0.891	
-1.522	0.129	0.057	-0.207	-1.115	-1.709		
1.691	-1.614	-1.377	-1.665	-0.392	-0.129	-0.605	-2.321
-2.824	-2.160	-1.071	-1.337	-0.305	-0.892	-0.451	
-1.495	-0.190	-1.219	-1.597	-0.611	-1.247		
0.607	-2.216	0.566	0.099	-1.044	-1.615	-0.148	0.941
-0.441	-1.030	-1.244	-1.604	0.456	-1.425	-1.037	
0.590	-0.376	-0.097	0.603	0.075	-1.724		
-1.102	-2.035	-1.897	0.905	-1.677	-3.218	0.543	-0.375
-1.639	-0.553	-0.376	-0.879	-0.109	-2.185	0.167	
-1.117	-1.271	-2.451	-0.631	-3.102	0.960		
0.947	-0.902	-0.666	1.412	-0.934	-1.889	-0.816	-2.424
-3.380	-3.035	-1.306	-0.955	-0.836	-0.139	-0.882	
-0.897	-1.667	-0.750	-0.645	-0.797	-2.096		
0.407	-1.717	-0.361	0.139	0.025	-2.351	-0.585	0.377
0.656	0.943	-1.033	0.137	-2.123	0.211	2.235	
-0.334	-1.773	-0.810	-0.785	-0.310	-0.185		
0.214	-1.196	-0.807	-0.477	-0.333	-0.610	-0.781	0.021
-2.313	-0.107	-1.017	-1.990	0.075	-1.826	-1.021	
-1.012	0.509	0.417	-1.244	0.167	-0.875		

Table36.txt

0.994	-1.233	-1.083	1.125	-0.121	-1.180	-1.049	-1.930
-1.449	-1.176	-1.592	0.929	-0.604	0.663	0.237	
-2.480	-2.164	-1.927	0.378	-0.396	0.152		
-0.122	-0.273	-1.323	-0.863	-0.607	-1.072	-2.588	-2.061
-0.337	-0.991	-2.005	-3.278	-0.530	-0.345	-0.923	
1.821	-0.512	-2.048	-1.867	0.026	-0.774		
-0.256	-2.172	-0.329	0.516	-0.282	-1.247	-0.917	-2.472
-0.116	-1.248	0.606	-0.800	-1.544	-0.211	0.220	
-1.260	-0.884	-0.159	1.111	-1.027	-0.889		
0.704	-2.146	-1.319	0.163	-0.248	-0.709	-0.771	-2.352
-1.563	-0.291	0.584	-1.922	1.122	-0.410	0.456	
-1.808	1.208	1.345	0.615	-0.010	-0.913		
0.624	-2.374	1.292	0.696	-2.123	-3.025	0.007	-1.980
-0.360	-2.315	0.224	-2.230	-1.525	-1.756	-2.721	
-1.447	0.129	-0.388	-2.379	-0.615	-1.236		
1.084	-0.737	-1.791	-0.584	-1.660	-1.246	-1.580	-2.016
0.771	-0.870	-0.488	-0.761	-1.517	-1.082	-0.282	
0.360	0.153	0.059	-0.295	-0.569	0.636		
-0.306	-0.635	-2.179	0.003	-0.916	-1.281	-0.045	-0.486
-0.327	-2.457	1.510	-0.441	-0.810	-2.920	-0.458	
-0.678	-0.603	-0.289	-1.347	-0.430	-0.640		
0.915	-2.149	0.213	-0.659	-0.715	-2.255	-0.138	-1.929
-0.431	-0.698	-0.761	-1.473	0.658	-1.719	-0.338	
-1.405	-0.202	1.100	-1.358	-0.709	-0.641		
1.504	-1.424	-0.282	-0.532	-1.195	-0.663	-0.846	-0.178
-0.404	0.077	-1.557	-1.968	-0.553	-1.032	-1.859	
-1.543	-0.821	-0.788	-0.693	-2.411	-1.989		
0.073	-2.197	-0.759	-1.349	-0.525	-1.177	-1.930	-1.370
-0.260	-2.866	-0.975	-1.059	-1.336	-3.041	-0.461	
-2.753	-1.832	-0.730	0.202	0.455	-1.591		
0.290	-1.468	-1.385	-0.938	-0.394	-3.016	-0.337	-1.956
0.784	-0.472	-0.655	-1.655	-0.165	-1.549	-1.716	
-0.578	1.490	-1.369	1.929	-0.259	-1.658		
1.227	-2.859	-0.576	-0.102	0.101	-2.390	-0.516	-1.509
-0.171	1.404	-0.789	-1.519	-0.118	-1.566	0.274	
0.200	-0.134	-0.967	1.361	-0.628	-2.322		
1.108	-1.007	-0.829	-0.243	-0.728	-0.255	-0.243	-0.152
-0.638	-2.510	-1.391	-1.608	-1.407	0.019	-0.913	
-1.428	0.372	-0.290	-0.719	-0.959	-2.530		
-0.007	-2.956	0.465	2.321	0.100	0.166	-0.179	-0.212
0.209	0.179	0.021	0.390	-0.497	-1.631	-1.096	
1.339	-0.636	-0.059	-0.221	0.189	-0.129		
0.807	-1.446	-0.414	-0.397	0.236	-1.205	-0.764	0.618
-0.775	-1.903	-1.843	-1.116	0.487	-0.717	-1.093	
-0.335	-1.665	-0.552	-2.202	-2.588	-0.273		
1.079	-2.387	-0.764	-1.008	-0.205	-0.496	-1.058	-2.117
-1.365	-1.876	-0.566	-0.249	-2.039	-0.940	-0.199	
0.857	-1.123	-0.209	-1.430	-0.100	-1.977		

Table36.txt

0.206	-2.110	0.384	-1.447	0.297	-1.061	-0.821	-0.661
0.846	-1.245	-1.905	-2.155	0.238	-1.702	-0.240	
-0.201	-1.937	-0.133	-2.424	0.638	-0.076		
-0.054	-1.116	-0.236	-1.839	-0.520	-3.210	-1.916	-1.859
-2.403	0.236	-0.554	-2.328	-0.405	-4.026	-0.256	
-0.627	-0.300	-1.234	-0.831	-2.507	-1.773		
-0.177	-2.309	0.917	-0.549	0.299	-0.412	0.670	-0.420
-0.196	1.603	0.901	0.309	0.082	0.499	-2.324	
-1.654	0.904	1.451	0.155	1.199	0.134		
-0.512	-0.334	-0.724	-1.517	1.153	-1.398	-2.566	-0.329
1.393	0.024	0.319	-0.320	0.013	-1.354	-0.628	
-0.079	-0.501	0.066	0.628	-1.788	1.257		
-0.612	-2.700	0.682	-0.255	1.382	-1.205	-0.297	-0.152
1.477	-0.804	0.767	1.592	-1.769	1.909	-0.536	
1.700	-1.301	-0.704	1.580	-1.111	-0.855		
-0.833	-2.486	-0.270	-2.212	0.204	-1.955	-1.642	-1.977
0.683	-1.157	-1.354	0.443	-0.173	-1.109	-1.353	
-0.708	-0.081	-2.351	-1.066	-1.549	-0.460		
-0.605	-1.619	-1.111	0.209	0.278	-2.304	1.284	-1.723
-1.458	-1.115	0.660	0.447	-1.040	-1.935	-1.459	
0.230	-0.593	-1.033	0.489	-1.693	-0.773		
0.148	-1.239	-0.323	0.713	0.997	-2.672	-1.637	-0.493
-3.587	-1.322	-1.744	-1.170	-1.303	-1.444	0.650	
-0.392	0.564	0.883	0.420	-0.457	-2.515		
0.640	-0.045	-0.380	-1.869	0.742	0.650	0.357	-0.649
-1.193	-2.356	-1.103	-0.622	0.133	-1.486	-0.809	
0.450	-1.997	-1.244	-0.523	-1.109	-0.593		
-0.622	-0.743	0.335	1.262	-1.242	-1.608	-0.949	-2.196
-0.450	1.737	1.082	0.847	1.459	0.848	-1.080	
2.358	-1.338	-1.826	-1.593	0.479	0.067		
0.086	-0.412	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
-0.267	-2.753	-0.259	-0.251	-1.763	-1.876	-1.700	1.256
0.869	-0.747	-2.635	-1.563	-1.225	-1.479	-0.923	
0.830	-1.696	-2.459	0.350	0.735	-0.967		
0.434	-1.184	0.005	1.481	-1.448	-2.540	-1.603	-1.507
-0.144	-1.140	-0.430	-1.373	-0.744	-0.250	-1.548	
-0.562	-1.068	-1.985	-0.827	-2.483	0.974		
1.581	-3.260	0.158	-1.076	-0.932	-0.481	-1.198	-1.325
-1.142	-1.756	0.236	-1.603	0.172	-3.500	0.964	
-0.440	0.727	-0.689	-0.236	-0.633	0.182		
-0.120	-0.720	-2.235	-2.637	-1.804	-1.070	-2.718	1.160
-1.395	-1.161	0.183	-1.158	1.608	0.437	-0.412	
-2.673	0.170	1.938	-0.777	2.417	-1.771		
-0.894	-0.543	0.392	2.329	-1.664	-1.330	1.685	0.405
0.764	0.169	-0.659	-0.888	-0.583	0.828	-0.413	
1.920	-1.245	-1.167	0.087	-0.723	-0.818		

Table36.txt

-0.515 -1.366 0.357 -0.564 0.845 -0.226 -0.801 -1.310
-0.066 -1.025 0.569 -1.397 0.515 -1.283 0.976
-0.118 -1.871 -0.680 -1.709 1.104 -0.461
0.275 -0.647 0.091 -1.403 -1.960 -1.191 -0.174 -1.475
0.803 -2.147 -0.971 1.102 0.287 -1.621 -0.822
0.272 0.223 -0.077 -0.427 -0.620 0.774
1.243 -3.142 -1.062 -1.114 -0.821 -1.022 0.393 0.621
0.062 -0.664 -0.080 -1.313 0.570 -1.339 -3.428
-0.112 -0.757 -1.816 1.246 -2.154 -2.956
0.771 -1.037 -0.374 -0.375 -1.438 0.065 0.508 -0.486
-1.194 -2.322 -0.876 -0.315 -0.656 -1.450 -0.613
-1.391 1.750 0.764 -1.880 -0.880 0.788
1.115 -2.518 -0.902 -2.429 -1.016 -1.422 -2.438 -2.788
-1.183 -0.353 0.676 -0.583 -3.064 -1.926 -1.668
0.431 -1.460 -1.540 1.079 -0.205 -0.352
1.750 -1.789 -0.824 0.261 -0.786 -1.360 -1.375 -1.634
-0.911 -0.979 0.888 -0.152 0.589 -2.026 -0.756
0.714 0.658 -0.361 -0.901 -2.772 -1.558
1.331 0.284 -1.337 -0.735 -2.185 -2.652 -0.623 -0.506
-0.203 0.032 -3.274 0.125 -1.653 -0.919 -1.293
-0.278 0.520 -2.625 1.481 0.378 -0.371
1.152 -1.101 -1.010 1.531 0.414 -0.883 -1.066 -0.991
0.766 -1.888 0.540 -2.423 0.625 -1.114 -0.119
-1.667 -0.259 -0.875 -0.280 -1.586 -0.355
0.275 -2.319 -1.999 1.634 0.351 0.463 -0.732 -1.481
-0.371 -1.796 -1.297 -0.848 -0.454 -1.748 -0.070
-0.844 0.638 -0.723 -0.223 0.585 0.632
1.864 -2.636 1.196 0.454 -0.742 -2.844 0.432 -0.396
-0.837 -1.586 -0.603 -3.584 1.604 -0.947 -1.545
-0.369 0.949 -0.873 -1.255 1.140 0.144
2.036 -2.237 -0.993 -0.420 -0.587 -1.747 -0.770 -1.237
-0.297 0.042 -1.433 -1.127 -0.489 1.009 0.086
0.920 0.060 0.072 1.120 0.323 0.132
1.046 -1.397 0.245 -1.147 -1.372 -1.632 0.027 0.458
-0.651 -0.545 -1.042 -1.486 -0.635 -1.894 -1.002
1.691 -0.381 0.660 -1.369 -0.205 -0.998
0.739 -2.521 -1.150 0.533 -0.095 -2.177 -0.110 -1.334
0.096 -2.274 -1.904 -1.009 0.583 -3.093 0.542
0.726 -0.447 -1.828 -1.595 -3.343 -0.321
0.649 -1.119 0.574 0.318 1.086 -1.610 0.683 0.209
-1.726 -0.728 -1.459 -0.012 0.294 -0.881 0.899
0.267 -0.380 -0.484 -0.019 0.579 1.029
1.062 -3.116 1.249 -0.087 -0.214 0.369 0.968 -2.689
-0.481 0.382 -1.035 -2.301 -1.239 0.424 -1.054
-0.786 -0.608 -0.117 -0.976 -0.554 -1.125
0.471 -2.724 1.314 1.796 -0.352 -0.321 0.027 -2.312
0.487 -1.057 0.159 -0.333 -0.905 0.037 -1.443
0.764 -0.332 0.415 0.706 0.703 -1.703

Table36.txt

0.679 -2.228 1.980 -0.482 -0.982 0.153 -0.718 -0.213
1.343 -0.807 -1.423 -0.512 -0.691 1.412 -0.193
1.261 -0.256 -0.053 -0.517 2.169 -1.748
-0.095 -1.577 -0.132 -0.462 1.642 -2.206 0.720 0.171
-2.539 -1.012 -1.016 -0.692 0.412 -0.258 -0.711
-0.508 0.305 -1.309 1.202 -0.897 -0.287
0.918 -1.593 0.993 2.818 0.796 1.103 -0.051 -1.422
1.385 -0.919 -1.411 -0.935 -1.470 -1.472 -0.073
-0.276 -0.428 -1.388 0.937 -1.529 -1.149
0.333 -1.445 -0.658 1.200 0.252 -0.872 -0.510 0.076
-2.094 1.193 0.046 0.663 -0.821 0.561 -2.515
-2.816 -1.802 0.781 0.880 0.133 -0.159
1.712 -1.889 -0.317 -2.393 0.058 -0.034 -1.512 -1.381
-2.480 -1.046 -1.759 -0.924 -0.581 -0.557 -0.186
0.019 -1.375 0.501 -0.777 -1.674 -1.434
0.549 -2.881 -0.548 0.201 -0.387 0.087 -1.722 -1.261
-0.147 -1.005 -0.384 -1.826 1.113 -2.060 -1.745
1.156 1.003 0.940 0.079 0.816 0.276
0.445 -2.554 -3.127 -0.209 0.121 0.035 -3.524 -0.088
-2.125 -1.577 0.183 -0.757 0.079 0.309 -0.821
-0.636 -0.748 -0.343 -0.059 0.153 0.292
0.294 -2.673 -0.659 -1.015 -0.673 0.170 -0.640 -0.687
-0.076 -1.379 -1.097 0.334 -2.542 -0.190 -2.045
-0.603 -2.425 -1.466 0.539 -0.539 -1.652
0.247 -1.498 -0.449 2.034 0.738 -1.900 -0.451 -0.834
-1.517 -0.589 -0.103 0.786 -0.213 -1.385 0.231
-1.691 0.728 -0.788 0.165 -0.115 0.269
0.370 -2.516 -0.276 -0.065 0.916 0.006 0.772 -0.292
0.026 -0.598 -0.636 -0.415 -0.429 -2.210 -1.241
-0.190 -0.556 -1.608 1.385 -0.521 -0.280
-0.233 0.135 0.756 0.102 -0.974 0.816 -2.486 0.320
-2.375 0.196 -0.829 0.113 1.570 -1.189 -0.835
0.803 1.395 -0.748 0.005 -0.251 -0.974
0.217 -1.709 0.092 -1.436 -0.633 -1.737 0.258 -1.093
-1.377 0.701 -1.131 0.352 0.536 0.672 0.468
0.003 1.064 -0.162 0.688 0.678 -0.645
-0.081 -2.002 -0.209 -0.380 -1.023 -1.466 1.039 -2.201
-0.696 0.147 -1.041 0.128 2.188 0.820 -1.652
0.562 0.551 -1.324 1.502 1.712 -2.011
0.182 0.051 -1.716 -2.005 -0.543 -0.015 -1.887 -0.896
-0.742 -1.456 -1.201 -1.235 -0.726 -1.989 1.489
-1.898 -1.329 0.620 -3.193 0.645 -0.124
2.254 -3.181 -0.599 0.916 -3.074 -1.490 -1.600 -0.991
1.082 -2.044 -0.581 -1.053 0.452 -1.397 0.137
-0.727 -0.757 -0.114 -3.062 0.790 0.480
0.577 -2.320 -0.376 0.547 0.384 0.204 -0.759 -1.650
-0.653 -1.033 -0.713 -2.156 -1.432 -0.365 -0.918
-0.765 0.743 2.303 0.698 1.061 1.547

Table36.txt

1.055	-2.671	-0.485	0.893	0.501	-1.418	-1.111	-0.837
-0.079	-1.123	-0.719	-1.318	0.464	-1.380	-0.131	
-1.481	0.036	1.562	1.288	1.014	-0.111		
-0.327	1.537	-0.767	-0.221	-1.235	-2.685	1.186	-2.237
-1.565	-0.291	-0.391	-2.168	-2.261	-1.367	-0.140	
-0.546	-0.785	-0.611	-0.334	-0.696	0.854		
-1.014	-2.073	-1.953	-1.073	-1.285	-0.744	-1.107	-1.388
0.659	-3.033	-1.305	-0.361	-0.962	-1.782	-0.201	
-0.173	-1.426	-0.419	-0.076	1.073	0.703		
0.017	-0.623	1.432	-0.784	0.514	-0.323	-0.760	-0.830
-0.568	-0.825	-1.953	-1.597	-0.234	-0.640	-2.301	
-1.285	-0.662	-1.484	-1.003	-0.869	-0.952		
0.379	-0.646	-1.696	-1.245	-0.177	-1.681	-0.018	-0.680
-1.169	-1.105	-0.595	-1.140	-0.287	-1.155	-1.477	
-1.955	0.747	-1.044	-0.869	-0.914	0.437		
0.145	-0.911	1.500	1.105	-0.476	1.289	-0.092	-1.723
-0.321	0.091	-2.398	0.183	-2.749	-1.266	-0.851	
-1.583	0.391	1.117	1.143	1.475	-1.654		
0.678	-0.928	-1.865	-1.017	-0.270	-0.753	0.594	-0.282
-0.077	-0.918	-1.904	-2.015	-0.178	-1.702	-0.542	
-0.386	-0.212	-2.277	-0.488	-0.621	-1.565		
-0.474	-1.124	0.021	-0.192	-0.866	-1.613	-1.794	-2.040
0.066	-2.262	-1.102	-0.716	-1.115	-2.217	-1.292	
-1.239	-1.214	0.357	-2.257	-0.823	-0.882		
-0.262	-2.777	0.954	-0.803	-1.547	0.678	-0.523	-2.092
-0.881	-0.780	0.345	-0.906	-0.078	-0.483	0.153	
-0.177	-0.486	0.300	2.465	-0.414	-1.055		
0.775	-1.941	-0.067	0.774	0.342	-0.166	0.190	-1.504
-0.925	-0.755	0.595	-1.248	0.994	-0.415	-0.605	
0.474	-0.369	-0.880	-0.995	-0.159	-0.220		
0.608	-1.150	1.041	-1.014	-0.261	-1.120	0.212	-2.209
-0.868	0.582	-1.686	-0.752	-1.727	-1.851	-1.534	
-1.236	0.820	-2.389	0.907	-2.853	-0.164		
0.650	-0.853	-1.705	0.597	0.199	-1.458	-1.029	-3.135
0.284	0.429	-1.531	-0.670	-0.873	-1.905	1.585	
-0.446	0.885	-2.569	0.119	1.034	-1.670		
0.988	-1.458	1.474	-0.553	-0.173	-1.804	0.052	-1.217
1.308	-1.331	-0.956	-2.015	-1.649	-1.426	0.438	
-2.263	-1.597	1.157	-1.232	-0.749	-0.363		
0.369	-3.020	-1.295	0.399	0.121	-1.220	0.256	-1.428
0.360	-1.684	0.027	-0.923	0.075	-0.175	0.197	
-3.729	-0.071	1.064	-1.403	0.065	-1.161		
1.207	-2.043	-0.745	-0.588	-0.521	0.605	-1.522	-0.453
0.884	-1.718	-0.625	-0.808	-0.673	-1.150	-0.683	
-0.612	-0.484	-0.045	0.180	-0.513	-1.248		
0.869	-1.344	-1.463	-0.402	-0.343	-2.028	0.354	0.367
-1.668	1.356	-0.726	0.089	-0.767	-1.884	-0.424	
0.794	-1.388	-0.373	-0.105	0.861	-0.571		

Table36.txt

0.251 -0.976 -0.246 0.088 0.269 -0.433 0.223 0.672
0.368 -2.298 -1.542 0.352 0.054 -1.507 -1.614
0.558 -1.074 0.809 0.846 1.412 -0.771
1.621 -0.737 -3.583 -0.153 0.839 -1.962 -0.527 -1.499
-0.072 -1.169 -0.413 -1.046 -0.763 -0.284 -1.005
0.926 -2.510 0.400 -0.439 -1.987 -2.419
1.431 -1.139 -0.055 -0.522 -0.334 -0.843 0.144 -2.817
-1.343 -0.495 -0.134 -0.564 0.075 0.526 1.145
0.505 0.492 -1.528 -0.293 0.213 -1.863
-0.261 -1.205 -0.074 0.343 0.387 -0.767 -0.944 -0.929
-1.148 0.168 -0.469 0.513 0.261 -1.521 0.903
0.472 0.981 0.972 -0.786 2.081 -0.636
0.830 -1.351 0.830 0.496 1.163 -1.501 0.880 0.020
-0.552 -0.160 -0.334 -0.894 0.145 -0.578 1.358
0.314 0.081 0.405 -0.223 0.749 -2.167
0.309 -0.480 -2.984 -0.759 -1.813 -1.072 0.149 -1.829
-1.722 -0.859 -1.562 -0.598 0.435 -2.152 -0.418
-0.519 0.905 -0.549 -0.011 -0.063 -1.104
-0.157 -2.047 -1.239 -0.480 -0.377 -0.029 -0.345 -1.388
-0.498 -3.140 -1.331 -0.438 -0.304 -0.801 0.655
-1.448 -1.196 0.994 -0.228 2.589 -1.484
0.174 -2.665 -0.328 1.594 -1.946 0.574 0.257 1.207
0.070 -1.801 -1.287 1.114 1.180 0.756 0.948
0.515 -0.731 1.575 1.654 1.881 0.056
-0.027 -2.870 0.320 1.706 -0.976 1.298 2.121 -0.707
0.585 -2.563 0.208 1.216 1.410 0.373 0.002
1.158 -0.440 2.424 0.595 2.544 -1.353
-0.039 -1.033 -0.409 0.180 0.222 -1.480 -1.058 -1.301
0.063 -0.297 -2.690 -2.055 -1.267 -1.379 -1.203
-0.383 -0.770 0.672 -2.450 -0.105 -0.316
-0.213 -0.661 -0.059 -0.307 -0.896 -2.174 0.414 -0.088
-0.449 -1.516 0.391 -1.323 -1.076 -0.240 0.487
0.457 1.561 -0.369 -1.330 -0.573 -0.431
0.790 -2.016 -0.030 0.513 -1.217 -1.276 1.443 0.433
-0.010 1.448 0.596 0.594 0.462 -0.805 -0.839
1.273 0.714 -0.650 1.513 0.935 1.099
0.728 -1.932 -0.100 0.572 -0.526 -0.158 0.800 1.092
-1.077 0.355 -1.054 -1.124 -0.215 -2.018 -0.778
-0.407 -0.345 -0.932 1.313 0.544 0.213
-0.518 -1.926 1.602 1.506 0.203 -0.992 0.691 0.915
0.277 0.213 1.742 -0.830 -0.420 -2.179 -1.253
-1.034 -1.298 -0.074 1.589 -0.106 0.275
0.791 -1.527 0.512 0.221 -0.012 -1.551 -0.793 -0.058
-2.012 -2.133 -1.996 -2.803 -2.551 -1.419 0.782
-1.153 -0.238 -3.520 -0.833 -2.034 -0.604
1.149 -3.127 0.292 -0.642 -0.864 1.826 -0.061 -2.052
0.368 -0.723 -0.451 -1.699 -0.557 0.443 -0.129
1.475 0.989 0.761 1.691 1.116 0.889

Table36.txt

-0.022 -1.981 -0.824 -2.192 0.124 -0.985 -1.234 0.149
-3.443 -3.925 -0.251 0.445 0.746 -1.128 -2.355
-1.144 0.118 -0.571 -1.043 0.010 -2.306
-0.147 -2.150 -0.919 -0.383 0.249 1.320 -1.093 -0.219
-0.499 0.028 1.206 0.097 -0.426 -0.522 0.761
0.193 -0.223 0.067 -1.044 0.714 -0.610
0.471 -0.849 0.234 0.042 -1.329 -0.442 -0.842 -0.704
1.052 -0.104 -1.093 -2.027 -0.182 -1.473 -1.284
0.128 -1.510 -1.183 -0.617 -2.088 0.174
-0.940 -1.953 0.263 -0.616 -0.366 -2.287 1.007 -0.373
-0.430 -0.429 -1.537 0.512 -0.793 -0.403 0.482
0.511 -0.896 -1.738 0.572 -1.702 -0.183
-1.521 -2.651 3.224 -0.855 0.416 0.782 -0.878 0.364
-0.517 -0.031 1.381 -1.525 -0.327 -0.624 -1.828
0.473 -0.049 0.535 0.572 -0.525 -0.967
-0.398 -2.574 1.037 1.332 1.032 1.555 0.478 0.018
-0.212 -0.543 0.218 -0.779 0.688 0.460 1.288
1.722 -1.136 -0.022 -0.726 -0.465 0.240
-0.378 -1.409 -1.153 -1.933 -1.241 -1.303 -1.865 -0.586
0.444 -1.414 -0.284 -0.608 -0.831 -0.593 -2.065
-1.313 -0.911 -0.255 -1.109 0.384 0.692
0.614 -1.633 0.935 2.379 2.735 1.415 0.999 0.314
1.533 -0.932 1.448 1.059 1.281 0.199 0.603
0.527 0.032 -0.508 1.271 -0.122 -0.465
-0.553 -0.799 -2.295 0.089 -2.251 -1.718 -2.212 -1.687
-1.224 -2.253 -0.189 -1.198 -1.759 -1.196 -0.603
-0.489 0.604 -1.093 -1.041 -0.342 -1.486
1.571 -0.593 -0.416 -0.839 0.490 0.136 0.755 0.408
-0.471 -1.440 -0.631 -0.589 -0.202 -1.276 -0.271
0.977 0.371 -0.355 -1.480 0.609 2.586
0.304 0.007 0.553 -0.524 -1.788 -0.527 -0.793 -2.287
0.127 -0.324 -1.381 -2.778 -2.542 -2.286 -0.064
-0.718 0.509 -0.054 0.476 -0.945 -1.274
-1.399 -1.344 0.715 0.140 0.488 0.606 0.221 1.814
0.975 -0.642 -0.784 -1.080 -1.617 1.221 0.867
0.460 1.129 0.592 1.242 0.200 0.182
-0.738 0.213 -0.884 0.679 -0.064 -1.100 -1.546 -1.043
0.306 1.032 -0.817 -3.122 -0.911 -2.228 1.508
-1.343 -0.654 -2.057 -1.492 -3.420 1.259
1.347 -0.474 0.201 -2.367 1.377 -2.296 -1.611 -2.252
-0.871 -1.243 -0.191 -1.748 -0.640 -0.504 -0.979
0.561 -0.486 -0.282 0.385 -1.568 1.043
1.156 -2.787 -2.038 -0.570 0.171 -0.454 -1.566 -1.261
-0.187 -0.702 0.468 -1.361 -0.179 -2.565 -2.034
0.578 0.863 -2.004 -0.916 -0.123 -0.060
0.550 -1.605 0.185 -1.439 0.915 -1.215 -2.323 -1.400
0.499 -1.818 -0.553 -1.280 -0.158 0.116 -1.367
-0.350 -0.140 1.024 -0.098 -0.272 0.565

Table36.txt

0.883 -1.891 0.439 -0.817 0.221 -0.694 -1.199 0.032
-0.657 0.036 -1.473 -1.650 -0.042 -1.430 -0.479
-1.959 -0.701 -0.142 0.568 -0.104 -1.168
-0.507 -0.818 -0.138 1.170 -0.511 -0.681 -1.590 -1.991
-0.691 -0.121 -0.628 -1.005 -1.088 0.763 0.129
-1.266 -0.104 -1.498 0.010 -2.133 -0.134
-0.609 -2.224 0.877 -0.585 0.029 0.355 -1.844 0.101
-1.417 -0.202 -2.144 0.675 -0.014 0.777 -0.358
0.242 -0.327 0.374 0.370 1.190 -0.990
0.579 -1.889 0.323 -1.312 0.550 -1.588 -0.719 -1.133
0.859 -1.982 -0.465 0.186 0.243 -0.225 0.704
-1.968 -1.981 1.378 0.270 -0.142 -0.165
0.762 -1.040 0.468 0.414 -1.617 -0.507 -2.095 -0.510
1.385 -1.114 -1.159 -1.149 -1.400 -0.444 2.537
0.814 -1.549 -1.721 2.157 -1.196 -0.271
-0.591 -1.436 -0.213 0.918 -0.648 -2.221 -0.147 -1.029
-1.972 -0.721 -1.438 -0.049 0.390 -0.433 1.508
0.897 0.131 -0.666 -1.319 1.040 -0.905
0.363 -3.106 -0.227 -1.053 -0.835 0.616 -0.110 -1.505
0.215 -1.517 -0.191 0.014 -0.549 -0.456 -3.430
-0.530 -1.914 -1.805 -0.838 -0.309 1.623
-0.969 -1.900 0.468 1.170 0.570 -0.550 -0.733 -0.238
-1.350 -0.500 0.666 -0.771 -0.966 -0.793 -0.026
1.651 -0.719 1.581 0.001 2.726 0.717
0.148 -2.107 2.209 -1.694 1.704 2.071 -0.749 0.287
1.477 0.791 0.485 0.461 0.992 -1.336 -0.048
2.389 0.172 1.306 0.142 2.000 -0.207
0.804 -1.246 0.273 1.543 -0.512 -0.077 -0.213 -1.172
0.383 -2.593 0.528 -0.704 0.022 -1.596 0.410
-1.266 -1.087 -2.883 -2.223 0.347 -0.355
-0.184 -2.609 0.017 -0.747 0.323 -2.600 -1.976 -1.695
0.499 -1.128 -0.158 0.057 -0.580 -1.256 -0.165
0.200 0.507 -0.506 0.632 0.148 -0.740
1.997 -1.570 -0.889 -2.331 -0.518 -0.858 -0.553 -0.861
0.047 -1.260 -1.826 0.681 -0.634 -2.382 -0.172
-1.132 -0.817 -1.227 -0.047 -0.355 -3.077
0.180 -2.134 -0.318 0.994 -0.562 0.108 0.308 -0.241
0.418 1.585 -1.329 -2.060 0.344 0.722 -0.551
-1.712 -0.563 2.227 -0.040 1.093 -1.495
0.394 -2.079 0.209 -1.189 0.857 -1.073 0.235 0.293
-1.134 0.680 1.097 -0.024 -0.744 1.457 -0.806
-0.319 -2.176 -1.317 0.823 1.262 -0.831
0.348 -2.708 -0.529 2.280 0.834 -0.463 0.644 0.497
2.514 1.072 -2.152 1.673 1.312 0.964 -0.381
0.481 0.936 -0.870 0.562 0.886 -0.133
-0.455 -0.799 -0.887 -1.335 -0.033 -0.287 -0.407 -1.330
-1.447 0.271 -0.533 -2.775 -0.699 -1.665 0.341
-1.532 -0.976 -1.590 -0.225 -0.102 -0.602

Table36.txt

-0.716 -1.477 -1.082 -0.954 -2.294 -2.469 -1.075 -2.446
-2.026 0.727 0.777 -0.519 -2.924 -0.603 -1.359
-1.058 -0.966 -1.494 -0.499 -0.484 0.837
-0.510 -1.856 -0.898 0.092 0.223 -1.364 -0.092 -1.890
0.900 0.623 0.553 0.426 1.791 1.105 1.255
-0.344 1.373 0.275 0.611 0.013 -0.356
-0.570 -2.519 0.621 -0.961 -0.644 -1.055 0.287 -0.276
-0.782 0.877 -1.012 -1.094 0.184 -0.279 -1.398
-0.374 0.333 -0.403 0.303 -0.190 -0.839
0.243 -0.071 -0.988 1.087 -2.090 -1.930 -1.785 -0.588
-0.926 -0.970 -2.027 -1.186 1.976 -0.802 -0.985
0.102 0.518 -0.816 -0.303 -0.910 -0.381
0.749 -1.098 0.165 0.333 -2.854 -0.963 -2.173 -1.459
-0.117 -1.548 -2.455 -1.578 0.943 -3.270 -0.681
0.132 -0.174 -0.765 0.032 -0.295 -0.241
-0.267 -2.095 -0.546 -0.060 -1.312 -1.253 -0.654 -0.311
-0.640 -1.726 -1.130 -0.762 -0.492 -1.259 0.108
0.009 0.525 -2.527 0.755 -1.362 0.403
-0.824 -1.028 0.933 0.174 1.333 -1.047 -0.650 -3.138
-0.123 -1.972 -1.686 -0.720 -0.047 -0.724 -4.380
-0.699 1.131 -1.884 -0.322 -1.405 -0.598
1.351 -1.544 -1.858 -0.845 -2.070 -1.738 0.867 -2.850
-1.618 -1.801 -0.925 -2.283 -1.500 -0.797 -0.546
-1.284 -0.675 -1.187 -1.589 -1.445 1.724
-0.858 -1.509 -1.939 -1.358 -0.482 0.547 -1.367 -2.359
-1.084 -2.132 -0.518 -1.947 -1.680 -2.218 -0.036
0.815 -0.981 -0.645 -0.657 -1.346 0.103
-0.391 -1.562 -1.369 -1.612 -1.041 -0.994 1.511 -0.997
-2.117 -0.412 -2.267 -3.547 -1.195 -1.097 -0.321
-0.883 -0.225 -0.121 -0.443 1.160 0.139
0.546 0.017 -0.826 -1.332 0.357 0.068 -1.249 -0.473
-2.184 0.656 -1.175 -1.548 2.217 -0.238 0.523
-0.703 0.048 -2.220 -1.657 -0.735 -1.765
0.963 -3.215 -1.443 -0.305 -1.998 -2.186 -1.449 -0.529
-1.011 -0.966 0.236 -0.449 -0.768 0.673 0.080
-1.245 0.204 0.246 0.653 -1.663 -0.444
0.835 -0.543 -0.655 1.141 -0.256 -1.199 -0.881 0.970
-0.245 -0.575 -1.674 -2.951 -0.825 -1.212 -1.898
-0.919 -0.202 -0.300 -0.616 -1.142 0.066
-0.341 -1.959 -1.799 0.571 0.534 -0.833 -0.166 -0.904
-0.208 -1.807 -1.712 -0.728 0.357 0.024 -1.314
0.966 0.624 -0.012 1.167 1.554 -1.019
1.151 -1.072 -0.121 0.143 -1.783 -1.200 -2.120 0.494
-0.277 0.150 -0.941 1.378 -0.381 1.090 -1.302
1.009 0.142 -0.487 0.255 -0.632 -0.705
-0.328 -0.639 0.566 0.391 -0.455 -2.464 0.092 -0.501
0.293 -0.603 -3.069 -0.591 -0.165 -0.660 -1.399
-1.454 -0.092 0.452 -0.295 -0.371 -0.302

Table36.txt

0.701	-3.145	0.789	2.247	2.381	0.564	1.288	-0.108
1.778	2.286	-0.647	3.315	2.228	1.114	0.232	
0.247	-0.262	-0.242	1.181	0.162	0.573		
0.078	-1.333	-0.603	-0.524	-0.309	-1.478	-0.529	-0.724
-0.996	-1.201	0.756	-2.214	-1.062	0.127	-0.831	
-1.341	0.874	-1.639	-2.195	-2.244	-0.716		
0.852	-0.747	0.918	0.279	0.732	-0.099	-0.515	2.828
0.097	2.317	-0.720	1.770	0.652	1.943	1.468	
1.362	1.025	1.935	-1.208	-0.005	1.008		
0.029	-1.782	0.741	-0.991	-1.309	-0.625	-0.116	-0.538
1.219	-0.655	-1.100	-0.423	0.121	-0.219	-1.112	
0.015	0.739	1.316	-1.024	-1.216	0.956		
0.659	-0.264	-0.223	-0.392	-1.435	-1.167	0.405	-1.043
-0.811	-1.615	-0.747	-0.395	0.345	-1.027	-1.164	
0.746	-0.306	-0.753	-1.486	-0.360	-0.021		
1.152	-0.391	-1.029	-0.611	0.048	-2.865	-1.039	-2.033
-1.860	-1.797	0.913	0.155	0.463	-1.051	0.686	
0.502	-1.015	1.468	-2.163	-0.406	-1.597		
-0.252	-1.848	-0.592	1.753	0.242	-0.803	1.040	-1.813
0.805	-1.808	-0.061	-1.033	0.058	1.163	0.370	
-0.615	0.258	-0.779	-0.756	0.701	0.663		
-0.762	-2.710	-0.990	0.938	-0.400	-2.247	-0.977	-1.864
0.458	-2.078	-1.414	0.147	-0.066	-3.425	-0.109	
-0.518	0.320	0.547	-1.450	-0.791	0.221		
-0.861	-1.540	-1.832	0.492	0.806	-0.197	-0.683	-2.365
-1.306	-3.143	-1.885	-0.008	-1.144	-1.423	-0.632	
-1.839	0.498	-0.618	0.280	-1.393	-1.205		
1.382	-1.430	-1.727	0.419	-0.100	-1.132	-0.780	-0.032
0.066	0.662	-1.130	-1.773	0.411	1.462	-0.768	
-0.352	2.084	0.364	-0.470	0.662	-1.307		
1.338	-2.109	1.437	-2.562	-0.083	-1.404	-0.154	-1.527
-1.006	-0.773	-0.029	0.002	-1.383	-1.427	0.677	
-0.949	0.047	-0.948	-0.844	-1.805	-1.097		
0.136	-2.634	0.057	-1.729	0.003	-0.914	-0.442	0.342
-0.903	0.670	0.313	-0.311	0.039	-0.789	0.355	
-0.557	0.264	1.150	-0.834	0.635	-0.231		
0.002	-1.244	0.332	0.207	0.040	1.525	-0.239	-0.902
0.518	0.053	-1.243	0.817	0.617	-1.680	-0.770	
2.220	-0.045	0.535	0.702	-0.543	-0.745		
-0.750	-2.389	1.104	0.098	-0.604	-0.819	-0.090	0.566
-1.146	0.225	-0.102	-0.871	-0.050	-1.135	-1.413	
-1.655	-0.217	-0.980	-3.074	-1.732	-1.713		
0.074	-0.870	-0.988	0.052	-0.034	-1.802	0.030	-0.216
-1.601	-0.709	0.967	-0.844	-1.079	0.505	-1.367	
-1.548	-1.048	0.265	-1.985	-0.745	1.270		
1.006	-2.468	-1.732	0.702	-0.709	0.269	-1.291	-1.626
-0.342	-2.104	-0.975	-0.813	-1.394	1.457	-0.799	
0.029	-0.261	-0.352	-0.051	1.052	0.285		

Table36.txt

-0.247 -2.465 1.907 0.694 1.848 1.241 0.253 -0.799
0.328 1.135 -1.298 -0.648 1.072 0.617 -0.355
-0.326 -1.493 2.780 -0.037 1.106 -0.658
0.600 -1.641 -0.313 -1.309 -2.047 -0.680 -1.741 -0.417
0.610 0.138 -0.563 -1.100 -0.280 0.160 0.195
-1.488 0.308 -0.831 0.532 -0.578 -2.902
0.636 -1.354 0.794 0.497 0.986 1.358 -0.563 0.441
-0.769 0.044 1.025 0.538 -0.189 -0.745 0.560
0.509 0.934 -0.262 0.949 0.031 0.095
0.126 -2.546 0.214 0.221 0.944 1.113 0.192 0.365
-0.701 0.895 -0.068 1.686 0.006 -1.321 -1.094
1.304 -0.862 -1.040 0.539 0.459 -0.349
0.216 -2.039 -0.023 0.646 -0.339 -1.866 -0.499 0.471
0.041 -0.189 -1.264 -1.977 -0.734 -0.229 -0.642
0.157 0.005 0.535 -0.969 -0.513 -1.018
-0.303 -2.782 0.694 -0.868 0.580 1.572 3.073 1.386
0.345 -0.443 -0.699 0.152 1.923 1.885 1.286
0.081 1.254 0.914 2.766 1.392 -0.653
-0.254 -2.671 2.500 -1.169 0.289 0.266 -0.690 0.241
-0.177 0.083 -1.247 0.143 2.374 1.114 -0.031
-0.719 0.373 1.674 2.509 2.187 -1.063
0.798 -2.559 0.148 -1.632 -0.329 -1.922 -0.539 -1.380
-1.291 -1.695 -1.793 -0.498 -2.424 -2.590 -0.708
-0.980 -0.138 -0.192 1.215 -1.085 -0.409
0.349 -0.795 -0.989 -0.248 -0.374 -1.175 -0.839 -0.644
-0.923 -0.024 0.431 -1.533 -1.061 -2.320 -1.491
-1.520 -0.547 -1.881 -0.170 0.336 -0.080
0.501 -1.418 -1.066 -2.544 -0.966 -1.209 -1.848 -1.124
-2.705 1.077 -0.960 -1.917 -0.085 0.187 0.046
-2.324 -0.603 -0.667 -0.206 -2.715 0.214
0.574 -1.861 1.537 -0.916 -1.365 -0.390 -1.336 -2.324
-1.517 -1.297 -1.918 -1.690 -0.411 -0.814 -1.076
-2.642 -1.199 -1.365 0.088 -1.937 1.124
-0.547 -1.559 -0.339 0.481 -2.009 -1.348 -0.967 -0.022
-1.646 -0.518 -0.541 -0.581 0.863 -0.335 -2.251
0.738 -1.192 -1.587 0.529 0.919 0.501
1.136 0.498 -0.398 -2.683 -1.630 -0.254 0.378 -1.772
-0.014 0.401 -0.944 -1.374 -0.779 -0.501 0.205
-2.528 -0.236 0.893 -1.046 -0.120 -0.497
0.393 -2.459 -1.796 -0.723 -1.104 -2.162 -0.424 -1.762
-1.807 -2.052 -2.316 -1.220 -0.603 -0.765 0.252
-1.631 -0.250 -1.967 0.980 -2.305 -0.845
-1.100 -2.945 -0.422 -0.739 0.115 1.367 -1.246 -0.666
0.169 -1.098 -0.900 -0.466 -0.399 0.900 1.368
-1.922 -1.531 -0.334 1.157 -1.028 0.323
0.075 -2.417 -0.075 -1.090 -1.798 -1.501 -1.070 -0.966
0.152 -0.304 -0.436 -2.112 1.918 -1.748 -1.645
-1.534 -0.989 -0.200 -0.911 -1.513 -0.474

Table36.txt

-0.451	-0.784	-1.823	-2.072	-0.108	0.123	-2.001	-0.802
-2.017	-0.863	-0.462	-2.856	0.164	-2.030	-0.953	
-1.375	0.251	-0.531	0.135	0.679	-0.947		
0.517	-1.534	0.950	-1.372	0.111	-1.064	1.391	1.009
-0.304	0.031	-1.979	-0.238	-0.964	-1.461	1.064	
-0.634	0.287	-1.199	-1.054	-0.034	0.881		
1.847	-0.780	-1.297	-1.572	-0.701	-1.769	-1.529	-3.369
0.229	-0.435	0.000	0.380	-0.462	-1.858	-0.538	
-0.904	0.698	-1.787	-2.182	0.667	-1.015		
-0.432	-2.143	-2.543	0.992	-0.425	-1.132	-0.985	-1.951
0.196	-2.237	0.760	-2.233	-0.002	-1.294	-0.614	
-0.456	0.656	-1.370	-2.241	-1.097	-0.332		
-0.359	-1.634	-0.801	-0.435	-0.659	-1.232	-0.943	-1.450
0.160	-1.388	-1.781	-1.235	0.891	-1.001	-2.047	
0.110	-0.005	0.203	0.918	-1.256	-1.365		
0.695	-1.590	-1.441	-0.684	-0.253	-2.017	-1.415	-0.084
-0.427	-2.070	-0.248	-0.956	-1.551	-0.272	-1.181	
1.277	-1.999	-1.165	-0.467	-0.194	0.047		
0.913	-1.576	-3.047	0.288	-1.666	0.722	-2.140	-1.872
-1.046	0.523	-0.019	-1.146	0.967	-1.830	-2.647	
-0.282	-2.106	-1.284	-1.176	0.557	1.062		
0.921	-1.666	-0.200	-0.332	-0.382	1.329	0.813	-1.068
0.911	-1.044	-0.212	0.098	1.246	-0.918	-1.331	
-2.030	0.013	1.044	0.881	-0.967	0.550		
0.562	-1.875	0.194	-0.219	1.052	0.872	-0.182	-1.421
-1.683	-0.184	-0.881	-0.114	0.823	-0.566	1.898	
1.357	-1.731	0.833	0.230	0.477	1.098		
0.134	-2.832	-0.395	-2.409	0.461	-1.569	-1.073	-0.318
-1.374	-2.055	-1.302	-1.540	-0.933	-1.353	-0.716	
-1.509	-0.387	-0.428	-1.855	-2.606	-0.548		
-0.016	-1.363	-2.437	-2.276	-1.652	-1.113	0.504	-1.539
-0.757	-1.620	-0.037	-2.171	-1.019	-1.288	-2.309	
-1.243	0.897	-2.682	-0.015	-0.721	-0.569		
0.628	-0.241	-2.376	-0.684	-2.014	-2.145	-2.922	-0.495
-0.815	-2.692	-0.956	-1.412	-3.298	-0.889	-1.583	
-1.158	0.343	-0.726	-0.081	0.971	-1.569		
1.383	-3.324	-0.470	-0.758	-1.204	-0.318	-2.895	-0.641
-1.667	-2.651	-0.226	-1.383	0.139	-0.710	-1.970	
-0.738	0.480	-0.982	-0.052	0.149	-0.847		
1.188	-1.469	-2.510	-1.213	-2.315	-2.228	-0.560	-1.072
-2.148	-2.890	-1.109	-3.467	-0.190	-0.968	-1.040	
-1.851	-0.508	-0.690	-1.132	-0.846	-1.972		
-0.154	-2.223	-1.098	-0.024	-0.172	-2.331	-1.665	-1.764
0.424	-1.108	1.153	-1.619	-2.038	-1.014	-1.790	
-0.408	-0.656	-2.507	-1.768	-1.396	-0.388		
-0.692	-1.641	-1.961	0.723	0.433	-1.476	-1.903	-2.011
0.358	-0.632	-0.250	-0.101	-0.046	-2.514	-1.019	
-0.774	1.233	-0.919	-0.039	-1.288	0.242		

Table36.txt

0.463 -2.135 -0.942 0.096 0.535 -0.775 -0.820 -1.765
1.539 -2.723 -0.904 0.291 -1.626 -0.394 -1.070
0.004 -1.104 -1.925 -2.247 0.473 -0.709
-0.118 -0.412 -1.089 1.125 0.779 1.609 -0.665 -0.277
-2.135 0.025 0.378 -0.102 -1.562 0.391 -2.298
1.010 -0.835 -1.942 0.105 0.839 -1.461
0.356 -1.098 -1.880 -2.638 -2.266 -2.943 -1.943 -1.940
1.024 -1.994 0.405 -1.417 -0.598 -1.889 -1.731
0.590 0.186 -0.655 -1.164 -0.282 -2.558
0.793 -0.790 -1.904 1.699 -2.441 -0.430 -1.602 -1.357
0.244 -1.905 -2.990 -1.650 -0.969 -0.466 -0.851
-1.604 0.011 -1.106 -2.784 1.210 0.739
1.839 0.333 -1.444 -0.680 -1.142 -2.071 -1.833 -1.239
-0.579 -1.166 0.280 1.158 0.574 -0.949 -0.502
-0.899 -0.744 -0.249 -0.176 0.164 -0.626
0.004 3.131 -0.551 -0.352 -1.835 0.144 -0.027 1.427
0.263 0.679 -2.441 -2.575 -0.907 0.512 -1.781
-0.947 -0.718 -1.590 0.369 -2.166 -0.815
0.691 -1.799 -1.307 -0.018 -0.983 -1.680 -1.024 0.154
-0.510 -0.804 0.112 -0.027 -1.673 -1.410 -0.815
-0.340 -0.295 -1.974 0.165 -0.989 -2.167
0.411 -0.026 -2.199 -2.005 -0.526 -3.169 -2.037 -4.100
-2.100 -1.767 -0.611 -2.900 -2.821 -2.820 -2.428
-1.571 -0.931 -2.645 -1.899 -1.972 -0.765
0.458 0.319 -0.412 0.513 -1.259 -0.747 -1.244 -0.935
-0.297 -0.021 0.142 -1.436 -1.402 -1.622 -0.845
0.206 -0.463 -1.390 -0.563 0.139 -0.826
0.248 -0.235 -0.037 0.418 -0.111 -1.431 1.304 0.157
-1.877 1.028 -0.891 0.019 0.091 -0.613 0.387
1.368 1.112 -0.544 -0.297 -0.458 -0.055
0.518 -1.599 -2.329 -1.916 0.174 -3.845 -1.381 0.339
0.050 -0.237 0.432 -2.443 -1.417 -1.906 0.033
-1.586 0.002 -1.918 -1.193 1.638 -1.405
-0.460 -1.877 -2.916 -2.412 -0.700 -0.446 -1.292 -1.908
0.168 -0.724 -0.125 -2.327 -0.209 -1.058 0.725
-1.220 0.574 -0.015 0.254 -0.493 0.508
-0.003 -1.761 0.558 -1.369 -0.918 -1.092 -1.200 -0.919
-2.705 -1.327 -0.881 -0.608 -0.785 -0.973 -0.054
-1.418 0.525 -1.294 -0.380 -1.172 0.319
0.210 -0.141 -0.188 0.682 -0.326 -0.640 -0.538 -2.780
1.937 -1.001 -2.507 -0.619 -1.197 -1.136 -0.586
-2.101 -1.782 -1.221 -3.097 -3.771 -1.119
1.112 -0.910 -0.454 -0.876 -1.544 -1.740 -1.065 -1.923
2.129 -3.085 -1.434 -2.710 -2.240 -1.484 -0.686
-0.859 -0.993 0.429 0.623 0.301 -0.134
0.558 -2.016 14.114 16.397 15.598 14.490 13.293 18.395
11.795 20.379 11.365 19.799 12.147 20.193 11.192
15.596 12.596 18.232 11.935 13.595 9.446

Table36.txt

1.335	-1.135	-2.358	-1.415	-0.819	-2.387	-0.508	-0.944
-1.555	-2.715	-0.426	-2.353	0.533	-0.892	-2.462	
-1.095	-1.001	-1.891	-1.702	0.855	0.994		
0.198	0.456	-1.228	0.826	-0.156	-1.193	-0.635	-0.166
-0.976	1.044	-0.834	-0.297	-0.675	-0.522	0.908	
-3.515	-1.419	-1.139	-0.051	-0.827	-0.012		
-0.952	-0.615	-0.995	0.871	-0.416	-0.308	-1.689	-1.454
1.153	-1.092	-1.163	-1.417	1.088	-1.092	-0.130	
0.530	-0.840	-1.132	-0.068	-2.866	-1.782		
-1.456	-1.978	-0.408	-0.444	-2.124	-1.322	-0.991	-1.083
-1.231	-0.853	-1.724	0.228	-1.615	-1.956	-0.585	
-0.687	-0.547	-0.616	-0.528	-2.534	-0.069		
-2.139	0.728	-1.703	0.323	1.653	-1.667	-1.687	0.151
-0.950	-2.496	0.214	-2.351	-0.556	-0.152	-0.200	
1.846	-2.335	-0.017	-1.275	-0.351	-0.500		
-0.104	-1.102	-1.513	-0.963	-4.466	-1.428	-0.734	-0.508
-1.305	-1.996	0.531	-1.913	-1.565	-0.610	-1.729	
-2.060	1.434	-0.421	-1.453	-1.970	-0.900		
-0.138	-2.084	-1.234	1.248	-1.094	-0.827	-0.944	-0.328
-0.887	-0.942	-1.104	-3.244	-2.314	0.439	-1.392	
-1.043	0.710	-1.537	-1.551	-1.021	0.591		
0.909	-2.266	-3.031	0.077	-0.483	-3.492	-1.953	-1.247
0.187	-1.519	-1.068	-3.116	-1.487	-1.159	-0.763	
-0.507	-1.949	-2.477	0.206	1.104	-0.830		
1.261	-1.250	-1.891	-1.278	-1.457	-0.658	-3.880	-2.405
-0.536	-2.147	-0.532	-2.054	-1.033	-1.802	-2.166	
0.134	-0.649	-1.124	-0.331	-1.169	0.836		
0.245	-2.386	-0.689	0.637	-2.928	-0.122	-0.446	-0.764
-0.534	0.165	-0.087	-1.553	-2.223	-1.001	0.910	
-0.995	1.233	-0.773	-0.585	-0.387	-1.353		
1.272	-0.691	-1.456	0.706	-1.096	-2.207	-0.284	-1.188
-0.634	-2.760	0.735	-0.086	-0.955	-0.402	-1.932	
-3.097	-0.628	-1.007	0.077	-0.731	2.089		
1.196	-0.022	-2.613	-2.626	-0.130	-2.312	-1.153	-1.385
-2.463	-0.925	-0.801	-2.505	-1.052	0.188	-1.481	
-1.655	-1.925	-1.368	-2.949	-1.128	-3.308		
1.501	0.787	0.149	0.022	-1.662	-1.664	-0.368	-0.956
-1.184	-1.509	-0.365	-2.057	-0.354	-1.557	-1.050	
-1.105	-1.207	-1.120	-2.238	-2.374	-0.164		
1.016	-2.470	-2.908	-1.463	0.228	-0.234	0.251	-0.628
-0.787	0.290	-1.279	0.129	-1.920	-0.980	-0.738	
0.522	0.375	0.318	0.393	-2.576	0.719		
0.224	-2.945	-0.124	2.924	1.094	1.234	0.286	-0.993
0.081	1.278	-0.707	0.374	0.282	1.411	0.688	
1.303	-0.703	1.413	0.979	0.966	0.309		
0.806	-1.122	-0.110	-1.079	-0.692	-1.120	-1.206	-3.691
-1.289	-3.288	-0.897	-1.746	-1.077	-1.878	-1.901	
-1.795	0.626	-0.278	-2.155	-1.541	-1.476		

Table36.txt

-1.174	-1.977	-1.379	-2.441	-0.903	-1.872	-2.206	-3.331
-1.575	-0.533	0.425	-1.544	-0.407	-1.662	0.556	
-1.109	-0.228	-0.059	-1.737	-0.886	0.643		
-0.875	0.481	-1.024	-1.589	-1.054	0.548	-2.295	-0.827
1.680	-1.823	-0.794	-1.074	-0.357	-1.163	-1.195	
-0.437	-1.306	-2.303	0.217	0.375	-1.563		
-0.115	1.773	-1.154	-0.091	0.097	-1.743	-0.767	-0.697
-1.492	-2.169	0.022	-2.414	-1.033	-1.676	-0.492	
-0.596	-0.846	-0.035	0.219	-0.335	-1.129		
0.767	0.504	0.662	-1.191	0.122	-0.816	0.159	-0.801
-1.212	-1.803	0.129	0.539	-0.325	-3.246	-2.213	
-0.062	-1.584	-2.301	-0.732	-1.572	-0.638		
-0.150	-0.505	-1.730	-0.569	-1.522	-0.705	-1.354	-1.930
-0.854	-3.254	-1.240	-1.357	-0.998	0.774	-0.668	
-2.261	-0.777	-2.453	-0.289	0.189	0.806		
-1.303	-0.584	-1.150	-1.197	-1.150	-2.267	-1.008	-2.383
-1.123	-1.827	-0.937	-2.233	-0.030	-1.463	1.083	
-2.109	0.284	-2.041	-1.063	0.860	0.279		
1.013	-0.159	-1.522	-0.226	0.048	-2.337	-1.122	-1.797
-3.113	-1.382	-0.508	-0.867	0.482	-1.338	0.145	
0.496	-2.380	-0.172	-1.313	0.000	-2.145		
1.151	0.184	0.593	-0.319	-1.114	-0.695	-1.156	-2.446
-0.847	-3.099	-0.231	0.330	-0.474	-3.829	-1.199	
-0.349	0.292	-2.488	-0.198	-0.739	-1.128		
0.215	-0.976	0.922	0.213	-1.364	-1.660	-2.809	-1.830
-0.718	-2.201	-0.117	-1.462	-1.883	-1.847	0.118	
-1.506	2.908	-2.769	-0.114	0.789	-2.043		
1.206	0.941	-0.037	-1.170	-1.316	-2.122	-0.333	-1.987
-0.435	-0.243	-1.422	-2.547	-0.380	-0.412	-0.006	
-0.293	-0.805	-1.412	-2.418	-1.239	-0.166		
-0.043	1.137	-1.270	0.303	-1.447	-0.422	0.252	-2.109
-1.654	-1.503	-1.294	0.619	-1.160	-0.369	-1.035	
0.605	-1.180	-0.226	1.071	-1.120	-1.040		
-0.249	1.100	-0.234	0.553	-2.878	0.417	-0.627	-1.204
0.186	0.236	-0.804	-1.348	-1.475	-0.578	0.649	
0.068	1.603	0.376	-0.749	-0.948	0.120		
-2.416	-0.326	-3.364	-0.224	-0.897	-1.814	-1.173	-3.430
0.366	-0.636	-2.289	-2.863	-0.547	-2.298	-0.436	
-2.854	-0.422	-1.747	-2.944	0.794	-1.720		
-0.113	-1.266	-2.881	0.871	-0.445	-0.965	-1.150	-1.861
-0.014	-0.923	-0.502	-1.994	-0.616	-1.215	-0.247	
-1.528	-1.117	-2.040	-0.407	-1.206	-2.327		
0.828	-0.729	-1.311	-0.323	-0.738	-2.734	-1.660	-0.729
-1.386	-0.316	-0.537	-0.794	-1.233	-1.044	-0.553	
-1.822	-0.444	-1.145	-1.708	1.232	-0.197		
1.085	-0.055	-0.986	0.352	-0.244	-0.504	-1.555	-0.696
-0.041	-2.645	-2.077	0.683	0.245	-0.588	1.368	
-0.045	-0.199	-0.913	-0.161	0.494	-0.403		

Table36.txt

-0.824	-1.246	-1.011	-1.697	-0.913	-1.090	-0.389	-1.502
-0.597	0.472	-1.589	-1.545	0.246	1.402	-2.050	
-0.057	-0.165	-1.954	-2.190	-1.110	0.463		
-0.996	1.168	-1.922	0.299	-0.672	-1.056	-0.264	-2.703
-1.175	-0.413	-1.399	-1.614	0.865	-1.125	-1.125	
-0.703	-0.025	-2.765	-2.010	-0.938	0.147		
0.165	0.773	-0.381	-1.648	-1.886	-1.348	-0.240	-0.970
1.328	-2.975	-0.619	-2.967	-1.771	-1.967	1.146	
-0.884	-0.772	-0.934	-0.193	-0.949	0.373		
1.195	1.517	0.004	0.505	-1.129	-1.340	-2.017	-0.867
-1.872	-1.265	-0.953	-0.793	0.276	0.552	-0.460	
-2.170	1.128	0.054	0.936	-1.771	-0.461		
-0.630	0.464	-2.789	-0.956	-0.294	-1.758	-0.771	-1.124
-0.119	-0.523	-2.531	0.729	-1.210	0.012	1.151	
0.926	-0.313	-0.629	-0.644	0.463	-0.179		
-0.575	0.117	-0.045	0.392	-0.592	-0.391	0.808	0.133
-2.151	-0.732	-1.726	0.654	-1.590	-1.568	-2.135	
0.799	1.125	-2.881	-0.717	-0.634	-0.428		
0.657	0.888	-0.109	-1.491	0.527	-1.320	-0.726	-1.244
-1.247	-1.490	-1.959	-1.263	-0.863	-1.976	-1.350	
-0.654	-1.324	-1.684	-0.863	-0.236	-0.533		
0.587	0.988	-0.448	-1.085	-1.009	-2.202	-1.032	-2.791
-0.822	0.785	-0.008	-2.885	-0.706	-1.530	-1.431	
-0.510	-0.580	-2.535	-0.794	-0.485	-0.086		
-1.533	1.054	0.296	-2.285	-2.687	-0.654	-1.843	-2.274
-1.618	-2.369	-1.259	-1.553	-0.657	-0.209	-1.380	
-0.401	-1.132	-1.267	1.317	-1.227	-1.421		
1.186	-1.527	0.173	-0.206	-2.652	-1.226	-1.539	-3.525
-2.196	-1.937	-1.911	-1.267	-0.627	-0.927	-1.055	
-1.098	-0.491	0.681	-0.194	-1.423	-0.945		
0.339	-0.239	-1.684	-1.710	0.730	-2.213	-0.380	-1.513
-0.342	-1.221	-1.876	-3.075	1.434	-1.352	-1.502	
-3.076	-0.094	-0.125	-0.577	-1.727	2.078		
0.894	-0.471	-0.933	-1.480	-2.277	-0.274	-1.506	-2.538
-2.621	-1.869	0.872	-2.858	-0.680	-2.260	-1.268	
-1.172	-1.632	-1.807	-0.258	-0.520	0.633		
-0.643	-1.041	-0.633	-0.597	-1.608	-1.050	-1.470	-0.740
-1.575	-2.385	-0.974	-0.816	1.098	-1.614	0.365	
-2.004	-0.021	-0.571	-2.186	-2.106	-1.224		
0.840	0.300	-0.842	-1.020	-1.303	-1.818	-1.320	-2.102
-0.174	0.097	-0.914	-3.508	-1.600	-1.785	-2.003	
-1.115	0.022	0.129	-1.146	-1.571	0.759		
-0.514	0.265	-1.377	-0.359	-2.170	-1.738	-0.195	-1.819
-3.325	-2.468	-1.602	-2.536	-0.603	-0.877	1.094	
-0.657	0.110	-2.156	0.642	-0.591	-1.092		
-0.152	-0.005	-0.127	-1.420	-2.977	-0.747	-2.332	0.201
-3.400	0.051	-0.488	0.378	0.239	-3.050	-0.274	
0.305	0.335	-2.883	0.344	0.179	-2.019		

Table36.txt

0.606	-0.311	1.369	-1.279	0.029	-0.951	-0.377	-3.146
-1.099	-0.146	-2.612	-1.771	-0.602	-0.641	-0.641	
-0.156	-1.247	-0.443	1.368	-0.058	1.814		
0.353	-0.259	-1.097	-1.114	-0.816	-3.299	-0.082	-2.834
-1.161	-1.428	0.080	-2.624	-1.359	-1.091	-0.572	
-1.441	-0.759	-0.882	-1.599	-1.037	-0.424		
1.374	0.139	-0.347	-2.178	-2.903	-0.916	-1.347	0.061
-0.566	-2.782	-3.145	-1.856	-0.870	-1.101	-0.047	
-0.193	-3.548	-0.047	2.116	-2.785	-1.395		
1.238	0.254	-1.168	-0.458	-0.565	-1.762	-2.415	-2.442
-2.343	-0.644	0.438	-1.231	-0.806	-0.746	0.169	
-1.363	0.435	-0.853	-0.591	-0.564	0.107		
1.083	0.813	0.453	0.531	-0.205	-2.038	0.330	-2.812
-0.403	-3.190	-1.230	-3.203	-0.096	-0.482	-0.456	
-0.736	-3.859	0.119	-0.228	-1.040	-3.141		
-0.048	-0.845	0.300	0.936	-1.424	-1.369	-1.310	-3.454
-0.920	-1.654	-0.896	-2.045	0.856	-0.799	-0.222	
-0.969	1.566	-2.060	-0.037	1.087	0.122		
0.473	0.461	-2.765	-0.894	-0.418	-1.967	-1.645	0.031
-1.038	-1.797	0.065	0.644	1.746	-1.017	-0.212	
-0.386	0.989	-2.181	-1.416	-0.870	-0.130		
-0.233	-0.122	-1.253	-0.707	-2.976	-1.163	-0.422	-1.773
-1.223	-1.165	-1.969	-1.596	0.103	-1.379	0.852	
-0.676	-0.606	-1.547	0.464	-0.872	1.119		
-0.134	-1.912	-3.002	0.125	0.392	-1.146	-0.888	-0.138
-0.565	-2.878	-1.481	-0.626	-1.244	-0.827	-0.655	
-0.175	-1.858	-1.180	-0.468	-0.026	-1.421		
-1.436	0.539	-1.059	-2.104	-1.190	-0.018	-1.541	-1.415
-2.004	-2.745	-0.015	-2.710	-1.826	-2.179	-0.110	
-0.572	0.026	-1.696	-0.001	-0.602	-0.290		
1.285	0.330	-1.453	-0.593	-0.290	-1.901	0.316	-1.600
-2.253	-2.294	-0.854	-2.803	-2.207	-0.627	-0.521	
-1.222	0.840	-1.477	-2.294	-0.002	0.167		
-0.792	-0.015	-1.145	-0.453	0.649	0.984	-2.094	-0.425
-1.158	-2.983	-1.411	-1.643	-1.017	-1.766	-0.040	
-1.713	-0.588	0.210	-0.819	0.389	-0.963		
0.419	0.522	0.048	-0.908	-1.196	-1.917	-1.339	-1.816
-0.432	-2.294	-1.586	-2.142	-1.210	-1.204	-0.431	
-1.243	-0.961	-1.116	1.182	0.347	-0.136		
-0.282	-1.333	-1.444	-1.760	-1.525	-2.596	-0.245	-1.533
-0.782	-1.832	-0.038	-0.468	-1.900	-1.111	-0.532	
-0.832	-1.561	-1.836	-1.405	0.339	-0.305		
0.405	0.045	0.846	-0.927	0.622	-0.033	-0.799	-1.893
1.147	-1.101	-0.848	-1.144	-2.172	-1.513	-1.183	
-0.279	-1.973	-1.044	0.434	-0.199	-1.153		
-0.171	-0.337	-0.996	-0.924	-1.031	-0.708	-1.513	-2.218
-1.435	-0.216	0.757	-2.208	-1.724	-2.041	-0.262	
-0.760	-0.089	-0.789	0.956	-0.234	-0.295		

Table36.txt

-0.484 -1.435 -0.819 -0.500 -1.743 -0.953 -0.241 -2.059
-1.131 -2.060 0.479 -2.287 0.510 -3.759 -1.040
-0.685 0.212 -3.695 0.249 -1.801 -1.069
0.272 -0.368 -1.141 0.629 -0.442 -2.248 -3.278 -0.974
-0.283 -1.357 -0.794 1.601 -0.701 -0.430 -2.147
-1.047 -2.520 -1.501 -1.937 0.688 -1.814
-1.702 0.383 -2.237 -2.649 -0.818 -0.411 -0.800 -1.117
-1.440 -1.909 0.687 -1.854 -0.953 -1.557 -0.178
-2.211 -1.133 -1.359 -0.335 0.678 -0.327
0.561 -0.966 -0.890 -0.795 -0.354 -2.564 -1.602 -2.223
-0.433 -1.501 0.443 0.209 -1.270 -2.163 -0.249
-1.916 -0.175 1.493 -1.445 -0.178 -0.876
3.168 1.343 0.491 -0.414 4.055 0.780 0.768 1.661
-0.890 0.828 -1.031 1.047 0.836 -0.400 -0.944
2.467 1.061 0.737 0.775 -1.708 0.557
-1.146 3.067 -1.085 -0.232 -2.176 -0.914 -2.732 0.483
-0.309 -2.170 -1.701 0.433 -1.117 -0.822 -0.413
0.874 -1.754 -0.593 -1.857 -0.736 0.161
-1.786 1.018 -2.256 -2.936 -1.856 -1.266 -0.143 -1.921
-2.353 -0.383 -1.618 -1.246 0.544 -0.422 -0.266
-1.233 -0.032 -1.711 -2.127 -0.860 -0.829
0.267 2.134 -0.705 -1.196 -1.660 -3.309 -0.484 -0.878
1.408 -2.110 -0.289 -1.181 0.364 -2.589 -0.499
-3.159 -1.355 0.494 -1.713 -0.230 -0.101
-1.106 -1.015 -0.334 -0.551 0.367 -2.310 -1.983 0.000
-1.059 -3.014 -0.197 -2.688 -0.525 -0.854 -0.890
-0.335 -0.329 -3.364 -0.155 0.213 -0.226
-0.524 -1.094 -1.981 -1.002 -1.262 -0.912 -0.440 -1.992
-1.309 -1.747 -1.071 -2.426 -3.523 -1.155 0.011
-0.796 0.694 -1.724 -1.194 -0.204 -0.099
-1.216 -1.139 0.978 0.486 0.308 0.557 1.441 0.218
0.890 -0.318 -0.332 0.193 -1.311 -0.621 -0.090
-0.707 -0.603 -0.945 0.891 0.873 0.008
0.329 0.306 -1.328 1.487 0.283 -0.619 -2.474 -1.868
-0.713 -2.157 -1.831 -0.921 0.578 -0.799 -0.598
-0.757 -2.575 -2.672 -0.354 -1.910 -0.592
-0.002 -1.785 -0.139 -1.920 -0.571 -0.826 -1.908 -1.191
-1.567 -2.951 0.844 -0.439 -1.634 -1.306 -0.100
-0.678 0.948 -0.867 0.563 -1.697 1.206
-0.448 0.502 0.654 -2.529 1.075 -1.332 -0.926 -2.218
-0.709 -3.700 -0.803 -0.659 0.441 -0.905 -0.387
-1.805 -1.483 -1.721 -1.912 -1.146 -0.704
1.082 -0.219 -0.915 0.266 -2.946 -0.433 -1.453 -0.164
0.167 -0.880 -2.694 -0.562 -0.644 0.013 -0.612
-1.086 -1.681 0.094 0.405 -1.913 -1.100
0.299 0.824 -1.961 -0.230 -1.865 -1.469 -0.289 -0.162
-0.676 -1.495 -2.210 -0.587 -0.505 -1.091 -0.535
1.796 -0.974 0.189 -1.056 0.357 0.453

Table36.txt

0.763	0.453	-1.618	-0.791	0.340	-1.240	-0.511	-0.833
-1.009	-0.160	-2.759	-2.078	-0.234	-1.447	-2.555	
-1.529	-1.726	-1.803	-1.232	1.195	-0.529		
0.538	-0.376	1.400	-0.456	-1.460	-1.420	0.224	-1.977
-2.254	-1.435	-2.082	-0.912	0.840	-1.707	-1.182	
-0.667	-0.060	-0.350	0.116	-1.210	-0.894		
0.290	0.625	-0.634	1.220	-0.933	-2.112	1.606	-1.246
-0.057	-1.597	1.039	0.960	-1.959	-2.893	0.249	
-0.294	-1.692	-2.759	0.062	-0.225	1.135		
1.592	-0.952	-1.246	-1.474	-2.488	-1.388	-1.324	0.936
-2.195	-1.014	0.978	-0.570	-1.911	-1.490	-0.688	
-0.153	-0.255	-1.455	0.510	0.261	-2.444		
1.215	1.171	-1.590	-0.344	-1.304	-0.168	-0.026	-1.502
0.198	-0.591	-1.799	-2.461	-1.201	-1.150	-0.923	
-1.229	-1.533	-0.945	-1.232	-1.411	-0.444		
-0.397	0.382	-1.069	-0.658	-1.554	-0.336	0.613	-0.455
0.258	-2.746	-0.143	-1.694	-1.154	-0.815	-1.131	
-1.872	-0.940	-0.716	0.207	1.965	-0.302		
1.802	-1.373	0.572	-0.234	0.320	-0.650	-0.274	-0.809
-0.237	-0.920	-0.736	-2.401	-2.710	-2.294	0.886	
-0.296	-0.020	-1.609	-2.445	-0.231	0.340		
-1.248	-0.073	-0.823	1.840	0.713	-1.280	0.774	-0.711
-0.851	-1.643	-1.132	0.253	2.176	1.063	-0.744	
-0.444	0.751	-1.132	-1.365	1.475	-0.756		
0.239	-0.685	0.209	-1.834	-2.155	-0.258	-0.512	-0.222
0.206	-1.384	-2.001	-2.593	0.878	-1.970	1.699	
-1.142	1.108	-1.409	-0.245	-0.574	-0.207		
-0.300	-0.481	-2.000	-0.218	-0.258	-1.464	-1.924	-0.062
0.128	-0.061	-0.442	-0.740	0.691	-1.957	2.013	
0.918	0.506	-0.025	-0.266	1.013	0.059		
-0.278	-0.434	-2.587	-1.358	-0.954	-2.349	0.089	0.441
-0.871	0.411	-0.842	-0.255	0.169	-1.784	0.423	
-1.660	-1.393	-0.758	-0.242	-1.307	-0.726		
-0.197	-0.395	-0.671	-0.933	-0.516	0.241	-0.418	-1.230
-4.542	-1.855	-2.012	-3.345	1.332	-2.963	-2.392	
-1.507	0.303	-0.482	-1.723	-0.384	0.403		
-0.175	-0.816	-1.809	0.852	-2.544	-0.474	-0.423	-0.361
-1.717	-1.762	0.303	-1.871	-0.935	-0.725	-0.152	
-0.092	1.004	-2.109	-2.129	-1.805	-3.234		
1.064	1.317	-0.724	-0.111	-1.377	-1.949	-2.851	-0.139
-2.078	-1.236	-0.297	-0.590	-0.234	-2.125	-0.637	
-0.401	-1.253	-1.143	-1.376	-0.805	-0.475		
0.745	-0.793	-1.736	-0.763	0.078	-1.505	-1.254	-0.732
-1.980	-2.845	0.539	-0.643	-2.272	-0.659	-0.688	
-2.859	-0.586	0.269	-1.529	0.739	-1.258		
-0.105	0.449	0.000	-1.092	-0.872	-1.978	0.311	-1.034
-1.354	-3.554	-1.873	-3.029	0.689	-0.477	-3.220	
-0.534	-0.469	0.290	-0.109	-1.630	-1.094		

Table36.txt

-0.550 -1.991 0.131 -1.990 -0.013 -1.125 -0.140 -0.939
-1.302 -1.288 0.233 -1.881 -0.219 -2.289 -2.286
-2.143 0.216 0.110 -0.842 -2.077 -1.162
0.882 -1.507 -1.850 -0.583 -1.153 -0.802 -0.882 -1.671
-1.676 -1.354 -0.757 -2.552 -2.402 -0.624 -0.481
-0.462 -0.432 0.301 -0.901 -0.812 0.539
0.289 -1.323 -0.749 -0.454 -1.125 -3.046 -1.811 -0.183
-0.266 0.374 -1.372 -2.782 0.707 -1.034 -1.185
-0.951 -2.642 -0.604 -0.997 -0.328 -1.348
-0.409 1.818 -0.447 -0.447 -1.111 -1.398 -1.098 -1.294
-0.689 -0.841 -3.014 -1.287 0.007 -0.549 0.900
0.811 -3.516 1.101 0.468 0.277 0.416
0.014 0.267 -2.976 -1.826 -0.580 -0.518 -2.033 -1.892
-1.302 -1.800 -0.558 0.400 -0.055 -2.141 -4.005
-1.676 -0.474 -0.298 -1.213 1.115 -1.864
0.496 -0.163 -0.692 1.063 -2.205 -1.031 -2.256 -0.588
-0.733 -1.514 0.010 -2.164 -1.564 -1.420 -0.569
-0.783 0.309 -1.546 -1.483 -0.318 0.246
0.379 -0.996 -1.215 -1.082 0.326 -0.843 -2.548 -1.603
-0.062 -1.430 -2.959 -2.677 -0.050 -0.024 -2.649
-0.762 -0.224 0.928 -1.636 -1.356 -0.139
0.272 -1.495 -0.675 -1.906 -0.327 -0.535 0.390 -1.434
-0.873 1.387 -2.280 0.603 -1.587 -0.414 0.111
-2.090 -1.465 -0.170 0.339 0.784 -0.013
-0.238 -1.585 -0.089 0.112 0.493 -1.637 0.503 0.530
0.450 0.288 -0.240 -0.495 1.297 -0.181 -0.588
-1.094 -1.007 0.009 0.126 0.843 -0.555
-0.806 -1.508 0.472 -0.523 -0.123 -1.552 -0.473 -1.069
0.521 0.437 -0.897 -1.815 -0.461 -1.995 1.074
-1.912 -0.085 -1.660 1.340 -1.391 -1.116
1.084 -1.381 -0.904 -1.443 1.468 0.077 -2.347 -1.119
-1.006 -2.244 -1.577 -1.836 -0.917 -0.315 -0.098
-1.297 -1.411 0.100 -0.186 -0.095 -1.162
0.827 -1.375 0.810 0.857 -1.350 -0.714 2.047 0.035
0.880 -0.187 -0.226 -0.669 0.473 -0.452 -0.239
-0.196 -0.720 -0.185 1.979 -0.124 0.099
-0.431 -1.194 0.287 -0.784 -2.006 -0.231 -0.012 0.426
-1.423 0.061 -0.549 -1.429 0.780 -0.564 -0.762
-1.122 -0.241 -1.306 -1.812 0.390 -1.376
0.074 -4.461 -1.157 8.565 -1.630 1.338 -0.061 -1.508
0.361 0.123 -2.244 1.497 2.209 2.833 0.863
-0.789 0.682 0.677 8.190 0.497 -1.054
-0.387 -1.169 -0.250 -1.488 0.663 -0.916 -2.408 -1.085
-2.644 -1.102 -1.050 -0.587 -0.335 -0.900 -0.611
-2.385 -0.496 -0.616 -0.414 -0.346 -1.322
-0.842 -2.652 -0.135 -2.384 0.460 -0.225 -1.364 -2.044
-0.803 -3.081 0.346 1.499 0.378 -0.048 -1.469
-2.485 -0.541 -2.510 0.005 -0.435 -1.592

Table36.txt

-0.228	-0.355	-1.871	-2.941	0.317	-1.599	-2.228	-2.349
-0.101	-2.148	-1.445	-1.066	-0.579	-3.855	-0.391	
-1.602	-1.133	0.316	0.322	-1.191	-0.766		
0.679	-2.154	0.183	-0.335	0.202	0.698	-0.490	0.208
0.163	-1.234	0.618	0.384	-0.402	-0.905	-0.028	
0.134	0.463	-0.526	-0.109	-1.596	0.101		
1.153	-1.504	-1.064	0.313	-1.537	-1.902	-0.071	-1.556
0.083	-3.218	0.123	-1.389	-1.337	0.436	1.132	
-0.514	0.795	-0.281	-3.675	-1.559	-0.849		
0.706	-1.755	-1.015	0.628	-1.402	-1.122	-1.222	-0.712
-2.014	-0.235	-1.715	-1.231	0.768	-2.924	-0.534	
-1.542	0.902	-1.768	-0.611	-1.228	-0.841		
0.313	-2.070	0.094	-0.470	-0.306	-1.372	-0.944	-0.534
1.384	-1.195	-1.566	0.394	-1.434	-0.950	-1.961	
2.298	0.475	-1.387	-0.729	-0.515	-0.435		
-0.491	-2.055	-1.009	-1.012	-1.992	0.273	-2.216	-0.500
-0.154	-3.845	-1.421	-3.257	-0.652	-2.012	0.560	
-0.787	-1.794	-1.817	0.261	0.223	-1.314		
-0.515	-1.230	-1.608	-2.232	1.218	0.464	-0.343	-3.755
-0.794	-3.014	-0.288	-1.373	-1.784	-1.670	-0.210	
-0.158	-1.065	-1.434	-4.103	-1.784	-0.314		
-0.722	-2.282	-1.991	-2.220	-1.959	-2.265	-0.854	-2.401
-2.054	-1.535	0.989	-1.672	-1.387	-1.036	-0.261	
-0.168	1.236	-2.145	-1.083	-0.630	-1.086		
1.072	0.097	-1.142	-1.062	-0.337	-1.327	1.398	-0.100
-0.870	-2.701	0.238	-2.155	-0.071	-1.571	-0.098	
-2.224	-0.597	0.536	-1.178	-0.825	0.392		
0.826	-2.194	-1.960	0.283	-1.883	-3.259	0.323	-3.563
0.231	-2.174	-1.927	-1.149	0.045	-1.344	-1.101	
-1.675	-0.210	-0.156	-1.802	-1.375	-1.423		
-0.249	-0.547	-0.031	-3.062	-1.972	-0.728	0.194	-0.218
-0.621	-3.478	-0.901	-0.914	-1.307	-0.680	0.140	
-1.644	1.714	-0.714	0.025	-1.681	-2.102		
0.974	-1.043	-1.694	-1.650	-0.778	-1.135	0.342	-1.694
0.035	-2.733	-2.773	-1.262	0.649	-1.841	0.979	
-1.873	1.090	-1.738	-2.912	-2.016	-1.033		
-0.560	-2.166	1.837	-0.279	0.635	-2.208	1.995	0.441
0.054	0.252	-2.265	-0.350	0.720	-1.091	-1.594	
0.969	-0.379	1.970	-0.482	-1.059	-0.545		
-0.830	-1.827	-2.871	-3.473	-1.505	-2.497	1.069	-1.207
-0.935	-1.575	-0.957	0.020	-0.353	-0.711	0.333	
-1.443	-1.136	-1.898	-0.996	-1.249	-1.361		
0.088	-2.206	-1.073	-0.686	-1.704	0.126	-1.426	-1.646
-0.683	0.108	0.472	-1.155	0.532	-1.013	-0.094	
-1.644	0.494	-0.455	1.096	-2.282	-0.438		
0.453	-0.499	-1.499	-1.740	-0.242	0.008	-2.552	-2.238
0.240	-0.471	-0.774	-1.111	0.119	-1.994	1.762	
-0.398	0.125	-0.495	-1.219	-0.503	-1.550		

Table36.txt

0.156	-0.636	-0.906	-2.446	-1.813	-1.252	0.143	-2.364
-2.136	-1.842	0.267	-1.638	-0.125	-3.157	-2.759	
-1.635	-0.162	-2.673	0.032	-0.627	-0.452		
-0.232	-0.022	-0.096	-0.683	-2.064	-0.176	-2.086	0.079
-1.499	-0.673	-1.326	1.666	0.625	0.516	0.339	
-1.666	0.316	0.631	-0.584	0.375	-0.944		
0.044	-0.267	0.350	-2.690	0.461	-0.293	-1.114	-1.030
-0.415	0.532	-0.095	-0.728	-1.897	-0.295	-2.011	
-1.801	-0.041	-2.313	-0.754	1.003	1.076		
-1.182	0.956	-0.921	-1.387	-0.138	0.412	-0.944	-0.475
-2.516	-3.078	-0.779	-4.003	-0.710	-1.569	-0.749	
-1.341	-1.779	-0.937	-0.627	-0.729	-0.391		
0.737	-1.843	-2.096	-0.841	-1.710	-1.015	-1.868	-1.428
-0.728	-1.407	-2.914	-0.170	-1.114	-0.839	-2.585	
-1.188	-0.546	-0.315	-0.651	0.003	-0.464		
0.037	1.378	-1.337	-1.135	-2.305	-0.002	-0.104	0.032
0.919	-2.255	-2.450	-0.960	-0.823	-0.276	0.400	
-1.211	-0.271	-1.778	-1.512	-2.820	-0.926		
-0.049	-2.487	-0.136	0.393	0.316	-0.895	-0.435	-2.543
-0.973	-1.011	1.763	0.820	-0.355	-0.823	0.010	
-0.847	-0.225	-0.288	-0.891	-0.164	-0.785		
-0.431	-1.602	-1.797	-1.371	-1.548	-0.178	-1.471	-2.675
-3.700	-2.501	-1.834	-0.698	-0.579	-0.363	-1.348	
-1.525	-0.450	-2.125	-2.858	-1.440	-0.564		
0.264	0.206	-1.381	-0.339	-1.178	-1.428	-1.440	-1.220
-1.509	-0.322	0.423	-0.071	-0.352	-0.299	-0.135	
0.520	-0.591	0.364	-1.629	-2.058	-0.837		
1.176	-1.074	1.575	0.019	0.430	-0.480	0.404	0.014
-2.074	-1.907	-1.930	0.124	1.821	0.850	-0.767	
0.263	0.489	0.123	-0.701	0.768	-0.660		
1.456	-0.805	-0.825	-0.028	-2.986	-2.033	-1.472	-2.817
-3.236	-3.024	-0.472	-1.199	0.595	-1.344	-1.100	
-0.581	-0.561	-0.708	-0.791	-0.148	0.035		
-0.653	-0.915	0.583	-0.473	-2.207	-2.267	-0.510	-2.230
-0.862	-2.421	-1.143	-2.131	-1.844	-1.416	-0.029	
-0.556	-0.566	-2.279	-0.284	-0.552	-0.890		
0.009	-1.403	-0.688	-0.829	-0.511	-2.578	-1.411	-2.101
1.056	-1.009	-0.968	-3.302	0.208	-1.573	-1.057	
-1.894	0.679	-0.559	-0.195	-0.529	-0.518		
0.426	-1.628	-0.425	-1.707	-0.486	-0.293	-1.123	0.056
-0.010	-1.285	-0.512	-2.782	-0.664	-0.507	-1.752	
-2.322	-2.068	-0.815	-2.153	-1.572	-0.289		
0.436	-0.642	-1.170	0.759	-2.407	-1.990	-1.632	-0.412
-0.764	-2.065	-0.601	0.332	0.683	0.245	0.374	
0.173	1.305	-0.868	-0.690	-0.384	-0.425		
-0.150	-0.996	0.820	0.150	-0.914	-1.000	1.277	-0.361
-1.767	-0.824	-0.549	-0.597	-1.211	-1.659	-1.026	
-0.978	-1.161	0.871	0.869	1.275	-0.982		

Table36.txt

0.284 -1.907 -0.146 -0.936 -1.070 -2.429 0.717 -0.389
-1.161 -1.325 0.561 -1.086 -0.236 -0.645 0.542
1.849 0.805 -0.168 0.162 -2.610 -0.982
0.322 -0.208 0.347 -1.054 0.176 -0.509 -0.401 -1.600
-0.749 -1.164 -2.801 -0.579 -2.494 -1.664 -2.389
-0.518 0.121 -0.716 0.155 -0.718 -0.341
1.267 -0.227 -1.201 1.229 -0.827 0.801 -1.458 -0.851
-0.945 -1.284 0.379 -1.114 -0.006 -2.430 -0.188
-2.521 -0.265 -2.089 0.486 -0.456 -0.679
0.118 -0.351 -1.142 -0.746 0.074 -1.231 -1.166 -3.247
-1.975 -1.327 0.409 -1.724 -0.002 -2.431 -1.376
-2.022 0.344 -0.253 0.539 -2.066 -1.401
-0.787 -2.433 0.677 0.449 -2.051 -2.213 -1.029 -3.420
0.299 -2.163 -0.821 -1.183 -0.765 -0.494 -1.156
-0.061 0.801 -0.961 -2.675 -1.243 -1.222
-0.198 -1.726 2.016 -0.184 0.101 -0.218 0.304 -1.530
-0.865 -0.436 -0.281 -0.532 0.597 -0.373 -0.426
1.080 0.255 -0.446 -0.004 -1.277 -0.033
0.444 -2.016 -0.542 -1.481 0.150 -0.402 -0.494 -2.193
-0.529 -1.069 -0.751 -0.389 -3.058 -2.632 -0.836
0.345 0.277 -0.466 -0.089 -0.985 1.289
-1.096 -1.239 -1.751 -1.795 -2.165 -0.714 -1.114 0.135
-1.915 -0.409 -0.906 0.065 -0.541 -1.710 -1.467
-0.932 0.327 -1.077 -0.670 -0.674 -3.040
-0.212 -2.036 -0.559 0.339 -0.932 -2.056 -1.689 -2.303
0.885 -1.132 -1.254 -1.688 -1.549 -1.474 -0.646
-1.275 -0.431 -0.762 0.143 -0.115 -0.099
-0.447 -1.612 -2.105 -0.661 -0.854 -2.418 -3.205 -2.333
-0.941 -3.043 -0.809 -2.302 -0.676 -1.253 -1.518
-2.530 -0.121 0.339 -1.660 1.353 -1.290
-1.062 -1.767 -3.226 -1.547 -1.494 -0.297 -0.201 -0.644
-0.877 -1.209 -0.514 -1.063 -0.725 -1.875 -1.258
-1.521 -1.530 -2.924 -2.433 -1.575 -0.108
-0.069 -0.236 -2.966 -0.762 -0.842 0.577 0.226 -1.045
-1.323 -0.914 -1.872 -0.585 0.281 -2.743 -0.014
-0.843 -0.394 -0.062 -0.425 -2.065 0.665
0.159 0.797 0.477 -0.083 0.319 -1.547 0.210 0.556
-1.499 -2.122 -1.465 -0.787 -1.694 -0.145 -2.091
-0.576 -1.107 -0.255 -1.035 -2.695 -1.439
0.140 -1.499 0.453 0.676 1.556 -1.055 -0.161 -2.120
1.489 -0.748 -0.163 -1.772 0.292 -0.414 -0.170
-1.165 0.211 0.942 -0.370 0.792 -0.185
0.068 -1.249 0.531 -1.621 -1.038 -1.016 -2.622 -1.679
-1.001 -1.463 -0.759 -0.227 1.595 -2.673 2.115
0.668 -1.127 -1.103 0.479 -1.160 -1.109
1.384 -0.167 -1.118 -0.656 -0.398 0.518 1.605 -0.959
0.094 -1.113 -0.944 -0.725 -0.939 -0.115 -0.803
-2.075 -0.520 -0.538 0.839 0.344 -1.554

Table36.txt

-0.149 -0.394 -3.269 0.713 -1.863 -0.708 -2.263 -1.740
-1.110 -0.749 -3.235 -2.093 -0.872 -1.102 -1.363
-1.330 -0.183 -0.344 -2.889 -0.546 -0.576
0.464 -1.267 -0.880 -0.206 -0.221 -2.561 -0.412 -2.078
-1.360 -1.179 -1.145 -2.125 0.358 -2.200 -1.271
-0.772 1.293 -0.658 -0.370 -1.552 -1.200
0.975 -1.347 0.362 -2.163 -0.448 -2.110 -0.442 -0.154
-0.349 -1.812 -2.042 -2.190 -1.145 -3.470 -0.387
-0.789 -1.694 -1.679 -2.534 -1.584 -0.703
0.242 -2.800 -1.408 0.153 -0.944 -0.983 -1.603 -1.074
0.755 -1.499 -0.425 -1.280 -0.184 -2.220 -1.036
-1.030 -0.695 0.366 -2.146 -0.469 -0.002
0.767 0.042 0.953 0.483 -0.620 -1.241 0.347 -1.841
-1.838 -1.944 -0.999 -0.229 0.959 0.325 0.092
-2.690 1.612 -0.727 1.514 -0.273 0.496
1.295 -2.668 0.328 -2.619 -0.127 -1.132 -0.804 -2.449
-1.361 0.064 -0.988 -2.696 1.166 0.237 -1.479
-2.649 -0.679 -0.632 -2.601 0.703 -2.508
1.166 -3.105 0.972 0.090 0.515 -0.516 1.709 -0.534
0.729 0.718 -2.658 0.247 -1.856 0.891 -0.416
1.312 -0.617 2.040 0.637 1.220 1.675
0.646 -1.766 -0.289 0.388 0.093 -1.724 1.768 -1.031
1.068 -0.464 0.428 0.735 0.582 -0.453 0.946
-0.224 -0.769 0.448 -0.553 1.964 -0.293
0.615 -1.971 -0.208 -0.721 0.261 -0.561 0.105 -1.259
-1.256 -2.171 -0.030 -1.322 -1.794 0.456 0.476
-1.903 -0.843 -1.833 -0.016 0.405 1.041
-1.163 -3.085 -2.189 0.681 -0.121 -1.126 -1.411 -3.088
0.290 -2.189 -2.492 -1.213 0.702 -0.708 -0.805
-0.920 0.609 -1.512 -0.829 -0.961 0.134
-0.577 -2.094 -0.366 -0.011 -1.001 -2.671 -0.630 0.276
-1.655 -2.005 0.084 -2.200 1.335 0.613 -0.839
1.030 0.839 -1.354 -0.685 0.747 0.560
0.612 -1.370 -0.866 -1.136 -2.145 -2.331 -1.428 -1.482
-0.422 -0.618 -0.803 0.117 -0.962 0.927 1.060
-1.648 -1.781 -0.357 -0.140 0.653 0.059
1.553 -0.548 -1.423 -1.209 -2.449 -1.896 -1.430 -0.839
-1.387 -1.720 -0.300 -1.683 -1.440 -0.977 0.529
-1.928 0.794 -1.113 -0.970 -2.013 -0.507
0.690 -1.961 0.345 -0.495 -1.312 -0.724 -1.115 -1.297
-0.356 -1.261 0.162 -2.958 0.044 -0.955 0.579
-1.145 -1.290 -1.240 -0.758 -0.231 -0.022
-1.344 -0.831 0.126 0.815 -0.277 -0.713 -0.872 -0.380
-1.600 -1.041 -1.922 -0.353 0.895 -0.779 -0.975
-2.047 0.239 -2.041 -1.335 -0.326 -1.221
0.690 -1.634 -0.902 -0.591 -0.471 -0.980 -0.166 -0.190
-0.330 -3.759 0.434 -0.514 -0.387 -1.958 -1.854
-1.420 0.841 -0.565 1.335 0.482 -0.761

Table36.txt

0.675	-0.073	0.430	-1.247	-0.899	1.394	0.839	-1.636
-0.588	-1.642	-0.680	-0.547	-0.202	-1.543	1.625	
-0.008	0.721	0.387	-0.790	-0.735	-0.941		
-0.124	-1.181	-0.730	-0.147	-2.442	-1.277	-0.917	-0.768
-0.301	0.272	-0.028	0.871	-2.882	-0.898	-0.712	
0.031	1.487	0.090	-0.726	-0.403	-1.263		
-0.381	-0.389	0.308	0.241	1.845	-0.059	-0.182	-1.505
-1.233	-1.064	-1.626	0.312	0.832	-1.014	-1.745	
-0.167	-0.428	-1.276	-0.664	-0.446	-0.238		
0.623	-1.856	13.245	15.323	11.328	19.094	12.540	18.517
9.723	20.844	7.162	20.533	10.496	18.033	13.106	
14.519	10.345	15.129	11.205	12.175	11.129		
0.319	-1.500	-2.855	0.307	-1.588	-0.090	-1.118	-3.645
-0.015	-1.474	-1.460	-1.020	0.372	-1.572	1.434	
-1.218	1.630	-1.934	-0.324	-0.671	0.020		
1.243	-1.999	-1.044	-0.120	-2.672	-1.134	-0.671	-1.082
0.279	-0.649	-1.423	-0.084	-1.984	-0.253	-0.079	
-1.079	-0.031	-1.073	0.501	-0.520	-1.475		
-0.009	-0.107	-0.265	-1.452	1.282	-0.366	-0.366	0.209
-0.906	-1.660	-1.255	-2.841	-0.355	-2.935	-0.685	
-1.679	0.188	-0.690	-0.106	1.969	2.315		
0.714	-0.858	0.489	1.762	-0.519	-0.809	0.439	-1.631
-0.758	0.768	-1.722	-0.460	0.112	1.998	-0.092	
0.541	-1.262	-0.533	0.005	-0.530	-0.544		
0.994	-0.537	-1.010	-3.118	-1.418	-1.847	-0.190	-2.954
-0.663	-0.216	-2.933	-1.637	0.964	-2.835	0.145	
-0.979	-0.379	-0.928	-1.752	-0.382	-1.043		
0.558	-0.771	-1.792	-2.154	-1.509	0.153	-0.625	-1.007
-2.128	-2.653	-1.932	-2.253	0.615	-0.089	0.439	
1.669	-0.020	0.286	-0.021	-2.098	0.524		
0.828	-0.288	-3.506	0.733	-0.285	-1.713	-0.802	-2.076
-1.091	-1.618	-0.723	-2.562	-1.688	-2.729	-0.790	
-1.087	-0.967	-0.156	-0.668	-0.765	-0.568		
0.237	-1.604	-0.720	-1.214	0.286	-2.098	-1.082	-2.005
-1.000	-1.394	-0.344	-0.604	-0.418	-0.111	-0.217	
-1.893	-0.043	0.461	0.122	-0.248	-2.103		
-0.441	1.426	0.201	1.744	1.058	-1.712	-2.072	1.286
-1.279	1.550	-0.099	-1.202	-0.440	-1.934	-0.103	
-2.058	0.461	-0.172	-1.864	-0.830	-0.229		
-1.555	-1.766	0.046	-0.089	-2.431	0.673	1.327	-1.062
0.251	-1.649	-1.391	-1.237	-0.725	0.863	-2.066	
-0.200	-1.697	-0.137	1.101	0.686	1.863		
1.148	-0.340	0.577	1.238	-1.492	-0.446	-0.477	-1.564
-0.915	-4.355	-0.135	-2.293	-2.518	0.035	-1.228	
-0.264	-0.563	-1.037	-0.115	0.585	-1.900		
0.368	0.268	-0.954	0.327	0.507	-1.109	-0.293	-1.508
-1.227	-2.086	-0.084	-1.669	-0.385	0.218	-1.772	
-0.983	-1.082	0.287	-2.593	-0.026	0.081		

Table36.txt

0.028 0.202 -1.679 0.637 -0.758 -1.074 -1.702 -0.467
-0.286 -1.672 -0.299 -1.322 -1.269 -1.066 -3.482
1.595 0.745 -1.318 -1.132 1.253 -0.767
0.658 -2.922 -1.007 -1.919 -0.887 0.077 -0.881 -1.403
-0.594 -1.263 0.746 -2.765 -0.353 -1.096 -0.919
-0.629 -0.740 0.504 -0.316 0.559 -0.586
0.998 -0.620 -2.356 -1.991 -2.507 -0.565 -1.616 -0.930
0.141 -1.068 1.542 -1.558 0.378 -1.907 -0.481
-0.914 -1.331 -2.620 -1.808 -0.777 0.007
0.859 -0.865 -1.553 -0.079 -1.430 -2.306 -0.211 -1.117
-2.385 -0.356 -1.331 -0.474 -2.320 -1.355 -1.555
-0.080 -1.768 -0.402 -2.205 -0.169 -1.237
0.615 -0.086 -3.672 -0.605 -1.530 -1.498 -1.496 0.132
-0.459 -0.218 -1.377 -0.645 0.118 -2.496 -1.544
-1.059 -0.417 -1.628 -1.747 0.268 -2.057
-2.450 -0.799 -1.152 -0.874 0.654 0.162 -1.387 0.068
-0.122 -0.250 -0.320 -1.549 1.282 -1.477 1.057
-0.811 -0.524 -1.582 -0.378 0.118 1.541
-0.454 -1.277 -0.528 -2.641 -1.016 -0.090 0.608 -2.365
-0.872 -2.557 -0.720 -0.388 -0.670 -1.647 0.113
-0.627 0.106 -0.673 -1.178 -0.763 1.457
0.113 0.234 0.350 -1.650 -2.348 -1.633 0.044 0.962
-1.154 -1.088 0.452 -0.105 -0.759 -0.222 -2.169
-0.483 -0.318 -0.867 1.083 -0.830 -2.475
-0.188 -1.636 0.082 -0.622 -1.306 -1.322 -1.284 -3.258
0.102 -2.218 -1.025 -2.820 -0.978 -1.115 -0.458
-1.424 -1.743 -0.866 -0.545 -1.448 -0.488
1.356 -0.246 -1.629 -0.599 2.077 -1.265 -1.202 -1.464
-0.902 -0.986 -1.639 -0.766 -0.255 -0.213 -0.446
-0.883 -0.719 -0.389 -0.999 -0.048 -0.797
0.850 -1.658 -1.345 0.300 -0.207 -1.025 -2.994 -2.525
-0.866 0.111 -0.995 -3.011 -1.720 -2.444 0.376
0.656 0.499 -1.382 -1.336 -0.128 0.204
0.234 0.600 -1.670 -0.907 0.126 -1.820 -0.737 -2.335
-3.789 -2.155 -2.143 -3.346 -1.499 -1.892 -0.343
-0.907 -1.636 1.318 -0.002 -0.707 -1.324
-0.080 -2.338 -0.718 -0.824 -1.877 0.690 -0.249 -0.161
-1.346 -2.227 -2.301 0.808 0.955 -0.002 0.109
-2.338 1.172 -1.654 -0.762 -0.364 -0.347
-0.177 0.963 1.729 1.277 -1.417 -2.590 -0.571 -3.133
-3.264 -1.841 0.524 0.863 1.368 -1.582 0.369
-1.723 -0.552 -1.835 0.059 0.650 -0.387
0.026 -0.077 -2.725 0.159 1.730 -1.234 -0.104 -2.204
-0.583 -2.909 -2.100 -1.251 -1.432 -0.792 -0.343
-1.186 -2.099 -2.578 -1.138 -0.177 -0.509
-0.344 -1.064 -2.181 -1.132 0.367 -3.112 -0.142 -1.188
-0.739 -0.485 -0.556 -3.813 0.260 -2.864 -1.001
0.217 -3.228 -2.305 -1.834 -0.864 0.298

Table36.txt

-0.215 -0.177 -2.397 -2.103 -2.525 -2.798 -2.067 -2.997
-2.497 -1.208 -1.214 -2.726 0.661 -1.616 -0.240
-1.533 -0.448 -2.159 -0.225 -1.564 -1.871
-1.350 0.020 -1.467 0.304 -1.168 -2.420 0.619 -0.726
0.103 -0.289 -2.408 -3.024 -0.583 -2.067 -1.133
-1.139 -0.199 -0.122 -0.950 -2.808 -1.698
0.894 -1.300 -0.723 -0.945 -1.176 -1.496 -2.638 -0.038
-2.474 -0.087 0.087 -2.382 0.066 -1.933 -1.093
-1.057 -1.951 -0.528 -2.677 -0.772 0.352
1.497 -1.181 -1.256 -0.088 -0.548 -1.805 -1.108 0.343
-0.493 -1.163 -1.088 -1.620 0.385 -1.311 -1.735
-0.861 -0.292 -1.253 -0.539 -0.185 -0.982
-0.116 -0.248 -2.489 -1.569 -0.278 -0.421 -2.005 -1.022
-1.004 -2.563 0.590 -0.723 -2.991 -1.953 -0.846
-2.201 -0.887 -2.466 -2.182 -1.386 -0.736
-0.906 -1.663 0.365 0.486 1.235 -3.080 0.379 -0.137
0.032 -0.925 -0.261 -1.544 0.950 2.903 -0.799
2.155 -1.223 0.293 1.092 -0.612 1.139
0.426 -1.028 -0.158 -0.204 1.631 -0.711 0.099 -2.843
-1.056 -1.210 -0.126 -2.542 0.381 -0.849 -0.286
-0.539 -1.225 -1.963 -0.770 -0.200 -1.642
0.233 -1.488 -2.687 -1.954 0.093 -1.244 -1.826 -2.661
-0.822 -2.842 -1.354 0.559 1.529 -0.325 -0.803
-2.113 -0.393 -2.153 -1.397 -0.939 -1.032
1.255 0.244 -0.297 0.639 -1.040 -0.454 0.311 -0.990
-2.880 -3.027 -2.904 -0.930 0.269 -1.457 -0.628
0.499 -0.995 -0.692 -0.736 -1.541 0.929
0.826 -2.927 -3.213 -1.387 -1.326 -1.759 -3.336 -2.448
0.506 -3.179 0.334 -2.736 -3.438 -2.000 0.643
-2.635 1.350 -1.443 -0.265 -2.454 -1.567
0.386 -1.274 1.099 -0.798 -0.756 -1.082 -0.117 1.156
-0.855 -0.440 1.135 -1.779 1.613 -1.072 -0.399
-2.587 0.950 -0.375 -0.766 0.860 0.060
-0.403 -0.795 -0.768 -0.675 -1.313 -0.533 -2.162 -1.470
-1.671 -0.853 0.272 -1.529 -1.818 -2.102 -2.367
0.867 -2.301 0.451 0.986 0.580 -0.332
-0.239 -1.251 0.959 -0.751 -0.141 -1.400 -1.373 -2.450
0.080 -1.672 -0.715 0.269 -0.443 -1.302 -0.988
-0.783 0.603 -0.083 -1.444 -1.168 -0.673
0.611 1.584 -1.940 -2.040 -2.230 -1.224 -1.514 -0.930
-1.334 -1.336 -1.229 -2.445 0.841 -2.413 -0.444
-1.221 -0.847 -2.723 -0.884 -1.764 -0.525
-0.458 -0.332 0.813 -0.706 -1.031 -0.828 -0.836 -2.354
-2.093 -2.030 -0.364 -1.320 -0.346 -0.396 -0.981
-1.012 -1.626 0.453 0.443 -0.658 -2.056
0.347 -0.777 -0.527 -1.094 0.625 -0.910 -2.687 -0.561
-1.960 -0.674 -1.869 -0.226 -0.549 -2.841 0.240
1.718 -0.561 -0.404 -0.044 0.316 -0.181

Table36.txt

0.178	-0.321	-1.070	-0.220	-0.102	-2.035	-3.282	-1.300
-2.452	-1.130	-2.882	-1.272	-0.687	-0.415	-1.057	
0.503	-0.132	-0.381	-2.425	0.475	0.043		
-0.116	-0.212	-1.476	-0.481	-0.807	-2.528	1.143	-1.400
-0.454	-0.787	-1.453	-2.045	-1.618	-0.907	-1.067	
0.052	-1.725	-1.581	-1.341	-2.366	-1.945		
0.360	-0.687	-2.005	-2.318	-1.412	-1.329	0.005	-1.512
-0.859	-1.069	0.668	-1.116	-0.044	-2.087	-1.098	
-0.064	-0.297	-2.344	0.212	-3.874	-0.207		
-2.101	-2.570	1.615	0.545	2.508	1.721	0.983	-0.018
-1.668	0.477	-0.346	0.674	3.234	-1.378	-0.086	
-0.950	0.931	-0.569	-2.086	-0.994	0.853		
-0.094	0.055	-3.182	-1.334	-2.337	-0.671	-0.576	-2.344
-1.541	-2.927	-2.112	-2.180	-2.274	-1.781	-0.822	
-0.245	-2.250	-1.358	-0.923	-2.534	-0.435		
0.303	-0.567	-0.326	-1.547	-1.001	-1.377	0.234	-2.959
-1.076	-0.362	-3.278	-1.341	-1.817	-1.745	-2.274	
-3.032	-2.134	-1.808	-0.744	-1.049	0.586		
-2.016	-0.883	-0.791	-1.729	-1.150	-1.290	-1.976	-1.111
-0.314	-1.899	-2.083	-0.792	1.236	-3.028	-1.581	
-2.486	-2.110	-1.803	-1.475	-1.672	0.655		
-0.425	-0.655	-2.122	-1.076	-1.039	-0.851	-0.902	-1.530
-1.235	-2.070	-1.102	0.265	0.178	-1.442	-0.551	
-2.722	0.231	-1.492	-0.810	-1.312	-0.698		
0.611	-1.955	-2.696	-1.189	-0.902	-2.229	-1.581	-1.390
0.310	-1.358	-1.575	0.110	-0.193	-1.853	-1.651	
-1.520	-1.887	-1.249	0.809	-0.459	0.255		
0.075	0.694	-2.296	-2.162	-2.015	0.607	-1.552	-1.189
-2.023	-1.075	-2.109	-1.510	0.163	-1.598	-1.494	
-1.519	-0.443	-0.582	-2.593	-2.371	0.326		
0.589	-0.987	-0.399	-0.546	-1.955	-0.661	-3.450	-1.367
-0.639	-2.463	0.228	-1.524	-0.456	-1.008	-3.907	
-0.561	-0.320	-1.960	-0.234	-1.189	0.189		
0.357	0.855	-1.358	-0.429	-0.128	-0.449	0.150	-0.596
-1.172	-3.330	0.910	-0.879	-2.205	-2.664	-0.182	
-1.194	-1.393	-2.770	-2.139	-0.666	1.492		
1.035	-0.288	-0.027	-1.223	0.276	-2.274	-0.413	-4.297
-1.848	-3.556	-0.945	-0.889	-1.768	0.823	-1.434	
-2.475	-1.635	-1.719	-0.582	0.483	-0.301		
0.278	0.265	-2.185	-1.355	-0.160	-1.172	-1.503	-0.850
-0.624	-0.848	-0.740	-1.442	-0.927	0.310	-0.164	
-1.632	-2.153	-1.676	-0.413	-1.815	0.100		
-1.043	-1.325	-0.673	-1.939	0.956	-1.269	-0.961	-0.206
-2.056	-2.454	0.670	-2.218	-1.895	-1.073	0.299	
-0.622	0.550	-0.595	-1.871	-2.163	2.242		
1.115	-0.957	-1.308	-1.061	0.017	-0.527	-1.844	-0.674
-1.178	-1.816	0.544	-1.769	-1.626	-0.738	-0.196	
1.347	-0.377	-1.352	-0.513	-1.347	1.075		

Table36.txt

0.040	0.965	-0.518	1.572	-0.830	-1.648	-1.044	-2.153
-2.381	-0.939	-0.707	-2.541	0.381	-1.124	-0.033	
-0.537	0.657	-0.672	-1.268	-1.614	-1.495		
0.195	-1.087	-1.603	-1.087	-1.708	-1.181	-1.510	0.376
1.099	-2.170	-0.815	0.284	-0.733	-0.487	0.821	
-1.899	-0.314	-1.087	-1.740	0.924	-1.470		
1.615	-0.238	-1.366	-0.316	-1.057	-0.327	0.509	-2.394
-0.359	-1.624	-2.074	-1.101	-0.295	-3.035	-1.108	
-0.503	0.255	-1.914	0.346	-1.675	0.694		
0.529	-1.214	-1.509	-0.516	-0.220	-3.133	-1.829	-0.228
-0.894	-0.303	-1.212	-2.675	-0.128	-2.819	0.806	
-1.080	-0.475	-1.162	-0.955	1.073	-0.357		
-0.363	0.241	1.429	-1.944	-1.113	-0.618	-3.253	-0.457
-0.054	-0.070	-1.692	-2.885	-1.990	-0.474	0.928	
0.999	-0.571	-1.312	1.117	-2.305	0.240		
0.316	-1.842	-0.014	-0.303	-0.737	-0.742	-2.799	-1.659
-0.636	-1.020	-1.062	-1.231	-1.333	-3.245	-2.631	
-0.504	-0.561	-2.448	-1.818	-1.713	-0.865		
1.556	0.440	-0.783	-1.659	-2.018	-1.010	-1.919	-0.704
0.502	-1.424	0.510	0.235	-0.092	-2.006	0.287	
0.122	0.145	-2.108	0.193	-0.690	1.287		
0.118	-0.282	17.221	15.264	10.530	20.734	14.473	17.276
13.427	21.223	9.512	16.786	12.188	17.777	12.393	
19.216	10.180	17.083	12.489	11.105	8.842		
-0.521	-0.986	-1.588	-1.154	-2.076	-1.211	-0.046	-0.978
0.422	-2.542	-1.109	-0.565	-2.960	-1.480	-1.931	
-1.906	-0.312	-0.606	0.023	0.018	0.120		
0.050	-0.696	-1.192	-0.432	-0.863	-3.637	-1.149	-2.170
-1.059	-2.411	0.128	-2.924	-1.707	-1.602	0.676	
-0.782	-1.486	-1.491	-1.641	-0.487	-1.650		
0.844	-2.187	0.408	1.774	-0.632	-2.222	-2.475	0.450
0.717	0.421	1.754	-1.195	0.805	0.511	0.567	
0.645	-1.339	0.331	2.063	-1.173	-2.236		
0.952	-2.460	-0.375	-1.816	0.148	0.057	-0.440	0.257
-0.936	-0.294	-1.649	1.027	-2.604	1.226	-0.220	
-0.080	-0.899	-0.253	-0.609	0.472	2.356		
1.159	-2.881	0.869	-1.597	-0.731	0.183	-2.309	0.499
-1.999	0.893	-0.826	1.366	-1.160	0.740	-0.081	
0.710	-1.405	-0.057	-0.237	-1.206	0.413		
0.636	-0.983	0.522	-1.423	-1.477	-0.565	-0.166	-1.516
0.252	-1.400	0.478	-0.406	-0.929	0.863	-0.010	
-0.726	0.156	0.501	-0.687	-0.024	-0.768		
0.285	-3.133	-1.195	1.426	-0.630	-0.626	-1.054	0.653
-0.255	0.895	-0.966	-1.394	-2.541	-0.773	-0.525	
1.466	-0.323	-0.464	-0.317	1.115	-0.274		
0.996	-1.919	0.562	1.414	0.550	0.004	-2.510	1.553
-0.239	1.169	0.856	2.055	-0.251	1.225	0.279	
1.002	-0.491	-0.834	0.281	-1.125	1.342		

Table36.txt

0.122	-1.654	-0.139	0.426	0.248	0.123	-1.623	-1.717
-0.839	-0.178	-1.674	-0.015	-0.789	0.164	0.579	
-0.373	0.682	-0.554	-2.212	1.257	-1.454		
-0.602	-1.653	-0.395	1.940	-0.605	-0.963	-1.308	-1.290
-1.187	-1.584	-1.130	-1.509	2.842	0.474	-0.659	
-0.117	-0.763	-0.422	-0.834	1.972	0.213		
0.450	-2.426	0.483	-1.505	-0.270	-2.186	-1.227	-0.940
-0.849	-0.628	-0.341	0.480	1.287	-1.043	-0.414	
-0.595	-1.828	-0.476	-0.460	1.066	-0.029		
-0.761	-1.359	0.702	-0.476	-1.343	-0.472	-1.287	-1.593
0.324	-0.471	0.048	0.303	0.750	-1.576	-0.036	
0.081	0.818	-0.308	-1.660	0.829	0.582		
-1.038	-4.882	6.284	5.032	2.369	5.065	10.213	12.967
2.586	3.360	3.092	10.645	-0.206	1.960	8.445	
3.632	6.394	17.487	4.728	7.632	7.109		
-0.016	-1.976	-0.425	0.234	-2.304	-0.269	-2.648	-0.418
0.024	1.565	0.055	-1.568	-0.373	-1.624	-0.682	
-1.273	-1.659	0.189	0.879	1.797	-1.972		
0.429	-1.205	-0.620	-0.781	-0.929	1.211	-0.424	-0.892
-0.079	-0.555	-2.583	-0.640	-0.261	-0.746	-1.199	
-0.757	1.354	-0.907	-0.655	-0.907	-1.245		
1.521	0.060	1.079	1.040	-1.048	-1.109	0.246	-1.782
-2.615	-1.131	-1.386	-2.539	-1.344	-0.602	-0.937	
0.167	0.400	-0.403	-2.378	-0.570	0.289		
0.937	-2.835	3.194	0.810	-1.041	-0.588	-1.859	-1.162
1.456	-1.329	1.273	-1.112	1.442	-1.101	0.098	
-1.201	0.568	1.700	1.505	0.292	1.484		
0.797	-2.468	-1.299	0.647	-0.087	-0.693	-0.784	-0.190
0.181	-1.389	-1.314	-0.136	-0.832	-0.133	0.854	
0.402	-0.742	1.203	1.583	0.767	-1.095		
1.419	-2.488	1.252	0.120	-1.590	-0.354	-3.112	-2.804
-0.074	0.449	-0.592	-1.672	-1.142	-0.301	-1.745	
-0.323	-0.262	0.385	-0.243	-0.269	-0.188		
0.859	-3.328	0.112	0.600	1.903	-0.241	1.694	0.514
1.621	1.663	-3.241	-0.279	-1.714	0.615	0.701	
-0.435	0.698	0.143	1.291	2.819	0.282		
0.356	-1.896	0.809	-0.904	0.195	1.071	-0.960	1.908
0.213	0.383	-0.498	0.816	-0.493	0.753	-0.178	
2.561	0.895	1.081	-0.605	-1.824	0.768		
0.747	-1.702	1.813	0.275	0.738	0.023	-1.161	-1.419
0.752	0.276	0.759	0.721	-0.261	-0.348	-1.343	
-0.417	-1.924	-0.207	-0.418	0.549	0.417		
1.239	-2.263	1.048	-1.850	1.752	-1.193	-0.283	-0.752
-0.600	1.670	0.834	0.087	0.031	0.094	-0.463	
2.336	-0.668	-0.570	0.043	1.140	1.169		
1.632	-2.421	-0.205	0.136	1.134	0.665	-0.263	0.470
-1.328	-2.056	-0.947	0.495	-0.086	-0.674	-1.463	
1.069	-0.682	2.777	0.518	0.343	0.115		

Table36.txt

-0.338 -2.408 -1.896 0.141 -0.488 0.637 -0.126 -0.957
-0.531 -0.454 -1.106 -1.143 -1.265 -1.248 0.415
1.697 -0.004 -1.682 0.485 -0.363 0.940
0.696 -2.838 -0.520 0.382 2.671 -0.474 -0.578 1.609
-0.133 1.696 -1.721 -0.055 1.293 0.249 1.049
2.082 -1.563 -1.146 -0.805 -0.371 0.411
0.927 -2.852 0.138 0.119 0.751 -0.463 1.191 -2.110
-0.012 -0.049 -2.245 1.137 0.105 0.228 0.073
0.638 -1.334 0.145 0.516 -0.316 -1.162
-0.221 -1.243 -1.552 -1.425 -0.167 -2.679 -1.352 -1.261
-2.652 -0.448 -0.216 -1.171 -1.468 -0.199 0.011
-1.242 0.399 -0.907 -1.861 -0.995 1.053
-0.863 -0.976 0.334 -1.612 0.575 0.311 -0.736 -2.058
-0.111 -1.924 -1.654 -0.786 -2.690 -1.683 -0.590
-1.933 -0.020 -1.590 -1.093 -0.653 -0.283
1.694 -1.046 3.079 3.381 -0.074 -0.546 1.732 -1.034
0.784 -1.461 -0.250 -1.316 -0.318 4.706 -2.192
0.113 0.906 -1.348 1.081 -1.391 -0.046
0.475 0.666 0.533 -0.801 0.074 -0.846 -0.290 -0.505
-1.206 -0.197 0.614 -2.054 -0.846 -1.953 -0.471
-0.069 -1.070 -0.434 0.946 -0.300 -0.775
0.678 -0.632 -1.293 -2.564 1.207 0.304 -1.272 -0.520
-0.426 -1.650 -0.689 -0.717 -1.512 -0.414 -0.443
-0.086 0.440 -1.682 -0.015 -1.194 1.224
0.601 -1.417 -0.457 -0.907 0.140 -0.655 -1.197 0.151
0.575 0.899 -0.347 -0.385 -0.326 -1.103 1.338
-0.578 -1.222 0.181 -1.279 -1.744 1.088
0.860 -2.226 -1.547 -1.854 0.294 -0.030 -1.509 -1.128
-1.057 0.104 0.167 -2.269 0.854 -2.917 -1.003
0.256 -1.318 -0.664 -0.640 0.663 -1.907
-0.588 -1.276 0.232 -1.233 0.623 -1.382 -0.682 -1.194
-1.047 -0.453 -0.307 -0.242 -1.122 -0.879 0.208
0.467 -1.991 0.734 -1.007 0.437 0.202
-0.583 -0.677 0.288 0.360 -0.702 -0.130 -1.639 -1.157
0.498 -1.804 -1.703 -1.780 -1.026 -2.611 -0.741
-1.088 -0.144 -1.301 0.172 -0.561 -0.357
0.080 -2.689 -0.397 -0.961 -0.886 -1.068 -1.541 -2.208
-2.038 -1.180 -0.780 -1.794 -2.401 -1.006 0.348
0.430 -0.845 0.643 -1.400 0.501 0.145
-2.458 -4.485 -0.291 3.178 0.961 4.730 -0.355 -0.594
1.798 1.534 0.441 12.705 6.236 8.397 1.094
0.755 6.781 17.073 0.171 0.978 0.705
-7.034 -2.602 7.066 0.374 -0.298 0.211 15.058 6.357
10.297 21.519 9.722 17.372 11.854 19.472 3.370
6.207 6.935 19.147 13.190 12.167 1.170
0.031 -2.511 -2.598 -0.344 1.169 1.673 -1.826 0.883
0.606 -0.940 0.260 -1.447 0.160 0.285 -0.904
0.069 0.273 -1.010 2.061 1.121 -1.363

Table36.txt

1.143	-2.757	0.513	1.168	-0.225	-0.240	-0.009	-2.518
-2.420	-0.330	0.316	1.079	-0.293	2.350	1.415	
-1.313	-0.578	0.237	1.231	-0.019	1.225		
0.486	-1.592	0.804	2.234	0.403	-0.167	-0.090	-2.425
-1.387	-1.046	-0.679	-1.147	0.112	-1.103	-2.372	
-0.905	0.615	0.741	-1.161	0.199	-0.499		
0.660	-1.689	1.785	2.077	-0.636	1.098	0.536	0.093
-0.389	1.783	0.933	0.224	-0.082	2.066	0.462	
3.113	0.184	0.312	-0.566	1.155	2.204		
0.464	-2.461	-0.025	0.190	-0.939	-0.853	-1.131	-0.734
-1.109	-0.012	-1.368	-0.649	-3.103	0.745	1.072	
0.269	-1.812	-0.905	0.040	0.956	0.663		
0.670	-2.092	0.917	-0.149	-2.210	-0.801	-1.441	-2.548
-0.486	-3.886	-0.095	-1.371	-1.149	-0.611	-0.623	
-1.318	-0.123	-0.184	0.364	0.390	0.111		
1.877	-1.403	3.930	5.834	0.053	1.502	-0.381	-2.608
1.214	1.144	0.922	1.103	0.220	2.162	0.286	
7.298	0.518	4.078	2.426	2.033	2.891		
1.704	0.151	-2.602	-0.609	-0.976	0.672	-0.633	-1.203
-0.190	-0.345	-0.079	-2.075	1.041	-2.710	-0.608	
-0.007	1.354	-2.626	-1.169	-1.191	0.262		
-0.459	-0.674	-1.345	-0.566	-0.700	-0.977	-0.739	-1.066
-0.069	-1.306	0.571	-0.425	-0.503	-0.200	1.379	
-1.771	0.467	0.472	-0.053	0.087	0.032		
-1.024	0.299	0.170	-1.978	-0.547	0.251	-2.963	-2.890
1.189	-0.466	-1.898	-0.546	1.467	-1.319	-1.159	
0.929	0.715	-0.668	0.155	0.217	-0.482		
0.403	-1.344	-0.894	3.264	-0.694	-0.297	1.855	0.413
-1.338	3.282	-1.486	-1.002	1.955	1.655	-2.232	
-0.812	3.433	-0.810	1.882	4.255	-0.732		
-5.434	-0.059	-0.041	-0.722	1.003	2.013	-1.941	0.002
-0.985	1.577	1.460	12.379	1.121	-2.183	1.691	
3.328	4.887	7.474	4.170	7.760	0.968		
-2.528	-1.663	1.429	0.339	2.287	-0.626	0.139	-2.011
0.589	-0.668	-1.313	0.037	0.279	-0.690	-2.593	
1.064	-0.767	-1.444	-0.111	1.134	0.745		
-0.090	-1.639	-1.253	-0.411	-0.290	0.275	-2.130	-1.608
0.149	-3.250	-2.394	-1.047	-2.408	-2.410	-1.429	
-0.285	0.270	-1.216	-0.027	-0.190	-0.004		
0.090	-2.915	-1.392	-1.070	0.767	-0.259	0.501	-0.192
0.460	0.993	-1.459	-0.413	0.502	0.661	0.473	
0.872	-1.260	-1.488	0.365	-1.322	-1.036		
-0.006	-1.356	0.332	0.156	1.996	1.591	0.023	0.950
0.663	1.430	-1.991	-0.043	-0.343	0.205	0.217	
0.871	1.291	1.397	0.374	0.470	-0.625		
-0.211	-1.364	8.250	8.979	9.564	15.753	11.860	12.219
12.855	17.090	9.109	12.361	6.153	16.955	8.256	
9.726	8.855	14.231	10.120	10.883	5.140		

Table36.txt

0.266 -1.193 -2.245 0.666 0.599 -0.792 -1.493 -2.005
0.510 -0.538 -1.791 0.536 -2.300 -0.068 -0.623
0.363 2.177 1.100 0.806 -0.058 -0.016
-0.221 -2.379 -0.777 -1.794 -0.329 -2.142 -1.846 -0.616
-0.281 -0.571 -1.505 -0.881 -0.484 -1.305 -1.941
-3.283 -2.359 -1.484 0.007 1.825 -0.964
0.072 -1.937 -2.334 1.259 0.448 -0.286 -0.940 -0.217
-1.311 0.472 0.647 -0.726 -0.749 -1.087 -1.276
0.862 -0.068 -1.953 0.677 -0.875 -0.750
0.440 -2.127 -0.659 -0.183 -0.127 -0.256 0.296 -1.379
1.421 -0.835 -1.853 -1.060 -1.255 -0.023 0.548
-0.616 0.548 -0.707 -1.265 -0.588 0.032
1.105 -0.993 0.323 -0.613 -1.318 -1.223 -0.493 0.536
0.167 -1.524 0.659 -2.212 -1.312 -2.296 -0.881
-0.606 1.103 -0.698 -0.363 -0.365 0.611
-0.024 -2.218 -2.854 -2.121 -1.410 -0.953 -0.899 -1.230
0.030 -0.190 -0.777 -0.594 -0.466 0.573 -0.403
1.077 0.332 -2.059 -0.490 0.483 -0.077
0.305 -2.064 0.268 1.836 0.935 -1.618 0.493 -1.115
-1.184 -2.522 -2.326 -1.634 -0.629 -2.133 -1.944
-0.990 1.499 -0.089 -1.564 -0.972 -0.706
0.241 -1.962 -0.007 -1.313 0.378 -1.917 1.783 0.577
-0.493 -0.607 0.542 -1.684 -0.996 -1.511 -0.934
-0.448 -0.511 -0.848 0.527 -1.824 -1.194
-0.173 -0.971 -0.643 0.050 -1.643 0.099 0.462 -1.881
0.229 -2.970 -1.813 -1.223 -1.790 -0.471 -0.910
0.659 -0.255 0.411 -2.471 0.036 0.054
-0.182 -1.310 -0.471 2.454 -0.393 1.033 0.291 -1.192
0.715 -1.978 -1.492 -0.791 0.998 -1.556 -0.362
1.434 0.456 -0.078 -1.181 -0.550 1.013
-0.458 -0.865 -2.398 -1.750 -0.477 -1.044 0.214 0.050
-1.330 -2.559 -1.086 -0.152 0.558 -0.120 -3.644
-2.793 -1.565 -1.672 -0.804 -2.253 -0.351
0.552 -1.338 -0.431 1.125 -1.280 0.056 -0.341 -2.323
0.535 -0.274 -0.236 -1.071 0.556 0.103 0.745
-0.449 2.371 -0.473 -0.082 -0.624 0.623
0.563 -2.621 -1.333 0.789 -0.908 -0.732 -1.413 -1.440
-0.354 -0.457 -0.785 -1.185 -0.367 -1.762 -0.164
-1.354 -0.354 0.714 -1.712 -0.016 -1.135
-0.289 -1.733 0.512 -0.791 -1.053 0.024 -1.803 -0.304
-0.390 -0.701 0.679 -1.276 -1.237 -1.392 0.271
0.781 0.401 -1.059 -0.155 -0.079 0.468
0.861 -2.332 -2.315 -1.801 -1.205 0.107 -0.164 -3.304
-0.131 -2.247 -0.760 -2.144 -0.317 -1.324 -2.863
-2.075 -0.888 -0.807 0.866 1.302 0.385
-0.412 -0.958 1.042 -2.047 -1.302 -1.937 -1.195 -1.049
-1.368 -2.942 -2.238 -2.663 -0.226 -2.946 -1.014
-0.520 -0.442 0.334 -0.150 1.399 -1.537

Table36.txt

-0.457	-1.289	-0.187	-0.139	-0.768	0.160	-0.061	0.278
-2.902	0.279	-1.718	-1.553	-2.345	-0.058	0.459	
0.158	-1.745	-0.245	-0.964	-2.328	0.416		
0.283	-1.831	-0.738	0.507	0.257	0.058	-1.103	-2.064
-0.940	-0.238	0.906	1.400	1.984	1.400	-0.513	
2.035	0.161	0.986	2.350	0.227	0.032		
0.893	-2.347	-0.687	1.128	-0.565	-2.270	-1.473	-1.565
-0.691	0.328	-0.626	0.923	1.136	-0.777	-0.113	
-0.604	-0.896	1.911	-0.505	0.298	0.357		
2.465	-1.893	-0.498	0.582	-2.148	-1.181	-0.178	-0.555
0.327	0.121	-2.628	-0.759	0.790	-1.506	-0.256	
-1.514	-0.084	0.296	-0.098	1.081	-0.235		
1.710	-2.248	-0.233	0.755	-1.919	-0.248	-0.900	0.355
0.293	-0.540	-0.256	-0.313	-0.018	0.208	-2.264	
-0.040	-1.510	0.321	-1.062	-0.159	-0.876		
-0.165	-1.316	-0.395	-1.135	-0.922	-2.840	-2.136	-0.369
-1.442	1.026	-0.342	-0.157	0.249	1.588	-1.172	
0.876	-1.883	-1.318	0.980	0.303	0.247		
0.421	-2.260	0.264	0.408	-1.281	-2.034	-0.503	-2.230
-1.256	-1.748	-0.119	-2.331	-0.702	0.290	-0.864	
-1.364	-0.415	-2.088	-2.095	-0.868	1.514		
-0.122	-3.443	-0.153	-0.241	1.598	-1.217	-2.292	0.029
-2.489	-1.710	-0.543	-0.646	-2.128	0.698	0.596	
0.156	-1.510	-2.471	0.590	-1.846	-0.658		
1.161	-2.870	0.046	2.277	-0.058	1.054	-1.085	0.883
-1.269	-0.073	-2.505	2.263	0.026	0.130	-0.736	
0.911	0.110	1.863	-1.963	1.399	0.282		
-0.456	-1.730	2.004	1.595	-0.404	-0.427	0.257	0.083
-1.010	-0.438	-1.922	-1.328	0.603	-0.437	0.009	
0.261	-2.081	-2.447	-0.296	1.669	0.244		
0.937	-2.242	1.084	1.003	0.930	-0.720	-0.962	-1.356
-1.037	-1.569	-1.656	1.431	-0.854	0.703	-0.446	
0.681	0.461	-1.755	1.085	0.410	-2.850		
0.531	-2.111	-0.611	-0.983	0.769	-0.786	-1.932	-1.921
-0.318	-0.915	-1.413	-0.189	1.392	-1.484	-0.108	
0.049	-1.845	-0.421	0.390	0.346	1.202		
-0.086	-2.951	-0.635	0.151	0.433	1.689	1.786	0.955
1.211	1.007	-0.166	0.132	2.588	2.195	1.612	
1.200	0.757	2.221	3.607	-0.239	2.598		
-0.125	-2.277	0.015	-1.435	-0.188	-0.861	-1.498	-2.995
-0.519	-2.045	-3.400	-3.059	-1.086	-2.690	-1.933	
0.610	-0.790	-2.109	-0.790	-1.356	-1.306		
1.307	-2.771	0.571	1.594	-0.072	-2.087	-2.021	-0.710
-1.150	0.956	-0.201	-0.957	1.738	-1.141	0.524	
-1.718	-2.433	1.563	-0.191	1.416	-0.190		
-0.344	-1.226	0.290	-0.448	0.375	-1.570	-0.714	-1.592
-1.937	-1.029	0.145	0.681	0.227	0.776	-2.608	
-2.268	-0.464	-0.975	-0.469	-0.579	1.947		

Table36.txt

1.213	-2.761	1.184	0.975	-0.995	-0.724	0.445	-1.830
1.195	1.418	0.612	-0.735	3.123	-0.427	1.286	
0.508	-1.713	0.591	0.992	1.073	1.015		
0.716	-3.310	2.671	1.537	-0.313	-1.577	-0.920	-0.081
-0.250	0.096	1.405	0.178	1.194	-1.582	-0.826	
0.335	-0.368	-0.179	-0.004	1.298	2.527		
-0.298	0.014	4.625	3.296	4.559	4.769	2.247	5.858
4.944	5.776	1.694	1.607	1.426	5.383	4.375	
3.053	-0.953	5.176	1.962	3.145	-0.271		
1.815	-1.195	-0.476	0.699	-0.642	-2.466	-0.257	-0.714
-0.381	-2.622	-2.523	-1.173	-1.841	0.059	0.960	
-0.805	-2.907	-1.202	-1.437	1.267	-1.556		
0.156	0.749	-1.243	-2.819	0.141	-0.092	-0.782	0.956
1.642	0.200	-1.009	-1.736	-0.399	-1.712	-0.342	
0.993	-0.757	0.809	0.326	-0.352	0.005		
0.367	-0.585	-2.069	-0.860	-1.270	-0.932	-1.247	-1.128
0.334	-1.839	-2.509	1.490	-0.342	0.675	-0.271	
-0.477	-2.358	-0.242	-1.602	-0.188	-0.973		
1.089	-0.752	-2.144	-1.161	2.233	-2.400	-1.195	-0.479
-0.094	-0.581	-2.879	-0.333	-1.557	-0.550	-1.071	
0.481	0.893	-1.254	-1.050	-2.656	-0.420		
-0.038	-0.185	1.964	-0.180	-2.123	0.645	-0.210	-1.703
0.276	-2.443	-0.080	-1.121	-0.145	-0.459	-1.131	
-0.212	-1.678	-1.202	-0.428	-0.940	-1.557		
-1.422	-0.236	-0.724	-0.518	-0.958	-2.154	1.090	-0.035
-1.087	-1.339	-0.373	-1.171	-0.471	-0.614	0.408	
-0.054	-1.274	0.567	-2.595	-0.739	-0.107		
0.975	-1.081	-1.058	-0.255	4.099	1.384	1.571	0.738
0.115	0.142	-0.948	3.171	0.534	-0.267	0.140	
1.704	0.612	2.249	4.025	1.544	2.425		
0.299	0.767	1.446	-2.028	-0.964	0.019	-1.286	-1.414
0.276	-1.407	-0.923	-0.969	-2.449	-1.126	-0.813	
0.640	0.366	-2.495	-2.333	-0.236	0.518		
0.575	-1.895	0.919	0.528	-0.938	-1.303	-1.080	-1.815
-2.430	0.078	-1.508	-1.068	-1.629	-1.061	-2.393	
1.054	0.558	-0.304	-0.593	-0.302	0.221		
0.633	-1.843	-1.103	1.706	-0.456	-0.736	-0.210	-0.752
-1.002	-1.539	-0.304	-2.381	0.190	-1.496	0.619	
1.418	-0.930	-3.040	-0.964	-0.429	-1.243		
0.364	-2.645	3.753	4.351	2.045	1.332	2.315	3.172
2.506	5.974	-1.065	4.789	2.526	4.000	-1.098	
5.111	4.513	1.476	2.459	4.470	2.483		
0.397	-2.536	0.970	-0.197	-0.857	-0.692	-0.823	-1.360
0.873	-0.979	0.604	-1.595	0.144	0.647	0.630	
-0.281	0.128	-0.902	1.039	0.412	0.008		
0.257	-1.879	0.012	-0.706	-2.010	0.221	-1.045	-3.064
-1.512	-2.697	-1.983	-2.047	-1.225	-1.049	-2.379	
-2.184	-1.173	-2.034	-1.256	-0.940	-0.075		

Table36.txt

1.132	-2.171	-2.602	-0.179	-0.626	0.171	0.012	-0.656
-1.630	-2.596	-0.420	-2.351	-0.476	-1.433	-0.070	
0.333	-1.131	-0.431	-1.807	-1.250	0.407		
0.457	0.118	0.738	0.331	-1.221	0.278	-1.852	-1.271
-0.841	-1.026	-2.577	-0.786	-0.844	-0.413	1.016	
-0.752	-0.411	-0.143	-1.432	0.689	0.382		
0.580	-1.981	-2.385	-1.172	0.256	-0.227	-0.689	0.357
-0.268	-0.335	-0.692	-1.787	-0.766	-1.726	0.785	
0.784	-0.110	-1.188	-1.355	-1.294	-0.982		
0.882	-1.988	-0.285	-2.310	-2.123	-3.070	0.332	-1.399
0.899	-0.716	-2.045	-0.469	-0.313	-1.271	-0.382	
0.272	-0.989	-0.460	-0.862	-0.945	1.115		
1.110	-1.763	-1.745	-0.150	0.118	0.326	1.547	0.021
-0.827	0.900	-0.465	-1.975	0.500	-1.082	-0.614	
0.485	0.001	-0.406	-1.329	-0.170	-0.377		
0.004	-0.895	-1.219	0.668	-1.381	0.686	-1.857	-3.579
-0.288	-0.761	-1.780	-2.601	-0.887	-0.104	-0.613	
0.093	-0.129	-1.839	-0.128	-3.617	-0.686		
-0.412	-2.207	14.458	6.168	16.757	23.431	-2.316	-0.513
13.135	0.550	-1.050	-0.725	7.611	1.392	10.352	
2.329	-0.331	18.850	1.368	-0.447	0.879		
-0.329	-1.758	0.308	0.393	1.062	0.019	-0.975	-1.850
-1.451	-0.654	-1.646	-0.283	2.316	-2.289	-1.795	
0.156	0.683	-0.828	-0.512	2.165	-0.253		
-0.086	-2.856	-1.233	0.335	0.396	0.410	-0.716	-1.808
-0.501	0.647	0.329	-0.054	0.497	0.031	0.082	
0.968	-0.514	-1.655	0.274	-0.770	0.773		
-0.182	-1.258	-0.458	0.534	0.261	-0.319	0.231	-0.007
-2.307	-0.941	-0.269	-0.085	0.580	-0.936	1.192	
0.916	-0.784	-1.093	0.128	-1.405	0.619		
-0.763	-1.082	-2.402	-1.085	-1.183	-1.469	-0.941	-2.698
-0.700	-2.930	1.496	-2.025	-0.116	-2.673	-1.001	
-0.210	-2.013	-2.164	-0.874	-1.349	-0.768		
-0.525	-1.290	-0.701	-0.365	0.686	0.664	-0.418	-1.937
-0.917	-0.312	-1.782	-1.186	0.202	-2.167	-1.120	
-1.478	-1.740	-2.208	-0.339	-0.270	1.866		
-1.861	-2.168	-1.679	0.850	-0.287	-2.114	-1.881	-0.671
-0.892	-2.687	-0.827	-2.307	-1.543	-0.466	-3.185	
0.616	1.640	0.032	-0.861	-0.447	0.108		
0.451	-3.083	0.030	-1.174	-1.168	-1.069	0.029	-2.307
-1.381	0.037	-1.073	-0.993	-0.134	0.596	-0.406	
0.882	0.023	-0.047	0.718	1.924	-0.618		
0.582	-3.014	0.478	-0.547	-0.504	-1.760	-0.917	1.613
-0.812	1.442	-0.362	1.712	-0.195	-0.598	-1.231	
-0.269	-0.133	-0.861	0.755	-0.510	-0.162		
-0.018	-1.706	-1.147	0.897	-2.071	-1.616	-1.349	-0.382
-0.328	0.157	-0.446	-0.932	-1.668	-0.695	-0.499	
-2.648	-1.349	1.557	0.483	-0.832	-0.765		

Table36.txt

0.004	0.276	-0.236	-1.198	0.405	-1.343	-0.682	-2.232
0.252	-2.300	-0.247	-0.680	2.394	-1.390	-1.627	
-0.162	0.140	-0.112	2.061	0.003	1.166		
0.069	-2.416	1.176	-0.070	-0.481	0.083	-0.001	-1.661
-1.622	-2.530	-0.839	-0.887	-0.968	-2.430	0.621	
-0.612	0.667	-1.839	-0.827	0.963	-1.514		
-0.773	-2.763	1.626	0.814	-0.978	-0.787	0.382	-0.678
0.254	-0.966	0.358	0.875	-0.031	-0.539	-1.004	
-0.572	1.254	-2.156	0.417	-0.480	-1.874		
-0.031	-1.941	-0.863	-2.975	-0.589	-0.391	-0.880	-2.319
-0.489	-1.510	-0.115	-0.462	0.394	-0.066	0.225	
-1.443	1.886	-1.236	0.943	-2.495	-0.600		
0.059	-1.590	1.086	-0.868	-0.265	1.001	-0.463	-0.269
-2.522	-0.833	0.533	1.163	0.074	-0.022	0.504	
1.204	-0.794	-1.887	-2.327	0.468	0.683		
0.204	-1.514	0.354	0.598	0.793	0.354	0.560	-0.913
-0.535	-0.991	-0.300	-0.706	-0.617	0.185	-1.791	
-1.252	-0.633	0.378	0.623	1.085	-1.027		
0.774	-1.064	0.033	-0.383	0.404	-1.475	1.217	0.173
-0.701	-0.578	1.271	-0.684	-0.346	-2.024	-0.925	
0.048	0.283	-1.585	0.871	-0.956	-0.300		
-0.490	-2.225	0.604	-0.635	-1.650	-0.593	0.389	0.453
-1.497	-0.972	-1.146	-1.220	0.803	-2.374	1.424	
-1.394	0.853	-1.373	0.358	-1.647	-1.119		
0.974	-1.057	-0.756	-1.996	0.104	-0.526	1.346	-0.271
-1.804	-3.621	1.173	-2.157	-0.375	-1.325	1.836	
-0.490	0.053	-1.663	-0.035	1.048	0.837		
-0.520	-1.475	0.696	1.527	-0.648	-0.110	-0.550	1.498
-0.013	-0.003	1.001	0.749	-1.181	-0.525	0.658	
2.093	-1.228	0.458	0.071	0.366	-0.798		
-0.004	-2.127	-0.555	0.139	-1.213	-2.143	-0.140	0.113
-0.897	0.123	-1.468	-0.928	0.120	-1.463	-0.763	
0.131	0.710	0.503	-0.806	0.971	1.776		
0.683	-0.859	-1.083	-0.799	-2.005	-0.063	-1.816	-0.640
-1.001	-1.599	1.315	-1.545	-1.387	-1.537	0.168	
-0.954	-0.374	-1.076	-0.526	1.709	-0.215		
-0.004	-1.748	0.111	-0.725	-0.231	-0.601	1.008	0.780
-0.866	-0.411	-0.207	0.866	0.100	-1.923	0.368	
0.683	-0.869	0.616	0.362	0.216	-1.281		
0.295	-2.056	-0.348	-1.576	-2.283	0.250	-1.930	0.143
-0.828	-0.881	-2.048	0.864	1.689	-1.772	0.627	
0.161	-1.118	2.319	-0.448	-0.846	0.920		
0.225	-2.367	-3.025	-1.959	0.024	-1.519	-3.263	-2.285
0.044	-0.881	-2.062	-1.588	-1.821	1.342	0.499	
-2.080	-1.937	-2.201	-2.605	0.147	-0.608		
0.933	-2.201	0.628	0.393	1.034	0.350	1.944	-0.606
0.096	0.584	-1.256	0.454	0.543	-0.736	-1.525	
0.475	-0.631	1.261	0.737	1.612	-0.335		

Table36.txt

0.290	-3.029	1.171	-1.090	-0.603	1.008	-0.952	-0.205
1.014	-1.152	1.165	0.016	0.245	-2.186	1.397	
0.245	0.887	-2.054	-0.001	1.780	0.896		
-0.071	-2.036	-0.205	-0.791	0.309	-2.414	-1.200	0.016
-1.161	-0.359	-2.739	-1.514	0.095	-0.759	0.883	
-1.882	-1.620	-0.361	0.245	1.257	-0.304		
-1.505	-3.138	1.401	1.119	0.780	1.822	-1.036	-0.875
4.711	5.885	1.800	-0.284	4.845	-0.040	3.711	
8.062	0.579	11.555	0.799	0.644	0.372		
-0.477	-2.027	1.463	-0.716	-1.777	-2.246	-1.294	-2.586
-0.028	-1.581	0.589	-0.914	1.407	-1.332	-1.769	
-0.704	-0.670	-0.975	-1.251	-1.099	-0.994		
0.900	-1.207	-0.097	1.370	0.244	-1.307	-1.871	-1.680
-2.156	-2.264	-2.332	-0.500	-0.335	-0.516	-1.531	
1.495	-1.065	2.261	-0.592	-1.487	-0.764		
0.828	-2.235	2.020	2.748	1.382	0.613	-0.423	-1.181
-1.163	-1.786	-0.335	-1.130	0.474	1.167	-1.213	
0.516	1.183	1.297	1.034	-0.167	0.633		
0.812	-2.871	1.730	0.465	0.916	0.973	-2.001	-1.020
-0.403	0.158	1.396	0.262	0.090	-1.894	1.022	
0.053	0.281	0.047	0.583	-0.919	-0.469		
0.891	-0.028	0.696	-0.659	0.610	-0.618	-1.183	0.244
-1.455	-1.336	1.733	1.230	1.429	-2.485	0.026	
-0.283	0.459	-0.476	-0.202	-0.491	-1.551		
-0.465	-0.228	-1.004	0.419	-0.808	0.189	-0.480	-2.286
-1.472	-1.762	-1.870	-0.656	-1.744	-2.169	-1.396	
-1.570	-1.545	0.124	-1.301	-1.500	-1.864		
0.145	-0.374	-0.726	-1.163	-1.647	1.655	-0.536	-2.027
-2.288	-0.604	-1.882	0.563	-0.371	-1.127	-1.732	
-0.321	-0.718	0.088	0.666	-0.719	0.406		
0.362	0.905	-0.926	-0.670	-1.186	-0.482	-1.570	0.209
0.852	-2.690	-1.282	-3.175	-0.826	-0.071	-1.080	
-1.072	-2.256	-1.474	-1.691	-1.618	-0.833		
0.906	0.427	-0.128	-0.480	-1.677	-1.309	-2.794	-1.002
0.008	-1.406	-0.501	-1.092	-0.504	-1.237	-2.408	
-1.773	-0.883	-0.615	-1.324	-0.308	-0.288		
-0.830	0.376	-0.456	-0.134	-1.374	-0.432	-0.772	-2.810
-0.825	-1.354	0.169	-2.331	-0.080	-0.160	-0.156	
0.189	2.280	-1.067	-2.411	-1.441	0.410		
0.153	-0.714	-0.508	-0.132	0.830	-4.118	-1.069	0.804
1.018	-2.282	-1.688	-0.919	-1.186	0.103	-1.442	
-1.790	-1.676	-1.639	-0.333	-0.042	0.633		
-0.125	-0.360	-1.382	0.223	-0.842	-2.434	-0.927	-2.070
-1.512	-0.899	-1.988	-0.798	-1.228	-2.762	-0.334	
-2.615	-2.651	-2.719	-1.279	-2.270	-0.248		
2.446	-4.042	5.213	12.706	-1.051	-1.123	13.480	6.278
7.896	1.524	4.221	17.693	4.977	-0.460	4.213	
-0.579	7.028	10.364	9.512	1.821	-2.182		

Table36.txt

0.955 -1.164 1.737 -1.547 -1.294 -1.421 -0.786 -3.366
-0.390 -0.798 -1.126 -1.280 -1.256 -1.880 -0.061
-1.498 0.061 -0.799 -2.807 -1.836 0.077
0.869 0.377 -1.226 -0.687 -2.526 -0.941 -1.759 0.170
-1.112 -0.998 -1.481 -0.170 -2.729 -1.752 -0.747
-0.565 0.332 -0.043 0.808 -0.405 -0.905
0.984 0.436 -0.290 2.004 -0.053 -2.238 -0.483 -1.135
-1.653 -1.944 -1.594 -1.715 0.286 1.445 -1.167
-1.466 0.520 -0.242 0.577 -1.112 -3.599
0.382 -1.504 -0.527 -0.821 -1.276 -1.002 -0.734 -0.234
-0.213 -0.588 -1.701 -1.525 -0.842 0.761 -0.624
1.800 0.130 1.029 0.521 1.603 0.129
-4.744 -3.228 1.436 3.816 -1.501 1.243 0.106 1.931
-0.609 1.876 2.935 4.826 2.857 0.800 -0.702
0.860 2.591 2.892 1.749 -0.901 0.683
1.056 -1.878 0.879 0.773 0.406 -0.640 -0.872 -1.368
-1.850 -0.428 -0.309 -0.233 -1.808 -1.648 0.102
0.209 -1.856 0.439 -1.969 1.033 0.214
0.924 -1.058 19.138 17.183 14.775 24.237 15.943 20.844
15.243 25.706 12.675 26.967 13.200 22.419 12.826
17.651 9.754 21.636 14.285 15.756 14.155
1.220 -2.410 0.456 -0.724 -0.383 -0.626 -0.041 -1.654
-0.219 -0.057 -0.129 -1.397 0.737 -1.577 -1.104
-0.064 -0.460 0.077 -0.817 -1.112 0.227
0.699 -1.021 1.027 -0.739 -1.137 -2.014 2.428 -1.088
-0.056 0.021 -0.121 -0.321 -1.409 -0.336 -1.284
-1.263 0.237 -1.767 -0.149 -3.486 -0.122
0.819 -2.771 1.138 -1.833 -2.477 -2.140 0.294 0.355
0.350 1.150 -0.137 -0.245 0.406 1.121 0.600
2.040 2.316 1.445 -0.261 -0.612 0.134
-0.752 -2.055 0.000 0.000 0.000 0.309 0.000 0.000
0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 0.000 0.000 0.000
0.184 -1.091 -0.166 -0.108 1.092 -0.479 0.536 -0.793
-1.559 -0.670 -1.573 -1.512 0.596 0.706 -0.347
0.097 -1.407 1.901 -1.157 -1.013 -0.901
1.508 0.379 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.000 0.000 0.000 0.000
1.500 -1.490 0.596 -1.803 0.086 -0.339 0.153 -0.289
-1.474 -1.244 -0.279 1.122 -0.342 0.783 -0.384
1.116 -0.261 -1.346 1.983 -1.334 -0.646
0.941 -3.459 -0.770 -0.106 -1.781 1.803 0.143 0.428
-1.326 -0.231 -0.041 -0.384 0.288 -0.637 -0.431
-0.724 0.179 0.179 0.836 -0.588 -0.265
1.011 -1.697 0.584 -0.230 0.134 -1.924 0.734 0.131
-2.002 -0.874 -0.582 -1.316 0.616 0.226 0.557
1.349 0.962 -1.676 0.764 1.005 -0.274

Table36.txt

0.875	-2.532	-0.144	-0.695	-0.086	1.146	2.919	1.097
-1.015	0.994	-0.308	-0.229	1.740	-0.567	-1.907	
1.415	2.378	2.073	-0.500	0.311	1.477		
1.381	0.256	-0.953	-0.655	-2.319	-1.774	-0.791	-2.121
1.198	-2.369	0.602	-1.039	-0.550	-1.085	-0.878	
-0.657	-3.512	-1.301	-0.238	-0.040	-2.095		
0.022	-1.865	1.131	-0.421	-0.816	-0.871	-0.410	-1.454
0.463	-0.962	-2.164	-1.399	-1.702	-2.248	-0.235	
-0.019	1.336	-1.983	2.223	0.532	0.967		
0.100	-4.124	1.204	-0.233	-0.102	0.116	0.615	2.735
-0.485	1.071	-0.047	-0.018	-1.580	-0.705	-1.128	
0.190	2.472	2.027	1.242	0.603	0.990		
-1.777	-0.844	-0.086	-1.646	-1.365	-1.391	0.592	-1.258
-1.630	-0.513	-0.633	-0.808	-0.434	-1.238	-0.554	
-0.747	-0.490	-0.242	-0.887	0.451	-0.870		
0.994	0.125	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
-0.389	0.872	1.278	-1.408	-1.243	-2.017	-0.227	-1.572
0.838	-1.519	-0.175	1.798	-1.493	-0.401	1.348	
0.266	-0.778	-1.426	-0.174	0.134	-0.505		
0.802	-1.534	-0.261	-0.261	-1.977	-1.749	-1.676	-1.415
-0.660	-0.662	-1.697	-1.048	0.322	-1.708	-1.232	
-1.662	0.734	-1.375	-2.136	0.350	-1.129		
0.102	0.987	-1.447	-1.436	-0.673	-0.469	-0.501	-0.769
1.751	-3.525	-1.392	-0.653	0.232	-0.178	-0.760	
-1.151	-0.771	-0.603	-1.173	-1.344	-1.064		
1.211	0.738	0.000	0.050	0.000	-0.868	0.000	-0.375
0.460	-1.169	0.000	-1.256	0.000	-1.145	0.000	
-0.378	0.000	0.000	0.000	0.000	0.218		
-5.677	-3.115	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
1.335	-1.548	0.560	-0.824	-0.882	-1.128	-1.192	0.269
-0.711	-0.572	-1.205	-1.199	-0.644	-0.797	-0.719	
-1.626	-0.423	-2.193	-0.977	-1.043	-0.661		
1.208	-1.817	2.419	2.824	-0.536	1.597	0.885	9.710
0.092	4.283	1.714	5.969	4.965	3.649	0.432	
-1.061	2.041	6.372	2.058	5.769	0.018		
0.432	1.132	-1.266	0.275	-1.254	-0.595	-1.185	-3.022
-0.436	-2.504	-2.297	-2.553	3.166	-1.298	1.097	
1.510	0.183	-1.993	0.456	-2.024	-1.060		
0.678	-0.812	-0.171	-1.576	-0.705	-1.669	-1.788	-2.309
-2.505	-2.353	0.167	-0.196	-0.004	-0.493	-2.766	
-0.031	-0.375	-3.252	0.369	-0.340	-0.883		
0.316	-1.303	-0.945	-0.957	-1.280	-1.425	-0.884	-0.373
-1.248	-2.826	1.521	0.755	0.138	-1.540	-0.196	
-0.838	-2.029	-1.422	-0.853	-0.554	0.343		

Table36.txt

1.341	-0.606	-0.084	1.232	0.356	-0.794	0.569	-1.283
-1.441	-0.203	-1.982	-1.165	0.793	-1.240	-0.243	
-0.646	0.563	0.127	0.405	0.403	-1.584		
1.716	-3.100	0.085	-1.204	0.967	0.856	0.105	-3.134
-0.426	4.967	-1.482	4.629	2.746	4.735	5.604	
1.016	3.545	-0.198	4.438	6.269	-1.153		
-1.024	0.590	-1.256	-0.492	0.829	0.745	1.498	-1.887
-0.513	-1.384	1.073	0.593	-1.486	-1.956	-1.784	
0.221	0.356	-1.861	-1.260	-0.632	-1.494		
1.182	0.378	0.729	-0.432	-0.031	-0.467	1.263	0.821
-0.307	0.214	-1.429	-0.873	-0.209	1.029	1.198	
-3.142	-0.529	-1.176	-0.770	-1.034	-1.372		
-0.284	-1.227	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
0.161	-1.586	-0.643	-1.144	-0.080	-1.942	-1.380	-2.015
-0.426	-1.992	0.790	-0.379	-0.778	-1.556	-0.727	
-1.426	0.548	-1.156	-0.155	0.395	-1.327		
0.694	-1.138	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
-0.315	-1.092	-1.625	-0.649	-0.188	-1.893	-1.596	-1.643
0.117	-2.893	-1.174	0.117	-2.095	-2.150	-0.326	
-1.236	-0.270	-2.330	0.419	-0.919	-0.578		
-1.702	0.369	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.309	0.000	0.000	0.000		
0.334	-0.732	-1.041	-0.423	0.733	-1.349	-1.021	-1.149
-1.191	0.227	-0.795	-0.995	-0.907	-2.932	-2.999	
-2.137	0.514	-0.528	1.117	0.540	-0.464		
0.147	-0.390	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
1.223	-1.362	-0.363	-0.542	-1.296	-2.317	-1.175	-1.870
-2.470	-3.243	1.194	-1.053	-2.264	-1.657	-1.462	
-2.783	-1.315	0.514	0.073	-0.787	-0.327		
1.460	-1.099	0.864	-0.896	-0.710	-1.624	-0.975	2.889
0.794	-1.589	-1.007	0.306	0.206	-3.778	-1.523	
-0.467	-0.336	-0.456	-0.108	-0.916	-0.127		
-0.552	-0.077	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000		
0.805	-1.852	-1.031	0.137	-0.736	-2.464	0.000	-1.368
0.000	0.000	0.000	-0.868	0.000	0.127	0.000	
-0.505	0.000	0.000	0.000	0.000	0.251		
0.239	-0.950	-1.288	-0.560	0.014	1.652	-1.270	-1.611
-0.445	-0.412	-0.173	-2.667	-1.504	-2.121	-1.197	
0.566	0.472	-0.765	-1.208	0.059	-1.407		

Table36.txt

1.051	0.151	1.632	-0.581	-1.210	1.369	-1.559	0.891
0.058	0.335	1.277	0.718	-0.633	0.822	-0.227	
1.268	-2.360	-0.544	-1.156	-0.731	-1.002		
-0.984	-1.109	-1.030	0.654	0.328	0.390	0.188	-2.161
-0.418	0.657	0.397	-1.283	-0.266	-1.356	-2.496	
-2.239	-0.506	-1.591	0.016	-1.414	0.845		
-1.057	0.398	-0.865	-1.087	-1.534	-1.817	-1.221	-1.452
-1.275	-1.456	-1.023	-2.359	-0.056	-2.965	-1.060	
-0.506	-1.261	-0.215	-0.948	-1.135	-2.313		
-0.155	-0.129	-1.564	-2.681	0.412	-1.591	-0.185	-1.382
-0.387	-1.883	-1.135	-1.478	-0.294	-0.375	-1.874	
-0.922	-1.010	-0.762	0.393	-1.473	-0.108		
-1.513	1.414	-1.717	1.282	-2.300	-3.012	-2.804	-0.974
-0.511	-1.540	-3.130	-2.656	1.008	-1.217	-0.268	
-0.800	0.567	-0.789	-1.687	-0.527	0.121		
0.914	-0.304	0.814	0.415	-1.595	-2.755	-1.860	-1.219
1.027	-0.414	-0.009	-0.996	0.641	1.522	-0.695	
1.579	-2.091	-0.667	0.243	0.310	-0.275		
1.415	0.105	1.430	-1.484	-1.027	-0.682	-1.156	-0.399
1.125	-1.003	-0.998	-0.629	-0.540	-0.811	-1.779	
-0.564	-0.597	-0.465	-1.108	-3.280	0.696		
0.946	0.363	-0.423	-2.494	-0.934	-1.163	-0.764	-0.654
-0.546	-0.639	0.232	0.304	0.058	0.881	-1.483	
-0.315	0.146	-1.655	2.100	-0.718	0.178		
0.216	-0.588	0.673	1.516	1.692	-0.935	-3.787	-0.824
0.190	-1.262	-0.034	0.837	-2.281	0.001	0.297	
-2.298	0.736	0.168	-0.806	-3.538	-2.361		
0.285	0.821	-1.705	-0.035	-1.290	-2.788	-1.126	-1.841
0.714	-4.114	-1.785	-0.539	0.048	-0.950	-0.219	
-2.222	0.106	-2.780	-0.055	-0.523	0.181		
0.001	-0.056	-1.825	-1.171	-1.653	-1.840	-0.236	-0.906
-2.001	-1.704	-1.559	0.623	-1.727	0.017	-1.360	
0.494	-2.344	-0.510	1.073	-2.743	-1.371		
0.230	-0.399	0.486	-1.074	-2.160	-1.771	-1.383	-1.866
-1.477	-1.078	-0.078	-1.241	-0.642	-1.474	-0.184	
0.374	-0.521	-1.354	-2.713	-0.806	-2.290		
1.053	1.735	-0.392	-2.582	-1.728	-0.496	-0.376	0.027
0.820	-1.665	-2.818	-1.231	-1.739	-1.540	-2.153	
-0.002	-0.956	-2.319	-1.358	1.020	-1.142		
0.638	0.671	-0.526	-1.888	0.674	-0.945	-2.249	-1.555
-3.069	-2.889	-1.097	-1.770	-0.665	-1.073	-0.160	
-1.869	0.298	-0.702	-2.212	-0.833	-0.838		
-0.504	0.271	-0.016	-1.197	-2.565	-1.496	-0.404	-1.078
-1.116	-3.230	-0.059	-1.187	-1.045	-0.285	-0.548	
-2.360	-0.772	-1.949	-1.615	-0.376	-0.505		
-0.207	-2.804	-2.227	-0.256	-0.574	-3.170	-0.629	-2.134
-0.965	-0.452	-0.925	-0.846	0.511	-2.597	-2.055	
-0.236	-1.844	0.749	-0.436	-1.600	-0.600		

Table36.txt

-0.791	1.152	-0.780	-1.508	-0.033	-1.342	-2.621	-2.235
-0.200	-1.390	-0.820	-0.006	-1.080	-1.656	-0.267	
-1.544	-0.014	0.169	-2.191	-0.556	0.648		
-0.656	0.685	-1.448	2.008	-0.539	-2.905	1.207	-0.785
-0.170	-1.180	-1.115	-0.616	-1.574	-0.090	-1.462	
0.813	-1.249	-0.927	-0.360	-2.326	0.481		
-0.514	0.319	0.173	-0.345	-1.889	-1.570	-1.133	-0.081
0.550	-1.611	-2.088	-1.747	-0.737	-1.089	1.172	
-1.388	0.614	-0.787	-1.909	-1.092	-2.202		
0.053	0.114	1.328	-1.518	0.566	-0.678	-1.358	-0.088
-0.868	-0.519	-2.786	-0.775	-0.047	-2.197	-0.362	
-0.992	-1.723	-2.163	0.545	1.119	-1.368		
0.328	1.488	-0.383	-1.311	-0.124	-0.887	-0.858	-1.008
0.248	-1.299	-1.223	-0.771	-1.755	0.076	-0.639	
-0.231	-0.295	-0.749	0.043	-0.188	-0.080		
-0.137	-1.937	-2.035	0.975	-2.440	-3.520	-0.921	-1.278
0.917	-0.416	1.251	-0.325	-0.576	-0.986	-1.503	
-0.471	-0.201	-2.003	-0.377	-0.312	1.517		
0.535	0.459	-0.525	-0.040	-0.313	-0.266	-0.877	-1.579
-0.442	-2.031	-0.495	-3.715	0.822	-1.756	-0.300	
-1.467	0.363	-1.556	-1.241	0.409	0.054		
0.991	0.606	-0.464	-0.687	-0.330	-1.133	-0.284	-0.647
-0.030	-3.510	-1.080	-1.061	1.025	-0.501	-0.615	
-1.522	0.081	-0.388	-3.850	-0.579	-0.850		
-0.425	0.740	-1.045	-0.675	0.639	-0.832	-0.303	-1.911
-1.958	-1.359	-1.249	-1.010	-1.646	-1.052	-1.053	
-1.452	-0.591	-0.151	-0.502	-1.748	-2.041		
1.213	1.950	0.631	-0.060	-1.973	-2.073	-1.020	0.485
0.599	-2.652	-0.200	-1.323	-0.640	-2.279	0.507	
-2.480	1.297	-1.159	-1.330	-0.329	-1.865		
0.530	-0.617	-2.361	1.366	-1.108	0.102	-1.724	-0.616
-0.987	-0.524	-1.712	-2.536	0.253	-1.584	1.529	
-1.996	-0.397	-1.849	0.198	0.149	-0.303		
1.089	1.533	0.013	-0.758	-2.163	-1.783	-1.400	-0.988
-1.883	-3.038	-1.135	-1.711	-2.099	-0.878	-0.345	
0.861	-2.258	-1.735	0.025	0.886	0.209		
0.354	-1.810	-1.031	-1.958	0.038	-1.491	-1.068	-1.377
-0.773	-1.497	0.168	-1.520	0.300	-1.221	-0.914	
-0.925	0.543	-0.662	-0.744	-1.065	-1.047		
0.596	-1.100	-0.909	-0.438	-0.070	-2.023	-1.109	-1.213
-0.536	-1.760	-1.472	-2.188	1.022	-1.589	-1.346	
-1.396	-0.418	-1.496	-0.659	-1.367	0.028		
-0.236	-0.679	-1.247	-1.263	-0.294	-1.309	-1.222	-0.731
-0.514	-0.900	-0.135	-3.172	0.112	-1.224	-0.236	
0.344	0.194	-1.007	-1.395	-1.481	-2.100		
0.014	-1.052	-1.227	0.432	-2.027	-2.336	-1.740	-0.356
-0.776	-1.399	-0.600	-0.799	-1.631	-1.589	-0.736	
-1.761	-2.034	-1.513	-1.860	-2.517	-0.265		

Table36.txt

-0.739	-0.841	-3.596	-2.683	-0.643	-1.477	-1.891	-2.767
-1.206	-1.126	0.130	-1.149	-0.927	-1.859	-0.650	
-0.498	-0.410	-2.342	-0.842	-1.636	-1.542		
0.978	0.714	1.675	1.345	-2.094	0.057	-1.106	-3.360
-1.934	-0.180	-0.630	-3.351	-1.844	-2.609	-0.079	
-1.327	-0.806	-3.243	-1.350	-2.129	0.597		
-1.798	-0.172	-3.477	-0.239	-0.763	-2.302	-0.899	-2.284
-0.870	-1.708	-0.605	-4.563	-1.286	-2.575	-1.706	
-1.774	-2.212	-2.479	-2.802	-1.332	-0.563		
0.183	-0.841	-2.097	-0.192	-0.605	-0.375	0.274	-1.796
-3.447	-4.013	0.930	-1.444	1.058	-1.596	-1.527	
-0.084	-1.339	-1.190	-1.484	-1.638	-0.716		
0.105	-0.810	0.590	-2.239	-0.079	-0.636	-0.309	-1.048
-1.331	-0.808	-2.762	-0.512	-1.326	-0.491	-1.921	
-0.891	-1.438	-0.723	-0.917	-3.676	-0.473		
0.999	-0.864	-2.396	-2.826	-1.202	-3.654	-1.505	-1.760
-2.804	-1.051	-0.919	-2.903	-0.274	-2.149	0.985	
1.293	-1.386	-2.397	-2.786	0.213	0.158		
1.410	0.479	-2.429	-1.961	-1.395	0.090	-0.484	-2.146
-0.009	-1.760	-1.037	0.019	-0.409	-1.237	0.551	
-2.899	-0.929	-0.539	-0.344	-1.013	-3.160		
0.316	0.917	1.374	0.039	0.323	-2.269	-2.595	-2.048
-0.321	-2.194	-0.969	-1.137	-1.189	-2.540	-0.819	
-0.941	-0.971	-1.315	0.324	-1.858	-2.371		
0.154	-0.475	-3.645	-1.399	-0.680	-1.631	-3.116	-0.741
-0.005	-0.094	-1.446	-1.049	-0.556	0.297	-2.654	
-1.552	-2.188	0.331	-1.758	-1.186	-1.068		
-0.108	-0.223	-1.315	-0.717	0.412	-2.299	-2.178	-2.246
-0.979	-3.894	-1.396	-1.416	-0.805	-1.419	0.784	
-1.430	0.110	-1.145	-0.901	-0.177	-2.118		
-0.325	-0.102	-2.441	-2.274	-0.983	-1.602	-2.047	-2.186
-1.308	-1.987	-1.001	-2.264	0.277	1.086	-1.368	
-3.616	-0.486	-0.003	-1.673	-0.437	-0.892		
-1.644	-2.890	-2.553	-0.246	-0.960	-3.071	-1.685	0.644
0.626	-0.780	-0.292	-2.650	0.106	-3.005	1.439	
-0.116	-0.710	-2.782	-1.293	-1.062	-1.368		
0.158	-0.341	0.985	-2.368	-3.409	-1.061	-1.742	-2.062
-0.786	-1.126	-0.494	-2.315	-1.130	-1.402	-2.715	
-1.328	-1.951	-0.549	-0.236	-1.657	-2.332		
0.497	0.401	-0.760	-1.408	-1.344	-0.450	-1.729	-0.525
-0.917	-0.240	-1.020	-2.558	-2.511	-1.561	-0.349	
-2.634	0.555	-2.451	-0.523	-0.562	-0.692		
0.075	-0.543	-1.082	-1.275	-1.588	-2.047	-3.576	-1.219
-1.544	-3.513	-1.880	-1.891	-2.017	-1.815	-2.329	
0.758	-0.984	0.166	-0.627	-0.790	-0.611		
-0.588	-0.767	-1.350	-0.976	-0.526	-0.624	-2.141	-1.937
0.870	-1.536	-0.414	-1.312	-1.379	-1.982	-0.980	
-1.682	-0.570	-2.152	-0.308	-2.094	-0.814		

Table36.txt

1.897	-0.880	0.123	-1.130	-0.228	-1.815	-0.255	-3.736
-1.841	-1.460	0.638	-0.075	-2.647	0.639	0.090	
-0.047	-0.928	-1.676	-1.124	-1.539	-0.692		
0.580	0.194	-1.152	-1.357	-1.229	-1.561	-1.637	-3.650
-1.170	-1.834	-0.907	-1.868	-1.284	-1.296	-0.709	
-2.974	-1.375	-1.136	0.531	-2.321	-0.840		
-1.192	-1.324	-1.569	-0.396	-3.372	-2.024	-3.389	-2.854
-2.903	-3.295	-1.760	-1.145	-0.755	-3.066	0.438	
-3.645	-1.172	-2.819	-0.978	-1.046	-1.175		
0.665	0.650	0.230	-2.156	-1.722	-0.367	-2.070	-1.565
1.174	-0.464	-0.297	-0.897	-1.303	-2.906	0.333	
-2.122	-1.635	-3.602	-2.139	-0.588	-1.371		
-0.750	-0.204	-1.885	-0.432	-0.527	-0.300	-0.717	-1.837
-0.442	-1.098	-1.779	-0.725	-2.024	-1.131	-3.001	
-0.035	-0.549	-0.102	-0.915	-1.040	0.293		
-0.280	-0.255	0.687	-1.339	-0.431	-1.565	-1.496	-0.446
-1.246	-0.712	-0.391	-1.502	-1.302	-1.514	-1.297	
-0.218	-0.645	-2.435	-0.222	0.141	-0.122		
1.361	-1.010	-0.774	-1.844	-1.794	0.097	-0.636	-3.728
-1.505	-0.481	-2.865	-1.430	0.678	-2.311	0.943	
-1.499	-0.863	-2.421	-3.022	0.759	1.126		
0.882	-1.414	-2.094	-1.244	-0.419	-0.667	-2.879	-0.048
-0.665	-1.612	-0.524	-0.994	-0.001	-1.422	-1.010	
-0.393	-0.412	0.655	-0.519	-1.427	-0.197		
0.076	-0.313	-1.420	-0.980	-2.375	0.993	-1.151	-1.241
-1.966	-1.753	-0.356	-2.052	-0.713	-1.170	0.638	
-0.339	-1.115	-0.822	-2.046	0.240	-0.407		
0.423	-0.808	-1.973	-0.222	-0.163	0.020	-1.131	-1.482
-1.118	-1.531	-2.685	-2.063	-0.478	1.528	-1.963	
0.880	-0.909	-0.922	-2.350	-4.284	-1.427		
1.725	-2.511	0.495	-0.712	-0.957	-1.846	-2.397	-0.313
-2.044	-0.506	-1.890	-0.926	-0.357	-0.194	-3.593	
-2.117	0.547	-0.847	-2.554	1.002	0.359		
0.452	-1.685	-1.222	-0.923	1.362	-0.591	-1.299	-0.373
-2.945	-2.356	-1.972	-0.090	0.003	-1.766	-1.364	
0.612	-1.300	-1.465	-0.473	0.000	-1.200		
0.320	-0.332	-0.704	-3.019	-1.650	-2.652	-1.639	-1.673
-1.989	-2.197	-1.889	-1.238	-0.088	-2.018	0.217	
-1.273	-0.331	-3.210	-0.378	-1.120	0.460		
-0.690	-0.552	-0.692	-3.136	0.905	-1.113	0.698	-0.952
-0.587	-2.326	0.290	-1.667	0.724	-0.086	2.124	
0.823	1.910	0.465	-1.801	-1.296	0.336		
1.128	-0.506	-1.226	0.144	-2.219	-0.237	-3.463	-1.160
0.013	-1.063	0.898	-2.336	-0.627	0.088	-0.435	
0.013	-1.550	-1.087	-2.014	-0.386	-1.398		
-1.046	0.389	-0.261	-2.347	0.935	1.053	-1.377	-1.464
-0.594	-0.456	-1.088	-1.759	0.298	-0.487	-0.570	
0.798	-3.246	-0.468	-0.770	-1.542	-1.825		

Table36.txt

0.024 -0.289 -0.495 0.378 -2.054 -0.551 -2.342 -0.006
-0.549 -2.013 0.190 -1.952 -0.850 -0.129 -1.284
-1.473 1.230 -0.910 0.322 -1.601 -0.630
0.124 -1.297 -0.363 0.832 -2.133 -1.344 -3.676 -0.652
-0.547 0.345 -1.083 -0.828 -1.322 -1.019 0.175
-1.387 -0.559 -2.248 -0.315 -3.048 -0.318
-0.836 -0.327 -1.047 -0.650 1.201 -2.911 -1.373 -0.262
-1.179 -0.604 -0.886 -3.207 -0.218 -1.657 -2.809
-1.204 0.065 -2.342 -0.183 -2.197 -0.675
0.474 -0.945 -0.915 -1.196 -1.151 -0.998 -0.893 -2.256
0.373 -1.283 0.593 -1.185 0.042 -0.696 -1.337
-0.703 -1.605 -2.286 -0.463 0.030 0.460
0.804 0.591 -2.533 -1.088 -0.500 -1.760 -1.534 -1.855
0.467 0.086 -0.977 -2.537 -1.158 -2.860 -1.593
-2.316 0.438 -1.496 -2.634 -5.404 -0.045
0.683 -0.069 1.951 -2.046 1.409 0.793 -0.035 -0.400
-1.767 -2.216 -0.895 -1.025 -1.144 0.289 1.878
-0.478 -0.736 -0.853 0.878 0.817 -0.096
0.945 -0.247 -0.539 0.115 0.340 0.470 -0.527 -1.498
1.639 -1.642 -0.041 -1.595 -0.959 -1.468 0.667
-0.420 -2.055 -0.821 -1.294 -1.774 -0.880
-0.221 -0.102 -2.187 -0.413 -0.289 -1.948 0.258 -2.382
0.141 -1.198 -1.384 -1.167 -2.009 -1.138 -1.224
-1.863 -2.164 0.417 -2.453 -0.086 -1.379
-0.446 -0.671 -0.628 -2.296 -1.207 -3.604 -0.406 0.474
1.249 -1.963 -2.214 -0.739 -0.081 -2.062 -0.367
-0.271 0.140 -2.693 -1.468 -0.261 0.282
1.452 0.484 -0.563 1.200 0.296 -3.540 -1.421 -0.931
-0.728 -0.663 -1.154 -1.810 -0.378 -1.158 -0.845
-0.012 -0.432 -1.025 -0.923 0.336 -0.101
-0.067 -0.282 -1.667 -0.986 -0.895 -1.141 -0.485 0.162
-1.186 -0.861 -3.349 -0.747 -0.525 -2.202 1.197
0.369 -1.024 -2.046 -0.618 0.474 -1.878
-0.088 0.228 -1.060 -1.180 -0.225 -0.370 -1.410 -0.993
-2.347 -1.154 -1.091 -0.176 0.861 -3.096 2.177
-1.455 0.058 -0.605 -2.083 -0.907 -0.591
-0.145 -0.220 -1.814 -1.577 -1.627 -4.021 -0.509 -3.255
-2.203 -1.603 -1.258 -1.323 -0.662 -4.435 -2.102
-1.186 -0.314 -0.724 -0.744 -0.404 -0.810
-0.467 -1.032 0.115 -1.370 0.840 -0.610 -0.869 -0.781
-1.693 -2.547 -0.998 -1.800 -2.160 -2.225 0.650
-0.531 0.831 -2.773 -0.462 -0.797 -0.909
-0.310 0.955 -2.171 -2.490 0.049 -1.299 -2.985 -1.181
-0.498 -0.103 -0.527 -2.384 0.392 0.355 -1.309
-1.952 -0.150 -1.892 -1.926 -2.185 -1.502
-0.047 0.279 0.486 -1.014 -1.684 -1.340 -0.484 0.237
-0.688 -1.133 -1.082 -1.320 -1.955 0.803 0.529
0.535 0.412 -1.689 -2.178 -2.939 -0.866

Table36.txt

0.194	-0.419	-0.268	-0.969	-1.586	-1.257	-1.625	-0.482
-1.700	-0.005	-2.182	0.471	1.190	0.257	-2.774	
-0.218	-2.259	0.304	-0.800	-1.344	-1.364		
-0.061	-0.614	-0.615	-0.543	-2.603	-1.061	-2.767	-2.420
0.087	-0.768	-2.092	-1.739	-1.637	-2.078	-0.049	
-2.469	-0.180	0.091	-0.929	-0.632	0.343		
0.061	1.000	-0.083	-2.773	0.965	-2.741	-1.958	-3.056
-0.737	-1.894	-1.498	-0.977	-1.372	0.009	-1.254	
0.195	-0.134	-0.832	-2.977	-1.428	-1.816		
-0.800	-0.046	-1.179	-3.036	-1.634	-2.890	-0.616	-1.982
-0.573	-3.033	0.409	-2.470	0.160	-0.969	-0.951	
-2.015	-0.343	-0.328	-1.328	-1.649	-2.234		
0.837	-0.285	-1.733	-1.243	0.331	-2.967	-2.744	-0.678
-0.423	-0.828	-0.393	0.432	0.053	-2.641	-2.552	
-1.029	-1.123	-1.185	-0.904	-1.282	-0.228		
-0.466	0.748	1.376	-2.826	-0.796	-2.820	0.087	-2.455
-1.404	-1.429	-0.752	-1.650	-0.210	-3.667	0.656	
0.647	0.444	-2.082	-0.374	-0.225	-1.806		
-0.959	-0.671	-0.748	-1.766	-0.439	-0.319	-1.003	-1.361
-1.056	-1.054	0.348	-0.821	-1.364	-1.930	-0.551	
-2.780	1.518	-0.247	-1.397	-2.481	0.219		
-0.692	0.543	-0.901	-1.415	-0.507	-0.662	-1.643	-2.055
-1.206	-0.827	-1.100	-0.234	-0.082	-1.005	-1.004	
-0.153	-1.513	-1.690	-0.877	-0.643	-1.559		
0.085	0.608	-0.370	0.885	-0.657	-1.455	-1.988	-2.002
-0.326	-1.840	-1.996	-3.174	0.265	-1.916	-1.395	
-1.856	-0.929	-1.737	0.416	-1.581	-0.909		
-0.395	-0.587	0.233	-0.539	-0.713	-1.764	-1.783	-0.018
0.483	-0.744	-2.620	-0.698	-1.834	-1.903	0.526	
-2.133	-0.811	-1.354	0.071	-1.106	-2.282		
0.301	-0.535	-0.061	0.610	-1.635	-2.073	-1.819	-2.294
-1.903	-1.358	-1.940	-2.720	1.382	-0.282	-1.273	
-0.174	-1.135	-1.416	-1.132	-0.956	-0.881		
-0.715	-1.692	1.219	1.556	3.048	4.033	2.397	3.408
2.388	1.621	1.023	2.439	2.382	3.497	2.269	
5.145	0.481	1.553	2.094	3.100	1.344		
-1.005	-0.813	-0.226	0.112	0.334	-0.883	-1.215	-0.059
-2.446	-2.110	-0.174	-1.602	-0.960	-2.165	0.349	
-0.108	-0.990	0.459	-0.859	0.385	-1.936		
1.268	-0.792	0.797	2.082	-1.374	-0.071	1.049	-0.695
1.335	-1.053	-0.691	-0.629	-0.775	-1.138	-1.185	
-1.709	-1.490	-0.066	-0.297	1.289	1.873		
-0.673	-0.534	-2.366	0.361	-0.859	-1.728	-0.981	-0.081
-1.540	-0.740	-1.355	-0.154	0.258	0.365	-0.802	
-0.235	-1.970	1.097	-1.474	-0.999	0.313		
-1.018	-2.407	-1.914	-1.527	-0.309	0.530	-0.121	-2.199
-0.953	-0.300	-0.506	-0.978	1.243	0.971	-1.122	
-0.374	1.209	4.192	-0.981	0.478	-0.541		

Table36.txt

0.789	0.596	-0.494	2.659	-0.911	-1.549	0.055	0.798
-0.244	0.401	-0.898	1.826	-2.146	-0.919	-0.773	
-0.368	-1.191	0.200	-0.220	-0.732	-0.225		
-0.106	-0.184	0.403	-0.395	-1.399	-2.404	-2.106	1.488
0.430	-1.974	1.420	1.135	-1.027	-1.361	-0.704	
-1.896	0.819	-1.547	-1.263	-2.157	-1.475		
0.428	-0.688	0.531	-0.848	0.098	0.806	-0.444	-1.744
-3.879	-0.851	-2.371	-1.155	1.046	-0.211	0.425	
0.441	-0.984	-1.883	-0.717	-1.098	-0.390		
0.115	-1.608	-1.932	0.402	-0.984	-0.405	-1.231	0.886
-1.062	-1.276	-1.698	-0.886	-1.321	-0.991	-0.726	
0.362	0.750	-0.750	0.257	-0.848	0.973		
-0.624	-1.744	-1.479	-0.442	-1.732	-1.980	-2.992	-1.359
-2.484	-1.739	0.382	-2.686	-1.142	-2.408	-0.814	
1.454	1.598	-1.165	-0.164	-1.941	-0.292		
-0.701	-0.028	-1.729	-1.003	0.071	-1.255	-0.584	-1.832
0.552	-1.320	-1.786	-0.352	0.204	-0.811	-0.363	
-0.388	-1.204	-1.383	-0.414	-0.307	-0.269		
0.748	-0.621	0.234	1.294	-0.722	0.366	-1.693	-2.021
-0.172	-0.404	-0.054	-1.615	-2.372	-0.937	-0.940	
-0.116	-0.187	-1.534	0.625	-2.496	0.794		
-0.466	-1.003	0.072	-2.279	-0.494	0.057	-1.795	0.271
0.920	-1.072	-0.879	1.333	0.575	-0.361	-0.481	
0.765	0.205	-0.873	0.055	-1.014	-0.472		
-0.195	-0.512	0.440	-1.292	0.002	-2.338	-0.671	0.052
0.320	-2.473	-1.117	-3.463	0.414	-1.715	0.471	
-0.281	-0.404	1.266	-1.612	1.871	-0.311		
0.165	-1.086	-1.286	-0.095	-0.870	1.565	-1.312	-1.855
-1.243	-1.180	-0.688	-1.685	1.249	-3.131	-0.036	
0.921	-0.247	-0.767	-1.760	-1.388	-2.325		
0.975	0.496	-0.119	-0.548	-0.027	-1.740	-1.249	0.222
-1.069	-0.479	-1.491	-0.183	-2.143	-1.851	-0.093	
-2.181	-2.495	-0.692	-0.368	-0.805	-0.102		
-0.613	-2.627	0.587	2.282	0.797	0.173	-2.147	0.932
-0.335	-0.991	-0.139	0.395	1.976	-1.288	-0.872	
-1.126	-0.557	-1.732	0.668	0.060	1.929		
-0.132	-1.087	-1.319	-0.897	-0.373	1.514	-1.428	-2.152
1.505	-1.213	-0.606	-1.736	-0.433	-0.118	-0.204	
-1.094	-0.466	0.033	-0.566	-0.048	-0.406		
0.422	-1.614	0.731	-2.626	-1.658	-1.110	-0.251	-2.928
-0.274	-2.350	0.239	-0.979	-1.980	-2.123	-2.211	
0.179	0.861	-2.563	-0.595	-1.066	-1.557		
-1.041	-1.380	-1.519	-1.226	-1.967	-2.143	-1.083	-2.593
-0.834	-0.175	-0.703	-0.789	-0.179	-0.311	0.470	
0.476	1.020	-0.214	0.271	0.276	0.826		
0.311	-1.830	-1.232	-0.739	-0.719	1.053	-0.319	-1.333
-1.008	-0.530	-1.651	-1.829	-1.826	-0.389	-0.109	
-4.068	-0.513	0.177	-0.769	-1.467	-1.550		

Table36.txt

-0.471	-2.732	0.013	-0.981	-0.259	0.224	-1.767	-2.121
-0.942	-1.849	0.298	-1.006	1.015	0.296	-0.438	
-0.303	-0.848	-1.483	-1.458	-0.236	-1.331		
-0.673	-1.743	1.728	-0.616	-0.440	-2.078	0.461	-1.949
-1.420	-0.380	-0.106	-3.554	-1.964	1.671	1.342	
-1.289	-0.094	-0.773	1.754	-0.736	0.696		
-0.301	-0.454	-1.641	-0.011	-0.561	-0.290	-1.270	-0.711
-1.539	-2.738	-2.240	-1.504	-0.486	0.810	-0.617	
0.178	-0.763	0.027	-0.123	-1.959	-0.806		
0.095	-0.003	-0.226	-0.046	-1.761	-2.834	1.045	1.460
-1.094	-2.136	-0.384	-0.960	-0.143	-2.287	-0.545	
1.221	-0.184	-0.319	-0.354	-1.210	0.115		
0.654	-1.092	-0.672	-0.969	-0.331	0.038	-2.513	-1.951
-1.554	-3.115	-0.174	-1.361	-1.393	-2.261	0.426	
-1.298	-1.145	-0.359	-0.960	0.193	-0.802		
0.891	-1.021	-1.095	-1.144	0.136	0.002	-1.367	-0.077
-0.609	-0.610	-0.891	-1.279	-0.623	-1.613	-1.601	
-0.243	-0.972	0.093	0.370	-0.228	0.375		
1.072	-0.882	-1.326	-1.155	-2.285	-1.137	-1.461	0.963
0.049	-1.967	-2.093	-0.716	-0.418	0.349	-0.232	
-1.570	-0.410	-1.883	0.372	-1.269	-2.930		
0.262	-1.792	-0.029	-0.921	-1.860	0.665	-1.910	0.869
-2.321	-0.361	-1.045	-0.134	1.118	-0.417	-1.090	
1.377	-0.616	-0.785	0.353	0.463	0.515		
0.140	-2.286	0.644	0.696	-0.734	-2.628	-0.392	-1.677
-1.105	-1.888	-1.573	-2.169	0.864	-2.210	0.438	
1.695	-1.214	-0.571	0.923	-0.318	-1.419		
0.226	-1.618	0.309	0.517	-0.774	-1.150	0.514	-1.357
0.497	0.711	-1.174	-0.983	0.239	-2.158	2.008	
-1.584	-0.792	-0.082	0.253	-1.245	-1.142		
-0.145	-3.619	17.618	16.447	11.753	21.295	16.507	19.395
12.093	22.571	11.987	19.559	11.897	16.799	11.967	
17.195	10.662	16.700	12.750	10.502	12.392		
0.830	-5.416	2.285	-0.827	0.080	-0.481	-1.229	-1.845
3.769	4.529	-0.033	19.212	-0.324	-1.508	-2.240	
0.555	5.481	1.892	3.265	3.376	0.355		
-0.284	-1.945	-1.324	-0.485	-0.062	0.335	0.112	-0.421
-0.819	0.103	0.545	-0.414	-1.606	1.084	-0.673	
-0.681	-0.497	1.186	-0.828	1.522	-1.823		
0.202	-1.648	-2.632	-0.116	-0.760	-0.596	-1.689	-1.567
0.419	-0.284	-0.870	-1.391	-0.822	-1.539	-0.834	
-0.968	-1.023	-1.055	0.633	-1.643	-0.416		
1.482	-2.296	-0.345	0.255	-2.037	-0.143	-1.023	-2.093
-1.548	-0.634	-1.897	-0.268	1.636	-1.568	-0.233	
-1.276	-0.751	0.093	-1.221	0.020	0.773		
0.632	-2.527	-0.625	2.180	1.167	0.429	-1.081	-0.049
1.229	-1.852	0.119	0.044	-0.396	-0.151	0.950	
0.347	0.197	-0.077	-1.295	-1.332	-0.658		

Table36.txt

0.382	-1.832	-0.477	0.515	-0.729	-0.225	0.866	-1.025
-0.508	-4.062	-1.226	-0.263	0.825	0.747	-1.054	
-0.703	1.464	-3.440	-0.668	1.099	0.305		
1.946	-3.090	8.220	8.909	8.507	14.628	8.091	11.037
9.225	14.860	6.839	11.041	8.277	10.852	5.950	
11.083	4.987	8.532	6.306	7.712	6.334		
0.935	-0.950	1.723	0.624	1.927	1.462	-0.555	0.981
1.791	2.860	1.282	2.580	1.156	2.734	0.895	
-0.413	-0.067	3.700	0.227	3.926	0.572		
0.969	-2.296	1.061	-0.115	0.321	-0.287	-0.415	-0.069
-0.357	-0.577	-0.312	-2.389	-1.324	0.367	-0.703	
-1.259	0.103	0.232	-1.142	0.228	-0.542		
0.558	-1.770	-1.897	-0.589	-0.792	-0.704	-0.461	-2.028
-1.524	0.342	0.087	-0.687	1.204	-1.757	-1.630	
-0.939	-0.825	-1.423	-0.159	-0.870	0.137		
0.704	-1.335	-1.369	0.719	0.244	-0.070	-0.503	0.857
-1.448	0.122	-1.431	-1.224	-0.105	-2.012	-0.096	
-0.414	1.589	-0.730	0.380	-0.845	-1.558		
-0.117	-3.284	-0.148	-0.479	1.334	0.324	-0.578	-0.240
-1.491	-1.776	-1.099	-0.067	0.471	-1.478	0.097	
-0.888	0.370	0.074	-1.601	-0.073	1.163		
-1.204	-0.216	0.044	-1.523	-1.659	-0.149	-1.846	-1.013
1.754	-1.851	-1.634	-0.967	-0.032	-1.865	2.387	
-0.560	-1.436	0.687	0.873	-2.270	-0.318		
-0.214	-0.943	0.363	0.982	-0.622	-0.310	-0.721	-1.400
0.040	-2.985	-0.097	-0.274	-0.660	0.273	-0.234	
-1.462	0.741	-0.062	-0.415	-0.279	-0.387		
-0.508	-0.771	0.677	0.304	-1.243	-0.890	-2.159	-0.795
-1.757	0.216	0.125	0.039	0.663	-0.081	-1.411	
-1.497	-0.636	-1.579	-0.770	0.681	-0.067		
0.447	-0.454	0.187	-0.945	-0.617	-1.245	-3.774	-1.308
-0.907	-1.901	-1.154	-0.594	-1.087	-1.124	-3.104	
0.209	0.670	-1.099	-1.071	0.143	-0.370		
-0.210	-1.219	-0.431	0.774	-0.787	-2.479	-1.045	-0.996
0.074	-0.157	0.917	-1.976	-1.337	0.571	-0.815	
-0.708	-1.265	-0.479	-2.002	-2.338	0.490		
0.249	-1.196	-1.005	-0.757	1.620	-1.393	-0.110	-2.261
-1.096	-0.716	-2.540	0.331	-0.344	-1.674	-0.588	
-2.015	0.332	-0.490	-1.421	0.180	-2.377		
-4.405	-4.545	-0.428	0.710	10.963	15.266	7.223	14.693
-1.162	0.762	-0.251	-0.064	12.407	10.321	13.648	
-0.808	0.010	11.353	8.653	8.150	0.203		
0.103	-1.345	-1.762	0.711	-0.113	0.071	-0.123	0.541
-0.324	-2.551	-1.097	-0.832	-0.327	1.289	-0.360	
0.221	-0.119	-1.471	-1.877	-0.156	-1.162		
-1.886	-0.355	-0.196	-0.677	-1.786	0.483	-0.201	-3.456
-1.991	-1.451	-1.575	-1.491	-0.046	0.169	-0.809	
-0.951	0.080	0.383	-0.562	-2.476	-0.351		

Table36.txt

-0.462 -0.177 -0.063 0.776 -0.077 0.685 -0.771 0.086
-1.293 -0.217 -0.612 -1.266 1.270 -0.160 -0.664
-0.256 -0.213 -1.596 -0.675 1.904 -0.092
1.366 -1.541 0.162 -2.757 0.380 -1.125 -0.768 -1.452
-1.257 -1.807 -1.216 -0.463 0.092 0.342 -1.369
0.898 2.335 2.070 -1.156 0.749 1.106
-0.651 -1.530 -0.576 -1.512 -0.269 -0.189 -1.120 0.268
0.086 -0.239 -1.115 -0.318 -1.929 1.113 -0.843
1.755 0.133 -2.685 0.262 0.768 -1.706
1.329 -1.836 -1.062 -1.572 -0.802 -1.261 0.369 0.067
0.609 -1.691 -0.504 -1.167 -0.366 -2.480 -1.311
-0.559 -1.148 -0.405 0.297 0.329 -1.100
0.184 -3.246 -0.643 0.480 -1.544 -1.649 -1.776 -2.112
-0.473 -2.117 -1.102 -1.014 -0.060 -0.626 -0.173
-2.056 -0.867 0.035 0.344 -1.345 0.355
0.495 -1.222 -0.054 -0.923 -0.198 -1.660 -3.052 -1.773
-0.793 -0.879 -0.083 -0.903 -0.726 -2.973 0.390
-0.192 0.808 1.672 -1.647 -0.118 0.191
0.598 -0.550 0.148 -1.723 -1.045 0.214 0.612 -2.054
-1.652 -0.811 -0.388 -1.105 -0.383 -2.047 -1.047
-0.359 -2.064 -0.543 -0.822 -0.549 -0.665
-1.994 -1.261 -0.124 -0.842 -0.936 -2.215 -2.327 -1.898
-1.880 -2.783 -1.056 -1.964 -1.163 -1.301 0.212
-1.658 -1.540 -2.200 -1.267 -1.955 0.593
-1.194 -0.872 -1.384 -0.663 -1.546 -1.293 -0.895 -1.768
-1.225 -3.134 -0.829 -2.191 0.183 -1.163 -0.781
-1.658 -0.221 -0.519 -0.879 -0.328 -1.213
-0.176 -1.196 -1.700 -0.719 -0.534 -0.564 -1.202 -1.968
-0.799 -0.819 -2.334 0.625 -1.300 -0.267 -2.515
-0.852 0.555 -2.630 -0.747 -0.490 -0.383
1.037 -1.781 1.289 2.606 1.406 0.122 -0.260 0.310
0.030 0.685 -1.869 0.455 -0.554 1.407 0.434
0.368 -0.554 0.612 0.514 -0.754 0.111
0.584 -1.041 0.802 -1.108 -1.030 -1.406 -2.965 -1.454
0.451 -1.213 0.095 0.559 0.709 1.454 -0.281
0.288 -0.163 -0.126 0.731 0.519 2.196
-0.340 -1.340 -0.338 -0.822 0.853 -0.606 -1.316 1.196
-0.249 -1.103 0.708 -2.041 -1.138 -0.493 -0.982
-0.709 -0.115 -1.384 1.129 -0.178 0.187
1.013 -3.166 0.718 2.878 1.497 -0.026 -1.075 -0.590
0.209 0.535 -0.660 -0.064 -0.038 -1.829 -0.676
0.793 0.812 -1.529 -0.887 1.616 0.358
0.196 -1.323 1.647 0.040 -0.958 -0.527 -2.094 -0.524
-1.626 -1.072 -0.345 -2.353 -0.984 0.161 -1.094
-0.462 -2.194 -2.056 -0.499 -1.837 -0.711
0.481 -0.529 -0.995 0.397 0.304 1.791 0.042 -0.842
-1.962 -1.125 -1.115 -0.880 -0.147 -1.880 -1.123
-1.053 -0.894 -0.050 -0.846 -1.202 -1.396

Table36.txt

-0.944 -1.176 0.120 0.427 -1.040 0.333 -0.428 -1.166
-1.587 -2.560 0.582 -0.341 -1.814 0.174 0.481
0.698 -1.145 0.157 -0.149 0.778 -0.985
0.277 -1.895 0.666 -0.506 1.026 -1.349 -0.570 0.555
-0.265 0.028 -1.832 0.455 -0.390 -1.494 0.393
-0.577 1.325 0.059 0.038 2.272 2.156
-0.061 -0.703 -2.707 -1.439 -2.974 -0.214 0.575 1.594
-1.077 -2.171 0.431 -0.195 -0.626 -0.347 -1.267
-1.022 -2.541 -1.665 1.164 -0.833 -1.096
1.169 -1.378 -0.386 -0.779 -1.320 -1.522 -1.101 0.115
-0.998 -1.586 -0.151 -0.298 -0.922 -1.174 1.362
1.954 1.252 -1.102 -1.413 -0.399 -0.019
1.016 0.255 -1.075 0.838 -2.887 0.835 -0.774 -0.631
0.106 -1.457 -0.528 1.466 -0.639 -1.642 0.321
-1.219 -0.027 0.701 0.259 -1.176 0.857
1.096 -2.657 -0.574 1.453 -1.736 0.315 2.312 2.463
-0.823 0.393 -0.625 0.517 0.042 -2.208 0.846
1.667 -1.055 -0.157 -1.225 0.395 0.350
0.966 -1.003 -2.003 -1.346 -0.038 -1.728 -0.160 -0.818
0.067 -2.443 -0.457 0.099 -0.536 -3.251 -1.490
-0.383 0.753 -0.672 -1.256 -1.150 -0.598
-0.091 -1.265 -1.390 0.243 -1.716 -0.936 -0.369 -0.488
0.175 -0.995 -0.482 -2.914 1.240 -0.328 -1.531
0.799 -0.655 -0.904 0.013 -2.225 -1.340
0.398 1.325 -0.728 -0.436 0.876 -0.471 -1.343 -1.104
0.704 0.042 -0.755 -0.038 0.358 -4.339 -0.481
-2.648 -2.098 -5.010 0.527 -0.605 -0.218
-2.556 0.024 -0.142 0.105 1.652 -1.893 -0.511 1.614
1.327 2.710 0.733 -3.704 -0.304 -0.439 -0.068
-0.073 -1.372 0.240 1.183 -0.947 -1.108
-0.382 2.356 -1.440 -1.846 -1.372 -0.960 -0.464 -1.166
0.220 -0.253 -0.759 -1.134 -1.820 -0.892 -0.113
-0.022 -3.002 -0.246 -0.655 -1.227 -0.433
0.414 -0.798 -2.114 0.272 -1.718 -1.915 -0.909 -1.938
-0.717 -1.423 -0.915 -2.108 0.251 -1.873 -1.605
-0.107 -0.015 -3.190 0.803 -0.259 -0.631
-1.257 -1.464 -0.770 -0.829 -0.095 0.539 -0.538 0.168
-3.412 -1.559 1.543 -1.222 0.703 -0.517 -0.118
-0.830 -0.805 -0.309 0.169 -1.920 0.092
-0.916 -0.548 -1.454 0.027 -0.663 -0.574 -2.198 -0.673
-1.449 -1.385 -0.186 -3.357 -0.547 -1.584 -1.906
-0.680 -0.963 0.017 -2.038 0.145 0.065
-0.504 0.055 -1.353 -1.814 -2.593 -0.226 0.476 -0.715
-0.691 0.412 -0.114 -0.537 -1.115 -2.666 1.214
-1.437 -0.198 0.386 -2.395 -0.820 -2.021
0.817 0.600 -1.688 1.087 -0.466 0.175 -0.348 -0.543
-0.881 -0.712 -1.959 1.037 0.190 -2.043 -2.004
-0.316 -0.115 0.896 -1.676 -0.262 -1.053

Table36.txt

-0.285	-0.006	0.474	-2.082	0.521	-1.688	-1.462	-1.136
-0.147	-1.916	0.023	-1.120	0.344	-0.792	-1.432	
1.159	0.021	0.089	-0.135	-0.263	0.007		
0.698	-2.483	-1.867	0.315	-0.865	-2.180	-0.174	0.220
-0.817	-1.216	0.444	-0.302	-1.499	0.384	-1.345	
0.817	-0.756	-1.460	0.115	0.328	0.526		
-0.061	-1.560	-0.994	-1.369	1.329	-1.372	-1.370	-1.868
-1.466	-2.805	-0.908	-1.732	0.809	-3.559	-0.333	
-0.759	-0.996	-0.650	-0.001	0.620	-0.711		
-0.054	-1.467	-0.327	0.268	-0.169	-0.633	-0.576	-2.234
0.641	-0.340	1.219	-0.731	-0.306	-1.247	-0.148	
-1.231	0.720	-1.431	-0.392	1.531	-0.275		
-0.166	-2.498	-0.533	0.537	2.648	0.899	0.149	5.294
-0.399	-1.632	-1.025	9.404	-1.302	0.766	1.007	
3.681	2.887	-1.381	6.759	-0.383	0.770		
0.454	-1.920	-0.292	1.302	1.325	-0.296	-0.130	-1.208
-0.612	-2.441	-0.949	0.016	-0.572	-0.313	-0.133	
1.315	-0.334	0.689	-0.374	1.799	1.495		
-4.213	0.134	11.561	9.454	12.428	16.841	10.507	14.501
8.231	16.745	8.805	10.217	6.971	12.653	1.063	
2.417	7.910	17.949	8.867	6.933	10.027		
-0.311	-1.043	-1.371	0.252	-0.252	-1.441	-0.319	-0.879
-0.133	0.044	-0.589	-1.955	-1.743	-1.109	-1.769	
-0.935	0.161	-0.511	0.723	0.330	0.059		
-0.134	-0.382	-1.515	-0.839	-1.120	-0.654	-0.845	-1.897
-1.163	-1.367	-4.130	-1.975	0.015	-1.141	-0.344	
-2.527	-0.626	-2.142	-1.379	-1.045	-1.216		
-0.617	-1.850	0.712	-1.058	-1.120	-1.573	0.979	0.634
-1.412	-1.348	-2.146	0.857	0.391	-1.616	-0.998	
-1.694	-0.566	-1.059	-1.298	-1.778	-2.280		
0.135	-0.160	-2.077	1.351	-0.569	-1.684	-1.767	-2.679
-1.018	-1.836	-0.014	-2.381	-0.800	-1.522	-0.512	
-0.150	-0.332	-2.624	-1.355	-1.061	-0.865		
-0.918	-0.328	-1.106	-2.691	0.422	-1.068	-3.132	-2.680
-1.351	-2.751	0.442	-1.757	-1.583	-1.596	-1.680	
-0.681	-1.288	-1.289	0.168	-0.345	-0.155		
0.483	-1.628	0.996	-0.246	-1.280	0.509	0.442	-0.883
-0.840	-0.056	-1.135	-0.413	-1.601	-0.362	-0.382	
0.295	-0.915	-1.699	-0.262	1.095	-2.495		
0.102	-1.393	-1.062	-1.215	-1.163	-1.236	-0.110	-0.105
-0.619	-1.723	-0.517	-1.840	-1.600	-0.136	0.777	
-0.824	-0.306	-1.560	-2.105	-0.547	0.157		
0.435	-2.056	0.529	-0.630	-2.823	-2.125	-0.884	-2.293
0.380	-1.584	-2.731	-1.956	-2.089	-2.988	-0.537	
-2.840	0.817	-1.531	0.686	0.478	-0.900		
-0.975	-0.481	-1.157	-1.660	-1.978	-1.436	-0.068	-2.524
-2.263	-2.768	-0.265	-1.455	-0.897	-2.868	-1.830	
-0.380	-0.417	0.328	0.485	-0.656	-1.077		

Table36.txt

-0.129	-3.089	0.003	0.022	-1.077	0.721	-0.454	0.275
-1.571	-0.320	0.245	0.183	-0.737	1.812	-0.937	
-0.015	-0.009	-0.859	0.022	1.129	-0.318		
0.674	0.649	-1.344	1.422	-2.130	0.508	0.475	-2.344
-0.874	0.546	-0.839	-1.255	0.231	0.621	-0.691	
-0.071	-1.669	-0.780	-2.598	-0.438	-0.128		
-4.052	-3.960	-0.384	0.302	4.864	10.691	1.423	2.117
-0.873	-1.383	1.660	-2.244	-0.344	3.771	1.326	
1.065	-1.032	1.353	0.832	2.093	-1.117		
0.048	-0.250	-0.331	-0.706	-0.792	-1.443	0.069	-0.579
0.199	-2.866	-1.880	3.327	1.087	-1.888	-0.929	
-0.507	-0.209	-0.902	0.343	-1.141	-0.673		
0.321	-0.362	-1.047	-0.275	0.127	-0.787	0.862	-1.716
0.216	0.400	-2.017	-1.549	-1.880	-0.426	1.357	
-0.870	-1.829	-1.801	-1.697	-0.492	0.992		
-1.589	-0.631	-1.766	-0.669	-0.561	-0.733	1.153	-0.966
0.155	-1.526	-1.680	-1.674	-0.664	-1.673	-0.892	
-1.823	-1.544	0.725	-1.720	-0.186	-0.006		
0.521	-1.263	-2.252	-0.436	-1.952	-2.506	0.377	-1.976
-1.635	-0.935	-1.347	-1.288	-1.071	-2.178	-0.985	
1.062	1.135	-2.152	-1.313	-0.854	-0.442		
0.270	0.101	-0.703	-1.383	-2.533	-2.328	-0.276	-0.869
0.227	-0.335	-1.822	-2.335	0.081	-1.679	-2.138	
-1.881	-0.583	-1.841	0.376	-2.344	-1.027		
-0.069	-0.318	-0.996	-1.928	-0.372	-1.156	-2.194	-1.541
-2.081	-0.367	0.228	0.380	-1.057	1.035	-0.863	
-1.990	-0.404	-1.679	-0.811	-2.301	-0.213		
0.254	-0.780	-1.279	-1.081	0.176	-2.460	-0.957	-1.165
-1.743	-1.468	-0.255	-2.795	-0.029	-1.555	-0.334	
-1.032	-1.483	-0.485	-0.952	-0.970	-0.593		
-0.359	-2.571	-1.761	-1.304	-0.913	-1.307	1.146	-0.792
0.374	-1.355	-0.449	-0.796	-0.543	-1.331	-1.157	
0.578	-1.894	-1.464	-0.541	1.904	-1.742		
-0.245	-0.448	-0.213	0.781	0.439	-0.456	0.929	-0.713
0.114	1.107	-1.815	-1.785	-0.867	-1.321	-0.257	
-0.205	-2.057	-0.210	-1.885	0.518	0.831		
-1.027	-1.600	-2.906	-0.195	-0.638	-1.476	0.254	-1.321
-1.605	-2.755	0.316	-1.460	1.013	-0.159	-0.494	
-1.619	1.767	0.834	-2.430	1.546	-0.803		
-0.093	-1.093	-1.304	-2.371	-1.280	-0.044	-1.057	-2.814
-1.449	-0.068	-0.585	-2.594	0.369	-1.715	-0.057	
-1.242	0.988	-1.122	0.015	-1.146	-2.008		
-0.422	-0.881	-0.451	-2.105	-0.463	-2.896	-1.132	-2.219
0.549	1.014	-0.870	-1.555	-1.148	-1.770	-3.520	
-1.541	-1.161	-0.935	-0.232	-2.376	-0.298		
0.512	-0.982	-0.677	-0.617	-2.071	-1.866	-0.428	-2.401
-0.261	-1.592	0.084	-1.390	-0.606	-1.152	-0.348	
-1.530	-1.523	-1.471	-0.943	-0.513	-0.835		

Table36.txt

0.755 0.204 -0.247 -1.139 -0.353 -0.493 -1.375 0.244
0.862 -0.742 -1.876 -0.852 0.204 -2.998 -0.366
1.283 0.508 -0.014 0.413 -1.279 -1.209
-0.075 -0.088 -0.122 -0.940 -0.364 -0.068 -0.671 -1.428
-1.615 -2.073 0.673 -0.736 -1.144 -0.981 -3.102
-0.532 -0.219 -1.883 -1.401 0.390 0.520
-0.188 1.272 -0.173 0.611 -1.068 -0.743 -3.949 -1.906
-0.246 -1.553 0.475 -1.405 -0.308 -2.499 -0.813
-1.073 -1.771 -3.435 -1.378 -0.925 -1.051
0.898 -1.554 0.247 -0.882 -0.801 -1.530 -0.268 -0.009
-1.259 -1.017 0.495 -4.377 -0.746 -1.295 -1.046
0.401 -2.176 -0.680 0.412 -1.296 -0.772
-1.150 -1.400 -0.009 -0.318 -0.888 0.662 -1.559 -1.249
-0.985 -1.508 -2.166 0.297 -0.775 -2.051 -1.866
-1.555 -0.018 -1.505 0.150 -0.451 0.617
-0.644 -0.331 -2.780 -0.070 -1.949 -1.456 -0.595 -1.635
-1.228 -1.139 -1.350 0.913 1.576 -1.040 0.242
-0.880 -0.929 0.305 -0.321 -0.561 -0.523
-1.345 -1.074 -1.987 -2.479 1.589 -1.115 -2.018 -0.479
0.142 -0.961 -1.586 -3.176 1.192 -0.280 -1.376
-2.568 -1.658 -2.524 0.816 -0.398 0.997
0.258 -2.034 -1.362 -0.518 -1.646 -1.190 -1.097 -1.960
-0.900 -1.471 -0.254 -1.066 -0.054 -0.210 -1.090
-0.487 0.362 -0.639 0.392 0.701 -2.202
-0.044 -1.980 -0.086 1.669 -0.550 -0.229 1.080 -1.063
0.288 10.230 0.693 -0.579 0.102 -0.792 0.627
0.851 0.242 0.439 -0.358 0.296 -1.363
-0.433 -1.946 -0.271 1.284 -1.460 -0.324 0.832 -1.714
0.063 -1.835 -0.873 0.912 -2.062 1.000 2.640
1.505 -0.160 0.299 2.172 -0.051 1.635
0.321 -2.855 9.811 8.718 9.257 12.745 8.455 12.517
7.964 12.104 9.322 13.104 6.411 15.634 8.807
7.641 5.714 10.252 8.280 8.866 8.494
0.434 -2.075 3.012 0.810 1.449 3.512 1.791 3.933
1.137 3.433 -0.751 4.311 2.298 2.072 0.818
1.700 0.839 2.520 0.573 2.853 0.626
0.469 -2.389 -0.355 -1.808 -0.097 -0.544 -0.790 -0.367
-0.542 -0.434 -1.206 -0.904 -1.911 -1.049 0.288
0.932 0.310 -0.165 1.613 0.568 0.000
0.250 -1.832 -0.786 0.099 -0.801 1.496 0.347 1.099
-0.019 -0.036 1.226 -1.637 0.858 0.031 0.651
-0.068 -1.008 -0.068 -0.077 1.879 -0.220
0.203 -1.987 13.431 14.340 12.193 14.436 11.774 14.674
11.717 19.824 9.676 17.198 7.980 14.130 9.933
14.589 9.273 17.536 8.155 11.711 11.225
0.073 -2.521 1.093 -1.072 -0.616 0.335 -1.488 -0.262
1.820 0.085 -0.236 0.849 -0.999 0.652 0.280
-0.124 -0.030 -0.391 1.654 -0.255 0.166

Table36.txt

0.483 -2.087 21.161 18.401 19.828 26.766 20.785 24.222
16.446 29.961 16.284 27.411 15.533 24.333 17.012
22.942 12.683 24.248 16.862 13.653 13.864
0.281 -2.345 -0.122 -0.759 0.491 0.121 -0.007 -2.762
0.959 -0.573 -2.102 0.074 0.111 0.846 0.690
0.906 1.020 1.389 0.744 1.154 0.843
1.071 -2.306 0.484 0.222 0.258 -1.776 -0.220 3.325
-0.352 -1.201 0.520 1.424 2.184 1.383 -1.527
2.065 -1.067 1.099 -0.284 -0.150 -0.284
0.114 -1.053 -0.022 -1.383 -0.479 -0.206 1.956 -1.369
-1.948 0.335 -0.623 -0.813 -0.995 -2.280 -0.650
1.060 -0.073 0.508 -1.304 -0.689 -1.496
0.201 -1.003 -1.590 1.308 -1.173 -1.530 -1.340 -0.671
-1.455 -1.690 -1.168 -1.585 0.410 -1.769 1.629
-1.765 -2.212 -1.559 -1.069 -0.431 -0.252
0.979 0.759 -0.199 -0.881 -2.270 -1.661 -1.432 -2.598
-0.289 0.678 -1.238 -2.152 -0.646 -1.012 -0.594
0.151 0.828 -2.944 0.077 -1.509 -0.878
0.956 -0.516 -0.972 -0.959 -0.820 -1.493 1.215 -1.662
-0.976 -1.469 0.064 -0.541 -0.183 -1.197 -1.552
-1.373 0.095 -0.712 -0.543 -1.538 0.921
0.684 -0.150 0.707 -0.664 -1.225 -2.667 0.527 -0.870
-1.311 -1.417 -1.212 -1.569 -0.798 1.983 -0.458
0.009 -1.534 -1.206 0.773 -2.219 0.525
0.135 1.499 -0.372 -1.445 -0.146 -0.978 -1.072 -1.117
1.086 -1.159 -1.262 -1.783 -0.430 -1.138 -0.760
-1.755 0.381 -2.527 -1.714 -1.774 -0.432
0.745 -1.584 -1.294 -0.638 0.144 -0.696 0.459 -2.087
-0.366 -0.525 -1.827 -0.239 -0.674 -0.981 2.063
-0.915 0.002 -0.414 0.341 -0.655 -0.409
0.086 0.820 -0.426 -0.191 -0.579 -0.477 0.329 -3.480
-2.789 -1.123 -3.034 -0.942 -0.632 -0.207 1.406
0.070 -1.165 -2.274 -0.958 -0.465 -0.411
-0.061 2.162 -1.120 -1.165 0.315 -1.166 1.044 -1.238
0.847 -2.185 -0.993 1.215 1.373 -1.040 0.373
0.009 -2.279 -0.275 -0.581 -1.189 -0.151
0.442 2.902 -3.013 0.299 -1.833 -1.003 0.064 -1.268
0.623 -1.495 -1.208 -0.389 0.237 -2.025 -0.354
0.804 -1.642 -2.745 -0.725 -0.339 -1.229
-0.926 0.751 -1.316 -0.667 -1.496 -2.085 -0.046 -0.983
-1.025 -0.196 -0.996 -2.209 0.756 -0.386 -1.737
-1.798 1.277 0.844 -0.730 0.332 1.030
1.568 0.560 -2.258 -1.313 -0.234 -1.317 -2.282 -2.012
-1.306 -1.767 -0.429 -1.030 0.185 -1.989 -1.268
0.467 -0.550 -1.547 -1.641 -1.166 -1.213
0.541 1.411 -0.960 -1.388 -1.314 0.685 -0.384 -2.643
-1.889 -0.660 -0.447 -2.204 -1.328 -1.778 -1.378
-1.667 1.031 -1.648 -2.665 -0.658 0.412

Table36.txt

0.240	-1.148	-1.514	0.181	-1.143	-1.134	0.025	-1.632
-0.876	-1.086	-1.166	-0.884	-0.591	-1.321	-0.995	
-1.171	-0.284	-2.402	-4.221	-0.658	-0.740		
-1.263	-0.192	-0.544	-0.949	-0.853	-1.318	-2.029	-1.334
-1.602	0.186	-1.310	-2.708	0.789	-1.047	-0.565	
-4.001	0.155	-1.629	-1.153	-3.093	0.227		
0.136	-1.557	-0.860	-3.035	-0.546	-1.418	-1.484	-2.144
0.036	-2.095	-0.738	-0.056	-1.816	-2.859	-1.457	
-2.496	-1.507	0.044	0.770	-0.706	-0.423		
0.568	-0.981	-3.713	-0.614	0.345	-2.076	-0.358	-0.944
0.820	-1.798	0.186	-0.395	-0.176	-3.653	-1.319	
1.385	-0.339	0.529	-0.817	-1.279	-0.281		
0.092	1.081	-0.771	-2.758	1.148	-2.122	-0.954	-1.784
-1.121	-1.726	-2.121	-2.589	-1.095	-2.433	-2.635	
-0.939	-2.115	-0.527	-0.275	1.064	-1.232		
0.838	0.988	0.252	-1.360	-0.509	-0.120	-1.760	-1.442
0.695	-1.050	-0.685	-2.259	-1.385	-1.086	0.325	
-2.055	0.715	-0.276	-0.791	-0.275	0.089		
0.240	-1.604	-1.567	-1.457	-2.744	-1.446	-1.086	-0.901
-0.756	-1.041	-4.046	-1.260	0.908	-2.558	-2.586	
-2.524	-1.398	-1.807	-1.000	-1.807	-0.623		
1.707	-0.245	-1.360	-1.231	-1.057	0.251	-0.034	-1.322
-0.093	-0.520	-0.191	-0.630	-0.276	-0.157	-0.707	
-1.017	-0.157	-0.214	0.023	0.015	0.029		
1.919	-0.668	-0.097	-0.228	-1.384	-2.040	-0.077	-1.210
-1.433	-0.890	-1.431	-1.888	-1.712	-0.730	-0.545	
0.003	-0.571	0.239	-0.073	1.608	-0.034		
-0.059	-1.483	-0.797	-0.277	-1.777	-0.092	0.088	-2.548
0.401	-0.530	0.221	-0.630	-1.073	-0.340	0.118	
0.233	-0.989	-0.447	0.184	-0.234	0.634		
1.069	-2.319	-0.673	-0.407	-2.295	1.101	-0.569	-1.183
-1.029	-2.070	-1.660	-0.626	-0.680	-1.377	-0.375	
-0.973	0.237	-1.274	-2.187	-0.464	-0.911		
-0.285	-0.202	-0.750	-0.408	-0.187	-0.766	-0.022	0.075
0.500	-2.563	-0.950	-1.537	0.127	0.288	0.427	
-1.198	-1.721	-0.331	-0.877	0.385	0.370		
-0.949	-0.199	-0.107	-1.438	-0.238	-2.770	0.323	-0.851
-0.604	-1.106	-0.402	-1.179	0.179	-0.854	-0.327	
1.527	-0.478	-0.541	-0.661	-0.359	-1.373		
0.062	-0.360	-1.518	-0.319	0.075	-1.761	-0.084	-0.307
-0.860	-1.105	-2.119	-2.172	-0.455	-2.715	0.884	
-2.031	-1.683	-0.713	-1.855	1.253	0.096		
-0.726	0.336	-0.037	-0.960	-1.058	-0.732	-2.439	0.213
-3.668	-0.769	-0.397	-1.897	-1.527	-2.075	-0.125	
-1.072	-2.638	-0.294	-0.980	-1.986	-1.317		
0.757	-1.290	1.095	-1.864	-1.693	1.544	-0.485	-0.142
0.402	0.034	-2.468	-3.863	-1.450	-2.674	1.063	
0.264	0.019	-0.970	-1.470	0.146	0.068		

Table36.txt

-0.632	-1.617	-1.544	-0.537	-1.514	-1.297	-1.281	0.188
-2.315	-1.401	-1.069	-2.907	-0.695	0.305	-0.538	
-1.274	-2.263	-1.466	-0.974	0.155	-1.327		
-1.297	-2.690	0.265	-1.158	-0.063	-2.144	-0.943	-1.167
-0.316	-1.704	-2.733	-2.535	-0.208	0.206	-1.774	
-1.548	-0.163	0.328	-0.689	-0.503	-2.417		
-0.126	-0.505	-0.728	-0.498	-2.074	-2.090	-1.004	-2.350
-2.115	-1.836	-1.361	-2.572	-1.056	-0.065	-1.114	
-0.880	-1.573	-1.622	-2.209	0.439	-0.555		
1.773	-1.133	-0.654	-0.240	-1.544	-1.680	0.321	0.420
0.241	-0.217	0.270	-0.862	0.507	0.482	-1.790	
-1.360	-1.220	0.007	0.493	1.258	-0.821		
-0.359	-0.601	-0.306	-0.722	-1.897	-0.637	-0.451	-0.777
-1.458	0.579	-0.939	-2.036	-1.046	-2.965	0.851	
-0.757	0.080	-1.064	1.007	-0.579	-0.060		
0.399	-1.858	0.098	1.369	-0.693	-1.001	-0.737	-1.205
-0.187	-1.886	-2.542	-1.027	0.203	-2.237	-0.496	
-3.094	0.746	-0.650	0.344	1.060	-0.748		
0.121	-1.487	-0.136	2.326	-1.768	-1.273	-1.691	-0.546
0.551	-0.209	-2.083	0.757	-0.025	-1.303	-0.090	
-0.552	1.836	-0.358	-0.225	-1.092	0.335		
1.998	-0.826	-0.200	-0.159	0.250	-2.223	-1.615	-1.527
-0.135	-0.916	-2.966	-1.546	0.367	-0.625	1.524	
1.459	-0.811	-1.643	-2.900	-0.799	-1.139		
0.153	0.088	-1.604	-0.356	-0.577	-1.572	-1.983	-1.974
0.001	-2.051	-0.963	-1.765	0.711	-1.277	0.590	
0.138	-0.746	-1.156	-0.949	0.053	-1.238		
0.230	-2.281	-0.249	1.436	-0.647	0.395	-0.661	1.020
-1.026	-3.425	-1.911	-0.289	-0.869	0.389	-1.023	
-1.858	-0.364	-1.050	-1.015	-0.038	-0.324		
0.540	-0.500	-1.897	0.522	-0.424	-2.069	-0.316	-1.117
-0.926	-1.152	-0.339	-1.315	1.961	-0.663	-1.187	
-0.424	0.454	-0.895	-1.314	0.747	-2.431		
1.503	-3.830	-1.013	-3.415	0.302	-0.889	-0.707	-0.490
-1.566	-0.258	-1.789	-1.229	-1.074	0.635	0.245	
-2.112	-1.503	-1.086	0.926	-0.571	-1.050		
0.104	-0.415	-0.632	-1.143	-1.858	-1.150	0.020	-0.389
-0.710	-0.616	-1.460	-0.917	-0.776	-2.464	-1.352	
-0.320	-0.254	0.207	-0.843	-1.988	0.335		
-1.445	-1.890	-0.578	-0.761	-0.401	-2.492	-1.593	-0.555
-1.275	-0.836	-0.197	-2.037	-0.657	-1.666	-0.400	
1.400	-0.841	-0.808	0.775	-1.675	-0.246		
0.570	-0.089	-0.037	-0.838	-1.668	-2.326	-0.731	-2.936
0.095	-0.151	-0.264	-1.281	0.054	-1.209	-2.210	
0.727	-0.238	-1.394	0.118	-0.130	0.293		
1.467	1.591	-2.365	-0.158	-0.883	-1.877	-0.497	-0.926
-3.366	-0.789	-1.455	-1.454	-1.337	-0.968	0.159	
-0.259	-1.572	-1.890	-0.221	-1.583	0.123		

Table36.txt

```
0.852      -0.924     -1.030     0.785      0.176      -1.775     -0.664     -1.845
    -1.522     -1.010     -0.601     -2.226     -1.099     -1.524     -1.755
-1.184     0.149      -0.086     -0.412     -1.232     -0.370
1.490      -1.057     -2.018     -1.952     -0.853     -1.995     -2.995     -2.607
    -0.873     -1.361     -1.451     -0.985     0.591      -1.515     -0.004
-2.938     -0.473     -2.398     -0.866     -1.703     0.649
0.325      -1.686     0.588      0.253      0.747      0.154      0.898      -0.462
    -0.719     -1.436     -1.079     -0.130     0.284      -2.952     -1.065
-1.366     -0.937     -0.514     0.988      0.548      -1.137
0.384      -1.362     0.460      -1.485     0.487      -0.749     1.215      -2.161
    -2.803     -0.154     0.194      -0.012     -0.926     -2.888     0.272
0.112      0.111      -0.783     -0.832     -1.366     0.698
1.135      -1.359     -0.114     0.008      -0.339     -1.327     0.300      -1.891
    -0.320     -1.523     -1.206     -1.675     -0.402     0.309      -0.823
-0.464     -0.633     0.136      -2.111     0.232      -0.086
-0.474     -0.534     -1.918     -1.025     -3.522     -0.798     -0.669     -2.896
    -1.533     -0.655     -1.870     -1.525     -0.579     -2.060     0.104
0.116      -0.950     -0.208     3.167      -1.573     1.145
1.046      -1.410     -0.883     -1.554     0.817      -1.815     -0.861     0.094
    -2.254     -2.740     -1.285     -1.619     -0.824     -3.195     -1.048
-1.645     -0.726     -0.491     -1.938     -1.605     -0.444
-0.383     -1.576     -0.968     0.090      -0.217     -2.058     -2.104     0.004
    -1.501     -0.548     -2.155     -2.396     0.005      -2.438     -1.091
-1.581     -1.050     0.345      0.414      0.211      -0.324
-0.428     -2.231     0.371      -1.349     -0.191     -1.916     -1.593     -1.916
    -0.354     -2.399     0.020      0.098      1.468      -1.449     -0.438
0.119      -1.341     -4.380     0.606      0.535      -1.252
-0.237     -1.966     -2.323     -1.271     0.091      -0.156     -0.562     -0.696
    0.775      0.185      -0.668     -1.433     -0.984     -1.396     -0.324
0.481      -0.081     0.181      -0.999     -0.049     -1.188
0.535      0.332      -2.093     -1.360     -0.374     -1.890     -1.818     -0.554
    -1.076     -1.738     -0.321     0.414      -0.874     -2.038     -2.347
-1.191     -0.955     -0.960     -3.468     0.062      -2.868
0.608      -0.727     1.574      -0.946     -1.157     -1.782     -1.023     -0.330
    -0.990     -1.059     -0.148     -1.098     -0.799     -0.428     -1.234
1.702      -0.568     -1.191     0.065      -1.060     -1.303
-0.039     -0.514     -1.347     -1.759     -2.196     -0.062     -1.064     -1.436
    -0.554     -2.688     -2.225     -0.832     -0.133     -2.190     -0.976
-0.206     1.063      -1.440     -0.189     -0.565     -0.508
0.369      -1.303     -0.773     -2.463     0.167      -1.740     -0.199     -1.110
    -0.776     -1.910     0.582      -1.921     -0.223     -0.032     -0.579
0.152      -0.113     -0.096     0.322      0.780      0.219
-0.001     -0.037     -1.048     -0.061     -0.876     -2.172     0.933      -0.297
    -0.903     -1.483     0.907      -1.779     -0.283     -0.975     -1.125
0.777      -0.081     -1.479     -1.096     -1.095     -0.178
0.183      -1.299     -0.944     -0.648     -2.420     -1.474     -0.361     -2.377
    -1.343     -1.025     -0.701     -1.259     0.105      -0.454     -1.967
1.127      -0.541     -0.805     -0.908     -2.338     -0.836
```

Table36.txt

-0.227 -0.131 -2.439 -0.165 -1.673 0.215 0.578 -0.515
-2.815 -0.597 -1.065 -2.334 -1.261 -1.659 -1.105
0.161 -1.137 -1.150 -0.747 -2.460 1.430
0.535 -1.783 -0.948 -2.671 -0.370 -1.372 0.225 -1.293
-1.533 -2.765 -1.503 -1.262 0.946 -1.670 -0.459
-2.375 0.258 -1.205 -0.333 -0.844 0.412
0.427 -2.821 -1.919 -0.586 0.487 -2.079 -2.004 -1.021
-2.495 -1.285 -0.870 -1.024 -2.673 -1.974 0.562
-0.991 0.592 -3.486 1.116 -1.011 -1.344
1.279 -2.726 -0.628 -0.180 0.181 0.279 0.418 1.066
-0.671 -2.022 -0.991 -1.176 -0.719 -1.837 -0.069
-1.599 -0.048 -0.754 1.583 0.447 0.235
-0.766 -2.418 -0.804 -0.686 -1.451 -2.341 -0.626 -0.125
-0.172 -1.197 -0.948 -1.968 -0.944 -2.123 -0.294
-0.100 -0.539 -1.468 -0.043 -0.675 -0.835
-0.020 -2.169 -3.630 -0.426 1.690 0.498 -1.129 -1.446
-1.304 0.637 -1.006 -1.385 0.124 -2.003 -1.091
-0.449 -0.448 -0.845 0.289 -0.897 -2.012
-0.816 -1.694 1.523 -1.687 -2.153 -1.177 -1.696 -1.251
1.788 -0.333 -1.739 -1.382 0.717 -1.737 -1.437
0.869 -0.335 0.416 -0.126 -2.206 0.638
1.012 -1.515 -2.394 -0.620 -1.248 -1.978 -1.029 -1.714
-2.233 -1.552 -1.179 0.050 0.361 -0.735 -2.203
-0.438 -1.568 -1.188 -1.520 0.920 -1.017
0.298 -0.378 -0.475 1.487 -0.836 -2.091 -1.680 -0.840
-0.529 -2.762 -0.944 -1.575 -0.045 -0.264 -0.487
-1.861 1.504 -2.492 0.187 -1.588 0.460
-0.580 0.246 -2.071 -1.887 1.128 -2.786 -2.537 -0.619
-0.812 -1.530 -1.521 -1.547 -1.144 -0.857 -1.100
-0.345 -1.729 -2.421 2.047 -1.371 1.434
0.213 -3.029 -0.504 -1.216 0.040 -1.603 0.036 0.608
-0.223 -0.142 -2.315 -1.607 -0.272 -1.924 -2.041
-2.086 0.374 -0.470 -2.663 0.694 0.671
0.031 -2.271 -0.083 -0.960 -0.408 -0.036 0.738 -2.458
0.374 -0.887 -0.966 -1.793 -0.150 0.067 0.573
-0.062 -0.833 -1.487 -2.683 -0.783 2.321
0.964 -0.889 1.271 0.353 -1.293 -1.490 0.892 0.908
0.179 -0.808 0.682 -0.513 -3.318 -1.346 -1.268
-2.250 -1.692 0.561 -1.997 -0.451 -2.206
1.515 -0.888 0.348 -1.251 -0.239 -1.113 -1.739 -2.185
-0.250 -1.482 -0.762 -1.038 0.801 -2.746 -0.254
-1.443 -2.143 -2.627 0.642 0.355 0.385
0.274 -1.185 0.129 -0.409 -0.278 -1.023 -1.136 -0.090
0.278 -2.013 0.329 0.433 -0.681 -0.991 -1.295
-2.547 -0.685 -1.256 -1.187 -3.555 -0.393
0.153 0.397 -1.308 -0.503 -0.248 -1.696 -1.576 -1.248
-2.703 -1.031 -2.765 -2.945 -0.112 -1.672 -1.761
-1.766 -0.720 -1.073 0.213 -1.879 0.433

Table36.txt

0.050	-0.159	-0.980	-1.044	-0.683	-1.825	0.481	-1.860
-1.239	-2.277	-2.298	-1.405	-1.219	-0.097	-1.374	
-1.533	0.457	-0.809	-1.140	-2.297	-0.446		
0.948	-1.370	0.575	-0.527	-1.875	-2.309	-2.154	-3.023
-0.214	-0.576	-0.027	-1.324	-0.832	-1.125	0.115	
1.053	-1.158	-1.547	-2.330	-0.377	1.109		
0.802	-1.979	-0.014	-0.425	-2.023	-0.790	-0.568	0.838
-1.009	0.348	0.004	-0.335	-2.111	-0.285	-0.444	
-2.052	-1.524	-2.213	-1.127	-0.663	-0.958		
-0.425	0.069	-0.873	-1.826	-1.238	-0.615	0.266	-3.342
-0.903	-0.605	0.370	-2.586	-1.365	-1.129	-1.657	
0.777	-1.775	-0.259	8.270	0.046	-0.888		
0.520	-2.900	-0.456	-1.201	0.028	-1.382	-2.897	-1.136
0.602	-1.212	-0.573	-1.134	-1.811	-1.111	-0.321	
-1.498	1.945	1.107	1.647	-1.299	-0.299		
-1.011	-2.532	-0.536	-0.722	-1.552	-1.122	-1.645	-2.411
-1.084	-1.187	-2.073	-2.005	-2.084	-0.351	-0.312	
0.771	2.298	-0.636	-0.717	-1.585	-2.586		
-0.193	-1.721	-1.102	-2.331	-0.992	0.317	1.081	-0.264
-0.426	-1.509	-1.961	-0.755	-1.352	-1.758	-2.410	
-0.228	-1.774	-1.300	-1.065	-0.832	0.316		
-0.271	-0.851	-1.301	-0.364	0.227	-1.419	-1.713	-2.447
-2.265	-2.057	-2.207	-0.078	-1.534	-1.150	-0.680	
-1.013	0.839	-0.874	-0.300	-2.132	-1.994		
0.424	-2.145	-0.755	-0.951	-0.361	-1.295	0.458	-3.227
-1.326	-3.222	-1.135	-1.487	-0.094	-1.887	-1.138	
-0.037	0.011	-0.128	0.592	0.040	-0.867		
-0.672	-0.543	-0.837	-1.608	-0.855	-3.086	-0.503	-2.013
-0.396	-1.640	-1.962	0.647	-1.984	-0.909	-0.376	
0.578	0.544	-2.825	-0.262	0.411	0.076		
0.313	-2.354	0.491	-0.594	-1.007	-2.006	-2.359	-1.313
-0.712	1.655	0.560	0.551	1.513	-1.045	-1.995	
-1.465	-0.751	-0.101	-1.022	-1.319	1.432		
1.154	-1.488	-0.903	2.058	-2.186	-1.153	0.497	-2.679
-0.338	-1.754	-1.916	-0.332	-2.006	-3.102	0.788	
-3.119	-0.731	-1.730	0.601	-0.504	-0.462		
-0.523	-1.325	-0.386	-0.811	0.019	-2.074	-2.481	-1.720
-1.284	-1.034	0.395	0.208	-3.042	-0.205	-0.274	
0.112	-0.944	-0.954	0.131	0.070	-0.022		
-0.074	-0.099	-1.626	-3.858	-1.052	-2.156	-0.674	-0.973
0.276	-0.898	-1.750	-0.471	-0.832	-2.326	-0.117	
-1.730	-0.404	-0.017	-2.038	-1.396	-1.931		
0.058	0.343	-1.103	-2.406	0.443	-1.733	-1.765	-2.022
-0.937	-2.013	-1.275	-0.540	-2.561	-4.614	0.217	
-3.638	-1.833	-0.861	1.338	-2.462	0.132		
-0.023	-1.818	0.265	-0.393	-0.352	-0.588	-2.278	0.685
-1.319	-1.408	-1.024	0.693	0.452	-1.360	-0.937	
-0.365	0.000	-0.170	-1.119	-0.563	0.167		

Table36.txt

```
0.374      -1.045     -2.160     -0.726     -0.225     -0.712     -0.946     -0.331
    -1.295     -1.734     -0.941     -0.490     -2.076     -0.780     -0.421
0.519      0.061      -1.129     -1.648     -0.790     -2.318
0.794      -2.442     -0.374     -1.219     -0.489     0.029      0.426      -2.404
    -1.176     -1.456     -1.023     -1.510     0.643      -1.746     -0.588
-0.257     1.366      -1.961     -2.776     -1.703     -0.524
-0.316     -0.882     -0.836     -0.978     -1.959     -1.616     -0.431     -2.442
    -1.306     -3.144     -1.352     -2.901     0.679      -2.407     -1.194
-0.208     -2.812     -0.394     -0.746     -0.681     -0.996
-0.188     -2.254     -1.339     -1.659     1.063      -0.544     -0.201     -1.887
    -1.014     0.023      -0.712     -1.128     1.768      -0.499     -2.046
-0.414     0.400      -1.179     -1.392     0.227      -0.224
-0.850     -1.808     -1.453     0.022      -1.092     -1.032     -1.414     -0.321
    -0.361     -0.049     -0.834     -2.202     -1.917     -2.478     -1.729
-0.990     -0.792     -2.311     -1.307     -0.836     -1.453
0.169      -2.307     -0.336     -0.271     -1.810     -0.178     -1.724     -1.154
    -1.858     -2.232     -1.837     -1.747     -1.034     -0.836     -0.879
0.939      -0.319     -2.010     -1.323     0.081      -1.096
-0.165     -1.473     -0.330     -0.545     -0.496     -0.916     -0.937     -1.637
    -1.644     -1.818     -0.180     -1.817     -1.671     -0.684     0.038
-1.761     -0.010     1.104      0.499      -1.018     -0.512
-0.453     -2.325     -0.744     -0.012     -1.307     -1.924     -2.764     -0.969
    -1.834     -1.563     -1.687     -0.555     -0.107     -2.568     -1.022
0.814      -0.718     -1.639     0.361      -0.628     -0.146
0.812      -0.755     -1.748     -0.986     0.186      -0.521     -0.381     -0.585
    -0.145     -1.105     -1.064     -2.224     -0.755     -2.607     -0.892
0.119      -0.501     0.554      0.514      -0.321     -1.069
0.162      -3.057     -1.587     -2.509     -0.141     -1.523     0.240      -1.185
    -0.121     -1.714     -0.170     -0.389     -0.217     -1.187     -2.492
-0.142     -0.417     0.031      -0.588     -0.570     -1.511
-0.198     -1.177     -0.111     -2.096     -2.123     -1.561     -1.137     -1.522
    -0.435     -0.022     0.314      -2.569     -0.449     -0.408     -0.198
-1.014     -0.388     -0.326     -0.195     0.101      1.039
1.161      -0.933     -0.960     1.140      0.086      -0.434     -3.607     -1.256
    -0.699     -2.309     0.164      -1.516     -0.666     -1.892     -0.645
0.090      -1.365     0.205      -1.341     -0.827     -1.956
1.237      0.269      -0.868     -1.188     0.333      -2.046     -1.242     -2.865
    -1.216     -0.359     -0.139     -2.587     -1.640     -1.666     -2.686
-2.800     -0.481     -3.597     -2.513     -1.288     -1.958
1.355      -2.275     -2.457     -1.728     0.084      -2.618     -0.408     -1.729
    -1.247     -1.116     -0.036     -0.848     -2.708     -2.229     -1.702
-0.564     -0.492     -2.101     0.035      -0.142     -1.311
-0.540     -2.057     -1.399     0.532      -0.097     -2.073     0.294      -1.512
    -1.735     -0.052     0.896      0.023      -2.363     -1.150     -0.810
-2.378     0.246      0.239      -0.364     0.835      -1.289
0.310      -2.956     -1.525     -0.352     -2.889     -2.577     -0.628     -0.736
    0.677      -2.198     -0.301     -1.409     0.343      -1.395     -1.466
0.261      -0.974     -1.024     -0.612     -1.418     -1.256
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Table36.txt

-0.945	-2.227	-0.860	-0.712	-1.403	-2.593	-0.353	-1.373
-1.382	-0.922	-1.466	-0.526	-0.835	-0.036	0.193	
-3.967	1.947	-1.818	0.360	-1.003	-1.452		
-0.200	-1.582	0.113	0.591	-0.938	-1.107	-0.749	-2.010
-1.234	-3.463	0.676	-0.909	-0.928	-0.400	-1.280	
-0.070	-1.409	0.826	-0.937	-0.233	-1.919		
1.085	-1.483	-1.596	-0.843	0.623	-0.033	-2.059	-0.849
-1.461	-0.125	-1.042	-1.053	0.590	-1.877	0.013	
-2.251	-1.687	-1.288	-0.873	1.852	-0.651		
0.588	-1.088	-1.398	0.853	-1.799	-2.332	-1.547	-1.514
0.519	-1.544	-2.177	-1.060	-0.978	-1.525	-2.015	
-3.098	-1.720	-0.540	-1.458	-1.501	-0.149		
-0.125	-1.273	-2.871	-0.098	-1.759	-1.426	-2.825	-0.916
-1.731	-0.758	-0.412	-1.105	-0.843	-0.399	0.388	
1.216	-1.490	-1.815	0.401	-1.528	-2.332		
0.297	-1.659	-1.892	-1.132	-3.972	-0.597	-2.233	-3.050
-2.094	-3.225	-1.049	-0.822	-1.305	-2.354	1.511	
0.594	-0.528	-2.521	-0.146	-1.855	-0.119		
-0.593	-3.339	0.347	-1.509	-0.207	-2.565	0.416	-0.796
0.584	-3.458	-0.438	-0.421	-0.749	-0.136	-3.691	
-1.806	-0.080	-1.097	-1.269	0.578	-1.880		
1.038	-1.183	-1.247	-1.849	-0.333	-3.169	-0.300	0.141
-2.134	-0.829	-1.290	-1.705	0.424	-1.760	-1.316	
-0.880	-0.068	0.369	-0.390	-0.983	-0.205		
0.537	-1.705	-0.882	0.035	0.201	-1.182	-0.992	-1.275
-0.523	-1.531	-0.759	1.026	0.014	-0.718	-0.448	
-0.388	-1.175	-1.350	-1.337	0.583	0.573		
0.533	-2.015	-1.581	-0.955	0.859	-3.067	-1.369	-3.404
-1.896	-0.362	-2.289	-0.344	0.610	-0.729	-1.335	
-0.242	-0.820	-2.418	-0.793	-0.829	-1.049		
-0.625	-1.704	-1.333	-0.476	-2.429	-1.422	-0.132	-1.538
0.613	-3.157	0.906	-1.761	-0.035	-0.301	1.013	
-2.168	-0.341	-0.960	-0.037	-2.923	0.768		
0.679	-3.017	-0.169	0.144	-1.891	-1.932	-2.905	-0.878
-1.869	-1.116	-0.748	0.205	-2.213	-2.096	-0.816	
0.152	-1.874	0.880	0.392	0.234	-0.020		
0.280	-1.843	0.342	-2.360	-1.633	-0.451	-1.128	-1.735
-1.743	-0.409	-0.970	-1.483	-1.673	-2.562	0.204	
-2.794	0.246	-1.644	-0.919	-1.332	-0.707		
0.456	-0.108	-4.640	-0.958	-0.775	-1.029	0.149	-3.102
-0.195	-1.434	-2.024	-1.873	-1.543	-4.096	-0.216	
-1.223	0.004	-1.458	-1.108	-1.178	0.431		
0.427	-1.956	-1.838	-3.450	0.858	-1.650	-2.956	0.400
-1.091	-0.437	0.271	-1.114	-2.006	-2.317	-1.354	
-0.420	-0.775	-0.117	-3.302	-1.089	-2.546		
0.548	-3.196	-1.080	-0.328	-1.155	-0.513	-0.734	-1.380
-0.481	-2.257	0.543	-2.416	-1.313	-1.671	-0.087	
-1.863	1.040	-0.265	-1.472	-0.531	-0.882		

Table36.txt

-0.377	-3.117	0.664	-1.321	-0.256	0.187	-1.985	0.572
-1.839	-0.181	0.385	-0.212	-0.544	-2.036	-0.324	
0.020	-1.694	-0.844	-0.887	-0.713	-2.294		
1.113	-2.194	-1.806	-1.821	-1.878	-3.200	-1.763	-2.000
-1.347	-4.107	-2.947	-1.540	-2.382	-2.274	-0.949	
-2.126	-1.310	-0.028	0.215	-1.019	-1.529		
0.413	-3.273	-1.673	0.577	-1.005	-0.099	-1.408	0.657
-1.244	-0.395	-2.513	0.211	1.462	-2.790	-1.502	
-1.950	-0.895	0.332	-0.631	-0.097	-1.026		
-0.161	-0.739	0.188	-0.694	0.004	-1.197	-1.642	-1.971
-1.487	-1.115	-0.410	-0.952	-0.567	-1.813	-0.301	
-1.602	-0.630	-2.440	-0.307	-0.761	-0.309		
0.321	-2.101	0.647	-2.341	1.032	-1.310	-0.491	-1.218
0.733	0.148	-1.000	-0.649	-0.908	-2.222	-0.504	
-1.253	-0.042	-1.240	-0.777	-1.566	-0.491		
-0.849	-0.954	-0.946	-0.428	-2.009	-1.856	-1.430	-1.402
0.570	-0.590	-0.668	-3.486	-1.306	-2.409	0.625	
-2.425	-1.465	-0.929	-1.278	0.343	-1.246		
0.508	-1.298	-1.610	-1.399	-1.189	-0.560	0.294	-3.115
0.179	-2.218	0.707	-1.929	-1.909	-0.444	-2.767	
-0.727	-2.046	-1.123	-1.481	-0.880	-0.699		
1.924	-2.180	-0.097	-0.114	0.309	-2.468	-1.588	-2.346
-0.883	-1.735	0.014	-1.553	-0.882	-0.911	-1.366	
-2.085	-0.541	-1.897	-0.013	-2.600	-1.966		
-0.063	-2.184	-2.747	-0.841	-0.385	-2.412	-0.728	-1.890
-0.402	-1.472	1.040	-2.553	-0.682	-0.322	0.078	
-1.194	-1.927	-3.700	1.400	-1.025	-0.734		
0.943	-0.254	0.396	-1.717	-0.719	-0.948	0.048	-0.859
-0.191	-1.339	-0.728	-0.809	-0.037	0.054	-0.529	
-2.834	-0.674	-1.326	-1.806	-1.841	0.235		
-0.667	-2.142	-0.796	-1.781	-1.643	-1.908	-0.602	-1.006
-2.064	-1.974	-2.007	-1.542	-2.742	-1.429	-0.512	
-1.026	-0.041	0.134	-1.293	-2.651	-0.340		
-1.170	-1.593	-1.277	0.082	-2.181	-2.452	-0.896	-1.984
-2.038	-0.375	-0.104	-1.730	-0.445	-2.361	-2.053	
-1.063	0.417	-1.579	-1.037	0.113	0.371		
1.571	-1.158	-1.873	-0.299	-1.727	-2.794	-0.230	-0.040
-2.706	-2.136	-1.152	-2.245	-1.289	-1.418	-0.663	
-0.945	-0.670	-1.303	0.272	-3.087	-1.744		
0.121	-0.610	-1.210	-2.462	-0.313	-2.288	-1.581	-0.963
-1.955	-2.986	-0.399	-2.989	-2.507	-1.362	-0.867	
-2.494	-1.308	-2.644	-1.308	-1.470	-0.963		
0.270	-2.528	-0.180	-0.914	-1.303	-1.826	-0.772	-0.834
-2.310	-1.719	0.425	0.321	0.590	-3.325	-0.658	
0.399	-1.296	-0.411	0.441	-0.117	-0.812		
1.134	-0.276	-0.863	-2.271	-0.617	0.713	-1.194	0.984
-0.513	-2.046	-1.318	-0.536	-1.127	-2.290	0.301	
-1.485	0.872	-0.114	-0.008	-1.237	-1.100		

Table36.txt

-0.249 -3.573 -0.732 -0.758 -0.971 -1.146 -1.605 -1.189
0.626 0.087 0.179 -1.622 -0.726 -0.254 -2.598
-1.844 0.292 -1.528 -0.527 -2.372 -2.318
-0.720 -1.856 -1.404 -0.038 -0.672 -1.325 -1.650 -2.094
-1.824 -2.288 -1.378 -0.551 -0.975 -2.174 -0.995
-0.377 -0.151 -1.461 -1.900 -0.601 -0.039
-0.874 -0.903 -1.788 -3.162 -0.457 -0.701 -1.955 -2.672
-0.182 -0.217 -0.454 -1.829 -1.516 -2.137 -0.415
-1.928 -0.957 -1.990 0.686 -1.156 -2.604
0.659 -0.741 -1.465 -1.945 0.182 -1.299 -1.161 -3.606
-1.056 -1.507 0.400 -1.948 -0.947 -2.139 -1.094
-0.059 -1.010 -1.976 -1.442 -1.729 1.632
0.683 -0.522 -0.940 -1.575 -0.445 -1.623 -1.663 -1.735
0.710 -0.004 -1.211 -0.520 0.074 -0.122 0.979
0.102 -1.560 -2.388 -0.342 -1.387 -0.151
-0.855 -1.833 -1.104 -1.353 -1.165 -1.126 -0.717 -1.127
-0.619 -2.247 -0.532 -2.285 -0.248 -0.450 -1.376
-3.153 -1.075 -3.199 -1.226 -0.704 -1.905
0.124 -0.892 -1.944 -1.474 0.278 -0.639 -2.844 -1.048
-1.343 -0.975 -0.634 -0.950 0.713 -2.271 -1.023
-1.584 -2.261 -1.053 0.017 -1.303 0.134
-0.729 -1.083 -0.971 -2.072 -1.375 -1.638 0.067 -0.622
-0.370 -0.919 -1.310 -0.986 -1.632 -2.342 0.795
-1.968 -0.375 -1.654 0.977 0.480 -0.060
0.223 -0.764 -0.735 -0.807 -1.690 -2.136 0.218 -3.007
-0.901 -0.365 -0.401 -2.114 -2.953 -0.146 0.463
0.954 -0.155 -1.431 -1.344 -1.634 -0.523
-0.831 -0.819 -1.890 -1.071 -1.750 -1.695 -1.827 -1.678
-0.608 0.089 -0.839 -2.393 -1.610 -2.411 -1.140
-1.159 -1.831 -1.796 -0.395 -0.965 -0.158
0.020 -1.513 -1.087 0.265 -1.073 -1.973 0.088 0.550
-1.105 -0.833 -0.721 -0.767 -0.596 -1.820 0.198
-0.894 -1.422 -1.118 -0.255 0.460 -1.089
-0.623 -2.693 -1.235 -0.977 -0.761 -0.788 -1.034 -1.544
-1.988 0.189 -1.173 -1.731 -1.051 -2.409 -0.937
-2.453 1.208 -0.366 -1.175 1.028 -1.572
-0.333 -1.897 0.819 -1.440 0.155 -1.168 -0.793 -1.675
-0.882 -0.912 -2.526 -3.612 -1.012 -2.452 -1.092
-0.163 0.888 -1.364 0.578 0.670 -1.255
0.680 -0.853 -2.189 -0.658 -0.954 -2.132 -0.842 -2.574
0.308 -1.259 -0.403 -1.202 -0.755 -0.830 -1.680
-2.199 -2.071 -0.997 -1.596 -0.870 -0.430
-0.779 0.342 -1.482 -0.689 0.405 -2.797 -0.793 -0.573
-1.037 -0.005 -0.994 -1.475 0.672 -0.679 -0.377
-1.577 -1.259 -0.988 0.392 -1.442 0.761
0.251 -2.305 -0.874 1.078 -0.011 -0.875 0.329 -0.738
-1.866 -2.339 -0.422 -1.541 -0.370 -2.225 -1.262
-2.106 1.754 -1.882 -0.754 -0.166 -2.229

Table36.txt

0.407	-3.010	-2.833	-1.702	-1.968	-1.420	-2.583	-1.649
-1.290	-3.726	-1.006	-1.043	-0.651	-1.751	-1.324	
-0.811	-0.218	-0.232	-0.188	-1.393	-1.775		
0.869	-1.677	0.747	0.528	-0.564	-1.429	0.651	-0.104
-2.258	0.813	-0.984	-1.716	0.711	-1.959	-1.724	
-0.957	-0.946	-1.043	-1.943	-0.555	-1.942		
0.121	-1.966	-1.358	-1.145	-0.865	-0.656	-2.113	-2.703
1.223	-1.666	-1.643	0.180	0.716	-4.472	-0.541	
-1.625	-2.422	-2.430	-1.069	-0.344	-0.031		
-0.050	-1.415	-0.479	-1.230	-2.593	0.090	-0.622	-0.449
-1.336	-2.202	0.487	-2.224	-1.426	-0.442	-1.317	
-3.064	-0.714	-0.123	-0.641	-2.420	-0.711		
0.634	-0.143	-0.351	1.415	-2.479	-1.707	0.441	-2.884
0.160	-1.024	-2.050	-1.196	0.396	-0.115	-0.869	
-0.748	-0.162	-2.421	-0.348	-0.518	0.572		
0.062	0.078	-1.496	0.000	-3.446	-4.830	0.076	-1.297
0.053	-0.941	-0.744	-0.030	-0.713	-2.406	-1.799	
-0.445	-0.382	-0.505	-0.580	-1.484	0.469		
-1.146	-0.326	-2.654	-1.340	-0.293	-3.306	-1.674	-1.512
-2.814	-1.512	0.115	-0.885	-1.280	-0.571	-1.274	
0.743	-1.258	-2.016	-0.077	0.438	-1.458		
-0.410	-1.327	-2.080	-0.038	-1.034	-1.957	0.199	-1.171
-0.921	-2.311	-2.293	-2.304	-0.142	-1.572	1.308	
-1.918	-0.654	-0.203	-0.266	0.247	0.835		
1.980	-1.503	-2.089	-1.464	-1.514	-1.839	-0.069	-2.408
-1.359	-1.939	-1.329	-0.866	-1.419	-1.597	-2.106	
-2.630	-0.780	-2.552	-1.441	-0.818	-1.397		
1.221	-1.579	-1.084	-1.753	-0.957	-2.258	0.449	-1.999
0.382	-0.111	-1.319	0.412	-0.211	-0.982	-0.434	
-1.769	-1.100	-0.678	-0.222	-0.080	-0.265		
0.161	0.222	0.411	-3.799	-3.232	-1.521	-1.225	-0.158
-1.599	-1.787	-0.092	-2.073	1.086	-2.115	-2.646	
-1.671	-0.649	-0.847	-1.303	0.052	-0.160		
-0.159	-2.719	-1.084	-2.169	-2.008	-0.983	-2.028	-1.312
-0.961	-0.625	-0.599	-2.796	1.439	-2.125	-0.612	
1.245	-1.310	-1.754	-0.059	-0.978	-1.242		
-0.085	-0.773	0.554	-1.750	-0.007	-0.899	-1.450	-3.492
-2.743	-2.415	1.228	-0.542	-0.319	-1.063	0.308	
0.552	-1.348	0.892	0.336	0.213	-0.423		
0.908	-0.081	-2.236	-2.248	-0.206	-0.729	-0.475	-2.873
-0.368	-4.160	-1.025	-2.242	-1.544	-1.454	-2.975	
-1.523	0.815	-3.716	-0.860	-0.969	-1.708		
0.320	1.469	0.843	1.118	-1.759	-2.030	1.419	-2.444
-0.934	-1.173	0.328	0.288	-0.645	-1.149	0.249	
-0.417	-0.942	-1.084	-0.379	0.585	-0.926		
0.143	-1.103	-0.507	0.266	-0.168	-2.213	-0.857	0.420
-1.343	-3.337	-1.525	-1.473	0.243	-2.892	-1.739	
-2.433	-1.266	0.615	-0.918	-0.148	-3.245		

Table36.txt

-0.005	-1.400	-1.995	-0.793	0.003	-4.038	0.113	-0.642
-0.528	-3.216	-1.167	-3.686	2.688	-1.746	-0.858	
-0.155	-0.451	3.368	-2.290	-3.396	0.199		
0.085	-1.539	-2.021	-3.121	-0.829	-1.745	-1.974	-0.358
-1.638	-1.197	-1.682	-1.723	-0.905	-1.650	-1.404	
-2.275	0.857	-2.959	-1.081	-0.524	-2.282		
-0.547	-1.119	-1.609	-1.643	-1.385	-3.793	1.263	-1.559
0.672	-2.308	0.719	-1.119	-1.186	-1.360	-0.342	
-0.598	1.476	0.044	-0.804	-0.174	0.964		
-0.464	-0.208	-0.557	-2.139	-1.236	-0.695	-1.175	-0.925
0.770	-3.054	-1.933	-2.219	-1.097	-0.369	-1.522	
-0.329	-1.637	-1.171	-0.423	-1.483	-1.735		
0.945	-0.093	-0.358	-1.375	-0.336	-1.722	-2.942	-2.119
0.629	-1.310	-0.440	-0.617	0.102	-3.528	0.097	
-1.458	-2.493	-1.673	-0.676	-0.692	-0.123		
-0.910	0.318	-2.900	0.179	0.261	-2.200	-1.043	-1.126
-2.268	-1.699	1.086	-1.201	-0.622	-0.938	-0.153	
-0.650	-0.182	-0.502	-0.329	-0.647	0.626		
-0.079	0.786	-1.095	-0.358	-1.405	-2.368	-1.964	-2.211
-1.318	-3.908	-1.968	-1.964	-1.488	-1.299	-1.312	
-0.389	-0.992	0.057	-1.941	-3.252	1.134		
-1.275	-0.062	0.046	-1.035	-0.440	-1.245	-0.596	-0.809
-1.257	-1.438	-0.779	-1.092	-0.519	0.191	-1.547	
-0.783	-1.698	-1.535	-0.135	-0.338	-0.991		
-3.146	-0.662	-1.146	0.072	-1.850	-1.094	3.997	-1.212
-2.410	-2.244	-2.441	0.474	2.452	2.211	0.571	
2.104	0.294	0.788	1.802	1.999	2.949		
-0.345	0.135	0.290	-2.046	-3.306	-3.712	0.269	-1.878
-0.553	-1.819	-2.627	-2.634	-0.565	-1.111	-0.597	
-2.856	-0.666	-2.515	-0.189	-2.559	-1.462		
-0.132	0.972	-1.880	-1.925	0.654	-2.579	-1.788	0.614
-0.373	-4.566	-0.790	-1.031	-0.258	-1.688	-1.398	
-2.854	-0.582	-1.139	0.144	0.114	0.021		
-0.463	-1.420	0.204	-1.443	0.355	-0.736	-0.424	-2.987
-3.275	-2.091	-1.242	-1.268	1.125	-2.692	-1.452	
0.618	-1.019	-1.525	-2.992	-1.301	-0.484		
0.179	-1.210	-2.669	-3.145	-2.533	-0.588	-0.986	-1.734
-1.353	-2.137	-2.285	-2.610	-0.717	-1.939	-1.975	
0.400	1.261	-1.088	-1.337	-2.624	-1.344		
-1.191	-0.581	-0.929	-1.887	-2.619	-2.700	0.139	-1.444
-2.366	-4.646	-0.024	-1.132	-2.460	-2.088	-1.230	
-0.641	-1.354	-2.296	0.245	-2.413	-2.304		
-0.908	-0.867	-0.329	-2.640	-0.532	0.214	0.071	-1.392
-1.025	-2.244	-0.736	-0.319	-0.070	-1.959	-0.959	
-1.276	-0.656	-1.045	-1.929	-2.039	0.057		
0.210	5.519	1.958	0.852	-0.517	1.310	-1.002	-1.572
0.191	-1.557	-0.522	-0.697	-0.426	-1.075	0.458	
0.593	0.860	6.560	-1.520	0.697	-2.995		

Table36.txt

0.262	-0.997	-3.497	-1.282	-2.689	-2.158	-0.822	-0.827
-2.216	-1.321	-1.711	-0.089	-1.883	-2.232	-0.098	
-0.926	-1.773	-2.555	-1.188	-0.735	-0.186		
-0.232	-0.269	-1.525	-0.452	-1.366	-0.388	1.601	-3.283
-1.762	-1.708	-2.114	-1.393	-2.273	-2.246	-1.481	
-1.556	-1.002	-2.598	-1.402	-1.903	-1.562		
0.576	-1.682	-2.648	-0.655	0.814	-3.824	-2.214	-3.239
-2.331	-1.298	-0.858	-1.387	-1.419	-1.333	-4.611	
-1.093	-0.248	-2.136	-0.796	-2.160	0.554		
-0.660	-1.083	-3.299	-2.867	-1.362	-1.511	-0.938	-4.099
-0.332	-3.638	-0.409	-3.387	-0.183	-1.549	-0.865	
-0.687	0.370	-2.754	-4.184	-0.924	-1.196		
-0.522	-1.489	1.091	-0.110	-1.383	-1.256	-1.106	-2.678
-2.092	-1.867	-0.932	-2.277	-0.276	-1.213	0.139	
-2.623	-2.569	-1.372	-1.857	-1.962	-0.392		
-0.531	-1.106	-0.597	-4.516	-3.564	-2.305	-1.876	-1.571
0.287	-5.136	-0.965	-2.274	0.280	-3.425	-0.529	
-2.375	-0.331	-3.667	-0.794	-2.767	-1.224		
0.036	-1.386	-3.795	-1.186	-1.055	-1.782	-1.492	-1.551
-0.068	-3.430	-0.759	-3.381	-0.526	-2.358	-1.689	
-1.594	-1.192	-3.486	-2.760	-1.104	-0.331		
-0.454	-0.202	-1.717	-1.776	-3.540	-1.839	-0.969	-2.777
-1.405	-3.717	-1.610	-2.409	-1.169	-3.227	-1.450	
-2.414	-1.003	-2.032	-1.607	-2.177	-1.281		
-0.496	0.671	-1.874	-3.137	-2.576	-2.235	-3.381	-3.116
-1.523	-2.988	-1.356	-6.385	-0.932	-1.404	-2.644	
-1.955	-2.514	-2.374	-2.661	-0.100	-0.690		
0.502	1.195	-2.584	-1.657	-2.113	-1.197	-0.763	-1.421
-4.162	-3.114	-1.814	-3.397	-0.805	-1.945	0.825	
-1.660	-2.877	-3.100	-2.568	-0.274	-3.063		
0.461	-1.193	-0.638	-2.416	-1.894	-2.203	-3.096	-3.868
-2.507	-2.527	-2.109	-2.604	-0.732	-3.223	-0.569	
-2.085	-1.130	-5.045	-2.521	-2.898	-2.413		
0.733	-1.085	-1.538	-2.517	-1.456	-0.922	-3.502	-1.519
-0.513	-3.383	-1.722	-4.758	-1.701	-2.236	-2.186	
-2.521	-1.591	-4.182	-1.428	-0.636	-2.731		
0.523	0.013	-1.463	-1.979	-1.840	-2.782	-0.549	-2.484
-1.454	-2.934	-1.688	-2.109	-2.332	-2.447	-0.700	
-4.544	0.047	-2.551	-2.817	-1.514	-0.844		
-1.013	0.570	-2.668	-1.443	-1.506	-2.113	-1.933	-4.461
-1.881	-2.886	-1.895	-2.350	-1.105	-2.371	-1.409	
-4.959	-1.816	-4.166	-2.598	-1.803	-0.346		
-0.502	-1.188	-3.138	-2.889	-1.847	-1.149	-0.598	-0.917
-1.730	-2.847	-0.701	-2.695	-1.978	-0.994	-1.819	
-1.441	-1.219	-0.342	-0.943	-1.918	0.015		
-0.644	-1.285	-1.912	-0.624	-1.631	-2.560	-0.567	-3.157
-2.541	-2.296	-0.664	-1.997	-0.719	-0.562	-0.982	
-2.776	-0.389	-4.303	-2.138	-1.944	-1.771		

Table36.txt

-1.069	-0.811	-1.570	-2.828	-0.330	-3.711	-4.080	-3.031
0.458	-2.080	-2.271	-4.634	0.184	-3.088	-2.175	
-3.095	-4.091	-3.039	-1.503	-2.649	-1.344		
-1.091	0.024	-1.547	-2.329	-2.016	-2.443	-1.195	-2.349
-2.845	-2.869	-1.344	-3.108	-1.009	-2.160	-0.257	
-2.478	-2.707	-1.001	-3.194	-2.599	-0.979		
-1.223	1.704	-2.263	-1.903	-1.128	-2.219	-1.598	-4.060
-0.164	-0.825	-2.625	-1.932	-1.959	-2.983	-0.202	
-2.288	-0.150	-0.352	-1.837	-2.593	-2.041		
-1.452	0.264	-2.640	-2.796	-1.641	-3.361	-3.087	-2.645
-1.885	-1.870	-0.807	-3.080	-1.298	-2.274	-2.710	
-1.815	-0.922	-1.958	-3.193	-0.352	-1.262		
-0.494	-0.194	-3.321	-1.721	-1.229	-2.104	-2.370	-2.406
-2.361	-5.059	-1.848	-3.663	-1.454	-2.252	-2.129	
-3.653	-1.770	-2.650	-3.686	-0.016	-0.071		
-1.166	0.265	-2.151	-2.720	-1.658	-2.556	-1.748	-2.668
-2.298	-3.962	-1.167	-1.203	-1.409	-2.318	-4.339	
-1.214	-0.091	-1.893	-0.730	-2.597	-1.000		
-0.468	0.933	-0.932	-3.364	-4.222	-2.073	-2.713	-2.926
-2.264	-2.994	-2.015	-2.759	-1.589	-1.170	-2.140	
-2.017	-2.427	-2.109	-2.430	-1.123	-4.656		
-1.244	-0.343	-2.621	-0.737	-3.046	-1.979	-1.570	-2.797
-2.312	-3.810	-1.452	-3.680	-2.057	-1.003	-0.869	
-1.241	-1.419	-2.230	-1.532	-2.171	-1.730		
-0.934	0.698	-2.108	-0.858	-1.540	-1.277	-2.791	-3.253
-2.631	-3.723	-1.794	-2.264	-2.630	-3.241	-1.504	
-3.195	-1.554	-1.990	-1.132	-1.911	-2.135		
-0.126	-0.294	-3.980	-2.191	-1.154	-4.780	-1.650	-2.243
-1.866	-5.507	-1.540	-3.253	-1.347	-2.788	-0.986	
-2.386	-1.380	-2.544	-0.937	-3.088	-1.242		
0.561	-0.374	-0.836	-2.140	-1.822	-0.428	-1.009	-4.143
-0.914	-2.965	-3.704	-4.597	-0.637	-3.295	-1.093	
-2.777	-0.126	-2.672	-0.563	-1.009	-1.990		
0.302	1.613	-2.651	-1.771	-1.165	-3.371	-1.801	-3.738
0.227	-3.972	-1.863	-2.560	-1.111	-2.423	-0.970	
-3.973	-2.528	-4.335	-2.093	1.078	-0.973		
-0.902	0.172	-1.215	-1.877	-1.600	-1.956	-1.653	-3.456
-1.033	-2.118	0.486	-0.789	-0.586	-1.972	-0.214	
-1.430	-3.166	-0.614	-1.176	-2.098	-1.170		
0.011	-0.823	-1.278	-1.303	-0.985	-3.520	-1.374	-1.242
-1.000	-3.509	-0.935	-2.820	-3.895	-2.757	0.258	
-3.008	-1.621	-1.582	-1.121	-1.490	-1.407		
0.617	0.188	-2.886	-2.216	-1.504	-2.057	-2.270	-3.893
-1.164	-1.216	-0.750	-2.607	-0.134	-2.969	-0.571	
-3.015	-2.377	-2.981	-2.869	-1.709	-0.820		
-0.025	0.260	-3.645	-0.665	-0.924	-1.363	-4.185	-1.116
-2.133	-3.576	-4.006	-2.120	-3.081	-3.424	-1.766	
-3.888	-1.151	-1.981	-1.139	-1.492	-3.451		

Table36.txt

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0.736      0.395      -2.747     -2.180     -1.276     -1.303     -2.357     -3.948
    -0.349     -2.671     -1.200     -3.672     0.654      -2.576     -0.145
-1.669     -1.194     -2.996     -1.299     -1.447     -0.732
-0.501     -2.034     -2.735     -1.138     -1.860     -2.386     -0.296     -0.835
    -1.911     -0.925     -1.025     -3.852     -0.337     -2.045     -0.220
-1.858     -0.086     0.625      -0.128     -0.580     -1.104
-0.934     0.047      -1.778     -1.632     -2.615     -2.380     -1.283     -2.843
    -0.981     -2.957     -1.335     -3.601     -0.971     -2.285     -2.903
-3.496     -2.746     -3.094     -2.857     -0.755     -1.427
0.982      1.071      -0.756     -2.754     -1.228     -0.884     -0.072     -1.670
    0.000      -1.101     0.000      -1.214     -1.598     -1.653     0.000
-1.214     0.000      -0.012     0.000      -0.941     0.000
0.075      0.021      -1.739     -0.738     -1.386     -1.471     -0.477     -3.373
    0.666      -3.211     -1.691     -2.034     -0.392     -2.676     -0.110
0.148      -0.507     -1.612     -0.986     -1.449     -1.383
-1.341     -1.420     -2.337     -0.243     -1.622     -0.928     -0.976     -4.401
    -0.498     -2.469     -2.443     -1.892     0.619      -2.181     0.132
-1.388     -1.703     -3.020     -0.907     0.191      -1.458
1.136      0.444      -1.848     -0.873     -0.911     -2.412     -2.285     -3.067
    -4.140     -2.859     -4.708     -3.420     -2.063     -3.188     -1.548
-0.925     -1.604     -0.847     -1.468     -2.821     -1.140
0.397      1.533      -0.858     -2.646     -1.285     -2.490     -0.640     -2.336
    -2.677     -3.318     -0.840     -2.667     -0.277     -2.595     -2.410
-1.912     -1.148     -2.873     -1.706     -1.710     -0.953
0.079      1.933      -3.449     -0.468     -2.032     -1.934     -2.401     -1.759
    0.213      -2.388     -1.992     -2.316     -0.691     -0.297     -2.550
-0.079     -1.155     -1.673     -1.396     -1.091     -0.484
-0.714     -0.268     -1.335     -2.304     -3.684     -1.347     -1.711     -4.140
    -1.996     -3.553     -0.340     -3.149     -1.764     -1.747     -1.361
-0.997     -1.953     -1.959     -1.076     -1.216     -1.779
-0.288     -0.761     -1.663     -1.465     -1.406     -1.864     -1.384     -2.576
    -2.166     -1.708     -3.328     -1.336     -0.225     -1.304     -0.722
0.667      -0.409     -1.661     -1.089     -0.832     -0.092
-0.336     1.456      -1.867     0.346      -0.350     -2.443     -2.172     -1.615
    -0.785     -2.251     -1.074     -1.929     -1.842     -1.327     -1.227
0.082      -2.949     -1.703     -0.149     -0.745     -0.834
0.293      0.398      0.136      -0.396     0.255      -2.746     -2.416     -1.258
    -1.446     -2.650     -1.300     -2.449     -1.726     -2.366     -1.253
-2.522     -1.132     -3.641     -0.460     -1.032     -1.531
-1.340     -1.262     -2.519     -1.644     -3.095     -1.634     -1.533     -1.528
    -1.703     -2.376     -2.225     -2.461     -1.890     -1.658     -2.513
-3.894     -1.441     -1.658     -1.839     -2.866     0.127
0.501      0.796      -2.270     -2.535     -0.860     -2.778     -0.595     -1.921
    -3.282     -2.371     -0.385     -2.577     0.108      -0.535     -0.750
-2.490     0.346      -1.958     -1.446     -2.558     -1.482
-0.590     0.519      -1.530     -0.512     -2.734     -2.926     -1.668     -3.523
    -0.698     -3.931     -1.066     -3.139     -0.719     -2.520     -1.490
-1.446     -0.579     -4.078     -1.521     -1.306     0.236
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Table36.txt

0.734	-0.777	0.853	-1.634	0.231	-3.027	-2.198	-2.972
-1.927	-0.655	0.218	-1.394	-1.708	-0.660	-0.386	
-1.211	-1.256	-0.905	-1.056	0.218	-0.108		
-0.049	-0.610	0.332	-1.417	-2.298	-1.542	-0.302	-0.904
-2.220	-2.298	-1.817	-2.573	-0.875	-1.471	-1.766	
-1.772	-1.142	-0.574	-0.872	-1.981	-0.028		
1.268	0.942	-0.648	-0.347	-2.399	-0.619	-0.493	-0.288
-0.868	-1.045	0.000	-1.091	-2.074	-1.861	-1.139	
-3.131	-1.955	-0.997	0.309	-0.290	0.772		
-0.727	0.315	-0.338	-1.198	-3.194	-0.790	0.000	0.651
0.000	-2.894	0.000	-0.040	0.000	0.000	0.000	
0.000	-1.198	0.000	0.000	-0.445	0.000		
0.333	-0.475	-1.038	-3.147	0.017	-0.567	-1.859	-0.295
-2.211	-2.193	-1.172	-1.680	-0.737	-3.982	-2.285	
-3.133	-0.581	-1.402	-2.595	-0.661	1.076		
0.614	0.133	-0.170	-0.790	0.000	-1.169	-0.634	-0.383
0.186	-1.214	-0.736	-0.475	-0.962	1.020	0.000	
-0.453	-0.539	0.765	-0.378	0.309	0.744		
-1.022	0.087	-1.970	-2.745	0.585	0.046	-0.796	0.036
0.438	-1.253	-2.142	0.297	0.218	-0.071	0.000	
-0.939	-0.293	-0.955	-0.396	0.085	0.000		
-0.161	-0.030	-1.472	-2.418	-0.239	-2.448	-2.507	-2.149
-1.853	-1.888	-3.379	-2.335	-1.414	-1.012	-4.233	
-2.658	-1.652	-3.226	-1.760	-1.701	-1.052		
-0.400	-0.165	-0.298	-1.003	-2.499	-0.296	-0.288	0.535
-0.587	-1.004	-2.667	-0.384	0.165	-0.835	0.190	
-0.779	-0.459	-2.034	-0.990	-0.796	-0.623		
0.370	-1.442	-0.426	-2.259	-1.311	-3.397	-1.424	-4.007
-1.141	-4.367	-0.582	-1.921	-0.931	-2.379	-1.079	
-2.712	-1.401	-3.407	-0.999	-1.793	-1.000		
-0.573	0.245	-1.065	-3.049	-2.628	-1.662	-1.953	-1.871
-0.435	-2.584	-0.465	-3.404	-1.155	-2.803	-1.188	
-0.500	-0.699	-3.136	-0.252	-0.976	0.945		
-0.351	-0.670	-1.361	-2.010	-1.798	-2.214	-1.366	-2.262
-0.754	-3.633	-2.157	-3.006	-2.418	-0.765	-1.258	
-2.268	-0.381	-1.085	-0.853	-1.439	0.027		
-0.430	0.201	-1.799	-2.370	-2.661	-3.839	-2.887	-3.977
-0.464	-2.723	-1.765	-1.986	-2.284	-2.401	-1.874	
-1.540	-1.391	-3.131	-1.798	-0.833	-3.246		
0.443	-0.341	-0.596	-0.383	0.224	-2.214	-1.103	-0.822
-2.141	-1.733	-2.138	-2.450	-1.349	-2.297	-0.245	
-1.221	-0.222	-0.691	-0.065	0.305	-2.691		
1.399	-1.232	-0.987	-2.021	-2.435	-1.765	-3.411	-0.934
-0.887	-4.479	-0.976	-1.683	-1.272	-1.083	-3.321	
-1.055	-1.478	-1.421	-0.588	-1.562	0.747		
0.723	-0.653	-0.977	-1.466	-1.462	-0.040	-1.291	-1.297
-0.945	-1.597	-0.004	-0.518	-2.697	-0.728	-0.784	
-0.195	-3.846	-2.673	-2.548	-0.380	-1.554		

Table36.txt

-0.041	1.228	-1.380	-1.792	-0.316	-4.869	-1.372	-1.335
-2.366	-4.415	-2.728	-1.196	-0.767	-0.907	-1.878	
-1.583	-2.167	-2.784	-2.599	0.633	-1.810		
-0.399	-0.634	-3.106	0.500	0.137	-3.264	-0.479	-1.057
0.000	-1.254	-1.169	0.230	-2.468	-2.289	0.000	
-0.058	-0.261	0.443	0.000	0.000	-0.384		
-0.630	0.890	0.000	-0.729	-1.214	-3.090	0.000	-0.170
0.000	-0.144	0.000	-0.950	-0.378	-0.144	0.000	
0.137	0.000	-0.790	0.000	-1.468	-0.492		
0.105	-0.211	-1.120	-0.169	-1.196	-0.335	-1.169	0.080
-0.027	-1.538	0.000	-1.206	-2.332	-1.466	-0.610	
-0.233	1.347	-1.493	-2.211	-0.541	0.786		
1.697	0.274	-0.541	-1.248	0.353	-0.973	-1.010	-1.242
-0.437	-1.400	-1.985	-2.419	0.374	-0.857	-0.002	
-0.768	-0.848	-2.532	-0.681	-1.093	-0.736		
0.583	1.024	-0.926	-2.204	-1.420	-1.717	-2.088	-2.336
0.544	-1.810	-1.532	-2.381	-1.165	-0.467	-1.767	
-1.217	0.881	-2.699	-1.340	0.637	-0.229		
0.626	2.021	-1.467	-1.098	-0.496	-2.489	-1.355	-0.249
0.160	-1.363	-0.428	0.562	-2.519	-0.362	-3.090	
-0.936	2.129	-1.300	-1.246	-0.440	-2.330		
0.738	1.416	-2.191	-1.031	-1.969	-1.660	-0.352	-1.978
-0.153	-1.922	-0.678	-1.436	-0.307	-2.340	-0.883	
-2.638	-0.858	-2.902	-1.132	-0.768	-0.545		
0.844	-0.245	-0.211	-2.064	-1.943	-1.498	-1.260	-2.310
-0.503	-3.025	-0.315	-1.228	-2.254	-2.045	-1.438	
-1.326	-1.608	-1.064	-2.507	-0.295	-1.335		
1.354	1.419	-0.180	-1.587	-0.645	-2.044	-2.122	-2.293
-2.474	-2.111	-2.603	-2.867	-0.516	-2.357	-1.339	
-1.537	-0.895	-1.509	-1.563	0.908	-0.198		
0.673	0.449	-1.256	0.218	0.000	0.069	0.529	-1.173
0.595	-0.373	-2.262	-1.841	0.011	-0.968	0.000	
-0.378	0.137	0.788	-1.528	-1.214	-0.998		
0.031	1.060	-3.050	-0.733	-1.564	-1.908	-2.525	-1.769
-2.618	-0.554	-2.705	-0.893	-0.061	-1.235	-0.259	
-1.303	0.197	-1.936	0.294	-1.279	-2.363		
-0.104	-0.432	-0.375	-0.733	-0.500	0.098	-2.664	-0.505
-1.120	-0.295	-1.714	-0.496	-0.445	-1.187	-3.474	
0.743	-3.090	-2.475	0.184	0.817	-1.256		
1.909	1.519	-0.356	-1.826	0.295	-3.623	0.648	-0.122
-0.133	-0.875	0.299	-0.260	-2.807	-0.708	-1.134	
0.130	-1.165	-2.938	0.000	-1.887	-0.228		
-0.909	-1.155	0.969	0.163	-3.090	0.000	-1.368	0.137
0.089	-0.914	0.000	0.000	-0.505	0.000	0.000	
-0.445	0.000	0.050	0.000	0.000	0.000		
0.896	-0.712	-1.069	-2.106	1.029	-2.449	-1.839	-1.249
-1.172	-2.504	-0.536	-1.564	-1.490	-1.572	-3.146	
-3.228	-0.526	-1.395	-1.177	0.403	-1.278		

Table36.txt

-0.522	0.245	-0.095	-0.170	-2.422	-1.003	-1.594	0.388
-2.564	-0.371	0.137	0.805	-0.541	-2.276	-0.765	
-2.078	0.724	0.500	-0.610	-1.694	-0.174		
1.094	1.494	-2.325	-2.191	-2.167	-1.983	-1.076	-3.479
-0.792	-0.531	-1.038	-3.146	-1.650	-2.255	-1.251	
-2.708	0.148	-0.749	-1.450	-1.049	-1.455		
0.649	-1.777	-1.321	0.696	-2.730	-2.927	-1.350	-2.705
-0.978	-2.332	-3.127	-1.859	-1.798	-1.684	0.843	
-1.527	-0.582	-0.092	0.212	-0.192	-0.146		
-1.607	-1.052	0.144	-2.191	-1.281	-0.695	-0.106	-0.949
-0.790	-0.264	-3.090	-1.029	-0.378	-1.204	-0.756	
-2.668	-0.378	0.000	0.000	0.979	-0.179		
0.195	0.874	-0.467	-1.160	0.034	-1.068	-1.594	-1.095
-1.038	-1.154	-2.339	-4.031	0.125	-2.279	-0.934	
-0.337	-0.136	-2.771	-0.307	-1.658	-0.634		
0.676	-0.189	-0.374	-0.299	0.023	-3.333	-2.170	-1.857
-2.550	-2.193	0.979	-1.827	-0.958	0.113	-0.395	
-1.335	-1.624	-1.276	-2.048	-1.000	-0.004		
-0.600	1.546	-0.984	-0.668	-0.778	-2.884	-1.192	-1.720
-1.882	-1.496	0.771	-0.973	-2.842	-2.106	-0.487	
-3.985	-0.070	-1.542	-0.106	-0.734	-0.492		
1.442	0.842	-1.952	-1.045	-1.862	0.767	-4.105	-1.925
-0.193	-0.664	0.154	-1.122	-1.369	-2.186	-1.286	
-0.454	-2.088	-1.742	-0.818	-0.562	-2.348		
-1.532	0.265	-1.192	-0.953	-2.348	0.158	-1.639	-0.689
-0.940	-2.038	0.232	-3.075	0.241	-2.209	-1.708	
-1.051	0.204	-2.884	-1.774	-0.153	-3.105		
-0.980	0.290	-2.137	-2.401	-1.497	-1.597	-1.594	-1.039
-2.027	-2.766	-1.058	-3.079	-0.920	-3.362	-0.603	
-0.676	-0.032	-3.129	-1.367	-2.173	-0.391		
0.483	-0.080	-1.342	-1.201	-2.062	-2.773	-1.065	-2.730
-2.392	-0.941	-2.158	-2.265	-2.800	-1.802	-0.826	
-1.535	-1.240	-0.970	-1.652	-0.148	-0.261		
1.354	-0.760	-0.890	-0.285	-1.214	-0.461	-0.237	-2.050
-0.456	-1.601	-0.217	-1.572	-1.188	-1.943	-0.217	
-0.924	-1.590	-1.314	-0.375	-1.673	-1.041		
0.197	1.239	-1.749	-1.497	-1.787	-1.921	-2.427	-1.089
-2.464	-2.620	-0.104	-2.589	-0.898	-1.321	1.362	
-1.101	-1.900	-0.147	-1.534	-2.307	-2.065		
0.009	-1.413	-2.993	-1.975	1.096	-0.287	0.174	-2.773
-2.118	-0.327	-0.227	-3.213	-1.028	-1.915	-0.700	
-3.097	-0.693	-2.722	-1.957	-2.274	0.546		
0.419	1.049	-0.791	-3.755	-2.204	-3.981	-1.529	-2.226
-1.196	-2.418	0.030	-2.547	-2.562	-1.679	0.369	
-3.555	-0.077	-0.915	-1.862	-2.241	-1.403		
0.538	-1.384	-1.669	-0.730	-0.562	-2.147	-1.533	-2.682
-0.715	-3.588	-1.381	-2.748	-0.896	-2.604	-0.556	
-2.127	-0.193	-3.161	-0.549	-1.132	-0.580		

Table36.txt

0.659	-1.640	-3.717	-0.659	-2.653	-1.290	0.065	-1.680
-4.300	-2.646	-0.099	-0.448	-2.272	-0.517	0.605	
-2.441	-1.777	-0.130	-0.786	-0.470	-0.350		
-1.066	-0.208	-2.614	-0.634	-3.396	-1.503	-1.819	-2.767
-0.180	-1.066	-2.123	-2.867	-1.290	-2.308	-0.588	
-1.320	-2.087	-1.343	-2.235	-0.559	-0.178		
-1.537	0.300	-0.217	-0.790	0.000	-1.169	0.000	-0.341
0.000	-0.519	0.000	-0.533	0.000	-0.302	0.000	
-0.823	0.000	-0.545	0.000	0.000	0.000		
-0.097	1.538	-0.435	-2.632	0.156	-1.456	-0.300	-1.400
0.702	-2.969	-2.004	-1.938	-1.166	-1.091	-0.548	
-1.188	-1.374	-1.881	-3.228	-0.153	-0.239		
-0.390	1.214	-1.642	-1.830	0.192	-1.098	-0.322	-0.978
-0.413	-1.699	-1.006	-1.404	0.000	-1.085	-0.266	
-1.364	-3.090	-0.450	0.192	-2.134	0.482		
0.517	0.199	-1.167	-2.326	-0.884	-0.806	-1.339	-1.059
-0.741	-3.208	-2.274	-1.189	-1.321	-0.294	-3.448	
-1.779	0.136	-0.441	-0.688	-1.047	-2.115		
1.665	-1.294	-1.109	-1.924	0.128	-0.984	-1.743	-1.897
-0.264	-1.500	-0.783	-3.739	-0.009	-0.653	-1.469	
-0.963	-0.904	-3.179	-2.830	-0.748	-3.487		
0.483	-0.145	-1.287	-1.331	-3.092	-3.162	-2.846	-1.589
-4.046	-3.427	-2.249	-1.094	-1.960	-2.797	-1.635	
-4.424	-1.848	-1.774	-0.495	-1.093	0.212		
-0.063	-0.257	-2.667	-0.249	-0.895	-1.814	-1.143	0.398
-1.717	-2.435	-0.300	-2.696	-1.677	-1.107	-0.439	
-1.214	0.366	-1.385	-0.724	-0.897	-0.151		
2.163	-1.256	-1.044	-0.687	-1.396	-1.686	-0.779	-0.709
-0.491	-2.455	-1.395	-1.809	-1.335	-2.630	-1.688	
-1.869	-0.778	-0.908	-0.545	-0.486	-2.143		
1.495	0.446	-0.790	0.116	0.000	-0.736	0.000	-0.798
-0.445	-1.174	-0.378	0.137	0.000	0.428	0.000	
0.000	-1.169	-0.249	0.000	0.000	-1.341		
0.487	0.051	-0.506	-2.365	-3.031	-2.412	0.612	-3.658
-1.514	-2.193	-2.624	-4.339	-2.551	-2.611	-1.435	
-0.234	-1.296	-1.794	-0.305	-0.695	-1.165		
0.963	0.051	0.018	-0.760	0.044	-1.283	-1.120	-1.374
-3.422	-0.711	0.157	-1.694	-0.294	-1.513	0.395	
-2.038	-0.539	-2.211	0.347	-0.096	-0.319		
-1.300	0.186	0.000	0.762	0.000	0.000	0.000	0.000
0.000	0.050	0.000	-1.214	0.000	-1.169	0.000	
-0.321	0.000	-0.736	0.000	0.000	0.000		
-0.096	0.353	-2.661	-2.103	-1.929	-2.306	-1.856	-1.606
-0.773	-3.035	-1.530	-2.868	-0.270	-2.910	-0.997	
-1.108	-0.968	-2.281	-2.711	0.217	-1.783		
0.791	0.365	-0.248	-2.236	-0.709	-0.521	-0.745	-0.069
-0.174	-3.108	-1.199	-0.391	-1.682	-2.144	-0.167	
-2.864	-0.794	-1.172	-0.604	0.413	-1.808		

Table36.txt

-0.992 0.891 0.000 0.651 0.000 0.651 -3.090 -0.009
-0.376 -1.476 -0.736 -0.378 0.000 -0.217 0.000
0.865 0.000 -0.736 0.000 0.000 0.000
0.334 -0.593 -0.060 -0.095 0.137 -2.404 0.307 0.188
-0.450 -1.423 0.154 0.936 -0.573 -0.624 0.128
-1.122 1.456 -0.702 -0.664 0.000 0.042
-1.049 -1.076 0.000 0.189 0.000 0.000 0.000 -0.378
-0.505 0.000 0.000 0.000 0.000 0.000 0.000
0.000 0.000 0.137 -0.823 0.000 0.000
0.851 -0.991 -0.253 -1.150 -0.650 -1.363 -0.568 -1.266
-1.304 -1.199 -0.529 -1.583 0.026 -1.217 -0.796
-0.654 -2.131 -2.046 -0.823 -0.570 -1.066
2.635 -1.416 -2.064 -1.934 -3.117 -1.349 -2.132 0.017
-0.407 -2.180 -0.319 -2.209 -2.225 -4.170 -2.550
-0.886 -1.601 -3.265 -0.105 -1.920 -2.419
0.526 -0.899 -0.389 -2.179 -1.536 -2.452 -2.929 -3.144
-3.048 -2.338 -1.744 -1.119 -1.421 -0.905 -1.135
-2.446 -1.590 -0.274 -3.668 -1.253 -2.002
1.061 -1.414 -0.520 -1.928 -1.046 -2.367 -1.369 0.094
-2.356 -2.826 -1.496 -2.295 -0.672 -1.029 -2.706
-1.243 -0.120 -0.873 -0.428 -1.163 -0.415
0.150 1.461 -0.645 -1.113 -0.725 -0.901 -3.085 -2.043
-0.818 -3.435 -1.166 -1.171 -0.634 -2.607 -1.617
-1.585 -1.285 -0.625 -0.506 -1.226 -1.980
-0.655 0.045 -1.657 -0.349 0.240 -1.484 -0.566 -0.894
-1.928 -1.602 -0.004 -1.027 -0.621 -2.729 -1.931
0.551 -0.788 -2.525 -0.058 -0.939 -0.414
1.125 -1.189 -2.528 -0.933 -0.708 -1.751 -2.129 -0.510
-0.136 -4.198 -2.605 -3.261 -2.218 -1.962 0.484
-1.811 -1.166 -4.073 -1.607 -2.455 -3.266
-0.174 -1.068 -3.886 -1.833 -0.520 -1.203 -1.923 -0.040
-1.289 -4.435 -1.468 -2.075 -2.692 -2.406 -2.116
-1.694 -0.741 -1.689 -1.749 1.748 -3.628
0.383 -2.211 -1.456 -2.180 -1.961 -0.785 -2.661 -1.661
-1.082 -3.746 -0.811 -3.320 -1.099 -3.861 -0.665
-1.618 -1.090 -2.906 -2.155 -3.080 0.135
-1.223 -0.976 -0.849 -2.205 -2.540 -2.222 -1.897 -1.622
-1.525 -2.499 -1.945 -3.616 -2.649 -0.928 -1.789
-2.496 -1.502 -4.552 -1.136 -1.062 -1.779
0.724 -0.227 -1.772 -2.927 -1.591 -3.795 -2.054 -0.936
-0.611 -4.336 -0.551 -2.987 -2.979 -3.295 -3.680
-2.319 -0.153 -1.320 -1.785 0.167 -1.648
-0.407 0.030 -0.318 -0.556 -1.926 -1.097 0.264 -0.735
-1.231 -2.034 -0.269 -1.175 -1.133 -1.720 1.353
-2.642 -0.253 -2.098 -0.684 -0.996 1.098
0.442 1.750 -0.528 0.300 -1.993 -1.892 -3.386 -1.310
1.287 -1.067 -3.602 -3.615 -0.483 -1.287 -0.762
-0.492 -1.087 -2.258 -0.828 -0.744 1.669

Table36.txt

0.166	0.178	-0.404	0.178	-1.257	-2.477	-1.496	0.008
-2.754	-0.835	-0.769	-2.233	-0.310	-3.159	-1.898	
-0.230	-2.341	-1.666	-0.054	-1.620	-2.736		
0.144	-0.317	0.622	-1.419	-1.743	-0.942	-0.525	-2.554
-1.903	-1.317	-1.047	-1.445	-0.459	-1.609	-0.299	
-1.938	-1.757	-0.860	-4.608	-2.446	-2.382		
-1.126	-0.685	-0.729	-1.389	0.178	-1.151	-1.456	-1.282
-1.268	-1.254	-1.917	-1.566	-0.475	-1.144	-1.748	
-0.818	-0.080	-1.248	-1.346	-2.571	-1.652		
0.615	0.624	-1.184	-2.571	-0.764	-0.418	-0.295	-2.634
-1.388	-1.670	-0.763	-1.475	-2.163	-0.718	0.078	
-0.562	-1.708	-0.592	-2.553	-2.469	-2.029		
2.406	0.967	0.260	-0.109	-1.310	-0.223	-0.363	1.318
-1.864	0.139	0.566	-1.625	-0.403	-1.452	2.262	
-0.445	-1.660	-1.273	0.396	-0.774	-0.337		
-0.237	-1.555	-2.605	1.949	-1.193	-0.451	-1.835	-2.470
-1.046	-0.869	-2.643	1.571	-1.851	-2.194	0.976	
-2.129	-1.108	-1.793	-1.440	-1.655	0.543		
-0.895	-0.347	-0.542	-0.610	-0.964	-1.500	-1.942	-0.491
0.518	-2.780	-0.916	-0.191	-0.701	-2.034	-1.569	
-2.843	-0.578	-1.400	-1.310	-0.940	-1.082		
1.363	0.241	-2.105	1.206	-1.610	-2.669	-1.758	-3.217
-1.356	-3.489	0.263	-1.609	-1.293	-0.936	-1.795	
-0.606	-1.088	-1.421	-1.113	0.095	-0.114		
0.127	-1.018	-2.296	-1.612	0.559	-1.861	-1.417	-2.110
-0.658	-1.407	-1.330	-2.973	-2.618	-2.421	-1.626	
-1.495	0.100	-1.615	-0.710	-0.519	0.392		
-0.343	0.732	-2.269	-1.635	-1.532	-0.170	-2.444	-0.960
-1.168	-0.523	0.266	-1.579	-0.775	-1.374	-0.607	
-2.192	-0.397	-2.312	-0.522	-0.997	-1.526		
-0.303	-1.406	-1.857	-1.300	-3.166	-2.118	-1.126	-0.725
-1.621	-1.832	-2.016	-2.818	0.721	-1.115	-1.855	
-0.589	0.878	-0.496	-1.991	-0.048	-0.267		
0.184	-0.867	-0.705	-0.919	-2.801	-0.383	0.006	-1.676
-0.391	-2.784	0.266	-1.204	-2.191	-2.239	-1.537	
-0.960	-2.368	-0.593	-0.446	-1.438	-2.647		
-1.495	2.599	-0.264	-2.686	-1.337	-3.891	-1.400	-2.493
-0.928	-3.402	-0.591	-1.414	-1.957	-0.766	-0.933	
-0.346	0.046	-1.815	-0.695	-1.622	-0.546		
-0.752	1.479	0.651	-1.004	-0.054	-2.034	-1.554	-0.571
-1.595	-2.676	-1.124	-2.002	0.206	0.475	-1.020	
-2.441	-1.582	-1.449	-1.359	-0.855	-0.750		
-0.968	-0.247	-1.491	-0.145	-0.802	-0.782	-1.766	-2.167
-0.305	-1.152	0.070	-1.616	-0.316	-2.603	-0.916	
-1.229	-1.828	-1.952	-2.044	0.459	0.515		
-0.338	-1.818	-0.229	1.769	-0.467	-1.657	-0.628	-0.730
0.336	-1.940	-0.975	-0.461	-1.439	-0.073	-2.317	
-1.517	-0.486	-1.231	-0.557	-0.429	-0.766		

Table36.txt

-0.237	-1.035	-0.540	-0.847	0.434	-2.065	0.254	-1.224
-1.965	-0.192	1.202	-0.608	-1.230	-2.860	-2.694	
-0.871	-0.593	-2.147	-0.981	-2.728	-0.234		
-1.075	0.750	-2.338	-1.337	-0.120	-0.317	-0.990	-2.490
0.748	-2.150	-1.097	-1.855	0.161	-1.844	-0.760	
-0.786	0.168	-4.009	-2.821	-0.847	-1.914		
1.638	-1.073	-0.848	-1.014	0.611	-1.816	-1.632	-0.392
-1.106	-0.454	-1.416	-2.513	-0.046	-0.070	-1.761	
-1.042	2.184	-0.465	-0.717	-1.183	0.819		
-0.180	1.673	-4.106	-0.106	-1.809	-2.006	-1.906	-0.449
-1.676	-2.893	-1.566	-1.668	-1.338	-1.989	0.335	
-1.078	0.011	-1.428	-0.440	-0.416	0.899		
0.981	-0.805	-1.492	-3.118	-2.135	-1.723	-2.283	-3.103
-0.068	-1.690	-0.212	-3.418	0.292	-2.676	-0.891	
-1.386	-1.404	-2.878	-1.181	-2.747	0.005		
0.166	-1.073	-2.546	-1.372	-1.015	-3.751	-1.575	-2.376
-0.507	-3.677	-0.784	-2.533	-0.427	-3.744	-1.008	
-3.767	-1.817	-2.275	-0.091	-0.081	-0.655		
0.065	-0.454	-1.005	-2.441	-1.260	-1.967	-1.397	-1.646
-0.321	-0.395	-0.698	-1.251	-1.215	-1.689	0.065	
-0.715	-1.594	-2.232	-0.860	-2.531	-1.817		
-0.776	0.038	-2.396	-1.025	-2.332	-3.688	-2.582	-2.572
-3.071	-2.447	-0.914	-2.909	-2.656	-1.701	-1.697	
-2.603	-1.546	-2.612	-2.799	-2.603	-0.483		
-0.778	0.556	-1.090	-2.628	-0.821	-2.015	0.122	-2.772
-0.443	-3.072	-0.457	-1.308	-1.432	-3.191	-0.125	
-2.557	-1.934	-1.979	0.960	-3.193	0.621		
0.519	-1.383	-0.553	-1.232	-0.650	-3.474	-1.204	0.253
-0.457	-2.496	-0.833	-1.618	-1.715	-0.713	-1.180	
-1.445	-2.980	-2.498	-1.707	-1.739	-1.421		
-1.494	-1.006	-0.680	-2.950	-1.623	-2.034	-0.556	-2.816
-0.152	-3.690	-1.283	-2.551	-2.412	-0.897	0.922	
-1.846	-1.431	-3.284	-2.240	-1.254	-1.727		
0.174	-2.128	-1.921	0.030	-0.232	-0.441	-0.997	-0.641
0.304	-0.496	-0.296	-0.545	-0.506	-1.732	-0.567	
-1.843	-2.129	-0.765	-2.584	-0.280	-1.144		
0.235	-1.185	-6.227	-0.135	-1.696	-2.582	-0.389	-4.124
-1.135	-3.674	-2.341	-2.628	-1.979	0.770	-0.966	
-0.970	-0.826	-2.545	-3.072	-0.762	-1.736		
-0.200	0.059	-0.288	-1.258	-0.484	-1.944	-2.306	-1.894
-0.554	0.638	-0.787	-2.581	-1.438	-0.251	-1.410	
-0.927	-2.388	-2.167	-1.814	-3.462	-0.305		
0.038	-0.654	-1.667	-2.952	-2.199	-0.558	-0.344	-2.682
-0.406	-2.367	-2.260	-2.090	-0.928	1.626	-0.553	
-2.439	-0.419	-2.231	0.251	0.257	0.686		
-0.182	0.044	-1.043	-1.698	-2.704	-2.218	-1.452	-2.737
-0.313	0.086	0.168	-4.305	-2.005	-2.601	1.130	
-2.448	-1.126	-3.699	-1.692	-2.089	-0.743		

Table36.txt

1.023	-1.537	-1.823	-3.096	-1.341	-2.648	-0.990	-2.473
-0.718	-0.544	-2.731	-3.006	-1.831	-0.586	-1.603	
-0.954	-0.331	-4.792	-0.637	-1.671	-0.591		
-0.804	-0.694	-2.041	-4.245	-1.967	-2.269	-1.940	-1.455
-2.613	-3.747	-1.527	-2.527	-1.780	-0.644	-0.974	
-2.391	-0.735	-1.459	-0.721	-1.789	-2.072		
-0.919	0.976	-0.697	-2.714	0.350	-1.290	-1.618	-1.209
-1.985	-2.264	0.591	-2.574	0.167	-2.014	-0.157	
-0.973	0.476	-1.809	0.279	0.074	-0.735		
-0.047	-0.762	-2.012	-0.975	-0.493	-3.280	-2.988	-2.824
-2.021	-3.105	-1.445	-2.985	-2.077	-1.868	-1.258	
-3.044	-0.684	-2.818	-2.034	-2.601	-2.629		
0.320	0.577	-1.831	-1.179	-0.839	-1.800	-0.813	-2.903
-1.067	-3.401	-2.095	-3.313	-2.463	-1.067	-0.367	
-0.763	-1.002	-3.036	0.381	-0.165	0.228		
-0.212	0.231	-0.496	-1.503	-0.650	-1.916	-2.273	-3.031
-0.031	-1.783	-0.180	-3.710	-0.980	-1.225	-0.409	
-1.025	-0.604	-2.279	0.221	-1.193	-0.549		
1.749	-3.084	-1.815	-1.887	-2.710	-1.873	-2.639	-2.539
-1.757	-3.308	-0.592	-1.881	-1.136	-2.038	-1.139	
-2.225	-1.491	-1.523	-0.606	0.660	-0.694		
-1.366	0.614	-1.994	-0.203	-1.264	-2.178	-0.785	-2.915
-0.711	-1.099	-0.056	-1.192	-0.255	-2.363	-0.671	
-1.157	-0.895	-0.784	-0.672	-1.224	0.320		
-0.066	-1.573	-1.651	-1.353	-1.827	-2.571	-3.231	-3.656
-0.702	-1.812	-1.948	-2.141	-1.536	-1.546	-2.521	
-2.411	-1.375	-1.873	-0.823	-1.270	-1.709		
0.312	-3.678	-0.310	-0.745	0.321	-0.626	-1.661	-2.488
-1.507	-1.244	-0.337	0.249	-0.532	-2.586	-1.333	
-0.533	-1.170	-0.602	-1.011	-2.543	-2.937		
0.890	2.231	-1.449	-2.985	-1.459	-1.201	-4.685	-2.900
-1.489	-1.961	-1.410	-1.169	-2.259	-1.100	-0.181	
-1.991	0.088	-0.241	-1.144	-1.828	-2.476		
1.645	0.327	-2.784	-0.296	-3.675	-2.281	-0.937	-1.878
-0.103	-0.363	-1.734	-2.093	-0.722	-0.628	0.325	
-0.528	-0.783	-1.339	-1.939	0.341	-0.243		
0.552	0.111	-3.048	-1.473	-0.849	-3.967	-1.531	-1.885
-0.795	-0.610	0.724	-2.328	-0.825	-0.969	-3.089	
-1.535	0.093	-2.639	-0.870	-2.158	-0.778		
-0.079	0.613	-1.797	0.142	-0.952	-2.784	-1.597	-1.380
0.716	-4.102	0.622	-0.497	-0.108	-3.956	-1.798	
-1.204	-0.871	-1.478	-2.264	-0.416	1.203		
-0.102	-0.230	-2.192	-0.727	-0.911	-2.225	-0.076	-1.972
0.032	-1.269	-0.063	-1.254	-1.314	-1.426	-2.972	
-2.347	0.220	-2.331	-2.959	-1.305	-0.479		
-0.036	-0.728	-1.200	-1.761	1.270	-2.241	-4.112	-3.368
-0.655	-3.143	-0.543	-1.678	-1.636	-3.044	-1.436	
-1.724	-0.357	-4.120	-0.392	-1.617	-0.961		

Table36.txt

0.219	0.381	-2.812	-0.303	0.828	-0.803	-1.144	0.121
-1.546	-2.811	-1.383	-1.129	-0.604	-0.952	-0.061	
0.937	-0.618	-2.483	-1.836	-0.118	-0.926		
0.622	0.615	-1.965	-2.138	-2.200	-1.659	-3.087	-1.064
-0.279	-2.189	0.240	-0.918	-0.968	-1.951	0.040	
-1.549	1.033	-2.060	-1.605	-0.799	-2.942		
-0.705	-0.473	-0.190	0.099	-2.271	-1.891	-1.994	-3.552
-1.003	-3.067	-0.996	-1.708	-0.916	-1.567	-1.326	
-1.648	-0.797	-2.481	-2.386	-1.521	-1.340		
0.136	0.547	-1.601	-0.861	-1.618	-0.689	-3.096	-1.576
-1.064	-3.233	-4.618	-1.585	-1.060	-1.722	-1.315	
-1.585	-2.320	-2.556	-1.540	-0.623	-1.134		
1.383	-0.900	-1.334	-3.287	0.649	-4.165	-2.530	-3.287
-0.575	-2.915	-1.587	-1.477	-0.612	-1.770	-0.884	
-1.100	-0.518	-2.777	-1.235	-2.127	-0.688		
-0.456	-1.881	-1.509	-2.347	-1.299	-4.522	-2.158	-2.592
-2.695	-2.594	-2.874	-1.091	-0.385	-1.608	-1.181	
-1.126	-2.167	-3.326	-0.146	-1.698	-2.055		
-0.080	-0.235	-3.971	-1.094	-1.289	-2.711	-0.625	-2.833
-1.567	-2.456	-2.267	-2.043	-0.926	-1.653	-2.491	
-1.610	-1.797	-3.136	-2.963	-0.793	-1.967		
0.671	-2.507	-0.963	-2.294	-2.704	-2.747	-2.797	-1.751
-3.846	-2.308	-0.367	-3.963	-3.332	-2.757	-2.405	
-1.285	-1.045	-0.830	-2.587	-1.829	0.170		
0.795	-1.525	-1.913	-1.304	-0.047	-1.677	-1.693	-1.371
-1.398	-1.305	-0.454	-0.605	-2.827	-2.868	-0.151	
1.534	-1.707	-2.250	-0.258	-0.402	-3.384		
-0.260	-1.499	-1.256	-1.369	-0.137	-0.205	-1.281	-0.176
0.366	-1.720	-0.954	-1.099	0.525	0.700	-0.201	
-1.935	0.596	-1.217	-0.462	-1.323	-0.312		
1.022	-1.057	-0.150	-1.320	-3.120	-3.800	-0.377	-0.669
-1.819	-1.542	-1.290	-2.276	-0.765	-2.744	-0.818	
-4.537	-2.502	-1.741	-1.168	-4.001	-1.438		
-0.820	-1.508	-1.595	-3.948	-1.999	-1.858	-2.648	-0.103
-0.499	-1.017	-1.323	-1.912	-0.134	-2.186	-2.209	
-1.432	-0.551	-2.062	-1.702	-1.851	-1.043		
-1.045	-1.522	-1.928	-2.293	-2.586	-2.262	-3.084	-4.069
-0.278	-4.167	-0.207	-1.552	-0.669	-2.150	-1.932	
-2.935	-0.885	-2.916	-1.903	-1.177	-1.167		
1.129	-1.391	-0.384	-1.133	-1.191	-0.566	-3.344	-3.024
-1.810	-3.042	-1.461	-0.434	-0.646	-3.309	-1.126	
-1.968	0.078	-0.925	-1.117	-2.722	-1.849		
0.214	1.182	-4.791	-0.598	-1.250	-3.247	-0.696	-2.144
0.327	-3.042	-0.402	-2.045	-2.176	-1.679	-1.313	
-3.816	0.179	-1.590	-0.756	-0.401	-1.335		
-0.139	-0.808	1.175	0.535	-1.890	-0.185	-0.673	-1.714
-0.139	-1.569	0.806	-1.092	-0.868	-1.929	-0.787	
-1.573	-0.035	-0.190	-1.049	0.081	-1.093		

Table36.txt

-1.649	1.623	-0.724	-1.027	-2.099	-0.693	-1.334	-0.153
0.050	-1.294	-0.027	-1.901	0.192	-2.258	-0.498	
-1.003	0.000	-1.177	-1.370	-0.366	-0.436		
0.784	-1.445	-0.342	-1.415	-0.086	-0.821	0.251	-2.721
-1.321	-0.788	-0.302	-3.340	-0.489	-1.310	-1.028	
0.110	-0.453	-2.560	0.955	0.307	-1.463		
0.200	0.704	0.043	-0.953	0.358	-0.961	-0.229	0.700
-0.070	-1.818	-0.917	-1.094	-0.134	0.720	0.100	
-0.395	-1.158	-0.097	-2.259	0.458	-0.591		
0.642	-0.408	-1.264	-0.732	-0.234	-1.350	-0.990	-2.234
-1.846	0.604	0.322	-1.822	-0.438	-0.586	-0.919	
-1.112	-0.298	-2.136	-2.056	-0.730	-0.457		
0.825	0.063	-1.841	-2.314	-1.597	-3.564	-1.547	-1.974
0.502	-1.932	-0.825	-1.270	-1.397	-0.314	-0.580	
-1.357	-0.655	-0.879	0.138	-1.489	-1.333		
-1.426	0.584	-2.772	-0.679	1.133	-2.779	-1.683	-1.071
-1.087	-1.600	-1.441	-3.756	-0.586	-2.631	-1.463	
-1.561	0.118	-1.361	0.109	-1.078	1.114		
0.896	-0.831	-0.790	-0.620	-2.669	-1.221	-1.575	-2.044
-0.981	-2.706	-0.055	-1.891	-0.887	-3.276	0.590	
-1.644	-2.706	-0.500	-1.217	-0.425	-0.206		
0.313	0.109	-2.494	-2.456	-2.684	-2.817	-2.225	0.250
-2.992	-3.439	-0.224	-3.834	-1.521	-3.738	-1.107	
-0.488	-1.316	-1.068	-3.043	-1.231	-3.169		
-1.207	0.183	-1.567	-2.334	-1.731	-3.062	-1.373	-2.525
-0.706	-0.723	-0.692	-3.244	-0.995	-1.817	-0.948	
-2.823	-1.051	-1.779	-0.947	-1.505	-1.113		
0.263	-0.966	-0.674	-2.436	-2.041	-1.601	-2.478	-3.741
-2.251	-1.359	-0.010	-2.060	-1.527	-3.211	-0.824	
-1.770	-0.125	-1.359	-0.690	-1.067	0.522		
0.793	0.041	-1.530	-2.384	-3.041	-0.273	-1.298	-1.203
0.177	-1.788	0.078	-1.139	-1.071	-3.201	-0.244	
-0.842	-0.095	-2.655	-0.267	-2.155	-1.133		
-1.148	-0.550	-2.242	-0.994	-0.285	-0.951	-1.371	-1.091
0.344	-1.034	-1.845	-2.367	-1.751	-1.555	-0.780	
-1.596	-0.159	-1.538	-1.549	-0.661	0.042		
1.495	0.059	-0.706	-2.262	0.225	1.368	0.565	-0.787
-1.915	-0.172	-1.467	-1.867	1.894	-1.057	-0.158	
0.216	-1.717	0.695	1.469	-0.089	0.080		
0.720	2.718	0.296	-2.043	-1.030	-3.203	0.007	-0.683
-0.973	-1.147	-0.587	-0.455	-0.698	-2.011	0.778	
-0.861	-0.371	-1.364	-0.379	-1.497	-0.058		
0.929	0.556	-1.423	-1.169	-1.458	-0.419	1.017	-1.698
-2.125	-1.925	-2.424	-2.042	1.244	-1.492	-0.143	
-0.707	0.144	-0.563	-0.168	-2.989	-0.019		
-0.542	1.413	-3.466	-1.825	-0.883	-0.834	-0.913	-0.959
-0.968	-2.534	-4.213	-0.269	-0.284	-0.808	-0.734	
-3.090	-0.605	-0.414	-0.680	1.330	-0.028		

Table36.txt

-0.318	1.177	-1.224	-0.079	-0.533	0.923	-1.721	-0.715
-1.654	-0.720	-1.109	-1.698	-0.111	-1.700	-1.052	
0.875	-0.356	0.416	-0.901	-0.288	2.039		
0.315	-0.720	-0.978	0.538	-0.335	0.421	-1.543	0.139
-1.161	-1.354	-1.858	0.640	0.460	-3.234	-2.166	
-0.289	0.217	-2.013	-0.719	-0.444	-0.636		
-1.557	1.310	-1.821	-1.042	0.964	-1.929	-1.233	-2.019
-2.783	-0.660	-2.462	-2.147	-0.685	0.568	-0.761	
-0.658	-0.317	-2.366	-2.329	-2.059	-0.795		
1.097	1.339	-1.597	-0.545	-1.776	-2.261	-0.832	-1.144
-0.578	-2.211	0.072	-2.447	-1.457	-2.127	-0.755	
0.400	0.015	-1.003	0.670	-2.045	-1.248		
-0.595	-0.338	-1.506	-0.595	-2.065	-2.005	-1.638	-0.799
-1.430	-2.768	-1.653	0.031	-0.505	-3.256	-1.405	
-2.235	-1.311	-1.688	-1.427	-0.030	0.068		
0.331	0.143	-1.483	1.783	-0.989	-0.098	0.658	-2.308
-0.918	-0.785	1.134	0.228	-1.838	2.392	-2.568	
1.002	2.411	3.950	-0.461	-1.511	3.261		
0.605	1.709	-1.614	-0.099	-1.121	-0.819	-0.972	-1.214
-1.922	-2.002	-0.045	-0.428	0.240	-0.977	-0.147	
-2.233	-1.958	0.512	-0.945	0.143	-2.154		
-0.454	0.558	-1.498	-2.581	-2.483	-1.836	0.502	-1.600
-0.345	-2.465	-0.602	0.252	0.216	-3.505	-2.611	
0.239	-0.941	-1.543	-0.161	-1.418	3.060		
-0.681	0.119	-1.587	0.369	0.066	-2.895	-2.305	-1.265
1.353	-1.530	-2.544	-0.327	-2.637	-0.449	-1.123	
0.001	-2.349	-1.262	-1.522	-1.534	0.905		
0.003	-0.294	-0.269	-0.407	0.892	0.316	-0.459	-1.419
-1.255	0.374	-1.101	-0.302	0.787	-0.156	-1.789	
1.078	-0.790	-0.547	0.758	0.988	-0.570		
0.326	2.168	0.224	0.789	0.198	0.117	-1.711	0.582
-1.649	-0.210	-1.682	-0.338	-3.705	-2.755	0.448	
-0.074	-1.258	-0.377	-1.778	-1.100	-1.795		
0.253	1.779	-1.888	0.549	-0.672	-1.776	-1.115	-0.368
0.487	-2.293	-1.534	-0.697	-0.866	-0.877	-1.210	
-0.654	-0.945	0.284	-1.138	-0.397	-0.827		
0.131	-1.393	-0.238	0.176	0.045	0.648	-2.968	-1.623
-0.984	-1.062	-0.403	-0.423	0.252	-0.613	-1.168	
1.254	-0.977	-2.926	-2.408	-1.536	0.360		
-1.220	-0.411	0.699	-2.632	-1.076	-1.647	-0.048	0.624
-0.939	0.107	-1.354	-2.349	0.968	-0.072	-0.130	
0.603	0.032	0.025	-0.849	-0.686	0.254		
0.222	-0.280	-0.260	-0.001	0.606	-0.886	0.260	-1.434
-1.044	-1.241	-0.674	-0.276	-1.657	-0.933	0.351	
-1.493	-0.320	-0.202	1.099	-1.368	-1.453		
-0.077	0.195	-0.589	-0.009	0.203	-0.694	-0.886	-2.184
-0.451	-2.181	-1.035	-3.367	-1.505	-3.810	1.063	
-0.764	2.448	-0.475	1.730	-0.068	-0.616		

Table36.txt

-0.168 2.134 -2.385 -2.173 1.458 -1.333 -1.847 -0.635
-1.395 -0.223 -0.722 -1.489 -1.348 -1.334 -0.309
-1.032 -1.386 -1.191 -1.772 0.235 1.194
-2.303 0.179 -1.938 -2.872 -0.435 -0.864 -1.969 -0.956
-2.194 -0.934 1.212 -2.409 -0.526 -2.062 -0.961
-1.021 0.295 -3.079 -0.354 -2.052 0.032
-0.463 -0.842 -2.233 -2.139 -1.631 -2.153 -2.588 -2.836
-1.487 -3.255 -0.757 -3.948 -0.890 -2.900 -1.358
-2.032 -1.683 -4.073 -0.950 -0.216 -1.308
-0.114 0.221 -2.401 -2.508 -0.785 -1.954 -1.722 -1.837
-1.115 -2.820 -0.624 -2.393 -0.505 -1.713 -1.263
-1.578 -1.335 -4.132 -1.574 -2.220 -0.560
-1.054 0.553 -0.031 -2.297 -2.769 -1.803 -0.452 -1.207
-1.856 -1.790 -0.585 -0.884 -1.054 -0.216 0.224
-1.697 0.892 -1.154 -1.698 0.861 0.212
-2.358 -2.510 -0.596 -0.997 -2.459 -0.316 -3.585 -1.939
-2.161 -2.435 -1.970 -3.029 -0.338 -2.094 -2.653
-2.038 -1.073 -1.135 -0.223 -0.933 -0.626
1.224 -1.794 -1.583 -2.354 -1.314 -0.264 -1.506 -1.920
-2.264 -0.895 0.024 -1.997 -2.417 -4.562 -1.588
-1.712 -1.920 -0.693 -1.664 -0.543 -1.048
-0.899 -0.287 -2.866 -0.207 -1.681 -0.085 -0.486 -1.471
-1.506 -2.313 -1.439 -2.354 -0.235 -2.094 -1.767
-1.171 -0.799 -2.388 -2.499 -1.185 -0.739
-0.526 -0.732 -1.978 -1.112 -0.745 -2.402 -0.090 -1.146
-0.772 -3.699 -0.722 -2.184 -1.042 -3.243 -1.445
-1.185 0.658 -3.877 -0.111 -1.113 -1.648
-0.537 -0.922 -0.690 -0.444 -0.730 -0.944 -1.802 0.142
-1.222 -0.376 0.156 -0.343 -1.797 -1.140 0.224
-0.446 -1.156 -2.658 0.789 -1.543 0.747
1.083 -0.084 -2.251 -1.874 -1.417 -3.134 -1.268 -0.186
-2.287 -2.192 -0.716 -1.681 -2.687 -1.862 -2.779
-1.515 -1.530 -1.254 -1.457 -1.171 -0.650
0.125 0.094 -2.434 -1.759 -0.451 -2.547 -1.745 -2.704
-0.460 -2.260 -2.558 -0.955 -0.502 -1.288 -1.633
-0.262 -0.953 -2.395 -3.108 -0.262 -2.612
0.253 -1.601 -2.593 -0.555 0.611 -2.962 -2.527 -2.872
-2.793 -0.612 -0.837 -2.699 -1.368 -2.793 -0.942
-2.166 -0.101 -1.627 0.333 -0.132 -0.174
0.447 0.278 -1.821 -1.789 -0.633 -2.130 -4.819 -1.523
-0.482 -2.549 -1.328 -2.860 -1.909 -2.605 -1.784
-3.312 -2.428 -3.455 0.240 -2.423 -1.846
1.976 -1.715 -1.558 -1.341 -1.371 -2.550 -3.684 -2.770
-1.342 -2.023 -0.248 0.602 -1.427 -2.041 -0.516
-0.833 -1.370 -3.685 -0.098 -2.380 -2.140
-0.614 1.386 -1.947 -1.545 -0.892 -3.071 -1.921 -2.720
0.440 -4.093 -2.242 -2.261 -1.984 -2.738 -2.228
-2.691 -1.486 -0.192 0.158 -0.677 -1.455

Table36.txt

-1.095	-0.493	-1.956	-1.580	-0.915	-2.601	-0.584	-3.062
1.274	-1.434	-1.640	-0.597	-0.529	-1.377	-0.214	
-3.535	-1.212	-0.416	-0.759	-2.066	-0.329		
-0.057	0.396	-2.453	-2.940	-1.129	-2.565	-3.214	-2.141
-0.825	-1.929	-1.209	-3.964	-0.926	-2.402	0.306	
-1.024	-1.098	-2.963	-1.225	-1.536	-0.392		
1.345	-0.141	-0.430	-1.400	-1.943	-2.996	-2.496	-1.490
-2.403	0.309	-2.923	-1.632	-1.048	-0.460	-1.600	
-0.805	-1.374	-1.455	-2.039	-0.830	-0.633		
-0.291	-0.973	1.492	-1.516	-0.963	-2.355	-1.679	-1.213
-0.842	-2.207	-1.405	-2.634	0.487	-1.501	-1.678	
-1.467	-2.333	-3.088	-2.529	-0.863	-0.452		
-0.606	-0.184	-0.949	-2.907	-0.231	-1.775	-1.398	-3.225
-1.701	-1.865	-1.572	-2.641	-0.599	-2.753	-1.043	
-2.565	-0.613	-3.762	-2.567	-1.405	-3.011		
-0.619	-1.160	-2.516	-1.005	-3.246	-1.865	-2.235	-0.755
-1.307	-2.409	-1.532	-3.450	0.030	-2.056	-1.380	
-3.872	-2.149	-1.995	-1.497	-2.484	-1.058		
-0.269	-0.857	-2.124	-2.410	-1.985	-2.222	-1.736	-4.619
-1.770	-2.892	-1.275	-2.248	-2.216	-3.530	0.037	
-1.351	-0.778	-1.190	-1.978	-0.149	-0.712		
-1.290	-0.672	-2.320	-1.985	-1.765	-2.207	-0.991	-3.994
-0.721	-1.793	-0.964	-1.916	-1.357	-2.136	-0.488	
-0.503	-0.772	-3.538	-1.116	-0.636	-2.123		
-0.451	-1.753	-1.494	-0.055	-1.548	-1.904	-1.776	-2.030
-1.150	-1.744	-2.034	-0.572	-0.285	0.561	-1.540	
-0.725	0.164	0.228	-0.051	-0.598	-2.167		
0.705	-0.558	-2.452	-1.483	-2.696	-3.015	-2.576	-2.387
-2.172	0.217	-1.157	-3.537	-0.361	-2.259	-2.338	
-0.921	-1.538	-0.547	-1.680	-2.257	-0.713		
-0.547	0.103	-1.791	-0.113	-1.130	-1.667	-1.370	-0.319
-2.347	-1.655	-0.163	-1.808	-1.345	-0.937	-2.598	
0.153	-0.178	-2.216	-1.382	-0.745	-0.410		
-0.451	0.770	-1.788	-1.895	-0.664	-1.551	-0.956	-2.531
0.126	-1.694	-0.071	-2.144	-1.486	-1.609	0.313	
-1.159	0.770	-3.946	-0.063	-2.826	0.261		
0.330	-0.587	-1.548	-2.915	-0.178	-1.361	-0.624	-1.908
-1.026	-2.258	-1.391	-2.410	-0.645	-3.746	-1.451	
-1.918	-0.670	-2.108	-1.498	-2.570	-1.013		
0.108	0.082	-2.025	-3.182	-2.537	-3.364	-2.799	-2.875
-1.637	-3.691	-1.770	-1.772	-0.241	-2.403	-1.773	
-1.697	-1.939	-2.299	-1.861	-1.867	-2.163		
-0.041	0.968	-1.235	-1.459	-3.028	-2.172	-2.403	-1.625
-0.604	-1.216	-0.375	-1.445	-0.086	-2.896	-0.641	
-1.971	1.113	-1.688	-0.206	-2.295	-2.604		
0.464	1.277	-1.516	-1.797	-1.322	-0.581	-1.686	-3.603
-2.249	-3.094	-0.473	-2.646	-2.132	-0.552	-0.023	
-1.667	-2.221	-1.371	-1.146	-0.748	-0.448		

Table36.txt

-0.277 2.193 -1.422 -1.204 -0.458 -2.356 -1.897 -0.742
-0.399 -2.656 -0.542 -2.868 -0.591 -0.547 -1.387
-2.041 -1.413 -2.683 -1.694 -1.025 0.302
-0.460 0.384 -2.228 -2.492 -3.268 -3.408 -3.080 -2.470
-0.740 -3.476 -1.335 -3.383 0.309 -2.425 -2.041
-2.883 -1.105 -2.645 -1.785 -2.471 -0.195
-0.340 -0.044 -0.562 -1.134 -1.147 -0.851 -3.442 -2.621
-1.310 -1.903 -1.387 -2.015 0.191 -1.270 -1.596
-0.957 -1.117 -1.742 -2.691 -2.467 -0.511
-0.232 0.727 0.765 -0.938 -1.160 -1.122 -1.454 -1.659
-1.028 -1.451 0.900 0.082 -2.086 -0.145 -0.858
-1.852 0.680 -0.354 -0.716 -0.822 -1.159
-2.309 -0.441 -1.224 -1.672 -0.233 -1.067 -1.473 -2.582
0.646 -1.446 -2.826 -2.761 -0.697 -4.384 -1.307
1.753 0.149 -1.044 -0.760 -2.332 -2.510
1.162 -0.140 -2.052 -1.718 -2.513 -3.703 -3.199 -2.706
-3.301 -1.741 0.190 -3.203 -2.115 -2.930 -1.941
-1.717 0.026 -2.198 -3.280 -0.651 -2.533
1.408 -0.620 0.570 -0.491 -3.315 -2.019 -1.326 0.074
-0.172 -2.234 -0.945 -1.582 0.278 -0.768 -1.569
-1.037 -0.008 -2.339 -1.154 0.431 -2.082
0.365 0.152 -1.433 -1.620 -0.414 -2.311 -2.434 -4.158
-2.263 -2.897 -2.662 -2.850 -0.959 -3.313 -3.278
-1.465 -1.279 -5.244 -0.979 -1.247 0.546
-0.624 0.258 -1.694 -1.696 -2.316 -0.248 -3.631 -2.729
-1.383 -4.160 -1.392 -3.207 -1.632 -2.246 -1.489
-2.230 -2.979 -1.352 -0.607 -2.254 -2.826
-0.906 -0.998 -1.194 -2.335 -3.267 -3.379 -1.935 -3.266
-1.188 -2.202 -0.143 -3.614 -1.254 -4.031 -1.823
-2.038 -1.688 -2.447 -2.392 -0.407 -0.725
-0.523 0.655 0.536 -0.582 -2.024 -0.309 0.007 -3.157
-2.335 -0.507 -0.883 -1.240 -0.196 -0.828 0.650
-2.823 0.636 -0.644 -1.381 -1.913 -2.176
1.587 -0.420 0.276 -1.740 -1.847 -1.622 -0.440 -2.184
-0.269 -3.196 1.463 -0.545 -0.683 -3.527 -0.264
-1.491 1.040 -1.661 -1.139 -1.201 -0.046
-0.855 -1.518 -1.440 -0.967 -0.974 -2.538 -2.231 -3.102
-0.612 -4.682 -0.869 -2.757 -2.422 -1.729 -0.193
-2.023 -2.691 -3.144 -0.571 -2.809 -0.949
0.984 -0.898 -2.289 -2.360 -0.440 -3.900 -1.387 -0.987
0.095 -1.649 -1.731 -2.369 -2.271 -2.098 -1.396
-0.772 -1.931 -2.339 -0.815 -0.238 -1.008
-0.727 -0.516 -1.401 -3.380 -2.560 -1.755 -1.703 -2.115
-1.794 -3.179 -2.680 -2.439 -0.849 -2.691 -4.098
-0.147 -0.446 -1.503 -2.326 -1.921 -2.882
0.198 0.287 -0.291 0.443 -0.436 -0.881 -1.410 -1.992
-1.398 -2.978 -1.746 -3.037 -1.074 -2.127 -0.303
-2.493 -0.414 -2.589 -2.419 0.688 0.038

Table36.txt

-1.089 -1.422 -1.742 -1.869 -0.560 -0.978 -1.820 -2.680
-0.867 -1.696 -1.180 -2.483 -1.767 -2.431 -0.957
-2.153 -1.756 -2.781 -1.981 -1.853 -3.059
-0.031 -1.671 -1.376 -0.889 -1.570 -1.031 -1.014 0.072
-1.466 -0.818 -0.420 -0.779 -2.976 -1.368 0.594
-1.846 -1.711 -2.059 -0.553 -0.732 -1.258
-0.169 -0.702 -1.929 -1.547 -1.140 -2.428 -2.596 -1.992
-0.329 -4.152 0.043 -0.884 -0.648 -3.019 -1.980
-1.758 -0.266 -1.061 0.075 -1.108 -0.931
-0.396 1.490 -1.646 -1.654 -0.331 -1.820 -1.445 -1.775
-0.365 -2.924 0.415 0.266 -0.766 -0.599 0.191
-1.921 -0.190 0.841 -0.113 -2.157 0.180
1.475 0.112 -2.245 -0.556 -0.415 0.046 -2.563 -0.928
-2.223 -1.705 -0.753 -1.179 0.314 -2.205 -2.110
-2.259 -0.109 -0.939 0.790 -1.461 -0.845
0.445 -1.232 1.076 -2.451 -0.950 -0.485 -1.641 -2.939
-1.948 -2.014 -0.791 -1.192 0.500 -3.575 -0.850
-0.328 1.063 -0.955 -0.500 -0.430 -0.916
-0.673 -1.181 0.896 0.732 -1.388 -2.400 -2.194 -0.559
-0.967 -3.345 -1.256 -0.359 0.219 0.538 0.441
-0.916 -0.751 -1.722 0.524 -1.026 -1.748
1.468 -0.249 -0.344 2.140 -0.010 -2.132 0.257 -1.660
-0.183 -0.387 -3.037 1.223 -1.072 -1.715 -2.601
-1.371 -0.443 -1.326 -1.297 -1.937 0.198
1.005 -0.795 -0.185 -1.860 -1.197 -2.228 -0.691 -1.412
-0.313 -2.199 -0.028 -1.777 -3.894 -1.478 -1.510
-1.010 0.345 0.124 -1.533 -1.650 -0.675
0.588 0.237 -1.301 -1.032 -1.505 0.149 1.377 -0.617
0.566 -1.199 -1.892 -1.357 -0.016 -2.215 1.051
-0.946 -0.141 -1.340 -0.627 -0.755 1.123
0.571 -0.811 -1.342 1.265 0.238 -0.857 -1.474 0.410
0.395 0.285 -0.700 -2.748 -0.935 -1.631 -1.518
-1.930 -0.314 0.087 -1.574 -0.939 -0.368
1.887 -0.236 -0.876 0.652 -0.611 -2.584 -2.097 -0.723
-1.495 -1.081 -1.825 -0.887 -0.929 -2.611 -2.239
-2.337 0.323 -2.524 -1.173 -0.076 -0.081
0.972 -1.185 -1.845 -0.401 -2.139 1.201 -2.680 0.923
0.866 0.023 0.423 -0.617 -0.428 -2.245 -1.524
-1.496 -1.550 -4.150 -2.093 -0.372 -0.726
-1.855 -0.321 0.305 -1.050 0.821 0.187 0.986 1.561
2.334 2.418 2.651 1.467 -1.271 -0.908 -0.603
1.254 0.333 0.139 2.334 2.057 0.652

chr10q_AI chr11p_AI chr11q_AI chr12p_AI chr12q_AI chr13q_AI chr14q_AI

Table36.txt

chr15q_AI	chr16p_AI	chr16q_AI	chr17p_AI	chr17q_AI	chr18p_AI	chr18q_AI	
chr19p_AI	chr19q_AI	chr20p_AI	chr20q_AI	chr21q_AI	chr22q_AI	Cancer	
-0.080	0.035	-2.449	0.219	-0.959	0.025	-1.420	-0.966
-1.203	-1.205	-0.167	-1.312	1.405	-0.382	-0.137	
0.556	1.339	0.105	0.065	-0.363	Pancreas		
-2.104	-0.957	-0.889	-0.703	-0.397	-0.502	-1.671	-0.726
0.437	-1.174	-0.412	-0.931	-0.595	-1.920	-1.166	
0.866	-0.898	-1.121	1.454	0.421	Pancreas		
-1.201	0.182	1.617	-1.286	-0.416	-1.076	0.569	0.366
-1.125	0.699	-1.979	0.225	-0.743	-0.198	0.004	
-0.827	0.200	-0.309	-0.058	0.825	Pancreas		
-0.335	1.282	-1.519	-0.340	-0.889	-0.201	-1.622	-0.605
0.452	-1.549	0.109	0.169	2.256	-0.026	-1.093	
0.324	0.920	-0.353	-0.111	0.309	Pancreas		
-1.640	-0.908	-1.911	-1.862	-0.209	-1.818	-2.533	-0.943
-0.150	0.337	-0.429	-0.236	0.123	-0.723	0.789	
-0.692	0.344	-2.148	-2.007	0.618	Pancreas		
0.229	0.057	-1.329	-1.117	-0.764	-0.852	-0.629	0.195
-0.733	0.805	0.151	-0.753	-0.189	-2.453	0.883	
0.983	-0.972	-2.013	-0.134	-0.918	Pancreas		
-1.333	-1.902	-0.370	-1.556	-0.223	-0.951	-1.813	-0.410
-0.694	-0.889	-1.711	-1.112	-0.784	1.424	-1.661	
-0.264	-1.103	-0.755	2.119	-0.837	Pancreas		
-0.058	-2.600	1.167	-0.437	-1.122	-0.209	-0.732	-0.279
0.298	-0.936	-0.316	-0.502	0.774	-0.317	0.887	
0.793	0.363	0.786	-1.530	-1.343	Pancreas		
-0.208	-1.160	0.262	0.020	-1.690	-1.132	-1.577	-0.232
-4.329	-1.197	0.365	-0.291	-0.024	-2.019	-0.625	
0.018	0.403	-1.983	-0.565	-0.347	Pancreas		
-1.212	-1.490	-0.989	0.632	-1.968	-1.216	-0.481	0.768
0.750	-1.981	0.330	0.135	-0.075	0.867	2.091	
1.163	-0.619	0.009	-0.696	-1.590	Pancreas		
-0.347	1.322	0.025	-1.392	-1.484	-1.770	0.703	0.407
0.610	0.474	-1.154	-0.105	0.873	-1.252	-0.491	
-3.101	-0.624	-1.269	-2.122	-2.027	Pancreas		
-1.035	-0.507	-2.390	0.145	-1.151	-0.499	-0.695	0.501
0.340	-1.208	-0.236	0.483	-1.732	0.169	-0.770	
-0.052	-0.862	0.800	-1.577	-0.910	Pancreas		
-2.083	-0.228	0.819	-1.158	-1.228	0.285	-0.979	0.427
1.117	-1.055	-2.059	0.558	-0.270	1.088	-0.295	
-1.302	-0.322	1.473	-0.114	1.848	Pancreas		
0.822	-1.700	-1.733	-0.923	1.410	-3.057	-0.374	-0.931
0.103	-0.291	0.930	-0.607	0.480	-0.620	-0.159	
-0.450	0.181	-1.635	-1.570	-1.862	Pancreas		
0.178	-0.680	-0.366	1.477	0.864	-0.335	-0.107	1.670
0.457	-1.189	0.004	-0.334	1.088	0.086	0.678	
1.295	0.769	-2.011	-0.886	-1.639	Pancreas		
0.733	-1.085	-2.437	-2.630	-0.408	1.108	-2.164	-0.698

Table36.txt

-0.132	-1.594	-1.011	-1.583	0.722	-2.174	-0.116	-1.014
-1.664	0.601	-1.200	-1.042	Pancreas			
0.075	-0.185	-0.485	0.425	-0.673	-2.068	-0.075	-0.034
-1.292	0.540	-1.767	-0.135	1.011	-0.165	1.302	-0.385
-0.114	-1.738	-1.819	-1.308	Pancreas			
1.272	1.762	-0.165	-2.232	-1.806	-0.340	-0.725	-0.271
0.072	0.171	-1.411	-0.530	1.042	-0.011	0.527	0.562
1.384	0.624	-0.669	-0.270	Pancreas			
0.945	-0.252	-0.779	-1.082	0.686	-1.548	-1.062	-1.474
-0.813	-0.930	-1.039	1.138	-2.677	-0.827	1.876	-0.932
0.150	0.395	-1.723	-0.703	Pancreas			
-0.850	-1.194	-2.516	0.262	-0.303	-1.106	-0.184	0.690
0.891	-0.701	-0.103	0.617	2.052	0.549	0.982	-1.642
0.490	-0.256	-0.790	0.147	Pancreas			
-0.311	-0.539	0.023	-0.515	-1.324	-1.267	0.174	-0.248
0.663	0.434	-0.085	-1.513	1.697	-0.288	-1.560	1.020
-1.058	-0.314	0.123	-0.725	Pancreas			
0.712	-1.744	0.583	-0.750	-1.585	-1.786	-0.811	0.437
-0.851	-1.228	-0.083	0.339	-0.457	-1.050	-1.648	-0.558
-0.546	-1.165	-0.947	1.165	Pancreas			
-1.292	-1.445	0.362	0.216	-0.480	-2.794	-3.406	-2.658
-1.230	-0.394	0.130	1.118	1.319	0.621	1.204	-0.946
1.703	-2.570	-1.322	0.349	Pancreas			
14.275	15.944	16.261	7.885	18.483	18.940	14.071	11.893
6.766	11.813	8.084	9.488	7.258	12.431	6.039	8.802
6.807	7.775	8.562	8.755	Pancreas			
-1.230	-0.207	-0.542	-1.146	-0.359	-2.589	-1.910	-0.460
-1.626	-2.316	0.061	-0.839	2.711	-0.157	0.213	-0.216
0.243	0.556	-0.396	-0.828	Pancreas			
-1.879	-1.324	0.236	-1.294	-2.374	-1.770	-1.920	-1.814
-1.413	-0.021	-0.074	-0.170	-0.624	-0.016	-1.182	1.661
-1.140	0.682	-2.083	0.875	Pancreas			
-0.783	0.654	-1.557	-1.512	-1.692	-1.583	-1.380	-0.914
-1.134	-1.192	-1.230	-0.827	-1.512	-2.176	-0.832	-0.839
-0.480	-1.960	-2.165	-2.906	Pancreas			
-1.302	-0.590	-0.694	-0.840	-0.231	0.482	-1.769	-0.863
-0.549	-1.735	-0.771	-1.091	0.812	-2.156	0.225	0.652
-0.989	-0.480	-1.850	0.342	Pancreas			
0.902	-0.458	0.988	-1.575	-0.051	1.183	-0.557	0.811
0.783	0.671	-0.452	1.300	2.250	0.745	0.881	-1.065
1.027	0.624	1.234	-0.417	Pancreas			
0.458	-1.131	-0.809	8.139	0.658	-0.592	0.132	0.342
1.229	-0.674	-0.128	-0.048	0.886	1.586	-0.049	-0.196
1.672	-0.781	2.824	0.785	Pancreas			
0.368	-0.579	-0.470	0.321	0.617	-2.402	-0.069	0.721
-1.542	-0.152	-0.010	-0.294	-1.765	-0.484	0.407	0.896
-1.149	1.012	-0.036	-0.866	Pancreas			
-1.552	-0.900	-1.234	-0.309	-2.609	-0.600	0.077	-1.000

Table36.txt

1.344	0.102	-0.177	0.260	0.359	0.382	-1.462	-0.947	0.908	-0.444
0.026	1.241	Pancreas	1.176	-1.940	-0.096	0.022	-0.894	-1.060	-0.948
-1.615	-2.320	0.276	0.086	-1.039	1.025	0.235	-1.429	0.151	0.838
0.152	-0.383	-1.851	Pancreas	-0.828	0.379	-0.859	-1.536	0.269	-0.701
-2.171	-0.622	-0.806	0.755	-0.317	0.480	-0.343	-0.736	-0.866	0.001
-1.077	-0.348	-0.672	-1.506	Pancreas	-1.192	-1.609	1.122	1.209	1.343
-0.417	0.957	0.886	-1.137	-0.898	0.761	1.074	0.969	-0.285	0.441
0.081	0.103	-0.204	0.401	0.245	Pancreas	0.114	-1.397	-0.858	-2.282
-1.107	-1.701	-0.485	1.021	0.998	-0.516	-0.694	0.411	-1.065	-1.141
-0.374	-0.674	-1.428	-2.012	-0.581	-1.863	Pancreas	-1.633	-0.837	0.529
0.783	-0.721	0.696	1.268	-0.704	-1.263	-1.571	0.017	1.852	1.229
-1.076	1.160	0.266	-0.189	0.367	0.668	0.421	Pancreas	0.602	0.301
-1.239	-1.018	-1.517	0.477	-1.083	0.234	1.322	-1.129	0.499	-0.083
-1.177	-2.083	-0.302	-0.295	-0.179	-1.552	-1.116	-0.779	Pancreas	-0.509
-1.767	-1.291	-1.012	-1.473	-2.643	-0.629	-0.300	-1.034	-1.628	-1.081
-0.909	-0.304	-1.312	-0.624	0.176	-1.429	-0.886	-0.841	-1.456	Pancreas
-1.340	-1.281	-0.379	0.606	1.302	0.225	0.472	-1.504	0.318	-0.937
0.209	0.407	0.004	1.227	1.127	0.654	1.619	0.930	-0.763	-0.120
Pancreas	0.439	-0.648	-0.490	-0.156	0.083	-0.412	0.522	-0.443	-0.164
0.180	-0.963	1.709	0.194	-0.454	0.742	0.306	0.641	-0.271	-1.982
-0.112	Pancreas	1.700	-1.909	-1.137	0.002	-0.835	0.899	-2.065	-0.425
-0.840	2.181	-0.566	-1.329	1.373	-0.538	-0.443	-0.863	0.600	1.591
-0.890	-0.755	Pancreas	-0.819	-2.177	-0.286	-1.632	-2.466	-1.838	-1.137
0.349	0.653	0.595	0.641	-1.228	-0.179	-0.114	-0.822	-1.716	-0.668
-0.706	0.565	1.013	Pancreas	0.020	0.494	0.279	-2.269	0.122	1.042
-1.433	-1.025	-1.147	-0.649	-1.740	0.201	1.316	-0.827	-0.746	1.517
0.144	-1.713	0.251	-0.997	Pancreas	-0.288	-0.955	-1.116	-0.490	-0.374
-0.934	-1.127	-1.092	-1.911	-1.230	-0.956	-1.012	-0.504	-0.831	-0.591
-0.578	-0.801	-2.255	-0.578	0.316	Pancreas	0.479	-0.027	0.790	-0.992
-0.697	-1.168	-1.357	-0.669	-1.687	-1.235	-1.547	0.122	0.018	-0.147
-0.128	-3.326	-0.690	-1.052	-0.507	-0.847	Pancreas	0.320	-0.980	-1.276
0.531	-0.588	-2.213	-0.061	-0.081	-1.105	-2.143	-0.745	0.060	-0.594
-1.497	-2.004	-0.558	1.078	0.334	0.408	0.172	Pancreas	-1.404	-1.133
-1.555	0.846	-0.794	-0.573	0.019	0.187				

Table36.txt

0.308	0.059	0.875	0.139	1.798	0.731	-0.790		
-1.989	0.710	-0.623	-0.285	-1.232	Pancreas			
-1.242	-0.598	-0.025	0.374	-1.095	-1.859	-0.968	-0.342	
0.373	0.314	0.299	2.236	0.010	-1.485	2.082		
-0.555	0.034	1.620	-1.034	-0.270	Pancreas			
0.693	-0.982	-0.271	0.408	-1.503	-0.030	-0.945	0.286	
-0.251	0.421	-1.355	-0.260	0.939	0.157	-2.143		
-0.843	-0.993	0.117	0.779	-0.031	Pancreas			
-0.077	1.026	-0.656	0.097	-0.672	-1.087	-0.510	-0.879	
0.156	0.037	-0.746	-0.224	-0.868	-2.002	-0.081		
-1.020	0.111	-0.894	-1.144	-0.805	Pancreas			
0.951	-2.112	-0.210	0.710	0.117	-3.787	-0.957	-1.337	
-0.602	0.107	-0.276	-0.768	-1.384	0.043	-2.125		
0.864	-1.505	-1.433	-0.146	-1.831	Pancreas			
-1.870	-0.916	-0.755	0.259	-1.187	-1.419	-0.367	-3.632	
-0.263	-1.163	0.068	-1.545	-1.740	-2.033	-1.010		
0.356	0.856	-0.524	-0.796	-2.127	Pancreas			
0.226	-2.799	-0.263	-0.754	-0.021	-0.486	-0.871	-0.716	
-1.978	-1.065	-0.299	-1.472	0.230	-1.320	1.031		
1.434	0.017	0.539	1.174	-0.220	Pancreas			
-0.518	0.428	-0.823	0.228	-0.019	-1.579	-0.192	0.291	
-0.256	0.124	-0.019	1.709	1.189	-1.658	-0.939		
-0.068	0.770	0.240	0.561	0.973	Pancreas			
-1.089	-0.767	-1.202	0.428	-0.514	-0.469	0.511	-0.064	
0.965	-0.235	1.115	0.937	0.281	-1.015	-0.201		
-0.715	1.444	0.093	0.941	-1.159	Pancreas			
1.677	0.616	-0.170	1.170	2.250	-0.401	-0.372	-0.155	
0.574	-0.771	-0.851	-1.078	0.709	0.811	0.550		
1.824	-0.249	-0.388	0.316	1.136	Pancreas			
1.094	1.081	1.993	0.673	2.538	-0.159	-0.697	3.430	
-1.351	-1.495	-0.758	2.269	1.683	0.350	0.956		
-1.206	0.720	1.221	-1.556	-2.270	Pancreas			
0.437	-0.631	0.247	0.050	-1.913	-0.293	-0.385	-1.991	
-1.930	-1.892	-1.262	-0.596	-0.917	-1.472	-0.235		
0.200	0.815	0.113	-0.301	-0.758	Pancreas			
-0.185	-1.838	-1.384	0.066	-0.511	-0.968	-1.555	-1.513	
-0.213	-0.070	0.734	-0.135	-1.436	-1.552	0.284		
-1.017	0.160	-1.027	-1.466	2.578	Pancreas			
1.262	-0.864	0.839	-1.005	0.227	-0.669	-0.892	0.122	
1.388	-0.218	-0.112	2.075	-0.136	2.433	0.624		
-0.919	-1.225	2.219	-0.091	0.293	Pancreas			
0.313	-1.404	-0.911	-1.838	-0.781	0.616	-0.951	-3.435	
-0.806	-2.174	-0.762	-0.892	-2.091	-1.383	1.285		
-0.718	0.491	-1.545	0.265	0.579	Pancreas			
0.186	0.948	0.303	0.071	0.880	-1.138	0.376	-0.303	
0.814	-1.837	0.289	-0.163	0.312	1.190	-0.684		
1.218	0.963	-0.649	1.506	-0.121	Pancreas			
-0.516	-1.139	0.190	-1.713	-1.593	-0.975	-0.894	-1.239	

Table36.txt

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    2.057     -1.719     -1.635     -0.752     1.071     -1.534     -0.694
0.234     0.703     -1.343     1.147     0.536     Pancreas
0.018     0.676     0.625     0.127     -1.256     -1.100     -1.923     -0.488
    -1.579     -0.431     1.192     -0.056     1.023     -1.409     0.534
-0.064     0.180     -1.378     0.212     0.094     Pancreas
-0.972     -0.317     -0.132     -0.575     0.288     -0.272     -0.819     0.599
    -1.936     0.120     -0.142     -0.464     -0.118     -0.195     0.816
-0.011     -0.448     -0.435     1.045     -1.285     Pancreas
0.765     -3.012     -3.548     -2.582     -1.846     0.478     0.026     2.055
    0.165     -0.490     1.393     -0.887     0.016     -0.443     -0.202
-0.101     -1.607     -0.149     0.541     -0.688     Pancreas
-1.027     -0.830     0.968     0.884     -0.437     -0.979     -0.635     -0.189
    -0.983     0.485     -1.427     1.018     -0.817     -0.093     0.829
0.744     -0.079     1.348     -2.038     -1.293     Pancreas
-1.775     -0.401     -1.429     -1.959     0.593     -2.226     -1.319     -0.576
    -0.157     -0.064     -1.449     0.780     0.756     -1.334     -0.654
0.183     0.954     -1.277     -0.776     -0.474     Pancreas
-0.210     -0.504     -0.429     -1.085     0.003     0.004     -0.925     -0.928
    0.397     -0.971     -0.601     0.710     -0.106     -0.063     0.771
-1.069     -2.616     1.519     -0.166     -1.499     Pancreas
-0.333     -0.514     -1.062     -0.028     -0.724     2.392     -0.793     -0.790
    -0.947     -0.284     0.331     -0.115     0.173     -0.737     -0.422
-0.160     -0.669     0.041     -0.077     0.399     Pancreas
-2.769     -1.775     -0.368     0.564     -1.539     -0.475     -1.956     -2.290
    -1.735     -0.120     -0.638     -1.018     -0.355     -2.477     0.839
1.154     1.495     -0.657     0.923     0.772     Pancreas
-1.242     -1.198     -1.263     0.556     0.912     -3.955     -1.608     -0.254
    -2.507     -0.805     -0.021     -1.459     0.934     -1.777     -1.782
-1.504     -0.701     -1.158     -0.192     -1.468     Pancreas
1.197     -2.346     -0.997     -1.021     0.406     -0.471     0.104     0.622
    0.002     0.002     0.214     0.398     0.706     -0.721     1.053
-1.419     0.871     -0.916     -0.886     -0.319     Pancreas
0.086     1.161     -0.810     0.338     0.134     -0.892     -0.938     -1.713
    1.239     -2.316     1.487     1.270     0.869     -0.515     -0.930
-1.450     0.272     1.007     0.787     -2.187     Pancreas
-0.885     1.012     0.939     -0.290     -2.554     -1.523     -2.051     -0.395
    -0.723     0.874     -0.817     0.315     -0.523     -0.974     2.600
-0.705     -2.404     -1.010     -0.579     0.155     Pancreas
-0.076     -0.511     -0.501     -1.109     -0.688     -1.081     -0.280     1.192
    -1.524     -0.955     0.287     -0.095     1.059     -0.428     0.052
-0.393     -0.108     1.020     -0.414     -0.003     NA
0.007     0.141     0.244     -1.228     -1.382     -1.669     -0.603     -0.656
    1.196     -1.130     -1.167     -0.616     0.920     -1.097     -1.390
-1.217     0.183     0.811     -0.072     -1.270     NA
0.338     -2.775     -0.860     -0.111     -0.159     -0.135     -0.818     -0.846
    -0.415     -1.502     1.414     -0.928     -1.433     -1.791     0.102
-1.524     -0.853     1.141     0.713     0.810     NA
-1.197     -0.714     -4.459     -0.489     -1.418     0.651     -2.639     -0.280
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Table36.txt

-0.559	-0.768	1.203	-0.357	0.057	-0.764	-0.345	
-1.768	0.269	-0.774	0.031	-0.984	NA		
-1.762	-0.528	-1.806	1.754	0.770	-2.376	-1.815	0.983
-0.930	-1.239	-2.352	-2.300	-0.693	-1.274	0.236	
-2.260	-0.190	0.259	-1.784	1.106	NA		
0.477	-0.874	-1.237	-3.247	0.219	-0.414	-0.942	1.145
-0.302	0.206	0.582	0.107	0.460	-1.976	-0.712	
-0.282	-0.764	-1.487	-0.279	-0.427	NA		
-0.031	-0.515	2.126	-1.123	-0.984	-2.050	-1.153	-1.805
-1.312	0.386	0.300	-1.025	-2.292	-1.365	0.289	
0.536	-0.813	-2.429	0.888	-2.285	NA		
-2.005	-1.672	-2.280	-0.712	-3.107	-2.267	0.277	-0.785
-1.609	-0.478	0.502	0.330	0.304	1.320	-0.189	
-1.051	-0.076	0.673	1.712	-1.016	NA		
-1.722	-1.506	-1.696	1.378	-1.248	-0.219	1.214	0.409
-1.795	-1.519	0.327	-0.594	-0.626	0.853	0.000	
-1.442	-1.367	-0.619	-0.381	0.097	NA		
-0.606	-0.344	-1.711	-0.452	0.627	-0.718	1.331	-0.721
-1.513	-1.183	0.411	0.313	-0.654	-0.634	-1.505	
-1.311	-0.244	0.636	-1.058	-0.893	NA		
-0.179	-1.401	-1.224	-1.719	-2.076	0.040	-0.746	0.342
-0.497	-1.081	1.271	1.081	1.367	0.166	0.627	
-0.805	-1.315	0.182	-1.389	0.112	NA		
-1.153	-2.743	-0.257	-0.640	-2.116	-1.671	-0.366	-0.407
1.291	-1.672	0.624	-0.341	-1.365	-1.276	0.082	
-0.137	-1.421	-0.336	-0.781	0.321	NA		
-0.615	0.200	0.104	-0.249	0.070	-1.559	-1.493	-0.861
-1.695	-0.788	1.319	-1.655	-1.563	-1.192	-0.885	
-1.074	-1.052	-2.376	-0.485	0.088	NA		
-1.172	0.390	0.120	-1.218	-1.080	-2.054	-1.697	0.128
-1.245	-1.382	-2.728	1.407	-0.580	-1.088	0.284	
-1.434	-0.947	1.470	-0.504	-2.450	NA		
-2.518	-0.346	-1.756	-1.769	-0.472	-2.756	0.364	-3.073
-0.770	0.677	-0.239	-2.001	-1.726	-1.833	0.081	
1.161	-1.007	-0.453	0.560	-0.236	NA		
-0.655	0.772	0.912	1.462	-0.505	-2.048	-1.824	-2.128
-1.516	-2.214	-1.436	0.542	1.781	-1.095	0.655	
1.327	-0.569	-1.832	-2.360	-1.410	NA		
-0.823	0.573	0.055	-0.807	-0.974	-0.109	-0.256	-0.454
-1.087	-2.173	-1.203	-1.220	-1.852	-1.996	-0.011	
-3.530	-0.933	1.192	0.826	-1.218	NA		
-0.231	1.707	0.368	-2.681	-2.785	0.597	-2.447	-2.783
0.627	0.193	4.159	-0.203	-0.234	-1.347	0.142	
-0.017	0.921	-0.497	-1.466	-1.748	NA		
-1.409	-2.108	-0.779	-0.490	-0.646	-0.016	0.120	-1.603
0.151	-0.523	-0.001	-0.155	0.992	-1.216	2.484	
0.398	1.389	0.960	-1.212	-0.132	NA		
0.599	0.282	-1.303	-1.544	-1.865	-0.192	-0.110	-1.216

Table36.txt

-0.929	-1.367	-1.671	-1.431	0.585	-1.066	-0.083	
-1.258	-1.640	-0.902	-0.995	-0.151	NA		
-0.371	-1.074	-2.032	-0.489	-1.606	-1.591	-0.593	-2.657
-1.068	-1.017	0.996	-0.392	-0.107	-0.047	-1.732	
-0.260	-0.087	-1.009	-0.368	0.201	NA		
1.655	-1.181	-0.671	1.524	1.150	-1.129	0.169	-1.046
0.957	-0.027	-0.698	0.748	0.213	0.284	-1.271	
-0.612	0.598	-1.306	-0.303	-0.660	NA		
0.548	-1.267	-1.839	-1.669	0.576	-0.889	-0.781	-2.517
1.801	0.151	-1.019	1.476	-0.103	-1.013	0.572	
-1.262	-1.118	-0.990	-0.824	0.137	NA		
0.332	-1.045	-0.784	0.000	-0.936	-1.441	-1.979	-0.466
1.663	-0.351	0.065	0.366	-1.603	-0.812	-0.653	
-0.419	-1.209	-2.350	0.466	-0.684	NA		
-2.177	-0.668	-0.690	-1.764	0.187	-0.991	-1.001	0.335
-1.444	-0.401	-1.257	-1.724	1.049	0.656	1.043	
0.442	-0.541	0.286	-3.015	-0.559	NA		
-1.318	-1.776	-1.034	1.331	-1.585	0.007	-1.792	-0.410
0.214	-1.713	-1.605	-0.038	0.070	-0.601	1.657	
-0.765	0.141	1.209	1.062	-1.421	NA		
-1.489	-1.625	-0.461	-1.386	-1.531	-1.443	-0.694	-2.331
-0.194	-0.258	-1.320	-0.096	-0.250	-0.868	-0.092	
-1.734	-0.559	-0.361	-0.467	-0.702	NA		
-1.273	1.266	-0.284	1.462	-1.526	-0.484	-0.230	0.001
-0.866	-0.437	0.458	0.957	-1.053	-1.350	-0.183	
-1.341	2.417	0.293	-1.914	-2.257	NA		
-0.621	-0.624	-1.100	1.479	-1.750	-0.781	-1.895	-2.070
0.604	-0.662	-0.531	-0.137	0.130	-0.679	-0.790	
0.025	0.510	-0.198	0.787	1.847	NA		
0.036	-0.221	-1.304	0.305	-1.397	-1.060	0.642	-1.373
0.500	-1.130	-0.332	-0.821	-1.799	-2.080	-0.660	
0.354	-0.137	0.663	-0.263	-1.966	NA		
0.153	0.347	-0.216	-0.879	-2.191	-1.595	-1.048	-0.781
-0.743	-0.619	-0.805	0.202	2.471	-1.689	0.236	
-1.532	-3.198	-3.148	-1.247	-1.436	NA		
-0.288	1.106	-0.497	-1.979	-1.172	-0.643	-1.212	-0.549
-0.176	-0.867	0.575	0.059	-1.637	-0.940	-1.972	
-0.165	-0.824	-0.669	0.678	-1.016	NA		
-1.736	-0.499	-1.982	-0.974	-2.595	-0.894	-1.604	-3.127
-0.759	-1.959	0.646	-0.632	-0.610	-1.383	0.284	
-0.298	-0.103	1.093	-1.290	-0.972	NA		
-0.737	1.675	-0.357	-0.322	-1.405	-1.030	-0.579	-0.640
-0.602	-0.654	-1.970	-3.101	-1.841	-0.129	-1.099	
-0.635	1.592	-0.236	0.129	-1.118	NA		
-2.026	-1.011	-0.642	-0.744	-2.597	-0.427	-2.755	-1.589
-0.505	-2.057	1.914	-1.489	1.619	-1.332	-0.185	
0.319	-1.078	0.444	-0.430	2.525	NA		
0.304	-2.775	-1.162	0.639	-1.283	-0.683	-1.492	-1.076

Table36.txt

-0.226	-2.383	-3.706	-1.188	-1.311	-1.307	0.051		
-0.653	-0.856	-0.470	-2.791	-0.642	NA			
-0.929	0.734	-0.228	-3.387	0.297	-1.772	1.406	-1.729	
-0.057	-0.780	0.346	0.093	1.213	-2.020	0.713		
-0.838	-0.491	-0.910	-1.061	-4.364	NA			
-1.073	0.209	-1.660	-0.910	-2.367	-0.135	0.293	-0.977	
0.119	0.150	-0.772	0.001	-1.375	-1.579	0.057		
1.341	-2.086	-0.604	-1.770	-1.036	NA			
-0.582	0.626	0.181	-0.599	-0.541	-1.730	-0.668	0.239	
1.121	-1.343	0.063	0.404	0.233	0.083	-0.837		
-0.403	-0.672	0.024	-0.763	-1.711	NA			
0.191	0.995	-0.385	-0.037	-2.466	-0.214	-2.075	-0.989	
0.889	-1.178	-1.046	-1.657	0.009	-1.655	0.486		
-0.596	-0.327	0.382	-2.438	2.400	NA			
-0.853	-0.720	-0.947	-1.071	-1.762	0.332	-0.783	0.811	
-2.378	-1.794	-0.930	-0.891	0.870	-1.335	0.272		
0.143	0.913	0.724	0.371	1.359	NA			
0.221	-2.137	-1.900	0.935	-1.606	-1.833	-0.488	-0.350	
-0.929	-0.811	-0.359	1.076	-0.706	-1.343	-0.494		
-2.507	0.223	-1.149	-0.259	-2.085	NA			
0.294	0.328	-0.320	0.078	-0.524	-2.124	-2.003	0.495	
0.543	-1.728	-0.449	-0.655	-0.028	-2.463	0.978		
0.021	-0.032	1.398	-1.354	0.449	NA			
-0.407	-0.647	0.603	-0.968	-4.196	-1.214	-2.911	-1.750	
0.900	-0.273	-0.248	-1.612	1.648	-0.274	-2.225		
0.523	-0.558	-1.098	0.180	1.370	NA			
1.304	0.493	-1.356	0.580	-2.343	-1.210	-1.051	1.180	
0.326	-1.477	0.659	-0.783	1.747	-2.053	0.601		
-1.340	1.690	-1.632	0.270	-1.189	NA			
-2.330	0.276	-2.622	0.474	-0.374	-0.529	-1.693	-0.113	
-1.398	-1.015	-0.505	0.340	1.206	-0.850	-0.803		
-0.843	-0.077	0.396	-1.813	0.736	NA			
1.136	-1.886	-1.097	-0.911	-0.807	-0.710	-0.093	-0.515	
-0.115	-1.171	-0.845	0.918	-0.410	-1.912	2.429		
-0.773	-0.633	1.790	-1.710	-0.474	NA			
-0.733	1.031	-0.560	-2.165	-1.384	0.763	-1.091	-1.162	
-0.273	-0.043	-0.086	-0.454	-0.814	0.744	-0.300		
1.269	-1.979	1.148	-1.446	0.157	NA			
-0.924	-0.502	-1.284	-0.286	-0.801	-1.259	-0.745	0.576	
-0.659	0.716	-1.502	0.014	-0.654	0.469	-0.166		
-0.226	-0.955	-2.226	-2.067	-0.240	NA			
-1.538	0.734	-0.597	-2.486	-0.699	-0.439	-0.988	-1.487	
0.998	-1.094	-0.595	-0.729	-0.600	-1.062	-3.299		
0.262	0.338	-2.369	-1.444	-0.523	NA			
-2.140	-1.413	-1.997	-1.555	-0.661	-1.298	-0.970	-0.999	
-1.717	-2.086	0.340	1.344	0.964	-1.621	0.613		
0.544	0.666	0.262	0.850	-0.099	NA			
-0.537	-1.643	-1.508	-0.763	-2.642	-1.294	-1.596	0.602	

Table36.txt

-2.287	-1.800	0.512	0.255	-0.941	-2.169	-0.880	
-0.625	-1.773	-0.593	-0.582	-1.361	NA		
0.469	-0.069	-0.447	-0.823	-2.461	-1.341	0.288	-1.378
0.503	0.502	-1.072	0.391	-0.040	0.318	0.543	
-0.318	1.510	-0.243	0.338	-0.999	NA		
0.000	0.000	0.000	-0.445	0.000	0.000	-0.445	-3.090
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	NA		
-1.434	-1.933	-0.692	-2.291	-0.797	-2.882	-1.252	-2.040
-1.180	-1.279	-1.088	-0.159	0.297	-2.481	-1.072	
-2.659	-0.018	-1.550	0.806	-0.698	NA		
0.084	-1.584	-1.171	1.542	-0.463	-1.842	-0.311	-1.184
-1.207	-2.065	-0.379	0.214	-0.242	-1.097	-1.723	
0.222	-0.033	-0.565	-0.058	-4.774	NA		
-0.629	0.681	-1.248	-0.722	-2.532	-1.155	-1.384	-2.917
-2.584	-0.298	-0.464	-1.769	-0.728	0.393	-0.120	
-0.064	-0.501	-0.271	-1.348	-0.346	NA		
-0.335	0.667	-3.642	-0.835	-1.074	-3.176	-0.945	-0.708
-1.475	-0.270	-1.166	-0.326	0.187	-1.086	-3.808	
-0.947	-1.138	-0.346	0.105	-0.501	NA		
-1.564	-1.055	-0.493	-1.422	-2.346	0.707	-2.800	-1.968
-1.128	-0.885	-1.040	-0.317	-1.202	-0.216	1.097	
-1.564	-0.668	-0.431	-0.335	-1.620	NA		
-0.990	-0.701	-2.113	-0.126	-0.094	-1.835	-1.042	-2.160
-0.750	-0.099	0.007	-0.551	0.313	-1.368	-0.894	
-1.105	1.183	-0.550	0.423	-1.494	NA		
0.652	-0.110	0.266	-0.876	-0.600	0.367	-1.628	-1.321
0.774	0.509	1.392	2.538	0.010	-1.133	1.356	
0.199	-0.212	-1.441	-0.117	-1.966	NA		
-1.128	-1.057	-1.303	-0.903	-1.829	-1.047	-1.022	0.464
-1.277	-1.307	-2.588	-0.871	0.746	-0.742	-0.316	
-0.866	-1.466	1.273	0.195	0.797	NA		
-0.326	-2.073	0.831	0.314	-0.950	-1.846	-1.397	-0.937
-2.160	-0.595	-0.499	-0.825	-1.600	-1.303	0.060	
-0.074	-0.412	-2.302	0.208	0.180	NA		
-1.027	-1.498	0.054	-0.246	-1.469	0.266	-0.579	-1.133
-0.373	-1.973	-0.322	-0.639	-2.869	-0.420	-0.480	
-1.349	0.650	0.747	-0.297	0.620	NA		
-0.354	-1.121	-1.170	0.069	-1.687	-2.007	-2.771	-1.177
-1.328	0.794	-1.088	0.259	-0.416	0.413	-1.140	
-0.269	-0.463	-0.845	0.272	0.347	NA		
2.094	-0.522	-0.186	-1.101	-1.152	0.406	-0.274	-0.011
-1.346	0.672	1.107	-1.216	-0.940	-0.432	-0.651	
1.859	-0.329	-0.989	-0.800	0.075	NA		
-2.063	0.585	-0.881	-0.605	1.012	-3.394	-0.250	-1.743
-2.387	-0.339	-0.686	-1.079	0.130	0.261	-1.938	
0.099	0.109	0.088	0.099	0.449	NA		
-0.241	-2.358	-0.002	0.304	-1.064	-1.243	1.207	0.466

Table36.txt

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    1.028      -0.394     -1.315     0.011      0.534      -0.454     -2.069
1.222      -0.724     0.109      -1.059     -0.233     NA
-0.316     -0.159     -1.002     0.503      -0.505     -2.341     -1.340     -0.188
    0.539      -0.159     -1.453     -1.557     1.107      -1.053     -0.750
-0.896     -0.022     0.281      -1.754     -0.918     NA
0.961      -0.845     -2.156     -0.296     0.340      -2.316     -3.317     -1.667
    -2.217     -0.841     0.006      -1.521     -0.945     0.611      -0.638
-0.075     -1.107     0.002      0.012      -1.042     NA
-1.832     -0.908     0.523      0.026      -0.933     -0.565     -0.732     -1.380
    0.107      -1.486     -2.098     -1.365     0.620      -0.760     0.428
-0.906     -0.742     1.515      -1.070     -1.963     NA
0.100      1.530      0.526      -1.598     -0.180     0.967      -1.241     -0.044
    -0.782     0.219      -0.359     -0.081     -1.123     -0.902     -0.197
-0.910     1.027      -2.003     0.617      -0.545     NA
-1.813     -0.291     0.521      0.262      -2.517     -3.573     -0.149     -1.539
    -1.596     -2.103     0.658      -0.392     -0.402     -1.820     -0.402
-0.607     -3.048     -0.008     -1.423     -0.970     NA
0.601      -1.187     -0.927     0.612      -0.830     -1.212     -1.805     0.799
    0.229      -0.446     0.079      -0.605     -1.287     -2.943     1.225
0.934      0.290      1.101      0.516      -0.062     NA
-0.393     -1.813     -1.785     -0.299     -2.397     0.657      0.735      -0.367
    -0.705     -1.132     0.124      -2.212     -0.176     -0.923     -0.853
-0.674     -1.483     -0.569     -1.206     -0.340     NA
-0.183     -1.182     -0.960     -1.030     -2.322     -1.006     1.546      -2.204
    -1.099     0.066      -0.349     0.119      -0.086     1.400      -0.185
0.915      -1.036     0.480      0.128      -0.592     NA
-1.320     -0.523     -2.756     1.139      -0.609     -2.883     -0.236     -1.093
    1.030      -1.194     0.479      0.212      -2.211     -1.122     -0.904
-0.882     -1.137     -0.274     0.171      -1.425     NA
-0.177     -0.847     -0.365     -0.820     1.665      -2.399     1.016      -0.171
    -0.210     -0.533     -0.643     -1.745     0.646      -0.223     0.448
0.190      -0.032     0.570      -0.803     -0.676     NA
-0.774     -0.239     0.763      -1.107     0.735      -1.168     -0.506     -1.465
    -2.058     -1.935     -0.741     0.978      1.869      -1.876     -1.796
1.143      -0.320     -0.927     -1.876     -0.409     NA
-2.087     -0.528     -1.702     -0.534     -2.189     -0.389     -0.294     0.082
    -2.071     -0.493     -1.094     -0.776     0.609      -1.324     -1.858
-0.944     -2.124     -1.061     -2.235     2.188      NA
-0.822     -1.279     -0.371     -2.313     0.106      -1.007     -0.085     0.076
    -0.973     -0.788     0.369      -0.360     -0.561     0.203      -0.974
1.661      -0.987     -0.323     -2.053     -3.101     Pancreas
-0.079     -1.366     0.519      -0.035     0.076      0.077      -0.466     -0.746
    1.042      0.197      0.174      1.050      -0.715     1.146      -1.509
-0.403     -1.188     -1.091     0.868      -2.108     Pancreas
-0.203     -1.457     -1.043     -1.419     0.790      -1.024     -0.975     -0.837
    -1.190     -0.866     -0.776     -1.163     0.184      -0.508     0.445
0.608      -1.467     -0.912     -0.074     -0.523     Pancreas
-0.257     -0.348     -0.882     0.442      -0.539     -0.768     -0.573     0.168
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Table36.txt

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    0.044      0.037      -0.220     0.431      0.866      -1.246     -1.525
0.127      1.588      -0.172     -0.385     0.996      Pancreas
0.203      0.294      -1.358     -0.512     -0.984     -1.607     0.979      -2.428
    1.543      -0.873     -0.359     0.133      0.770      -2.645     -0.217
0.309      2.145      -0.285     -2.891     0.332      Pancreas
-2.220     -0.973     -3.188     -0.089     -1.203     -1.158     -1.951     -1.288
    1.939      -2.264     -0.768     -0.014     -0.449     -1.041     -0.779
1.848      0.778      -0.907     -0.927     1.120      Pancreas
-1.644     -0.139     -2.244     0.913      0.947      -1.180     -0.279     -0.650
    -0.389     -0.835     -0.080     0.365      0.921      -0.889     -1.660
-0.700     -1.727     1.088      -0.248     -0.060     Pancreas
-1.190     -0.291     2.416      -1.976     -2.657     -1.485     -0.161     -0.692
    -0.396     -0.883     0.420      -0.133     -0.393     -0.654     0.205
0.254      -0.931     -2.184     0.138      1.377      Pancreas
-2.575     -0.275     -1.391     -0.758     -0.530     -1.635     -2.239     -1.801
    0.576      -0.780     -0.631     -0.916     0.577      -2.446     0.517
1.021      0.111      -0.539     -1.039     -1.242     Pancreas
-3.547     0.318      -0.946     -0.532     -0.394     -2.500     -2.509     -1.691
    0.129      -0.990     0.655      -0.623     0.016      0.128      0.226
0.709      -2.320     0.623      -1.273     -0.580     Pancreas
-0.540     -2.171     1.125      0.051      -1.966     -1.447     -0.434     1.624
    0.170      -2.387     -0.020     -0.191     0.642      -1.004     -1.043
0.074      -1.913     -1.104     1.284      0.260      Pancreas
-1.931     0.461      -2.485     -0.714     -0.150     -1.137     -0.479     -0.888
    -0.020     0.115      0.278      1.324      -0.868     0.214      -1.919
1.502      -0.500     -1.117     -1.389     -0.618     Pancreas
-0.261     -2.061     -1.739     0.261      -1.725     -0.687     -0.554     0.319
    -0.102     -0.634     0.561      -0.917     0.809      -2.336     -0.176
0.453      1.515      0.176      0.525      0.586      Pancreas
-1.393     -2.083     0.584      -0.517     -1.521     -0.107     -0.575     -1.745
    -0.313     -0.690     1.159      0.848      1.420      -0.927     -0.453
0.860      0.410      0.209      -0.276     -0.158     Pancreas
-1.063     -1.048     -1.265     -0.285     -1.305     1.041      -0.114     -1.751
    -0.914     0.478      -0.502     -1.652     -0.584     -1.916     -0.630
-0.321     -0.307     -1.566     -0.257     0.319      Pancreas
-0.907     -0.862     0.541      -0.337     0.323      -0.419     -1.078     -0.989
    -1.668     -1.032     0.375      -1.079     -0.293     -1.173     -0.267
-0.572     -0.421     0.020      -2.210     0.757      Pancreas
0.660      -0.511     -0.862     0.912      -1.205     -1.902     -0.638     1.193
    0.504      -0.779     -0.079     0.544      0.476      -0.439     -0.619
-0.005     -0.685     -1.106     -1.495     -0.806     Pancreas
0.171      -2.083     -2.149     -1.176     -2.342     -1.363     -1.387     -1.272
    -0.283     -0.944     0.040      0.556      -0.618     0.598      0.000
-1.222     0.066      0.247      -2.577     -0.662     Pancreas
-0.597     -0.264     -1.531     -1.521     0.247      0.683      -1.050     0.570
    -0.157     -1.989     -0.936     -0.321     1.740      0.366      0.555
-0.603     -0.903     0.539      -1.038     -0.093     Pancreas
1.141      -1.580     -0.801     -1.433     -0.255     -2.341     -1.799     0.551
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Table36.txt

-0.209	0.267	-1.125	-0.506	1.357	0.389	-0.002	0.185
0.544	-0.372	-0.252	-1.021	Pancreas			
-1.410	-1.956	-0.590	0.559	0.111	-2.034	-0.964	-1.622
-0.445	-2.881	0.447	-0.643	-0.994	0.575	-0.176	-1.391
-1.216	-2.711	-0.234	-1.776	Pancreas			
-0.958	-0.859	-1.732	-0.645	0.041	-1.200	-1.481	0.334
-0.051	-0.977	-2.345	0.045	0.511	0.055	0.723	-0.231
-0.455	1.895	0.072	0.795	Pancreas			
-0.039	-0.226	-0.560	-2.052	-0.962	-0.408	0.545	-0.117
1.144	-0.358	-0.902	0.887	-0.633	-0.692	-0.263	-0.786
1.115	-1.247	-1.005	-0.912	Pancreas			
-0.102	-0.789	-1.131	0.171	0.275	-2.009	-0.798	0.113
-0.712	-1.129	0.735	1.232	1.404	-0.520	2.042	0.007
-0.885	-0.012	-0.053	0.244	Pancreas			
-0.430	-0.539	0.251	-0.013	1.003	-0.483	-0.626	1.406
-1.588	-1.720	-0.803	-0.518	-1.206	1.024	-0.113	-0.164
-0.330	0.948	0.023	0.201	Pancreas			
-0.532	0.649	-0.430	0.221	-0.725	1.094	-0.888	-2.474
-0.794	-1.007	-1.526	0.532	-0.434	-1.651	-0.413	-0.094
0.063	-1.754	0.199	0.674	Pancreas			
-2.625	0.012	-0.979	-0.667	1.231	0.113	-2.626	-1.900
1.116	0.341	1.465	0.095	0.912	-0.135	0.197	0.332
1.711	0.370	0.107	-0.827	Pancreas			
-0.448	0.072	-0.361	-0.582	1.154	-1.020	0.122	-2.030
-0.717	0.130	0.618	-1.565	-0.206	0.617	1.581	-0.540
0.150	0.907	0.920	2.336	Pancreas			
-0.186	-0.179	1.343	-0.683	0.058	-0.129	1.491	-1.158
-0.906	-0.856	0.568	1.381	0.675	-1.709	1.557	0.665
-1.036	-0.268	0.466	0.765	Pancreas			
-0.345	-1.291	-0.032	-0.374	-1.971	-0.964	0.832	-1.782
0.143	-0.229	-0.574	0.011	-0.531	0.383	-0.261	-0.859
-0.041	-0.806	-0.466	-0.511	Pancreas			
-1.004	-1.707	0.711	-0.179	1.059	-0.951	-0.905	-0.995
-0.763	-1.843	-0.962	1.292	0.699	-0.175	0.970	-0.334
-2.067	-1.282	-0.425	-0.218	Pancreas			
1.203	-1.039	-0.244	0.637	0.947	-0.195	-0.965	-2.661
-0.878	0.827	-0.961	-0.714	0.345	-0.019	0.576	-0.042
-1.527	-0.834	-0.976	-0.484	Pancreas			
-0.761	0.587	-2.752	-0.097	-1.252	1.086	-1.460	-1.297
0.976	-1.220	-1.071	-1.149	-1.016	-1.113	-0.312	-0.607
1.001	0.553	-1.788	-0.830	Pancreas			
-0.596	-0.559	-0.337	-1.795	-0.405	-2.332	-0.201	-1.441
0.915	0.334	-0.347	0.300	-2.002	0.741	-0.305	0.399
-0.094	-0.104	-2.006	0.003	Pancreas			
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	-1.214	0.000	0.000	0.000
0.000	0.000	0.000	0.000	Pancreas			
-0.124	-1.235	-1.888	-1.536	1.300	-0.298	-0.372	1.548

Table36.txt

-1.851 0.169 1.354 -2.105 -0.426 0.509 -0.501
0.475 0.622 -0.631 -0.482 -0.854 Pancreas
0.180 -0.220 -0.996 -1.728 -1.178 0.204 -0.795 -0.570
0.195 1.159 0.292 0.855 -1.192 -0.327 0.066
0.108 -1.143 0.083 -0.406 -0.411 Pancreas
0.071 -1.550 -1.677 0.035 -2.049 -1.262 -1.237 -1.007
-0.826 0.665 -0.360 -0.400 -0.463 0.898 -1.227
0.393 -0.005 -0.422 -1.074 -0.921 Pancreas
-0.172 0.221 0.056 -1.867 -0.031 -1.227 -2.951 -0.702
0.849 -1.885 -1.588 0.001 1.611 -2.598 -0.778
-1.679 -2.302 0.340 -0.775 -0.161 Pancreas
1.571 -0.949 -0.173 -0.143 0.497 -1.382 -0.604 0.172
1.505 0.477 -0.592 1.461 0.225 0.849 -0.096
1.859 1.080 0.872 0.324 -0.051 Pancreas
0.647 -0.046 -0.371 -1.145 2.732 0.110 0.863 0.215
-0.253 0.073 -0.384 0.105 1.045 -1.854 -1.376
0.720 0.700 0.472 -1.861 1.540 Pancreas
-0.628 -1.154 0.475 -1.043 -2.178 -1.274 -1.304 1.927
-0.936 -0.811 0.047 -0.378 -0.532 -0.585 -2.052
0.233 0.097 0.765 -0.508 0.330 Pancreas
-1.052 -0.268 -1.957 -1.893 0.423 -1.175 0.154 -1.728
0.139 -0.619 -0.689 0.415 -1.117 0.246 -0.321
-0.318 -0.686 -1.220 -0.560 0.165 Pancreas
-0.795 -1.360 -1.627 -1.102 -1.144 0.285 -3.236 0.314
-0.091 -0.073 -0.982 0.371 0.910 -0.247 -0.661
-1.436 -1.039 -2.025 -1.699 -2.017 Pancreas
-0.028 -2.057 -0.177 -1.590 -0.194 -1.181 0.712 -1.487
-1.503 0.735 -0.296 -0.508 -3.231 -0.305 -1.549
-1.985 0.629 -1.076 -1.114 0.074 Pancreas
-3.113 0.188 -1.506 -0.461 -2.461 -0.457 -4.508 -1.324
0.262 -2.426 -0.123 -0.525 0.959 -0.520 0.156
0.714 -1.147 -1.284 -0.796 -1.966 Pancreas
-1.675 -0.888 -0.211 0.012 -1.609 -0.754 -0.282 -2.183
0.579 -0.434 -1.051 -1.842 -0.023 -1.267 -2.573
0.138 -0.969 -0.709 0.332 -3.629 Pancreas
-1.258 -1.259 -0.392 0.405 -0.441 -0.491 0.500 1.579
-2.156 -0.983 -0.152 -1.406 -1.026 0.538 0.004
-0.309 -0.939 -0.910 -1.734 -1.238 Pancreas
-1.051 -1.234 0.095 -0.559 0.120 -1.275 0.778 -1.341
0.775 0.736 0.694 0.860 1.330 -2.279 0.803
-0.134 -0.108 -0.240 -2.953 -1.273 Pancreas
-1.021 -1.510 1.631 0.524 -0.501 -1.063 -2.385 -1.229
0.171 -1.426 -2.399 2.583 -0.504 0.308 0.135
0.067 -0.828 -0.025 1.407 0.071 Pancreas
0.153 -2.009 -1.770 0.632 -0.369 0.304 -1.334 -0.524
0.765 0.286 -0.631 1.575 -0.315 0.026 -0.345
0.163 -1.989 -0.713 -0.983 -1.723 Pancreas
1.052 -0.873 -0.248 0.674 -0.851 -0.047 -0.137 -0.762

Table36.txt

-0.390	0.445	-0.560	1.978	-0.454	-1.276	1.865		
-1.452	0.702	-0.453	-0.270	0.762	Pancreas			
-1.806	0.045	1.572	0.030	-0.511	-2.343	-2.663	0.235	
2.232	0.283	1.138	-0.056	2.258	0.042	0.749		
-1.473	0.979	-0.523	-1.792	-1.395	Pancreas			
0.704	-0.756	0.491	-1.516	1.298	-0.761	0.721	-0.125	
1.576	-1.455	1.028	0.029	1.116	-0.565	1.146		
-0.129	0.589	-0.827	-0.711	1.627	Pancreas			
-2.269	-1.335	-1.133	-0.505	-0.922	-1.688	-0.207	0.113	
-0.742	-1.487	-0.700	-0.421	2.180	-0.643	-0.771		
-0.566	1.688	-2.074	-0.379	-0.417	Pancreas			
-2.130	-1.189	0.087	0.041	-0.304	0.981	-0.627	-0.941	
0.626	-1.314	-0.889	0.523	2.537	-0.086	1.485		
-0.532	-0.572	-1.345	0.749	0.517	Pancreas			
0.043	1.176	-0.842	-0.692	1.143	-1.726	-1.120	0.684	
-2.116	-1.503	-1.421	-0.178	1.224	0.417	0.712		
1.312	0.301	-0.859	-1.269	0.038	Pancreas			
-0.627	-2.264	-0.157	-0.716	0.085	-0.174	-0.997	0.584	
0.558	0.733	0.476	0.259	0.949	-1.307	1.158		
-0.560	2.116	-1.854	1.668	-2.225	Pancreas			
-0.467	-0.879	-0.367	0.594	0.012	0.048	0.496	-1.704	
1.842	-0.877	1.210	0.783	0.723	0.183	3.377		
1.057	3.678	2.135	0.764	-0.197	Pancreas			
0.117	0.205	0.264	-1.112	0.157	1.936	0.012	-0.810	
0.974	-2.252	0.023	0.625	-1.008	1.856	0.333		
-1.521	1.408	1.789	-0.943	-1.422	Pancreas			
-0.691	-0.680	-0.797	0.223	-1.350	0.172	-1.618	-1.307	
0.053	-0.423	-1.293	-0.086	0.337	-0.399	-1.367		
-1.774	-1.584	-0.550	-0.336	-1.386	Pancreas			
-0.753	0.281	1.152	0.050	-0.182	0.668	-0.040	0.340	
-0.336	-0.302	0.306	-0.808	1.430	-0.830	-0.686		
-1.366	1.505	-1.360	-0.901	0.110	Pancreas			
1.047	-1.749	1.012	-0.888	-0.665	0.915	-0.330	-0.997	
1.445	-0.696	0.210	2.506	1.382	-0.807	1.600		
1.550	2.008	-0.405	-1.606	0.497	Pancreas			
-0.528	0.186	-0.197	-1.766	0.362	-0.277	-0.602	-1.439	
0.080	-1.088	-1.273	-0.912	0.632	0.079	-1.115		
-1.033	0.681	-0.085	-2.363	-1.095	Pancreas			
1.474	1.187	-0.661	0.431	-1.496	-0.116	0.156	0.154	
-0.108	1.487	-0.911	-1.267	1.583	-0.785	-0.815		
0.609	1.125	-0.445	-1.112	0.240	Pancreas			
-0.692	-0.169	-1.117	-0.427	1.794	0.004	-1.697	-1.037	
0.701	-0.091	-0.402	1.178	1.522	-0.080	0.517		
-0.615	1.120	-0.280	1.277	-0.750	Pancreas			
-1.115	-1.217	-2.258	-1.024	-1.474	-0.585	-1.057	-0.043	
-0.281	0.123	-0.521	-0.571	-0.888	-1.598	-0.017		
-0.971	-0.603	1.851	-0.349	-1.264	Pancreas			
0.201	-1.428	-0.001	1.339	0.428	-0.486	0.036	-0.485	

Table36.txt

0.067	-0.338	0.607	1.435	0.989	0.295	0.302	
0.610	-0.667	-0.846	-1.733	-0.968	Pancreas		
0.035	0.622	0.497	1.911	0.734	-2.289	0.887	-0.040
-0.404	0.108	0.372	-1.486	2.787	-0.656	0.593	
1.301	1.762	-1.570	-0.744	-0.786	Pancreas		
-1.919	0.177	-1.137	-0.981	-0.635	0.759	-0.413	-0.960
1.338	0.981	-1.383	-0.468	-0.707	-1.144	-0.887	
-0.550	-1.760	-0.667	-0.178	-1.403	Pancreas		
-0.977	-0.025	-1.636	1.651	-1.595	-1.318	0.186	-0.555
-1.040	0.273	0.639	-1.874	0.014	-1.740	-1.308	
-1.160	0.187	-1.454	0.949	-0.726	Pancreas		
-0.137	0.373	-0.822	1.340	-0.212	-2.310	-3.507	0.110
0.343	-0.776	0.663	0.488	-0.339	-2.845	-0.514	
-0.092	0.181	-0.809	-1.098	-0.255	Pancreas		
1.177	-0.441	1.368	0.030	0.336	-0.694	-1.368	0.155
-0.104	-1.757	0.201	-0.003	-1.332	-0.665	-0.189	
-1.423	0.185	0.027	0.946	-2.074	Pancreas		
-1.434	-0.604	-1.629	-0.016	-0.842	-0.217	-0.790	-1.228
-0.601	-0.491	-1.343	-1.277	1.582	1.033	1.471	
-1.735	-1.728	-0.448	-1.075	1.286	Pancreas		
-0.322	-1.329	-1.439	1.169	1.148	-1.092	-0.899	-1.875
-0.049	-1.017	-0.031	-1.381	-0.003	-0.924	0.730	
0.161	0.600	1.232	-0.624	-1.387	Pancreas		
0.492	-0.084	-0.659	-2.101	-2.742	-1.528	-0.419	-0.154
1.613	-1.334	0.278	-1.053	0.336	-1.075	0.394	
0.470	-1.509	-0.048	0.149	0.486	Pancreas		
-0.643	0.128	-1.105	-0.546	-1.674	0.016	-1.829	-0.915
0.212	-0.453	-1.906	-2.461	-1.165	-0.387	-0.139	
0.945	0.421	-1.273	-1.331	0.793	Pancreas		
-0.474	-1.310	0.320	0.402	-1.472	-1.099	-1.140	-2.365
-0.757	-1.268	0.004	-1.000	-0.590	1.227	-0.472	
0.890	0.925	-0.457	1.049	-0.989	Pancreas		
-0.716	-1.419	-1.585	-0.458	-1.742	-1.671	0.004	0.268
0.749	-1.649	-0.080	0.606	-0.041	-0.984	1.252	
-1.340	-0.372	1.336	-0.680	0.805	Pancreas		
-0.301	0.666	-1.991	-1.256	-1.186	0.780	-0.853	0.554
0.649	0.003	-1.640	-1.892	-1.590	-0.829	0.857	
-0.995	0.270	-1.292	-1.347	-0.642	Pancreas		
-0.761	-1.319	0.807	-0.690	-1.720	0.255	0.623	-0.784
-1.148	0.885	-1.665	-1.150	2.034	-1.353	-1.156	
0.259	2.111	-1.016	-0.618	-0.012	Pancreas		
-0.227	-1.931	0.054	-0.300	2.869	-1.643	0.145	-1.910
-0.203	-0.846	-0.996	-1.210	0.137	2.171	0.145	
-0.685	1.329	1.201	0.437	0.366	Pancreas		
1.032	-1.034	-2.472	-2.062	-0.844	-1.972	-0.418	-1.820
-0.674	0.019	0.576	-1.855	-0.278	-0.576	0.922	
0.184	0.476	-0.430	-2.007	-1.246	Pancreas		
0.718	-0.603	-0.824	-1.019	-0.494	-0.086	-1.566	1.028

Table36.txt

-0.026	0.966	0.995	1.383	0.401	0.543	-0.596		
1.020	0.142	1.986	-1.685	-1.568	Pancreas			
-0.696	-0.912	-1.948	-2.155	-0.254	0.119	-1.895	-0.071	
0.670	-0.977	0.877	0.573	0.845	0.501	-0.118		
-1.586	-1.022	-0.226	0.157	-0.551	Pancreas			
-1.885	-2.331	-2.333	-0.332	-1.285	1.596	-0.222	-2.329	
0.368	-0.697	0.206	0.912	0.515	-0.520	-1.515		
-0.116	0.589	1.279	0.550	-0.812	Pancreas			
0.881	-1.035	0.349	-0.845	0.448	-1.459	-1.134	0.625	
0.870	-1.045	0.447	-0.289	-0.718	0.642	0.884		
0.014	0.532	0.008	-1.614	-1.058	Pancreas			
-0.537	0.875	0.138	-0.739	0.515	-0.324	-0.019	-1.805	
-1.887	1.235	-0.421	0.829	0.622	-0.018	-0.620		
1.729	-1.224	-0.014	-0.933	-1.614	Pancreas			
0.000	-0.666	0.636	1.323	1.472	1.064	-1.100	-0.022	
1.093	-0.712	1.632	1.212	0.722	-0.415	1.124		
2.265	-1.415	-0.560	0.007	-1.219	Pancreas			
-0.677	0.045	-0.777	0.020	0.650	-2.163	-1.847	-1.418	
-0.980	0.459	0.293	0.772	-1.005	1.323	-0.980		
0.589	-0.441	-0.976	0.396	0.710	Pancreas			
-0.605	0.513	-2.529	-2.721	-1.339	-0.295	0.049	-0.401	
-0.012	-0.915	1.139	-1.605	0.253	-2.838	0.000		
-1.408	0.379	0.221	-0.436	-1.169	Pancreas			
-0.170	-0.848	-0.685	-0.925	-0.263	0.294	-1.557	-0.827	
-1.622	-1.356	-0.741	-0.780	-0.551	-0.587	0.000		
0.226	1.825	-2.568	0.128	0.465	Pancreas			
0.246	-1.282	-1.500	-0.246	1.341	0.092	-0.027	-0.516	
1.557	-0.580	0.241	-0.659	-0.114	0.907	0.000		
-0.517	1.111	-1.609	0.037	0.726	Pancreas			
-2.220	-2.067	-0.205	-0.999	-1.304	-1.306	-0.923	0.541	
0.737	-0.816	-0.498	-1.617	-1.395	-1.563	-0.448		
-2.483	-0.059	-2.385	-0.116	0.662	Pancreas			
-1.437	0.451	0.130	0.078	-1.239	-0.941	-2.191	0.893	
-1.155	0.396	-0.290	0.884	-0.543	0.679	1.666		
-0.035	1.046	1.583	0.404	1.017	Pancreas			
1.863	2.291	2.363	0.583	1.234	0.862	-0.019	2.305	
1.289	0.351	0.781	1.493	2.253	0.884	1.236		
0.353	2.674	2.300	-1.209	0.795	Pancreas			
3.078	1.968	3.002	1.145	1.041	0.630	-0.633	1.072	
-1.009	1.321	-0.125	1.955	1.986	-0.068	2.773		
0.848	1.465	1.828	0.120	1.106	Pancreas			
-2.151	0.768	0.590	1.026	-0.998	-3.100	-2.022	-1.165	
0.581	0.085	-1.430	0.350	1.060	0.575	-0.554		
3.034	0.865	-1.058	-0.088	-1.023	Pancreas			
-0.132	-0.855	-1.904	0.314	-0.406	-3.211	0.624	-0.170	
-0.419	0.387	-0.669	-0.716	-0.532	-0.385	-0.136		
-1.015	-2.522	-1.484	-1.453	-0.452	Pancreas			
0.987	-1.412	-0.908	-0.336	0.350	-0.154	1.343	-1.022	

Table36.txt

0.528	-1.019	-0.568	1.009	1.206	0.758	1.364	
0.830	0.832	-1.245	-0.737	-0.334	Pancreas		
0.275	0.309	0.037	-0.024	-1.727	-0.887	-2.215	0.404
-2.364	-0.326	0.901	-0.493	2.004	-1.192	1.581	
0.896	1.190	-0.714	-1.281	0.614	Pancreas		
-0.980	-0.623	1.837	0.125	1.382	2.047	-0.735	0.812
0.834	0.008	2.114	-0.323	2.901	-2.540	1.406	
-0.084	0.971	0.773	-0.876	-0.050	Pancreas		
-0.627	-1.055	-2.235	-1.079	-2.424	0.582	-1.911	0.795
-0.467	-0.270	0.305	-0.750	0.137	-2.747	0.432	
0.817	1.398	-0.067	1.000	-1.406	Pancreas		
-0.860	-0.155	-0.284	1.259	1.192	-0.581	-0.676	-0.728
1.006	-2.503	0.247	0.926	3.185	-0.292	-0.058	
-0.057	0.186	1.683	0.071	-0.440	Pancreas		
0.080	-0.999	0.312	0.396	-1.080	0.302	-2.922	-0.954
-1.148	-0.514	1.596	-0.189	-0.125	-1.073	0.164	
-0.656	0.487	2.362	0.110	0.811	Pancreas		
0.215	-1.609	0.194	0.006	0.494	0.467	-0.090	0.107
2.638	-1.710	1.466	-0.820	-0.177	-0.780	-0.329	
-0.481	1.563	0.101	-1.842	-1.224	Pancreas		
-1.360	-1.149	-0.354	-0.377	-0.986	-1.268	-1.815	-1.251
-0.602	-0.832	-1.577	1.747	1.287	0.650	-0.562	
0.341	0.556	-0.789	-0.234	-1.136	Pancreas		
-1.407	-1.412	-0.836	0.338	-0.175	-0.290	-0.484	1.354
-0.894	-0.311	-1.655	-1.205	0.660	-0.848	0.388	
0.691	0.473	-0.098	-0.384	-0.122	Pancreas		
-1.585	-2.022	-1.362	-0.213	0.548	-0.438	-0.512	-1.630
0.113	-2.311	-0.656	0.031	0.137	-1.304	1.303	
-0.768	0.397	0.899	-0.142	0.273	Pancreas		
0.312	-0.316	-1.102	-0.722	0.088	1.139	0.257	-0.837
-1.200	-1.624	-0.036	-0.223	1.302	-0.303	0.688	
0.634	1.435	0.013	-0.831	-1.502	Pancreas		
-1.234	-1.163	-0.525	-1.048	0.948	-0.102	-0.410	-0.216
0.035	-0.053	-0.157	0.260	-1.050	-2.340	0.440	
-0.015	0.840	0.357	0.939	-2.898	Pancreas		
-0.324	-0.749	1.228	1.009	1.417	0.122	1.260	-0.086
-0.502	0.891	-0.653	0.180	2.278	0.786	-1.279	
-0.171	1.350	1.227	0.426	-0.720	Pancreas		
-0.863	-1.042	-0.161	-0.802	0.763	-4.142	0.109	-1.413
-0.147	1.251	0.671	-0.024	0.598	1.127	-1.113	
1.107	-1.124	-1.369	0.927	-0.883	Pancreas		
-0.076	-1.943	-0.408	-2.222	0.111	-2.468	0.916	-3.592
0.587	-0.750	0.388	-0.631	-0.766	-0.243	2.255	
0.863	0.873	-0.106	0.988	-0.475	Pancreas		
-1.444	-1.716	-2.029	0.015	-1.052	-2.672	-0.487	-2.328
-1.298	-1.148	-0.647	0.387	-0.419	0.950	-0.873	
-1.087	-0.853	0.979	-0.994	0.082	Pancreas		
-1.800	-0.182	0.412	-1.556	0.108	-0.356	0.221	0.535

Table36.txt

-0.091	-0.724	1.560	1.222	1.355	1.228	-0.693		
-2.121	1.355	0.545	0.077	0.875	Pancreas			
-0.600	-2.412	-1.852	-1.753	-2.595	-1.538	0.054	-0.241	
-0.200	-1.176	0.630	1.882	-0.476	0.275	0.575		
1.100	-0.147	1.509	0.450	-1.417	Pancreas			
-1.593	1.324	-0.711	0.238	0.650	0.472	-1.374	-1.023	
-1.816	-0.318	-0.012	1.474	0.609	-2.296	-0.574		
1.173	0.187	-1.092	0.618	-1.250	Pancreas			
0.093	-2.031	0.911	0.662	-2.653	-1.980	-0.379	-1.661	
-0.974	-1.303	1.291	-1.081	1.622	1.328	1.573		
0.222	-1.124	-0.738	-1.911	-1.402	Pancreas			
-2.306	-1.181	-0.367	0.368	0.886	-2.836	0.850	0.789	
0.783	-1.387	0.197	-0.802	-0.824	-0.896	-0.686		
0.792	0.682	-1.922	-0.661	0.001	Pancreas			
-0.998	0.693	-0.443	-0.565	-1.611	-1.385	-1.906	0.355	
0.167	0.755	0.537	-0.186	-0.314	0.953	0.589		
-1.803	2.214	-1.910	-0.833	0.237	Pancreas			
0.210	-0.331	-1.781	0.578	-0.679	-2.011	-1.313	-1.601	
-0.214	1.793	0.160	0.516	-0.517	-1.120	-0.002		
0.156	0.119	0.233	-1.292	-0.804	Pancreas			
1.656	-0.599	0.078	0.920	-1.250	-1.269	-0.231	-0.477	
-0.156	0.158	0.061	1.628	-0.780	-0.330	-1.034		
-0.034	0.551	-1.460	-0.978	-0.754	Pancreas			
-0.361	-1.764	-1.453	-0.754	-1.018	0.415	0.930	0.918	
-0.388	0.510	0.527	-0.630	-0.890	0.682	0.966		
-2.244	-0.565	0.925	-3.574	-0.283	Pancreas			
0.236	-0.350	-1.029	0.158	-0.033	-2.224	-0.720	-1.304	
-1.835	-0.959	-0.401	-0.225	1.929	0.893	0.339		
-0.027	-0.570	0.562	-1.563	-2.019	Pancreas			
-0.176	0.317	-0.054	0.422	0.439	0.130	1.185	-0.501	
1.219	-0.003	-0.851	-0.463	1.534	-1.430	0.731		
-0.306	2.518	0.744	0.490	-0.380	Pancreas			
-0.220	0.037	-3.013	0.820	-0.368	-1.773	-2.365	-1.552	
-2.117	0.171	0.480	2.152	-0.241	-0.628	-0.126		
-0.156	-0.623	0.943	-0.730	-0.683	Pancreas			
-0.616	-1.446	-0.317	0.147	-2.114	1.239	-0.651	0.075	
0.045	-1.564	-2.535	1.669	0.768	-1.926	-0.787		
-0.342	0.855	0.910	0.727	0.267	Pancreas			
1.089	1.141	0.624	-1.086	1.224	1.688	-0.328	0.670	
1.281	0.501	0.080	0.671	-0.301	-0.884	-0.721		
0.794	1.579	0.270	1.336	1.499	Pancreas			
-0.021	-1.714	0.489	-1.803	-0.501	-2.489	-2.728	-1.971	
-1.273	-0.357	0.888	-0.866	-0.379	0.273	0.045		
1.573	-1.820	-0.528	-0.847	-0.569	Pancreas			
0.998	-1.641	-2.671	-0.252	-0.533	0.021	-0.981	-1.447	
-0.179	-0.161	-1.659	1.551	0.567	-1.238	-0.016		
0.062	0.931	-0.511	-0.339	0.182	Pancreas			
-0.972	-0.507	-0.020	0.591	-0.383	-0.851	-1.926	-1.535	

Table36.txt

0.619	-1.352	-0.654	0.179	-0.468	-1.941	1.060	-0.436	0.021
0.128	-0.677	0.198	Pancreas					
0.229	0.538	-1.068	-0.617	0.579	-0.944	0.467	0.000	
0.788	1.131	-1.580	-0.670	0.823	-0.201	0.141	0.387	0.169
-1.187	0.424	-0.647	Pancreas					
-0.199	-0.630	-1.084	0.447	-0.034	0.289	-0.330	-1.015	
0.869	-1.273	0.010	0.352	1.880	0.525	1.443	0.006	-0.456
-0.729	0.547	-0.111	Pancreas					
1.131	-0.027	0.842	0.799	0.655	0.336	0.108	-0.626	
-0.108	1.218	1.051	0.052	3.433	1.363	-0.548	0.636	0.692
1.406	0.157	0.457	Pancreas					
-1.024	-0.471	-0.551	-0.359	0.349	-1.934	-1.456	8.122	
-0.157	-0.517	-0.233	0.170	-0.252	1.003	0.724	-1.720	0.354
-0.001	-0.243	-0.775	Pancreas					
-1.154	-0.641	-2.482	-0.316	-0.551	-2.277	-0.193	-0.753	
-1.454	-0.215	-0.031	1.426	-0.344	-0.522	-0.140	-0.380	-1.086
-0.788	-2.019	-1.022	Pancreas					
-0.215	1.164	-0.024	-0.088	0.584	-1.847	0.664	-0.624	
0.833	-0.372	-0.615	1.812	-0.437	-0.251	2.036	-1.275	1.414
-0.754	-0.961	-0.891	Pancreas					
-0.234	-2.434	-0.132	-1.650	-0.974	0.133	0.244	-0.482	
0.651	-0.806	-0.029	1.605	-0.781	-0.398	1.044	0.207	-0.565
-2.095	0.030	-0.239	Pancreas					
-0.299	0.169	-2.053	-0.238	1.391	-0.453	0.627	0.114	
-0.418	-0.533	-0.832	0.201	-0.768	-1.318	-0.563	0.206	-0.156
0.092	-1.211	1.034	Pancreas					
-2.167	-1.470	-0.707	-2.354	-1.070	-2.482	-1.138	-1.138	
-0.317	-0.989	-1.730	-1.038	0.054	-1.212	-0.318	-1.104	-1.114
0.187	-1.987	-0.280	Pancreas					
-0.055	-2.147	-1.151	-1.911	-0.196	-0.013	-1.034	-0.952	
-0.713	-0.501	-0.222	0.358	2.414	-1.609	0.029	0.348	1.240
0.159	-0.613	-1.131	Pancreas					
-1.083	-0.640	0.502	0.179	-1.356	-0.407	-2.307	-1.901	
0.823	-0.821	-0.481	0.888	0.313	1.151	-0.946	-1.175	1.220
-0.177	-1.441	-1.776	Pancreas					
-0.438	0.517	-0.796	-0.062	0.832	-1.140	-0.954	-2.077	
-0.077	-1.205	1.421	-2.211	-0.176	0.347	-0.734	-1.657	-1.049
-0.558	-0.476	0.027	Pancreas					
-1.757	-0.277	-0.325	-3.029	-2.064	0.437	-0.653	-0.421	
-0.786	1.027	-1.382	0.316	1.290	0.357	0.475	-0.403	0.660
-2.664	-0.757	-0.453	Pancreas					
-0.636	0.147	-1.389	-1.413	-1.927	-0.644	-2.518	-1.175	
-1.768	-0.846	1.008	0.073	0.707	-1.726	-0.837	0.243	-0.800
0.674	0.391	0.350	Pancreas					
0.510	-0.077	0.564	-0.981	1.257	-1.435	-1.628	0.046	
-1.759	0.571	0.901	-0.595	-0.317	-0.375	0.219	-0.270	-0.466
0.625	-0.045	-1.363	Pancreas					
-0.048	-1.703	-1.158	0.093	-0.833	-0.937	-0.917	-0.149	

Table36.txt

-0.387	-1.055	-1.741	-1.017	-1.538	-2.630	2.010		
-1.755	-0.247	-1.241	0.107	-1.055	Pancreas			
0.285	-1.184	-4.520	0.422	-1.104	-1.092	-0.700	-1.746	
0.675	-1.131	-0.505	-0.040	0.335	-0.104	0.428		
0.462	0.504	0.359	-0.290	0.070	Pancreas			
1.055	-0.325	-0.451	-0.806	-1.541	0.316	-1.643	0.372	
1.013	-1.975	-1.021	0.196	0.983	0.483	0.512		
-2.592	0.642	-0.145	-1.361	1.501	Pancreas			
1.482	-1.267	-2.867	-1.901	-0.627	-0.241	0.700	-0.377	
-0.438	-0.419	-0.009	-1.011	0.608	0.448	1.239		
0.188	1.799	0.442	-1.970	0.924	Pancreas			
-0.425	-1.371	0.497	-0.417	0.534	-0.058	-0.908	-1.686	
-0.161	0.214	-0.838	0.188	-1.134	1.001	-1.955		
0.046	0.647	-1.164	-1.204	-0.716	Pancreas			
0.327	2.142	0.002	-0.200	1.682	1.567	1.156	-0.756	
0.219	-0.125	2.090	-0.375	1.445	1.068	1.640		
1.172	3.779	0.081	2.501	-0.776	Pancreas			
-1.888	1.350	-0.536	-2.361	0.299	-2.267	-2.242	-0.908	
-1.200	-2.576	1.111	-1.490	1.315	-1.346	-0.302		
0.906	0.010	-0.188	-0.824	-0.635	Pancreas			
-1.519	-0.108	1.487	1.696	-0.808	0.267	-0.324	1.790	
1.079	-1.667	-0.152	-0.794	1.753	-1.559	1.208		
-0.498	0.209	1.405	0.606	-1.664	Pancreas			
-0.543	0.347	1.174	-0.052	-0.107	-0.253	-0.297	-1.159	
0.144	-1.942	-1.429	-0.997	0.418	1.831	0.817		
0.206	-1.583	0.222	-1.650	-0.541	Pancreas			
-0.864	-0.114	-0.718	-0.753	1.047	-1.882	-0.118	-0.179	
-1.431	-0.783	-0.629	0.868	2.368	0.126	-0.580		
0.893	0.652	-0.786	0.117	-0.512	Pancreas			
-1.259	1.447	0.010	0.365	0.579	-2.203	-1.901	0.169	
-0.820	-1.422	-0.473	-0.271	-0.361	0.544	-0.198		
0.768	0.094	-0.840	-0.763	-0.263	Pancreas			
-0.746	0.243	0.615	0.315	0.725	-1.725	-0.678	-0.625	
1.263	-2.371	-1.041	-0.183	-0.268	-1.924	0.259		
1.599	2.485	0.311	-0.550	-1.709	Pancreas			
-0.012	-0.007	0.154	-0.451	-0.144	-2.037	-0.781	-0.253	
-0.479	1.075	-0.533	-1.574	1.681	1.015	-0.530		
-1.312	-0.413	2.284	-1.669	-1.681	Pancreas			
1.311	-0.489	0.000	-1.801	-0.862	-0.002	-0.656	0.455	
-1.698	-1.584	0.353	-0.210	0.939	0.729	-0.226		
-0.141	-2.168	-0.900	-0.755	-1.549	Pancreas			
0.712	-0.908	-2.317	1.895	-1.709	-1.647	-0.234	-0.737	
0.941	-1.445	0.128	-1.461	-0.091	-1.135	-0.441		
-0.471	0.577	-3.045	-0.066	0.713	Pancreas			
-1.727	-1.937	-0.337	-0.971	-0.093	-0.849	0.786	-0.517	
0.972	1.873	-0.058	-1.330	-1.366	0.645	2.070		
0.825	-0.273	-0.381	-0.837	0.128	Pancreas			
-1.437	0.922	0.287	-0.648	-1.004	-2.397	-0.648	-0.024	

Table36.txt

1.174	-0.470	-1.018	0.294	0.155	-0.593	-0.746		
-1.120	0.184	-0.433	-0.858	-0.907	Pancreas			
1.817	-0.587	1.216	1.354	0.101	-1.224	-0.990	-0.862	
0.438	-1.786	1.092	0.127	1.506	0.240	-0.797		
-0.422	-0.511	0.821	-0.458	0.024	Pancreas			
-0.244	-1.472	-0.074	0.456	-1.202	-1.335	-1.082	0.278	
-0.189	-0.297	-2.860	-1.003	-1.300	-1.687	-0.334		
-1.038	-0.425	1.218	-0.417	-0.862	Pancreas			
-0.420	-1.212	-1.275	-0.447	-1.868	-2.317	-0.074	-1.330	
0.453	-1.085	-0.532	-1.094	0.254	-0.003	-0.943		
0.024	0.170	-0.277	-0.512	0.000	Pancreas			
-1.968	-0.224	-2.268	-0.256	-2.926	-0.282	0.139	-1.497	
1.482	-0.375	1.449	-2.770	-0.936	0.845	0.556		
0.422	-0.011	-2.426	-1.399	-0.801	Pancreas			
1.789	1.472	1.012	-1.283	1.422	0.930	0.137	-0.934	
-1.921	0.225	0.085	0.930	2.924	0.537	-0.846		
0.807	-0.766	-2.451	-1.646	-1.628	Pancreas			
-1.575	1.052	-1.058	0.925	-1.569	-0.364	1.522	-0.018	
0.441	0.838	1.834	0.688	1.775	0.884	-0.152		
-1.051	-1.531	-0.964	-1.041	-1.178	Pancreas			
-0.535	0.516	1.057	0.169	1.009	-0.089	1.296	1.163	
-1.822	-0.106	2.130	1.365	0.388	1.471	1.381		
-0.342	0.525	1.746	1.560	0.531	Pancreas			
-0.565	0.546	-0.017	1.985	-0.353	0.149	1.513	1.632	
-0.658	-1.449	2.033	-0.272	0.283	-1.858	1.918		
-0.921	0.364	-3.399	-0.219	0.735	Pancreas			
0.910	0.479	0.070	0.537	-1.245	-1.076	0.540	0.448	
-0.303	-0.931	1.893	-0.710	1.481	-1.547	1.794		
0.006	0.819	-0.358	-1.275	-0.362	Pancreas			
1.969	0.462	-0.110	0.485	0.720	0.820	0.436	1.087	
0.090	0.509	0.747	0.915	3.838	1.806	2.654		
-0.021	0.944	0.690	0.659	-2.796	Pancreas			
1.366	0.413	0.165	-0.875	-0.179	-0.744	1.298	0.465	
0.865	0.469	0.237	-0.143	2.738	0.121	4.020		
1.072	0.524	1.256	-0.757	-0.732	Pancreas			
0.903	-0.653	-0.755	1.040	-1.663	-0.931	-0.047	1.081	
-1.109	-1.256	0.307	0.748	0.604	0.043	0.667		
-0.105	1.054	-0.572	-1.311	0.376	Pancreas			
-0.164	-1.594	-2.122	-0.875	-1.026	-1.025	-1.149	-0.951	
-0.399	-0.418	-1.477	0.949	-1.011	-1.358	-0.878		
-1.328	-0.125	-1.125	-0.125	-0.357	Pancreas			
-0.360	-0.891	-1.911	-0.397	-1.769	-2.923	0.683	1.357	
-1.746	-1.147	-1.205	-0.554	0.457	0.970	-1.153		
-2.334	0.863	0.154	1.347	-1.078	Pancreas			
0.001	-1.236	-1.884	-1.603	-0.173	-0.395	-0.083	-0.087	
1.545	-1.428	0.223	0.884	1.382	0.162	1.022		
0.534	0.663	-1.043	-2.635	-0.427	Pancreas			
0.771	-0.296	-0.564	0.228	-0.829	0.359	0.280	-0.253	

Table36.txt

-0.308	1.308	-0.484	1.498	1.854	-0.496	-1.536	
-0.169	-0.039	-0.073	-0.543	-0.440	Pancreas		
-1.613	-0.268	-4.215	-0.509	0.298	-0.449	-1.645	-0.829
-1.011	-0.591	0.006	-0.209	1.910	-0.070	1.337	
-0.502	0.155	-1.498	-0.180	0.356	Pancreas		
0.002	-2.574	-2.196	0.230	-1.152	0.147	-0.349	-1.716
-0.778	0.408	-0.364	0.675	-0.021	-0.585	-3.594	
-0.674	-0.187	-3.089	-0.309	-1.660	Pancreas		
1.342	-0.699	0.223	-0.742	-0.008	-1.515	-1.171	1.252
-1.033	-0.576	-0.276	-0.809	-0.703	-0.493	0.594	
0.104	1.358	0.334	-1.905	-1.563	Pancreas		
-1.334	-0.580	-0.870	0.102	-0.148	-1.311	-1.579	-0.249
-1.553	0.003	-0.481	0.460	-1.470	0.864	-0.039	
-1.684	-0.620	0.940	-0.570	-0.489	Pancreas		
-0.485	-1.713	-2.017	0.382	-1.132	-1.133	-1.515	-2.017
-2.426	-1.134	0.803	1.167	0.285	-0.782	-0.416	
-1.225	-1.169	1.152	0.044	-1.211	Pancreas		
-1.219	0.119	-0.044	1.058	-0.736	-0.239	-2.779	-2.544
0.075	-0.943	-1.374	0.152	0.764	-0.308	-1.054	
-0.257	-0.803	-0.235	0.420	-0.755	Pancreas		
1.233	-0.342	-0.533	-0.757	-0.853	-1.274	0.236	1.637
-0.535	-2.180	-0.213	-0.523	-0.966	-1.314	0.927	
-0.324	-1.824	1.177	-2.088	0.091	Pancreas		
1.413	-0.105	-1.380	-0.289	-0.953	-0.916	-1.207	-1.410
0.058	-1.702	0.612	0.921	0.805	-0.552	-0.198	
0.590	-0.747	-1.237	-0.438	-1.230	Pancreas		
-1.622	-1.632	-0.589	1.004	-3.216	-2.669	-1.899	-0.855
-1.530	-1.567	0.079	1.013	0.416	-0.197	0.304	
-0.468	0.696	-0.007	-0.488	-2.194	Pancreas		
-1.748	-0.830	-1.983	-2.191	-0.455	-0.203	-0.250	2.141
0.882	-1.891	-0.790	1.640	1.582	0.373	1.782	
-0.761	-0.303	-1.953	-0.646	-1.074	Pancreas		
-1.202	0.093	-0.850	-0.562	-0.645	-2.827	-1.833	0.401
-1.965	0.112	-0.631	0.535	-2.104	-1.416	-1.308	
0.025	0.697	-0.410	-1.239	-0.334	Pancreas		
0.099	0.709	1.612	-1.475	3.280	-0.917	-1.801	0.889
0.131	-0.821	-1.268	1.078	0.036	0.913	1.478	
-2.449	0.162	-0.986	0.883	-2.442	Pancreas		
-0.973	-0.942	-1.164	1.820	2.121	1.448	0.045	-0.247
0.125	0.785	-0.506	0.612	1.950	-1.227	0.905	
-0.023	0.538	1.093	0.484	0.826	Pancreas		
-2.018	0.679	-1.077	-1.766	-0.537	-2.756	-1.532	-1.856
-0.602	-2.715	0.056	-2.664	-1.587	-0.147	-1.530	
1.909	-0.723	-2.390	-1.159	-0.231	Pancreas		
0.069	-0.077	-1.673	0.550	-0.673	-0.841	-1.235	-3.721
-3.423	-1.952	-4.455	-1.060	-1.466	-0.845	-0.171	
-1.959	0.204	0.727	-2.391	0.192	Pancreas		
-0.597	0.317	-1.928	0.544	-0.853	-0.439	-0.594	-1.147

Table36.txt

-2.616	-2.740	-1.710	-1.146	0.116	-1.935	1.691		
-0.797	0.075	-0.208	-1.715	0.304	Pancreas			
-1.561	-0.686	-0.982	-0.208	-0.711	-0.743	-0.319	-0.432	
0.589	-2.184	-2.242	-0.511	-0.065	0.661	-2.023		
0.354	-1.848	-0.248	-0.861	-1.165	Pancreas			
1.656	-1.059	-0.838	-1.094	-0.099	-0.877	-1.327	-1.732	
-0.811	-1.091	-0.003	-2.349	-0.870	0.096	0.656		
0.315	0.649	-1.577	-0.375	-0.902	Pancreas			
-2.123	0.553	0.829	-2.287	-0.327	-0.502	-2.412	-0.748	
-0.932	-0.182	-0.843	-1.162	-0.292	0.107	-1.668		
-1.574	-1.199	0.221	0.149	-2.842	Pancreas			
-0.008	0.089	-2.423	0.494	1.047	-0.353	-1.009	0.223	
0.901	-0.653	-2.237	-0.448	-0.759	1.064	0.355		
-0.211	1.410	-1.195	-2.108	-0.681	Pancreas			
-0.791	0.612	-1.486	-1.257	-1.752	-0.640	0.065	-0.582	
0.950	-1.566	1.626	-0.572	-0.589	-1.893	1.551		
-1.068	1.136	-0.659	0.802	-0.796	Pancreas			
0.365	0.174	0.440	-1.449	1.436	-1.315	-0.444	0.481	
-0.971	-1.271	-1.188	2.078	-1.097	-0.740	1.367		
-2.641	-0.428	0.604	1.008	1.693	Pancreas			
-2.401	-0.607	-0.931	-0.943	-0.062	-0.218	-0.476	-0.397	
-1.692	-0.833	-0.463	-2.045	2.705	-1.721	-1.723		
-2.129	-0.387	-1.051	-0.978	0.694	Pancreas			
-0.426	0.228	-1.582	-0.663	-0.560	-1.522	-1.181	-0.331	
-0.298	-1.147	0.770	1.386	-0.287	-0.477	-0.874		
-1.827	-0.255	-0.813	0.263	-1.114	Pancreas			
-0.519	-0.873	0.598	-1.511	-0.105	1.089	-0.296	-0.397	
-0.354	-0.510	-0.839	1.238	-0.532	0.927	-0.585		
-2.330	-0.228	-0.433	-1.107	-1.542	Pancreas			
-0.211	0.803	-1.864	-0.301	1.047	0.445	0.015	-1.687	
-0.717	-0.527	-3.351	-2.413	0.303	0.003	3.130		
1.888	0.765	-2.776	1.610	0.026	Pancreas			
0.312	-1.623	0.289	-1.000	0.353	-1.986	-1.525	-2.019	
0.419	-1.043	-1.634	-1.866	0.219	-1.026	0.222		
0.106	-0.569	0.215	-0.462	0.708	Pancreas			
-1.140	-0.725	-1.248	-1.611	-2.260	-3.326	-0.685	-1.167	
0.872	-1.968	1.431	0.498	-0.500	-2.386	-0.842		
-0.543	-1.324	-0.047	-0.851	0.528	Pancreas			
-0.909	0.513	-0.247	1.193	-0.835	-2.025	-0.474	-0.366	
-0.926	0.089	0.847	0.822	1.555	-0.880	-0.172		
-0.713	0.491	-2.064	-0.874	-2.057	Pancreas			
0.686	-2.236	0.324	-0.789	-0.045	-0.183	-2.133	-1.934	
0.565	0.724	0.386	-0.055	0.002	0.580	0.000		
-2.342	0.633	1.768	0.984	-0.893	Pancreas			
-0.372	-2.245	-0.710	1.384	-1.463	-1.007	-0.139	-1.103	
-2.659	-0.171	0.470	-1.252	0.249	-2.900	-1.642		
-0.813	1.705	1.718	-0.406	1.472	Pancreas			
-1.817	0.373	-0.561	-0.477	-0.387	-1.481	-2.298	0.017	

Table36.txt

-1.316 -0.226 -0.145 -2.547 -0.762 -0.954 0.728
-1.610 0.332 -1.956 -1.278 0.666 Pancreas
-1.644 0.383 -0.286 -0.868 -0.092 -0.336 0.068 -1.225
0.560 -0.757 -1.616 -1.010 -0.169 0.664 -1.372
1.661 0.176 -1.358 0.100 -1.480 Pancreas
-0.467 -0.873 -2.407 -1.625 -0.628 -1.523 0.841 -1.507
-1.128 0.284 -0.823 -1.240 0.000 0.670 0.467
-0.916 0.793 0.583 -0.520 -0.682 Pancreas
-0.912 -1.108 -0.339 -1.362 -3.211 -1.402 -1.945 -0.761
-2.997 -0.911 -0.499 0.372 -2.316 -1.257 -0.767
-0.884 1.004 -2.210 -0.536 1.253 Pancreas
14.183 11.494 13.009 9.029 14.514 17.100 13.168 9.968
10.484 10.074 5.292 9.371 2.840 11.837 6.935
9.089 8.433 6.176 7.557 6.836 Pancreas
-2.420 -0.552 -0.752 0.449 -1.510 -1.583 -0.019 0.145
1.337 1.555 -0.266 -1.202 -0.600 -0.593 -0.200
-3.227 -0.291 -1.498 -1.126 -0.719 Pancreas
-1.650 -0.679 -1.129 0.753 -0.706 0.626 -1.115 -1.367
0.816 -0.884 0.617 0.238 -0.773 -0.773 0.523
-0.516 0.639 -0.777 1.198 1.324 Pancreas
-1.046 0.328 -0.711 0.599 -0.605 -1.267 0.617 -0.982
0.981 -1.207 -1.416 1.067 0.777 -0.918 -0.425
-1.840 -0.831 -0.186 1.057 0.124 Pancreas
-0.677 -0.560 -0.560 -0.315 -0.571 -1.989 0.105 -3.464
-0.080 -0.122 -1.223 -1.118 -1.876 -0.528 0.002
-1.869 0.002 0.374 -1.190 -0.820 Pancreas
0.853 0.916 0.341 -1.339 -2.040 -0.772 0.968 -0.146
-1.376 0.630 -1.031 -0.031 0.497 -0.127 -0.519
0.049 -0.939 -2.228 -0.698 0.433 Pancreas
-1.454 -0.171 -2.562 -1.436 -2.291 -1.344 -1.727 -0.752
-1.073 -1.364 0.055 0.290 0.659 -1.708 -0.252
0.550 -0.958 -2.127 0.163 -0.667 Pancreas
-0.998 0.507 -1.200 -0.156 -0.196 -0.817 -2.082 -0.695
-1.522 1.222 -0.899 -0.652 -0.192 -1.894 -0.064
-1.857 0.102 0.368 -0.742 0.092 Pancreas
0.641 -1.285 -2.115 -1.056 -0.746 -2.057 -1.154 -0.893
-0.375 -0.231 0.252 1.649 -1.498 -3.260 -0.533
-1.028 -0.701 -0.618 -1.687 -0.288 Pancreas
1.068 -0.492 0.720 0.399 -0.379 -2.576 -1.596 -1.969
-0.343 0.850 0.763 -0.825 0.201 -0.514 -2.083
0.660 -0.262 -1.019 0.428 -2.194 Pancreas
-0.817 -0.446 -0.275 -0.750 -1.234 -1.762 0.873 -0.484
-3.012 -1.778 -2.475 -0.011 -1.778 -1.141 0.768
-0.223 -0.363 -2.178 -1.145 -2.237 Pancreas
-1.861 0.328 -1.923 1.180 -2.599 -0.505 -1.688 -2.914
0.041 0.760 -0.130 -1.610 -0.314 0.482 -0.820
0.208 1.046 -0.285 -0.369 -1.910 Pancreas
-1.301 -0.970 -1.399 0.212 -1.375 -1.165 -1.795 -0.861

Table36.txt

-0.857	-0.543	0.712	-2.266	-0.548	-0.931	-0.823	
-1.306	-1.719	-2.690	-2.228	-1.182	Pancreas		
-0.741	-1.159	-1.162	-0.795	-1.147	-2.542	-2.000	-0.457
-0.789	1.032	-1.162	0.316	0.345	-0.390	-0.218	
-0.343	-2.541	-0.249	-0.815	-0.538	Pancreas		
-0.682	-0.420	-1.194	-1.760	-2.143	0.102	0.546	-0.184
0.190	-2.548	-0.228	-0.764	0.306	-1.515	-1.177	
0.618	0.328	-0.031	-0.599	0.599	Pancreas		
-0.205	1.454	-0.797	1.444	1.594	1.066	-0.823	-0.195
0.499	-1.040	-0.374	-0.645	1.362	-0.486	2.432	
-0.010	1.105	1.921	1.296	-1.521	Pancreas		
0.077	-1.786	-0.728	0.205	-1.158	-0.390	-0.813	0.219
-0.656	-1.767	0.141	0.389	0.121	-1.906	-2.195	
2.399	-1.278	-1.275	-0.399	-2.088	Pancreas		
-1.950	0.695	-1.230	0.385	-0.920	-0.579	-1.202	0.463
-0.830	0.003	-2.003	-0.561	1.350	-1.657	0.000	
-0.403	0.775	0.396	-0.452	0.906	Pancreas		
-0.434	-0.256	-1.965	-1.193	-1.972	-1.813	-1.235	-0.287
-0.776	-0.107	0.959	-2.190	-0.302	-0.064	0.462	
-1.183	0.848	-0.446	-0.356	0.511	NA		
-1.552	0.992	-0.447	-0.168	0.167	-1.367	-0.842	-2.042
0.563	-0.874	-0.953	-0.881	-0.074	-0.933	0.101	
-2.285	0.539	0.271	0.389	0.057	NA		
0.180	0.617	-3.218	-0.990	-1.985	-2.278	-1.494	0.904
-1.216	0.080	-1.840	-0.372	0.555	-0.742	-0.690	
-1.550	0.604	-1.026	-0.235	0.016	NA		
-2.894	0.273	-0.486	-0.743	-3.905	-2.009	-1.531	-0.100
0.819	-1.708	-1.489	-1.234	-0.256	-1.119	0.086	
-2.327	-2.899	-1.706	-3.809	-2.417	NA		
0.607	-0.618	0.488	-0.549	-0.903	-0.630	-1.739	-1.843
1.038	0.315	-0.888	-0.715	1.055	-1.328	-1.953	
1.348	0.397	-1.339	0.557	-0.946	NA		
0.270	1.056	-1.704	-1.122	-2.399	-2.730	-0.819	-0.077
0.545	-1.911	-1.528	-0.751	-0.648	-1.938	-0.526	
-0.176	-0.057	-1.049	0.310	0.606	NA		
-1.515	0.130	-2.107	-2.483	-1.350	-1.667	-0.080	-1.553
-0.394	-0.574	-1.282	-0.701	0.148	-2.534	1.043	
0.502	0.882	0.297	-1.292	-1.985	NA		
-0.080	-2.218	-0.250	0.490	-1.540	-1.693	-0.437	-1.129
-1.587	-2.036	-3.231	-0.895	0.014	-1.042	-0.391	
-0.746	0.395	-0.819	-0.577	-0.032	NA		
-1.066	-1.355	-1.907	-0.155	-0.537	-2.095	-1.298	-2.783
-0.148	-1.774	-0.764	-1.174	0.007	-0.137	-0.017	
0.771	-1.922	-0.146	0.909	-1.602	NA		
-0.756	-0.747	-1.068	-1.201	-1.868	0.202	-0.081	-0.646
-0.577	1.275	-1.084	-0.714	-0.394	0.089	-0.567	
-1.259	-0.866	-0.634	-1.636	-0.361	NA		
-1.496	0.709	-1.242	-0.104	-0.501	-0.705	-0.771	-1.255

Table36.txt

-1.560 -1.018 2.720 -0.407 -0.550 -0.462 -0.735
0.141 -0.792 0.117 -1.848 -2.670 NA
-1.122 -0.721 -1.825 1.557 -0.600 -2.844 -0.325 -0.815
-0.692 -2.102 0.049 -0.102 0.811 -1.680 0.049
-0.687 -0.400 -0.886 0.869 1.887 NA
-1.189 0.961 -2.594 -0.864 -1.383 -0.710 -2.808 -0.798
1.214 0.264 0.589 -2.691 -2.212 -2.611 -1.277
-0.689 -0.934 -1.405 -1.376 -0.696 NA
-0.740 -2.414 1.078 0.004 -0.796 -1.262 -0.646 -1.690
0.386 -0.575 1.544 -1.116 1.197 -1.440 0.241
0.586 -0.863 -1.121 0.472 -0.246 NA
0.222 -0.640 -0.543 1.443 -1.425 -0.554 -0.518 0.669
-1.161 0.517 -0.148 0.287 -1.066 -0.980 -0.887
0.683 0.921 0.602 -0.636 -0.514 NA
0.369 1.627 0.990 -0.822 -0.299 -1.377 -1.785 -0.044
-0.768 -1.140 0.264 0.166 0.130 0.358 0.368
0.998 -0.349 -0.657 0.248 0.484 NA
-0.378 0.898 -1.616 0.473 -1.641 -0.210 1.670 -0.199
0.477 -0.923 1.149 -1.525 0.448 -0.936 -0.662
-1.461 0.444 -1.730 -0.396 1.097 NA
-1.785 -0.326 -0.249 -1.241 0.548 -2.298 -0.968 -0.621
0.484 -1.715 -0.697 -0.574 0.042 0.346 0.200
-0.087 0.091 -0.139 -0.134 0.560 NA
0.007 -1.137 -0.065 -1.798 -0.983 0.517 0.004 -1.990
-0.050 0.399 -0.350 -0.807 -0.145 -2.538 0.035
0.424 -2.027 1.433 0.624 -0.862 NA
-0.750 -1.331 -1.220 -1.531 -0.884 -0.489 -0.330 -0.625
-0.678 -1.292 -0.460 -1.838 2.170 -1.133 -1.513
0.259 0.611 -0.257 0.087 0.282 NA
1.273 -0.470 -3.046 -1.265 -0.438 -0.054 -0.747 -0.649
-0.734 0.466 0.118 0.394 -0.460 -0.981 0.224
-1.014 1.364 -0.083 -1.822 -0.008 NA
0.510 -1.125 -0.676 0.770 -0.470 -1.923 0.639 -1.999
-0.673 -0.363 -0.677 0.207 1.563 0.650 -0.360
-0.878 -0.328 0.390 0.191 -2.400 NA
0.487 -0.620 -0.673 0.681 -2.355 -0.148 -0.151 -0.407
-2.183 -1.051 0.548 0.519 0.183 -0.165 0.580
1.421 -1.531 -0.208 -2.879 -0.571 NA
1.168 -0.387 0.413 -0.192 -1.608 0.912 -1.817 0.467
-0.077 0.423 -0.886 0.500 -1.598 -0.382 1.179
-1.826 0.121 -0.265 -1.196 -1.975 NA
-1.180 -2.189 -1.000 -0.273 -2.055 -0.131 -1.473 -1.775
0.252 -2.399 -1.749 -0.152 -0.667 -0.388 -0.713
-0.808 -2.645 0.138 -0.932 -1.158 NA
-1.549 -1.680 -2.035 0.402 -1.937 -1.282 -1.270 -1.633
-1.225 -0.181 -0.803 -0.037 0.908 0.536 -1.744
-1.871 -0.822 -0.411 -0.783 0.076 NA
-1.533 -0.982 -1.477 -2.530 -0.728 -0.445 -1.441 -0.907

Table36.txt

0.074	-1.798	-3.375	-0.815	-1.883	-1.213	-1.905	
-0.589	0.219	-0.035	-0.021	-0.110	NA		
0.183	-0.210	-1.626	-1.065	0.574	0.115	-1.992	-0.705
-0.422	-0.047	0.908	-1.360	0.531	-0.354	-1.892	
-0.623	-0.193	-1.033	-0.986	-0.263	NA		
-0.506	-2.259	-3.401	-0.440	-1.797	-1.983	-0.441	-1.487
-0.426	0.352	1.373	0.077	-2.442	0.015	-0.383	
-0.872	-0.648	-0.053	0.302	-1.702	NA		
-1.987	-1.386	0.624	0.136	-0.893	-0.692	0.671	-1.485
1.251	-1.103	-3.621	-0.733	0.157	-1.147	-2.005	
0.286	-0.536	-0.081	0.402	-0.275	NA		
-1.454	-1.586	-0.528	0.025	-1.035	-2.721	-1.544	-1.955
-2.066	-1.002	-0.330	1.279	0.228	-0.569	0.922	
-0.057	0.638	-1.173	-3.510	-0.512	NA		
-0.978	0.881	-2.094	-1.111	0.450	-1.427	-2.007	-0.581
-0.271	-0.737	-0.789	-0.497	-0.651	-1.076	-0.206	
0.514	-0.028	-0.425	-1.059	0.081	NA		
-0.755	-0.646	-0.317	-0.204	-0.521	-0.824	-0.722	-0.729
0.926	0.631	1.086	-0.056	-0.674	-1.103	-1.426	
-0.621	-0.547	-0.124	-1.127	-0.689	NA		
-2.344	-0.556	-1.868	-0.843	-2.069	-1.900	0.039	-1.478
-0.322	1.971	-0.591	-1.271	0.402	-0.982	-0.759	
-1.302	-0.376	1.296	-0.774	-0.099	NA		
-0.073	-0.319	-1.285	-2.391	-1.697	-2.275	0.690	-1.753
-0.986	-1.257	0.560	0.979	1.716	-2.402	-0.980	
-0.237	1.189	0.105	-1.637	-0.687	NA		
0.372	-0.706	0.460	1.666	-0.342	-1.059	0.086	-0.788
-0.239	-0.573	-1.921	-1.174	-0.573	0.816	-0.071	
-2.652	-1.020	-0.055	-0.769	-0.612	NA		
-0.605	1.576	-0.194	1.689	-1.304	-1.473	-1.902	-1.619
0.490	-0.621	0.597	-2.104	-1.241	-2.401	0.493	
-1.210	0.102	-0.641	-0.086	1.563	NA		
-1.463	-0.051	-2.013	0.171	0.091	-0.610	-2.650	-0.924
-1.927	-0.901	-1.878	0.477	1.504	-0.860	0.555	
-0.023	0.600	1.015	-0.881	-1.208	NA		
0.690	-2.587	-0.089	-0.149	-0.104	-0.666	-1.360	-0.949
-0.051	-2.213	1.379	0.489	1.003	-3.135	-1.568	
-1.589	0.356	-2.100	0.406	-0.840	NA		
-1.258	-1.045	1.102	-0.177	-0.151	-3.688	0.621	-1.040
-0.480	-0.264	0.332	0.004	-0.738	-4.407	0.043	
-2.913	-1.014	-0.806	-0.765	-1.245	NA		
1.658	0.555	-0.703	-0.020	-1.328	-2.217	-2.052	-0.054
0.171	-0.871	1.045	-0.200	-1.263	-1.811	0.759	
-0.932	-0.162	-1.013	-2.823	-0.377	NA		
-0.610	-2.331	-0.692	0.245	-1.616	-1.259	0.818	-1.384
-0.655	-2.087	-0.504	-1.082	-0.760	-0.390	-1.805	
-0.262	-0.753	0.115	-1.784	-1.831	NA		
-1.248	-1.934	0.000	-1.095	-1.433	-0.950	-0.524	0.458

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-0.223	-0.131	0.697	-0.776	-0.182	-1.463	-0.196	
-0.293	0.972	-0.420	-0.976	-1.929	NA		
-0.728	-1.640	-2.303	-2.385	-0.132	-1.436	-1.442	-0.142
-0.174	0.438	-2.093	0.488	-0.092	-2.120	-0.647	
-2.358	-0.912	-0.094	0.025	-0.449	NA		
-1.113	0.123	-1.163	0.149	-0.188	-0.743	-1.466	-1.057
-1.271	0.780	0.115	-0.050	-0.323	0.724	-0.271	
-1.263	-1.076	-0.180	-0.025	-1.273	NA		
-1.545	1.017	-1.762	-1.219	-1.071	0.172	-1.147	0.003
-0.387	0.388	1.072	-0.097	-2.773	-1.722	-0.275	
0.263	-0.592	-0.508	-2.154	0.961	NA		
-2.034	-0.553	-2.300	-0.343	-0.171	-1.785	-1.151	0.231
0.212	0.969	-0.234	-0.462	0.825	-0.279	-0.854	
-1.414	-0.981	0.062	-0.674	-1.445	NA		
-1.811	-1.222	-0.974	0.240	-2.627	-1.804	-0.153	-0.403
-2.391	-1.411	-2.154	-0.539	-0.031	-0.192	0.102	
-0.994	0.154	-0.030	-1.637	-3.159	NA		
0.528	0.234	-2.177	0.298	-2.695	-2.329	-0.432	0.121
-0.602	-1.648	-1.576	-0.003	1.614	-1.808	-0.576	
-0.357	-1.134	0.037	-0.806	-0.568	NA		
-1.420	0.309	-1.161	-1.683	0.933	-2.676	-1.584	-2.458
1.183	-0.323	-0.324	-2.775	-1.017	-0.653	0.691	
-1.460	-2.366	-0.749	0.151	0.766	NA		
-0.180	-1.042	-0.766	-0.593	-0.447	0.460	-0.410	-2.411
-0.253	0.461	0.208	1.349	2.878	-0.790	-0.302	
0.309	-0.738	0.415	-0.757	-0.668	NA		
0.445	1.734	2.731	1.585	-0.196	0.880	-0.557	1.851
0.660	-1.099	1.219	0.546	1.303	1.601	-0.263	
1.217	-1.956	-1.835	1.028	-0.443	NA		
-2.139	-1.852	-2.713	-1.720	-0.124	-1.206	-2.505	0.656
2.340	-0.556	0.633	-0.814	-0.201	-2.346	-1.185	
0.977	-1.543	-0.317	1.240	-1.236	NA		
0.028	-1.031	-0.241	-2.542	-0.374	-2.282	0.018	-1.734
-1.658	-1.253	-0.748	-0.141	0.973	-1.425	-2.709	
-0.667	-0.332	-1.573	0.585	-0.691	NA		
0.116	-1.503	-0.773	-0.819	-1.461	-0.808	-1.437	-0.468
0.441	-0.941	-2.040	1.110	0.425	0.309	-0.087	
1.348	-0.649	-0.268	-2.193	-1.158	NA		
-0.172	0.078	-2.711	1.029	0.214	-1.832	-1.283	-1.850
0.428	-0.390	0.883	1.333	1.556	-1.100	-0.364	
0.756	-2.273	0.011	0.241	0.220	NA		
-0.026	0.547	-1.632	-0.884	0.176	0.115	-2.466	-2.232
0.338	0.201	-0.473	-1.299	-0.060	-1.501	0.392	
-2.286	-0.761	-2.726	0.299	0.381	NA		
2.663	0.027	-0.816	0.490	-0.070	-0.699	-0.903	0.573
1.197	0.208	-0.251	0.537	0.164	-0.575	0.368	
-1.324	0.968	-0.364	-0.946	0.203	NA		
-0.493	1.100	-2.225	-0.534	0.412	-2.689	-1.388	0.743

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-0.521	0.216	-0.445	0.138	1.345	-1.388	-0.416		
-2.161	-0.171	-0.168	-0.833	-1.233	NA			
-0.264	-1.340	0.687	-1.163	-1.599	-1.052	-0.028	-0.487	
-0.822	-1.442	0.217	0.318	-1.053	-1.627	-1.989		
-0.322	-0.064	0.781	-1.484	-2.860	NA			
-0.038	-1.048	-2.412	-1.229	-2.887	-1.149	-0.448	0.073	
-0.175	0.417	-1.152	-0.348	-0.120	-0.329	0.971		
-0.704	-1.805	0.405	-2.092	0.480	NA			
-0.856	-1.249	1.225	-0.498	-1.465	-0.430	-0.896	-2.015	
-1.815	-1.499	-0.467	-0.050	0.163	-1.100	0.352		
-0.025	-0.540	0.823	-0.652	-0.768	NA			
-1.156	-0.133	-1.329	-1.153	-1.670	-1.821	-0.112	-1.561	
-1.240	-0.446	0.790	-0.439	-1.285	0.153	0.071		
-2.103	2.030	-1.112	-1.971	-1.497	NA			
-0.717	-0.773	-1.007	-2.466	-0.512	-0.006	-1.188	-1.484	
-0.088	0.149	0.301	-0.150	-0.629	-0.023	-0.927		
0.258	-0.279	-1.875	-0.872	-1.377	NA			
0.319	-2.288	-0.701	-1.007	-1.259	-2.155	-1.009	-2.375	
0.496	-0.549	-0.369	-1.259	0.333	-0.940	-1.460		
-1.885	-0.606	-1.003	-1.403	-1.174	NA			
-0.208	0.453	-1.043	-0.412	-0.642	-1.893	-1.671	0.254	
-1.301	-1.997	0.150	0.198	-2.147	-1.882	-0.863		
-1.337	2.517	-0.320	-1.043	-1.476	NA			
-0.924	-1.653	-1.084	-0.541	-0.951	-0.365	0.158	1.377	
0.211	-1.432	-0.062	-0.313	0.222	-0.999	0.306		
-0.908	-0.058	0.784	-0.825	-0.934	NA			
-0.139	-0.991	-1.894	0.488	-0.466	-1.246	0.552	-1.211	
-1.112	-2.119	-0.086	-2.189	-0.621	-0.632	0.229		
-0.612	-0.547	-0.221	0.037	-0.827	NA			
-2.023	-2.849	-0.054	0.287	-1.300	-0.951	0.581	0.286	
-0.084	-2.062	-0.378	-1.554	-1.101	-1.484	-1.265		
0.697	-1.192	-0.277	-1.195	0.927	NA			
0.831	-0.138	-1.725	-2.316	-0.931	-3.305	-0.703	-0.744	
-0.224	-0.225	-0.018	-0.858	-1.782	-1.811	-1.184		
-1.359	-0.002	-0.676	-2.482	0.036	NA			
1.887	-0.593	0.857	-0.484	0.561	-1.777	-0.904	-1.106	
0.315	-2.465	-0.789	-0.817	-0.529	-0.756	-0.034		
0.000	-0.378	-2.703	1.064	-0.755	NA			
-0.226	0.279	-0.854	-0.140	-0.644	-1.048	-1.531	-0.575	
-0.742	-2.276	-0.639	-0.325	-0.824	-1.703	-1.580		
-0.880	-0.076	0.287	0.279	-2.040	NA			
0.765	-0.811	-0.082	-1.634	0.645	-0.313	-1.396	-0.837	
1.604	0.055	-0.102	-1.583	0.103	1.831	-2.470		
1.053	1.917	-0.568	-0.718	-1.408	NA			
1.435	1.307	-0.167	-0.385	0.252	-1.179	-1.566	-1.457	
-1.547	-0.896	-1.449	1.432	-0.356	-2.918	0.616		
-0.492	-0.501	0.145	-1.460	-0.298	NA			
-0.687	-0.524	-2.341	0.208	-0.271	-1.927	-1.678	-0.566	

Table36.txt

-1.266	-2.322	0.034	0.347	0.257	-0.088	0.929		
-0.488	-1.798	0.523	0.436	-2.267	NA			
-2.695	0.236	-2.059	-0.504	-2.665	-0.598	-2.251	-1.926	
2.020	0.626	-0.822	0.520	-1.717	-0.512	-0.077		
-0.327	-2.497	-0.250	-0.512	-2.121	NA			
-0.380	1.713	-3.510	0.205	1.202	-1.879	-0.089	-1.459	
-0.200	-0.790	0.341	-1.365	-0.759	-1.355	0.909		
-0.012	0.744	-2.206	-1.996	-0.259	NA			
-0.676	0.042	-0.741	-0.298	0.180	0.545	-1.118	0.207	
0.893	-1.817	-0.145	-0.409	0.397	0.080	0.453		
0.241	-0.553	-2.031	-0.447	-0.949	NA			
-1.472	-2.128	-0.358	0.350	-2.185	-0.186	-0.510	-1.423	
-2.278	0.720	-1.371	0.472	-1.517	-0.292	-0.201		
-0.861	0.161	-2.880	-1.800	-1.037	NA			
0.582	-0.854	-1.176	-1.340	-2.442	-1.690	-1.587	-0.435	
-3.227	-0.895	-2.601	-0.860	0.022	-2.315	-0.920		
0.834	0.862	-0.548	-0.342	-1.024	NA			
-1.070	-1.232	-0.962	-1.232	-0.539	-0.918	0.095	0.354	
-2.070	-1.163	-0.757	-0.843	1.395	-1.669	-1.293		
2.249	-1.733	-1.411	-1.201	-1.345	NA			
0.039	0.164	-0.331	1.292	-1.466	-1.807	-2.076	-2.030	
0.803	-0.665	-1.892	-0.580	-0.101	0.697	-0.859		
0.733	-0.171	-2.004	-0.657	0.716	NA			
-1.992	0.282	-0.612	-0.337	0.293	-0.450	-1.069	-0.752	
-0.498	0.348	-1.406	0.250	-1.614	-0.226	0.281		
-1.267	-0.027	-0.517	-0.887	-0.269	NA			
-1.676	-0.191	-0.038	0.445	-0.385	0.130	-1.043	-2.207	
-1.403	-0.792	-2.333	-1.143	0.231	0.178	-0.878		
-0.123	-2.037	-1.717	-0.862	-0.630	NA			
-0.496	-0.256	-0.846	-0.618	0.252	-2.276	-1.972	0.847	
-0.276	-0.278	-1.966	1.345	-0.202	-1.397	-0.015		
-0.134	0.145	-1.380	-0.632	0.754	NA			
0.486	-1.226	-1.334	-1.544	-1.723	0.285	-2.480	-1.368	
-0.683	1.145	-0.144	-0.536	-1.471	-2.010	-1.394		
-2.429	-0.374	-0.752	0.295	-1.316	NA			
-0.163	0.323	0.141	0.612	0.179	-0.944	-1.561	-0.979	
-1.434	-1.557	-2.164	-0.370	0.488	-1.459	-0.388		
0.610	0.650	1.074	-1.114	-1.123	Pancreas			
-0.498	-1.193	1.000	-0.146	0.689	-0.835	1.607	-0.802	
-0.712	-1.514	1.737	0.006	1.710	-1.684	-0.165		
-2.028	0.959	0.065	0.286	-2.066	Pancreas			
-2.595	0.262	-1.244	-0.192	0.020	0.330	-1.051	0.015	
0.431	0.378	0.829	0.393	-0.535	0.956	-0.739		
-1.582	0.476	0.490	0.289	-0.279	Pancreas			
-1.648	-2.617	-1.694	-0.477	-0.789	-0.258	-0.474	-0.417	
-0.898	-1.593	-1.396	-1.286	1.580	-0.604	-0.192		
-0.326	-1.536	1.267	-2.920	-0.955	Pancreas			
1.265	-0.920	-0.455	0.789	0.528	-2.247	-0.192	-0.441	

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0.920	-1.033	-0.761	1.503	-0.571	-0.127	-0.806		
1.540	0.159	0.317	-0.653	-0.938	Pancreas			
0.532	-1.826	-1.133	0.921	-2.270	-1.142	-0.165	-1.473	
0.477	-0.888	-0.003	-1.405	0.798	-1.033	0.721		
-0.368	-1.244	-1.819	-0.776	-1.845	Pancreas			
5.199	0.964	7.217	8.271	-0.675	9.811	3.551	5.029	
1.982	4.147	1.499	0.826	-1.045	4.788	-0.179		
0.487	0.471	-0.172	2.743	4.005	Pancreas			
-1.816	0.438	-1.557	-0.741	-1.819	-2.512	-2.603	-0.023	
-1.741	-1.569	0.117	0.109	0.269	0.471	-0.606		
-1.636	0.101	-0.643	-0.093	-0.435	Pancreas			
-1.294	-1.662	0.128	-1.203	0.127	-0.885	-2.731	0.355	
-2.666	-1.320	2.320	-0.281	-1.100	-2.117	-0.282		
0.541	-0.256	0.039	0.456	0.210	Pancreas			
-1.530	-0.189	-1.781	-0.560	-1.317	-1.528	-3.745	-1.948	
0.205	-1.400	0.166	1.283	-0.497	-2.677	0.908		
-1.121	0.287	-0.088	0.545	-0.743	Pancreas			
-0.334	-3.091	-1.244	-0.905	0.353	-1.908	-0.040	-0.065	
-0.062	0.322	0.024	-0.752	-1.253	-0.793	1.322		
-0.782	0.673	0.249	-1.187	-1.587	Pancreas			
-1.143	-0.940	-1.597	-1.257	0.144	-1.155	-1.952	-0.546	
-1.192	-0.646	-0.791	-1.978	-0.199	-0.628	1.741		
-1.656	1.153	0.386	-1.143	1.682	Pancreas			
0.103	-0.534	-0.811	-1.409	-0.629	-2.310	-1.688	-1.801	
-0.518	-2.568	0.291	0.698	1.470	-1.331	0.269		
0.256	-0.054	-1.257	1.655	0.330	Pancreas			
1.504	-0.782	0.434	0.281	-2.067	-0.869	-1.831	-1.400	
0.716	-1.205	-1.415	1.126	-1.537	0.355	0.165		
2.020	0.293	-2.561	-0.150	-0.231	Pancreas			
-1.316	0.452	-3.892	0.138	-0.279	-1.904	-0.547	-0.760	
-0.017	-1.108	-1.411	0.367	-0.070	-1.006	-0.353		
-0.456	-2.358	-0.359	0.120	0.228	Pancreas			
-1.536	-1.994	0.930	-1.281	-2.032	-1.741	-1.909	-0.384	
-0.179	-1.618	-1.056	-0.710	-0.042	-1.369	2.279		
3.104	-1.016	-0.379	-0.183	-0.973	Pancreas			
-1.645	-0.411	-0.993	-0.546	-2.686	-2.704	0.003	-0.544	
-1.754	0.321	-0.681	-1.013	0.330	-1.459	-0.751		
0.491	1.469	-0.422	1.151	0.173	Pancreas			
-0.660	-1.165	-0.610	0.639	-0.578	-2.365	-1.455	0.747	
1.073	-2.663	-3.830	-0.962	-1.379	-0.212	0.502		
-0.483	-0.119	0.807	-0.506	-0.241	Pancreas			
-0.961	-1.334	-1.614	0.759	-2.542	-0.581	0.233	-0.802	
0.281	-0.207	-0.851	-0.803	1.731	-0.211	-0.765		
-1.072	-0.095	0.109	-0.626	-0.706	Pancreas			
0.684	0.447	0.385	-0.002	-0.696	-0.019	-1.301	-1.407	
-1.678	-0.567	-0.914	1.114	-0.931	1.442	0.787		
-1.156	-0.235	1.064	0.179	0.531	Pancreas			
0.044	-2.294	0.115	-0.776	-1.679	-0.201	-0.461	-1.980	

Table36.txt

0.142	-1.026	-1.225	-1.185	0.745	-1.229	-1.492		
-2.242	0.562	-2.075	-0.783	-0.365	Pancreas			
-0.091	-1.404	-0.426	-0.676	-0.506	0.611	-0.881	0.906	
-0.393	-2.497	-0.953	-0.072	0.705	-0.314	0.849		
0.280	0.783	-2.541	0.079	-0.899	Pancreas			
-2.960	-1.096	-0.228	-2.591	-0.006	-1.603	-0.938	-0.086	
-1.135	-0.893	-1.731	-0.785	-0.015	-1.093	1.142		
2.856	-0.163	-0.306	0.319	-2.145	Pancreas			
-0.116	-0.564	-0.333	1.636	-0.560	-0.586	-1.646	-1.605	
-1.153	-0.481	-0.146	-1.254	0.866	0.214	-1.688		
-1.282	-0.368	0.019	-1.213	-0.409	Pancreas			
-2.037	-0.382	-0.116	0.296	-1.387	-2.846	-1.742	-1.490	
0.454	0.227	-0.556	-1.625	1.038	-1.842	1.028		
0.999	-1.922	0.479	0.118	-1.089	Pancreas			
-0.548	-0.810	-0.959	-0.634	-2.171	-2.690	-1.074	-0.666	
-0.760	-1.491	-2.352	1.272	-1.169	-1.529	1.963		
-0.929	-0.410	0.976	-0.756	-0.503	Pancreas			
-1.702	-1.336	-0.394	1.706	-0.157	-2.426	-1.019	-2.504	
0.465	0.855	1.342	-1.048	2.738	0.303	-0.289		
-0.894	-0.453	-0.318	-1.215	-0.813	Pancreas			
0.113	0.065	-1.499	-2.760	-0.522	-0.964	-0.446	-0.708	
-1.431	-1.128	-1.223	-0.636	-0.458	0.574	-1.182		
-1.030	0.749	-0.816	-1.595	0.628	Pancreas			
-1.976	0.137	-0.593	0.058	-1.374	-0.464	-0.018	-0.220	
-0.058	-1.390	-0.729	-0.798	1.235	0.273	-1.546		
-0.747	-0.431	-0.524	0.566	0.031	Pancreas			
-0.955	0.408	-1.240	-2.257	-2.814	-1.126	-0.316	-1.686	
-0.192	-1.126	-0.190	-0.136	0.598	-0.166	-1.585		
-1.986	-2.035	-2.942	-0.733	-0.384	Pancreas			
-0.566	-1.529	-2.509	0.273	-1.038	-1.395	-0.212	-0.417	
0.412	-0.287	-0.413	-0.901	-0.677	-0.216	-0.124		
1.382	0.712	-0.623	-0.120	-0.860	Pancreas			
0.499	-0.835	-0.645	0.259	-0.551	0.599	-0.511	-1.118	
0.404	-2.510	-1.605	-0.456	0.556	-1.443	0.235		
0.249	-0.645	-0.695	-1.235	0.599	Pancreas			
0.246	-0.308	-2.292	-0.826	-2.247	-1.037	-3.056	-1.404	
-0.912	-1.503	-0.993	-1.075	-1.609	-0.922	0.287		
-0.258	-0.489	-1.021	-1.745	0.087	Pancreas			
-2.004	-0.962	-2.861	-3.008	-1.030	-2.375	-1.164	-1.048	
-0.533	-1.689	-2.598	-1.047	0.727	0.898	-0.134		
-1.673	1.025	-1.144	0.479	-1.344	Pancreas			
-1.596	0.028	-0.289	0.381	0.945	-0.336	-1.891	0.008	
1.149	-0.662	-1.393	0.792	-0.254	-0.200	1.870		
0.812	1.270	-1.233	-1.487	-1.042	Pancreas			
0.032	0.073	-2.656	-0.852	-1.149	-0.582	0.874	0.498	
0.808	1.541	0.037	-1.988	0.645	-0.224	-0.478		
0.048	1.729	-1.264	-1.651	0.263	Pancreas			
-1.746	-1.168	-1.966	-0.897	-2.986	-3.198	-0.917	-1.239	

Table36.txt

-1.460	-0.073	-1.593	-2.513	-0.124	-1.063	-0.586	
-1.614	-0.821	-0.913	-1.454	1.247	Pancreas		
-0.722	-2.509	0.223	1.176	-2.387	0.165	-0.506	-1.292
-0.433	1.879	0.173	-0.786	1.249	-0.252	-0.246	
0.958	-0.110	-0.172	-1.063	-1.550	Pancreas		
-1.229	-0.842	-1.635	-0.011	-1.765	-1.785	-1.239	-0.349
-1.864	-2.268	1.474	-0.953	-0.891	-1.238	-0.071	
0.256	0.535	-0.636	-1.020	0.912	Pancreas		
-1.382	-1.301	-0.692	-0.450	-0.462	-1.273	-0.063	0.084
-0.345	-1.846	-1.004	-1.221	-0.195	-1.472	0.894	
-1.070	0.439	-0.123	-1.156	0.338	Pancreas		
-0.339	1.747	0.737	-0.499	-0.680	0.572	-1.708	0.361
0.196	-2.077	1.879	-1.624	2.273	0.104	0.786	
0.539	-1.067	-2.021	-0.621	2.132	Pancreas		
-0.197	-0.244	0.128	0.721	-0.129	0.328	0.304	-0.287
0.558	-1.678	-1.088	1.891	2.045	0.763	1.412	
-2.566	1.609	-0.432	0.966	-0.775	Pancreas		
0.011	0.746	-1.185	-0.902	-2.047	-1.596	-1.078	-2.596
-0.168	-1.605	-0.559	-0.242	-0.270	-1.138	-1.476	
-0.647	0.380	-0.301	-2.227	-2.209	Pancreas		
-2.622	-1.157	-0.484	0.836	-0.533	0.415	-1.565	-0.012
-0.129	0.189	0.289	0.580	0.323	-0.510	-1.447	
1.345	-0.241	0.381	0.317	0.497	Pancreas		
-0.338	-0.185	-1.877	0.743	-1.011	-2.822	-1.918	-0.871
0.478	-1.131	-0.098	-0.849	-0.590	-0.284	0.697	
-1.204	-1.268	0.734	0.916	-1.370	Pancreas		
-0.897	0.383	-0.991	-0.965	-1.363	-0.168	-0.390	-2.194
-1.480	-0.383	-0.487	-0.787	1.723	-2.488	-2.241	
-0.917	-0.154	-0.310	0.330	-0.907	Pancreas		
0.243	-1.315	0.227	0.753	-0.780	0.437	-0.282	-1.550
1.894	-0.866	0.051	-0.182	1.065	0.408	1.205	
0.781	-1.440	-1.310	-0.488	-1.433	Pancreas		
-2.037	-0.731	-0.693	0.080	0.220	-0.899	0.044	-1.691
0.271	-1.431	0.078	0.180	3.032	-0.511	1.153	
1.084	-0.207	-1.192	-1.439	1.115	Pancreas		
-1.163	-1.730	-0.578	-1.312	-0.942	-2.244	-0.611	-2.233
-1.917	-2.704	0.923	-1.227	-1.495	-2.468	-0.816	
0.619	-1.008	-1.027	-0.264	-1.097	Pancreas		
-0.818	-1.395	-3.220	-0.694	-0.539	0.608	-0.498	-1.069
1.176	-1.515	-0.128	-1.360	-0.652	-0.655	-0.696	
0.948	1.195	-0.662	0.641	1.305	Pancreas		
-0.678	-1.555	-1.975	-1.655	-1.833	-2.320	-2.404	-1.934
0.029	0.172	-2.340	-1.234	0.311	-0.251	-0.747	
-2.155	-1.136	0.027	-0.848	-2.306	Pancreas		
0.122	1.166	-1.817	-4.129	-2.457	-1.203	-0.291	-0.903
-0.253	-1.599	1.063	-0.710	-0.054	-2.513	-1.190	
-1.577	-0.050	-2.670	-1.557	-2.505	Pancreas		
-0.666	-1.912	0.041	-0.464	-1.123	-1.153	-0.540	-0.798

Table36.txt

-1.325	-1.938	0.119	-0.499	-1.057	0.352	0.226		
-1.751	-1.443	-1.649	-1.466	-0.722	Pancreas			
-1.169	-0.428	0.770	-0.354	0.467	-0.724	-2.509	-2.470	
-1.751	-0.766	-1.400	-0.551	-1.232	-0.988	-0.155		
-0.976	0.352	-0.300	-0.820	-0.232	Pancreas			
0.268	-0.650	-1.552	0.465	-0.459	0.236	-1.209	-0.106	
1.499	-0.340	-0.616	0.458	0.947	-0.405	1.620		
-0.886	0.346	1.067	0.378	0.809	Pancreas			
-1.046	-0.441	-1.143	0.108	-0.018	-1.525	0.861	-2.205	
-0.249	-1.246	-0.694	-0.460	-0.103	-1.269	-0.520		
0.387	0.187	-2.570	1.909	-1.906	Pancreas			
-1.777	-1.031	-0.733	-1.108	1.316	-2.691	-0.531	-0.384	
0.138	-0.863	0.610	-1.264	0.942	-2.668	2.405		
-1.350	0.284	-1.103	-0.363	-0.101	Pancreas			
-1.693	-2.615	-1.925	0.384	-1.395	-0.561	-0.386	-1.797	
-1.532	-0.593	-0.406	-0.466	-3.176	-0.443	0.168		
0.574	-1.861	-0.144	-1.360	0.544	Pancreas			
-0.646	-1.585	-3.747	-1.776	-1.113	-0.566	0.135	-0.242	
-0.963	-1.898	-2.096	-0.748	2.178	0.027	-1.135		
-1.336	-0.131	-0.415	-0.490	-0.995	Pancreas			
-1.185	-1.089	-1.110	-3.348	-1.135	-1.721	-0.190	-0.647	
-0.181	-1.254	0.784	-1.427	0.264	-0.052	0.509		
-0.088	-1.153	-0.228	-1.392	-0.486	Pancreas			
-0.392	-0.528	-1.207	-2.833	0.275	-1.157	-0.982	-1.782	
-1.966	-1.000	-0.244	0.868	-1.168	-1.298	-1.123		
-0.560	0.274	-0.361	0.063	-0.249	Pancreas			
-0.814	0.730	-1.216	-1.063	-1.614	-2.203	0.758	-1.296	
2.298	1.412	0.627	1.359	1.468	0.731	1.075		
1.327	-0.029	-0.758	-1.468	-0.915	Pancreas			
0.565	-1.262	-0.449	0.748	0.397	-1.536	-2.272	-0.918	
-1.482	0.663	-1.428	0.482	-0.984	-1.813	0.860		
0.029	-1.040	-1.237	0.073	-1.286	Pancreas			
1.547	-0.480	1.096	0.813	-0.212	-0.877	-2.201	-2.017	
0.303	-1.776	-0.207	-2.012	-1.496	0.634	1.829		
0.476	1.205	0.231	0.704	0.489	Pancreas			
-0.833	-2.865	1.065	-0.806	-1.195	0.707	-0.032	-0.460	
0.289	-0.513	-0.117	0.346	0.052	0.239	-0.268		
-0.534	-0.736	0.777	-0.057	0.422	Pancreas			
0.374	-1.700	0.522	-0.478	0.985	0.197	-0.711	-0.508	
-1.537	-2.390	2.086	-0.344	0.911	-1.649	0.342		
0.866	0.724	-0.246	0.348	-0.515	Pancreas			
-1.390	-0.800	-1.841	-1.743	-2.716	-2.109	-0.392	-1.867	
-1.394	-0.105	-1.359	-0.580	-0.268	-0.746	0.762		
-1.856	-1.011	-0.257	-0.699	1.534	Pancreas			
-0.565	0.205	-1.931	-0.260	0.031	-0.964	-0.054	1.705	
-0.587	-0.774	-1.780	2.014	0.749	0.505	1.319		
-1.666	0.495	0.467	-0.896	-2.039	Pancreas			
-1.068	-0.924	0.666	-0.943	-1.820	-0.478	0.641	-2.101	

Table36.txt

-0.791	-1.046	1.054	1.308	0.444	-1.396	0.934	-0.074	0.820
-0.992	0.228	-0.845	Pancreas					
-3.009	-1.656	-1.139	0.144	-2.511	2.095	-0.290	-1.969	
-0.957	-1.895	-1.260	-1.557	0.468	-1.390	-0.260	-0.247	-0.870
0.703	0.391	-1.144	Pancreas					
-0.201	0.451	0.499	-1.578	-1.344	-0.857	-0.292	-1.662	
0.286	-0.191	-0.060	0.268	-1.022	0.380	-1.995	0.839	0.427
0.577	-1.685	-0.301	Pancreas					
-2.288	-2.515	1.425	-0.740	-1.070	-1.057	-1.158	-0.344	
-1.275	-1.021	-0.626	0.157	0.002	-0.518	2.210	0.661	0.024
-1.285	-2.248	-0.298	Pancreas					
-0.628	-0.131	-0.322	-1.375	1.770	-2.316	-1.438	0.379	
0.152	-1.134	1.218	0.323	-1.759	0.117	-1.009	-1.028	-0.073
-1.842	-0.497	-0.580	Pancreas					
0.408	0.111	-1.277	0.098	-2.002	-1.957	-0.412	-0.995	
-0.728	0.852	-0.129	-0.038	0.032	-1.343	2.001	-2.642	-0.848
-1.988	-1.646	0.211	Pancreas					
0.157	0.219	0.244	-1.365	-1.977	1.081	-0.420	-1.466	
0.757	-1.073	-1.190	1.340	0.040	0.211	0.595	0.063	-0.004
0.122	-0.576	-1.873	Pancreas					
-1.891	0.883	-0.275	-1.322	-1.016	-0.776	0.143	1.290	
1.195	-1.947	-1.077	-1.263	1.632	-1.442	0.338	0.673	0.949
-0.571	0.322	-0.754	Pancreas					
15.263	9.329	12.354	7.875	17.410	17.939	12.534	13.871	
8.731	9.418	8.242	8.156	7.209	11.477	6.363	5.740	8.206
3.878	9.213	6.203	Pancreas					
-1.150	-0.072	-1.341	1.078	1.307	-2.062	-0.366	-1.161	
-0.008	-0.436	1.142	-0.935	-0.936	0.470	-1.556	1.090	1.364
0.220	-1.469	-0.667	Pancreas					
-0.507	-0.164	-0.019	-0.214	2.080	-0.001	-2.368	-0.458	
0.793	-0.718	0.998	-0.176	0.454	-1.662	1.583	-2.323	0.164
-0.363	2.183	-1.160	Pancreas					
-0.256	-0.370	-0.512	0.617	-1.545	-0.412	-1.121	0.552	
-0.980	-0.472	1.274	-1.335	-0.774	-1.502	-1.416	-2.597	0.982
-0.181	-1.712	-2.023	Pancreas					
0.089	-2.072	0.131	0.723	-0.277	0.160	-1.800	-2.108	
0.698	-1.512	-0.894	1.156	1.334	-0.080	-0.415	-1.357	3.385
0.195	1.383	-2.193	Pancreas					
-0.302	-2.841	2.413	-0.877	-0.478	-2.265	-1.169	-0.199	
-0.154	-0.452	0.423	-1.349	-1.138	-0.730	-1.043	-2.761	-0.609
-3.754	-2.198	0.857	Lung					
-2.133	-1.190	-1.193	0.986	-0.401	-0.415	-0.631	-0.493	
-0.192	-0.577	-0.544	-0.603	0.542	0.472	0.492	0.636	-1.234
-1.307	-1.571	-0.187	Lung					
-0.088	0.174	-1.083	-0.146	-1.151	-1.768	0.389	-0.913	
0.675	-1.712	-1.508	-0.090	-2.268	1.515	0.371	1.587	0.142
-0.330	-1.238	-0.858	Lung					
-1.563	-2.434	-0.778	-1.411	0.509	-0.898	1.230	-0.675	

Table36.txt

-0.139	-1.192	-0.532	0.512	-0.442	-0.415	-1.311	
-0.408	0.826	0.047	-0.596	0.863	Lung		
-0.916	-0.663	0.519	-0.513	0.578	-1.693	-0.680	1.056
-0.479	-0.570	0.535	0.598	2.294	-0.168	-1.036	
0.085	-1.753	-0.758	1.220	0.215	Lung		
1.298	0.102	-0.209	3.426	-0.391	0.472	-0.822	-1.928
1.071	0.750	-0.524	1.254	0.353	-1.387	-0.107	
0.095	-0.558	0.693	-0.096	0.511	Lung		
-0.360	-0.855	-0.317	0.164	0.216	-0.714	-0.763	-0.524
0.382	-2.147	0.616	-0.388	0.616	-0.369	-0.680	
-1.686	0.627	-0.491	0.949	0.821	Lung		
-0.530	0.675	1.105	-0.343	0.846	0.340	-2.183	-1.218
-0.150	-0.438	-0.555	-0.333	0.598	0.457	-0.705	
-1.320	-1.317	-1.537	0.481	-0.880	Lung		
-0.702	-2.649	-0.940	-1.641	-1.923	-1.659	-0.676	0.291
-2.651	-0.586	-0.119	0.176	-3.759	0.388	-2.015	
-1.685	0.736	-1.218	-2.629	-0.277	Lung		
0.238	-1.757	-1.936	-0.849	-2.553	-1.269	-2.554	0.499
-0.700	-0.272	-0.642	1.451	0.515	-0.718	-1.183	
-0.639	0.168	-2.789	-1.367	-2.000	Lung		
-0.098	-1.990	-1.966	-0.786	-0.521	-2.432	-0.865	-0.428
0.161	-1.156	-0.730	0.432	-0.628	0.121	-0.077	
-0.624	-1.420	-0.807	-0.446	-0.543	Lung		
0.512	-2.731	-3.794	-0.498	-0.946	-1.096	-1.672	-1.301
-0.548	-0.686	-0.708	0.150	-0.397	-0.725	0.380	
-1.105	0.026	-1.524	-0.053	-1.883	Lung		
-1.497	-0.439	-1.065	-0.580	-1.623	-1.280	0.084	-0.670
-0.018	-1.778	-0.521	0.123	2.207	0.255	-0.129	
0.055	-0.325	1.105	-0.623	-0.971	Lung		
0.943	-0.346	-1.632	-1.370	-0.265	0.140	-1.379	-1.353
-0.016	-0.570	0.710	2.079	0.910	-0.772	-0.931	
1.481	0.099	-0.365	-0.085	-0.888	Lung		
-1.312	-0.029	-0.535	-0.564	-1.920	-1.781	1.468	-0.184
0.367	-0.261	-0.353	0.133	1.735	1.439	-1.894	
-2.145	-0.303	1.247	-1.200	0.357	Lung		
-2.765	0.397	-0.506	0.540	0.321	-1.655	-1.754	-1.973
-0.916	0.250	0.631	-0.899	-2.384	-0.672	-0.981	
0.726	-0.027	-1.327	-0.645	1.075	Lung		
-1.271	-2.239	-0.149	-1.676	-1.602	0.110	-1.485	1.242
0.190	-1.442	-1.681	-1.161	0.440	-2.146	-1.249	
-0.533	-1.926	-0.536	-0.537	0.330	Lung		
-0.513	-0.187	0.471	0.164	-1.282	-0.135	-0.750	0.377
-0.292	-1.537	0.152	0.770	0.852	-0.503	-1.061	
-0.491	0.529	-0.578	-2.066	-1.864	Lung		
0.483	-2.691	0.124	-1.318	-0.863	0.466	0.333	-1.548
-1.004	0.683	-0.618	0.286	0.692	-0.075	-1.250	
-0.766	-0.720	0.777	0.865	0.579	Lung		
1.757	0.261	-1.024	-0.270	0.987	-1.090	-0.391	0.067

Table36.txt

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    0.095      -2.340     -1.899     -1.043     1.770      -0.207     -0.510
-1.687     -0.470     -0.580     1.023      -0.969     Lung
-0.219     -0.308     -0.805     -0.406     -0.376     -0.601     -0.723     -1.623
    -0.499     -1.449     -0.391     -1.120     0.440      -2.345     -0.839
-0.695     0.989      -1.076     -0.007     1.047      Lung
-0.556     -2.219     -0.095     -1.813     -1.485     0.125      -1.603     0.686
    0.809      -0.711     -2.637     1.982      0.454      -1.499     -0.322
-2.068     -0.504     -1.251     -1.320     -0.599     Lung
-0.200     -0.593     -0.707     0.897      -1.922     -0.674     0.525      -2.098
    -1.797     -0.401     -1.374     -0.773     1.364      -2.040     -0.471
0.691      0.384      0.520      0.053      -0.431     Lung
-0.605     -0.753     -0.493     -0.972     -3.258     -1.868     -1.931     -0.540
    -1.492     0.174      -1.415     0.423      -2.041     -1.963     0.484
-2.099     0.647      -0.762     0.434      -0.945     Lung
-1.259     -2.043     -2.453     -1.332     -1.890     -0.651     -2.397     -3.174
    0.091      -0.929     -0.987     -2.631     0.833      -1.806     -0.948
-1.026     -0.778     -1.372     0.243      -0.944     Lung
-0.919     0.069      -1.509     -0.020     -0.182     -0.351     -0.404     -1.321
    0.300      -2.016     0.973      0.913      -1.315     -2.423     -1.625
-0.721     0.701      0.050      -0.156     -0.568     Lung
-0.367     1.009      -0.535     0.368      -1.304     -0.392     -1.373     1.110
    -0.963     -0.727     -1.185     -1.370     2.815      -1.140     -0.122
0.586      1.053      -0.822     -2.358     -0.346     Lung
-0.047     0.208      1.013      -0.792     -1.680     -0.896     -1.968     -2.570
    -0.017     -1.568     -0.501     0.155      -0.805     0.782      -0.912
-1.523     0.884      -1.707     -0.002     0.397      Lung
-0.530     0.270      -1.197     -1.659     -0.563     -2.931     -1.722     -0.355
    -0.287     -2.043     -1.761     0.782      -0.523     -0.278     -1.480
-1.707     -0.877     0.040      -1.295     -0.961     Lung
-0.673     -2.287     -0.382     -0.298     -1.472     2.228      2.392      -1.572
    -1.811     -2.744     -2.589     -0.227     0.835      1.555      0.623
1.125      -0.562     -0.472     -0.478     -0.582     Lung
-2.121     -1.730     -2.407     -1.837     -0.696     -0.896     0.550      0.464
    -2.471     -0.807     -0.399     -2.661     0.153      -0.750     0.302
-0.548     -1.596     -0.341     -3.777     -0.561     Lung
-1.075     -2.994     -0.452     1.623      -0.745     -0.865     -0.117     -1.024
    -1.035     -1.920     -0.267     -1.147     0.017      -2.216     1.059
1.795      -1.284     -2.133     0.139      0.244      Lung
-0.261     -2.328     -0.689     0.725      0.111      -0.878     -1.494     0.143
    -1.857     -1.532     -0.726     -0.867     -1.192     -2.200     -0.375
-1.518     -0.930     1.535      -0.103     -0.987     Lung
-0.175     -0.477     -2.226     -0.022     -2.925     0.189      -0.633     0.470
    -0.358     -1.527     -1.852     -0.602     -0.825     -1.834     -0.275
-1.754     -0.814     -1.784     -0.090     0.167      Lung
-1.218     -1.637     -1.373     -2.525     -1.175     -1.004     -1.172     -0.335
    0.492      0.254      -0.530     -2.563     1.927      -1.048     -0.514
-1.757     -1.231     0.787      1.620      -1.110     Lung
0.010      -1.971     -1.268     0.438      0.449      0.772      -1.753     0.826
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Table36.txt

-1.634	-1.309	-0.510	0.451	1.426	-0.927	0.944		
-1.664	0.965	0.221	2.205	0.332	Lung			
0.320	-0.687	-1.027	0.616	-2.855	-2.545	-0.497	-1.795	
-1.096	-0.374	-1.666	-0.353	-1.328	-1.117	0.215		
-1.590	-0.599	-0.982	-0.178	-0.831	Lung			
-1.992	-0.885	-1.161	-0.882	-0.683	-1.830	-0.182	-1.755	
-1.285	0.181	-1.296	0.288	1.931	-0.747	0.276		
-0.572	0.600	0.384	-3.265	-1.200	Lung			
-1.034	-1.364	-2.642	-1.892	-0.639	0.212	-0.932	-0.293	
0.066	-0.744	1.331	-1.832	-0.101	-0.705	0.155		
-0.062	-2.930	-0.910	1.268	1.345	Lung			
-1.155	-0.327	-0.019	1.159	-0.716	-1.673	-0.808	-0.305	
0.526	-0.300	1.864	1.204	-0.093	-1.079	-1.062		
-1.282	1.068	1.926	0.859	-0.033	Lung			
-0.759	0.072	-1.017	0.893	-0.214	-0.715	-0.573	-0.281	
-0.559	-0.710	1.422	-0.855	1.493	-1.024	0.009		
0.909	-0.045	-0.693	0.554	-2.859	Lung			
-0.196	-0.906	0.011	-0.445	-2.749	-3.942	-0.915	-1.328	
0.639	-1.995	-2.303	-0.751	1.913	-0.421	0.673		
-2.511	-1.198	-1.375	-1.244	0.095	Lung			
-1.060	-1.936	-1.030	-1.393	-0.899	-2.113	-0.320	-0.693	
0.018	-0.300	-0.635	0.524	1.213	-1.050	0.786		
0.692	1.041	-0.938	2.387	-0.906	Lung			
1.269	-1.035	3.088	1.375	-1.402	1.227	-0.078	0.084	
-0.558	0.772	1.738	-0.431	1.514	2.829	-0.050		
-0.430	-0.196	-0.177	0.489	0.335	Lung			
-1.567	-3.634	-0.308	-1.679	0.112	-1.383	-1.265	-0.306	
-0.495	-1.195	0.243	-1.456	0.038	0.425	0.176		
-0.348	-2.400	-0.179	0.546	-0.678	Lung			
0.539	0.207	-0.198	-0.679	-0.055	-1.011	-2.345	-0.885	
-0.813	0.985	-0.752	-0.228	1.870	-1.181	-0.214		
-1.612	0.045	-2.573	-0.977	0.360	Lung			
-2.048	-0.956	0.693	-0.972	-1.744	-1.061	-2.697	-0.600	
0.807	-1.317	-1.223	-1.210	0.385	1.015	-1.271		
-1.896	-1.513	-0.788	0.106	0.084	Lung			
-0.895	-1.412	-2.510	-0.431	-0.836	-1.079	-1.583	-1.426	
-0.445	-0.516	-1.041	-1.027	-1.329	-0.704	-0.752		
-1.792	0.688	0.910	0.071	0.201	Lung			
-1.076	-0.678	-1.704	-0.934	-1.590	-0.990	-1.471	-1.553	
0.623	-0.308	-0.781	-1.323	-0.793	-1.388	-0.882		
-1.967	-0.380	-0.656	0.024	-1.216	Lung			
-0.457	-2.558	-1.018	-0.642	-1.434	-1.299	-2.103	-1.788	
-0.752	-1.126	-1.736	-0.394	0.881	-0.739	-0.031		
-2.473	-3.804	-1.477	0.300	-1.781	Lung			
-1.195	-1.666	0.470	-1.890	-1.957	-2.125	-2.506	0.211	
-1.796	-2.944	-0.717	0.801	-0.765	-0.456	-0.627		
-0.747	1.012	0.383	-1.620	-0.599	Lung			
-0.765	-1.784	-2.199	-0.187	-1.752	-0.938	-0.767	-0.410	

Table36.txt

-0.508	-0.572	-2.574	0.554	-1.477	0.055	0.154	-0.774	1.646	-0.315
-1.442	-0.114	Lung							
-1.759	-0.142	1.287	-2.464	0.953	-2.763	-1.241	-2.774		
-2.120	-0.144	-1.276	-0.725	1.148	-1.816	-1.065	0.551	-0.373	-0.508
-0.224	-2.657	Lung							
-2.508	-3.152	-0.091	-0.257	0.549	-2.329	-1.285	-1.268		
0.069	0.512	-0.999	0.463	0.056	-0.774	-0.281	0.167	-2.481	-2.329
-2.473	-0.833	Lung							
-0.963	-2.084	0.768	-0.144	-2.244	-2.479	-1.096	-0.544		
2.602	-1.351	-2.245	0.358	3.087	-0.207	0.713	-1.364	-0.702	-0.008
-0.278	-2.019	Lung							
-1.547	-2.135	-3.041	0.053	-1.157	-1.127	-2.469	-1.035		
-0.920	-0.191	-4.181	0.652	-1.215	-1.004	0.231	0.586	0.336	-1.591
-2.959	0.039	Lung							
-1.165	-0.691	-1.365	-1.074	-2.637	-0.997	-1.173	-1.975		
-0.901	-0.769	-0.297	-1.150	-1.042	-0.197	-0.357	0.455	0.330	-1.661
-0.383	-0.226	Lung							
0.246	-0.635	-1.237	-0.746	-0.020	-1.941	-0.105	-0.210		
-0.953	-2.004	2.725	-0.397	-0.261	-1.581	-0.057	-1.270	-0.853	-0.270
-1.178	0.151	Lung							
0.608	0.183	-0.664	-0.719	-0.278	0.735	-1.046	-0.140		
-0.083	-1.910	0.406	-0.503	-1.711	-0.822	-0.432	1.114	0.685	-1.552
0.233	-0.758	Lung							
-1.022	-1.362	-2.219	-1.939	-1.503	0.555	-1.466	-1.622		
-0.225	-0.937	-2.386	0.094	-0.882	-0.839	0.757	1.094	-0.261	-0.735
-0.595	-0.101	Lung							
-0.945	-0.424	-0.739	0.649	0.789	-0.891	-1.449	-0.405		
-0.083	-3.017	0.190	0.330	-0.392	-1.531	-3.759	-2.151	-0.035	-0.740
-1.214	-0.563	Lung							
0.382	-0.180	-0.589	0.235	-0.428	0.045	-0.652	0.142		
-2.304	0.076	-0.668	-1.183	-2.118	-0.518	-2.180	-1.027	0.014	-1.708
-1.987	0.259	Lung							
-1.725	-3.521	-1.193	-0.424	-1.753	-2.493	-1.001	-1.138		
-1.053	-2.559	-0.908	-2.248	1.829	1.200	0.779	1.321	0.428	0.035
-0.037	0.110	Lung							
11.083	13.052	16.326	8.204	17.739	16.728	12.697	10.754		
7.015	8.354	7.547	10.114	7.928	14.849	7.289	6.879	7.668	4.491
9.751	6.696	Lung							
0.375	-1.379	-0.572	0.408	-2.833	-1.085	-0.281	-1.713		
-2.131	-1.783	-0.691	1.085	-1.727	-2.407	0.358	-0.035	-0.287	0.036
0.426	-0.969	NA							
-2.159	-1.520	-1.382	-1.620	-2.354	-1.690	-1.047	-2.180		
-0.381	0.042	-1.148	-2.338	-0.572	-1.460	0.160	-0.457	-1.125	-2.434
-0.108	-1.854	NA							
-1.408	-1.059	1.032	-0.482	-0.534	-0.836	-1.046	0.753		
0.551	-0.453	-1.833	1.259	-1.657	0.226	-1.125	-0.623	0.701	0.691
1.708	-0.312	Liver							
2.065	0.709	-0.366	-0.073	-0.993	0.444	0.532	0.913		

Table36.txt

-0.282	-1.190	1.393	-0.851	0.461	-1.687	1.428	
0.005	1.587	-0.066	0.858	-0.537	Liver		
0.687	-1.229	0.155	0.405	0.596	-0.583	-1.254	-0.220
-0.607	0.918	0.076	-1.864	0.167	0.696	0.734	
-1.225	0.508	1.400	-1.865	0.497	Liver		
-0.955	-2.173	-0.222	-0.393	0.486	-0.590	-0.835	1.573
-0.124	-0.563	0.687	-0.944	-0.422	0.400	0.552	
-0.187	-1.635	-0.094	0.109	-0.981	Liver		
-0.433	0.181	0.125	-0.573	-0.483	-1.743	-2.562	-0.972
-0.358	0.577	0.280	1.790	1.379	-0.341	-1.059	
0.186	1.400	-1.278	0.101	1.845	Liver		
0.494	-2.199	1.318	1.365	0.529	0.613	-0.690	-0.553
-0.731	-0.796	-0.722	1.686	-0.116	-1.539	2.086	
0.164	0.866	2.382	0.228	0.620	Liver		
-1.318	-2.345	-1.886	0.179	-1.356	-2.053	-0.278	-1.721
0.275	0.478	-0.833	-2.124	-0.008	-0.454	-0.884	
0.056	-1.720	-0.202	0.606	1.857	Stomach		
-0.984	-1.417	-2.262	-2.196	-1.442	-0.720	-0.570	0.212
1.327	-1.273	-0.266	-2.815	0.585	-1.382	0.280	
-0.968	2.175	0.639	-2.660	-0.292	Stomach		
-0.161	0.246	-0.487	-0.627	-0.656	0.152	1.356	0.248
-1.037	-0.679	-0.156	0.498	0.699	-0.117	1.096	
-0.096	1.727	-0.694	-1.635	-0.659	Stomach		
-2.718	-0.216	-1.572	1.144	0.342	-2.380	-1.853	0.773
-1.383	-0.695	-1.230	-0.753	-1.148	0.451	2.838	
-1.510	2.592	0.822	-1.025	-0.369	Stomach		
9.159	7.227	8.999	4.232	9.124	9.161	14.827	10.987
3.236	13.132	6.555	-1.141	9.142	12.340	3.462	
6.885	2.298	4.108	7.969	-0.025	Liver		
0.207	-0.713	0.707	0.856	-0.638	1.070	-2.284	-0.644
-0.790	-1.215	-2.272	-1.354	0.268	-0.109	-0.286	
-1.060	-0.698	-0.202	0.961	1.076	Stomach		
-1.145	-0.339	-1.537	-1.111	-1.695	1.199	-1.277	-0.067
0.663	0.072	0.173	-0.871	-0.834	1.692	-0.166	
1.544	1.176	-0.296	-1.098	0.910	Stomach		
-1.305	-3.051	-1.186	-1.631	0.427	0.575	0.341	-0.781
-1.160	-0.044	0.010	2.364	-0.455	1.482	1.229	
0.649	2.970	-0.625	0.695	-0.922	Stomach		
-0.666	0.149	-0.326	0.292	0.470	0.197	-0.495	0.951
1.008	0.966	0.108	0.056	-0.428	0.106	1.096	
1.234	0.259	0.948	1.901	-0.254	Stomach		
1.021	-0.953	-1.811	0.089	-0.194	-2.241	-0.550	-1.899
-0.565	-0.073	-1.221	0.399	0.288	0.003	1.548	
-0.323	-1.503	-0.360	-0.974	0.875	Stomach		
-0.054	-0.785	-1.065	-0.421	-1.443	0.241	-1.153	0.564
-1.155	-1.000	0.593	-1.482	1.010	1.005	-2.340	
-0.773	0.185	-1.541	-0.287	-2.918	Stomach		
0.724	0.256	-1.858	0.390	-0.903	0.293	0.162	-0.129

Table36.txt

-1.168	0.837	-1.962	1.230	-0.502	-0.013	3.538	0.618	0.774
-0.321	0.165	-1.344	Liver	-0.199	-0.241	1.050	0.295	0.953
1.444	1.370	-0.816	-0.164	-1.045	2.867	0.196	2.835	-0.469
0.613	1.963	0.762	1.653	-0.332	1.633	Liver	2.481	-2.243
-0.067	-1.819	-0.265	-1.893	0.985	-1.033	0.467	-0.530	0.446
2.421	0.472	-0.246	2.513	0.297	-1.023	0.349	0.664	-1.385
Liver	-1.105	-0.970	-0.604	-1.037	-0.151	-0.495	-0.016	-0.102
-0.732	-0.302	2.420	-1.011	-0.635	0.283	0.167	0.472	-1.555
-1.260	1.016	-0.045	Liver	1.001	-0.980	0.022	-0.450	0.652
0.537	-1.110	-0.362	-0.131	0.975	-0.236	1.090	0.440	0.995
-3.090	-0.458	1.687	0.345	1.116	-0.190	Liver	-0.655	-2.075
-0.842	1.006	1.318	-1.689	-1.103	0.434	0.651	0.846	0.750
1.771	1.051	0.712	0.220	-1.447	1.636	1.455	0.001	-1.772
Stomach	-1.119	-2.062	-1.466	-0.887	-0.759	-0.383	-1.191	1.389
-0.909	-0.722	-1.960	-0.143	-0.107	-0.345	0.896	-1.432	-1.808
0.733	-1.394	0.352	Liver	-0.134	-1.334	-0.059	0.391	-0.492
-1.730	-1.085	0.168	0.847	0.210	0.768	-0.560	-0.658	0.202
-0.082	0.023	2.135	-0.803	-0.846	0.840	Liver	0.156	-2.137
-1.000	0.483	0.431	0.227	0.981	-0.796	0.158	0.395	-2.981
-0.641	-0.125	0.244	-0.207	-0.560	2.607	-1.391	-0.951	-0.880
Liver	-1.733	0.296	-1.624	0.535	-1.323	-1.110	-1.330	-1.814
-1.609	-1.031	-0.324	0.845	0.384	0.225	0.000	1.173	0.468
-0.580	-0.573	-0.549	Liver	-0.821	0.755	0.127	-0.024	2.575
-1.976	0.995	-1.636	-0.235	-0.526	-0.324	-0.675	1.613	0.561
0.097	0.795	0.865	1.567	0.303	-0.565	Liver	-1.282	-0.856
-1.393	0.542	-1.388	-1.848	-1.999	-1.406	0.171	-0.142	0.500
0.340	-0.596	-3.719	-1.749	0.917	-0.362	0.765	-1.571	-0.345
Colorectal	-3.551	0.077	-0.593	-1.415	0.681	-1.285	-1.191	0.128
0.438	-1.800	0.649	0.017	-0.242	-0.692	0.463	-0.465	-1.396
1.001	0.956	-0.885	Colorectal	0.219	-1.757	-1.177	-0.680	-1.239
0.158	-0.327	0.258	1.558	-1.886	-0.723	-0.151	1.761	0.198
0.905	-1.037	-0.509	-0.102	0.948	-1.334	Colorectal	-0.131	-1.007
-1.594	-0.266	-0.280	2.122	-1.136	0.132	-0.835	1.102	-0.104
-1.412	-0.608	0.810	1.432	-1.284	0.052	-0.271	-1.328	0.192
Colorectal	-0.625	-0.459	0.398	-1.028	-2.364	0.527	-0.162	-0.558
-0.435	0.419	-0.909	-0.580	-0.529	-0.653	1.838	0.251	1.508
-0.131	-1.442	-0.240	Colorectal	-0.275	-1.631	-0.840	-1.126	-0.380
-0.312	-2.201	-0.847						

Table36.txt

0.938	-0.665	-0.508	-1.491	0.995	-0.797	-1.251		
-0.618	0.171	0.887	0.340	-0.483	Colorectal			
-0.778	-1.535	0.847	0.580	0.686	-2.298	0.305	-0.973	
-0.305	-0.617	-0.868	2.830	0.408	-1.326	-0.314		
-0.088	0.658	-1.352	-1.586	0.025	Colorectal			
3.880	0.696	4.173	-0.015	0.934	2.079	6.808	7.311	
2.345	2.709	-1.227	0.817	2.139	6.474	4.516		
3.490	2.795	-1.943	6.536	4.561	Colorectal			
6.239	5.005	12.474	4.303	7.372	7.792	15.026	5.590	
4.373	4.142	7.331	-0.463	0.120	10.112	0.150		
2.144	4.408	1.994	-0.201	2.736	Colorectal			
0.715	0.237	1.989	-0.075	1.118	-0.057	-1.909	0.139	
1.339	0.239	-0.906	-0.006	0.233	1.222	0.090		
1.270	1.072	0.193	1.782	0.364	Colorectal			
-0.520	-0.594	-0.166	-1.242	0.127	-1.974	-0.675	-0.705	
-0.136	-0.169	0.211	0.904	1.372	-2.647	0.468		
0.442	-0.844	1.127	-0.770	-0.234	Liver			
-0.046	-0.609	-0.705	-0.766	-0.445	-1.554	0.974	-1.592	
1.495	-0.940	0.669	0.007	0.241	-0.847	0.565		
-0.167	-0.382	1.857	-0.479	1.196	Colorectal			
1.252	2.911	-0.200	3.324	0.800	0.849	-1.313	0.129	
0.146	-1.271	0.178	1.978	1.445	2.562	1.059		
0.202	1.217	0.020	2.228	-1.181	Colorectal			
-1.239	-1.927	0.244	-1.951	-0.497	-0.164	-1.506	-1.592	
-0.766	-0.718	-1.249	-0.152	1.866	-0.025	-0.856		
-2.636	0.845	1.016	0.535	0.127	Colorectal			
0.282	-2.108	-2.642	0.582	0.131	-2.519	-1.612	-2.185	
1.726	-1.936	2.661	0.012	-0.611	-0.837	-0.307		
-0.526	-0.286	0.386	-1.771	-0.737	Colorectal			
1.179	1.804	-3.356	1.785	3.270	3.902	-0.364	-1.506	
-1.819	1.675	0.152	-1.007	0.815	0.033	1.194		
1.381	-0.645	1.155	-0.146	-2.589	Liver			
1.392	-0.394	-0.662	-0.242	-0.048	0.216	-0.903	0.382	
-0.079	-1.626	-0.711	1.414	-2.579	-0.309	0.351		
-0.105	-0.854	-0.254	1.064	0.308	Liver			
-0.339	-1.103	-0.184	-0.678	-0.829	-0.661	0.459	-1.863	
-0.008	-1.846	0.174	-1.500	0.163	0.218	1.122		
-2.402	-1.103	0.416	-0.937	-0.367	Liver			
-0.229	-0.311	-0.626	-1.300	-1.655	-1.329	-0.197	-0.394	
-1.037	-1.359	-0.545	-0.730	1.557	-2.756	-1.527		
-0.125	-0.032	0.115	0.371	-0.260	Liver			
-0.999	-0.781	0.174	1.451	-1.061	2.885	0.401	-0.133	
0.709	0.998	1.894	-1.117	1.476	2.298	-0.593		
0.603	0.248	1.351	-2.116	-0.576	Liver			
-1.832	1.296	6.126	2.399	2.264	6.567	0.199	8.364	
0.584	4.849	5.088	2.510	5.268	4.301	0.972		
0.435	-2.130	-0.344	3.895	-0.795	Liver			
-0.535	0.720	2.849	1.362	0.709	1.168	0.400	-0.133	

Table36.txt

0.146	-1.131	1.033	0.288	3.377	0.781	1.363		
-0.809	-0.616	-1.022	-1.111	0.564	Liver			
-0.169	-0.671	-0.139	-0.186	-0.389	-0.357	-0.667	-1.504	
-0.823	-1.539	0.695	1.728	1.291	0.561	0.974		
0.793	-0.865	0.560	-1.446	-2.958	Liver			
0.651	-1.375	-1.333	-0.150	0.161	-0.239	0.698	0.116	
-0.065	-0.476	-0.534	-1.478	0.319	-1.438	1.531		
0.688	1.044	0.033	-0.476	0.023	Colorectal			
1.837	0.298	0.139	0.338	1.750	-0.518	0.075	-0.128	
1.528	-0.122	-0.093	1.323	1.610	0.828	1.688		
1.020	0.432	-0.053	-0.040	0.856	Colorectal			
10.988	7.691	11.144	3.564	12.623	12.323	8.285	8.947	
6.905	7.307	1.265	5.105	6.025	8.569	4.768		
4.574	3.591	6.267	10.129	6.054	Colorectal			
-0.587	-2.141	-0.761	-1.518	0.128	-0.120	-1.127	-1.134	
-0.907	-0.908	-0.958	-0.711	-1.367	0.152	0.096		
1.467	1.682	0.221	-0.812	0.741	Colorectal			
-1.281	-0.560	-1.452	-0.823	-1.071	-1.898	-1.449	-0.235	
-0.699	0.326	-0.426	-0.618	0.281	0.698	1.624		
-0.331	-1.358	-0.881	-1.754	-0.378	Colorectal			
-0.880	-1.536	-2.281	-2.009	-0.919	-1.867	0.224	-1.032	
-0.384	-0.314	-0.491	-0.484	-0.859	0.139	-1.259		
-0.063	-1.861	-0.310	-0.686	-1.268	Colorectal			
-0.292	-0.159	-0.753	-0.098	-1.292	-0.806	-0.796	-2.480	
0.875	-1.660	-0.009	0.219	0.984	0.143	-0.009		
-0.501	1.283	-1.642	0.308	0.385	Colorectal			
-0.267	0.342	-2.418	-0.804	-1.095	-0.760	-2.506	0.292	
-0.880	-0.663	-0.009	0.357	0.950	-0.608	-1.023		
-1.078	-1.411	0.031	1.377	-0.112	Colorectal			
-0.386	1.117	1.503	0.005	0.040	0.232	0.065	-1.755	
0.260	-1.080	-0.735	-0.130	1.213	-0.906	-1.916		
-0.498	-1.142	-1.175	1.703	-1.026	Colorectal			
1.318	-0.878	0.045	-1.789	0.426	-1.611	-1.542	-1.548	
-1.239	-0.369	-0.654	1.547	2.264	-2.611	-0.555		
-0.255	-0.043	-0.215	-1.149	-2.945	Colorectal			
-1.272	-0.400	1.111	-0.615	0.007	-1.126	0.176	-0.852	
0.305	-1.270	-0.924	-0.420	0.868	-0.482	1.354		
0.493	0.635	0.677	-2.613	0.716	Colorectal			
-0.955	-0.434	1.890	-0.354	1.136	1.044	1.146	0.439	
0.638	-0.378	1.310	-0.746	-1.109	-0.466	-1.558		
-0.297	-1.559	-1.990	-1.078	-1.069	Colorectal			
0.595	-0.859	0.538	0.270	-0.815	-1.643	-0.804	-0.792	
1.056	0.003	1.108	0.360	1.300	0.259	0.629		
-0.282	3.380	-0.626	0.487	-1.989	Colorectal			
0.546	1.562	-1.335	0.438	-1.197	-0.619	-0.378	-0.654	
-1.358	-0.255	0.320	-1.466	0.105	-0.154	0.928		
-0.522	-1.164	0.101	0.262	-0.233	Colorectal			
0.650	0.604	-0.409	-1.329	-1.055	-1.066	-0.107	-0.693	

Table36.txt

0.915	-0.701	-1.078	-0.171	0.701	1.097	0.408	-1.061	0.559	0.291
1.763	-0.846	Colorectal	-1.289	-0.843	-0.117	-1.238	0.525	0.074	-0.705
0.165	-0.191	-0.029	-0.290	0.158	0.529	-1.136	-0.057	-0.432	-0.726
-0.183	-2.083	-0.672	Colorectal	0.100	0.037	2.641	1.187	0.933	-0.144
-3.130	1.678	1.066	-1.394	-1.628	0.540	-0.636	-1.025	-1.400	-0.509
2.057	-1.430	1.900	0.721	Colorectal	-2.240	0.133	0.024	1.654	1.694
-0.326	0.140	-0.773	0.469	-0.639	-0.271	-1.357	-1.935	-1.008	2.098
0.615	-0.854	-0.255	-0.886	-1.225	Colorectal	-0.726	-0.392	-1.861	-1.161
-0.849	-2.060	0.697	0.277	0.145	-2.625	0.782	-1.543	-1.812	-2.554
-0.397	-0.130	0.338	0.982	0.701	-0.359	Colorectal	-1.214	-2.013	0.802
-1.496	0.241	-0.544	-1.964	-0.732	1.065	0.784	0.692	1.299	-1.021
-2.157	0.075	-0.299	0.156	-2.205	-1.088	0.311	Esophagus	0.483	-0.300
1.595	-0.866	-0.397	-1.127	-1.167	-1.487	-1.120	0.314	0.369	0.153
1.381	-0.520	0.810	-0.098	1.054	0.728	-0.547	-2.146	Colorectal	1.123
-0.224	0.017	-0.582	0.579	-0.164	-1.970	0.084	-3.184	-0.808	-1.234
0.592	-0.321	0.251	0.922	-2.419	-1.467	-0.233	-1.079	0.764	Esophagus
0.154	-1.946	-0.704	-1.660	-0.953	-0.094	-1.000	0.003	-0.393	-0.098
-1.222	-0.964	-0.296	0.000	0.709	0.134	-1.810	0.466	-2.112	-1.673
Esophagus	-0.655	-0.124	-1.810	1.061	0.354	-1.680	0.214	-0.573	-1.599
-1.346	-0.229	-0.702	0.410	-2.126	0.483	-0.775	0.974	-0.975	0.892
-0.860	Colorectal	-0.830	-0.259	0.389	-1.751	-1.348	-0.777	0.208	-1.827
-1.086	-0.343	0.465	0.705	0.623	-0.319	0.284	-0.746	-1.027	0.651
-0.285	0.236	Colorectal	-3.432	0.305	-3.027	-1.327	-1.354	-1.384	-1.421
0.363	-0.097	-0.701	-0.614	0.907	1.910	-1.606	-1.721	1.651	-0.371
-0.945	0.259	-0.191	Colorectal	0.100	-0.980	0.079	0.503	-0.164	-0.730
-1.142	-1.605	-1.159	-1.515	-0.837	-1.019	0.100	2.049	0.219	-1.547
-0.954	0.238	-2.596	1.729	Colorectal	-0.979	-0.995	-2.644	0.925	-0.067
0.653	-3.326	-0.384	0.032	0.574	-0.731	1.599	0.542	1.127	0.024
0.142	1.153	0.119	0.054	1.559	Liver	0.035	-0.687	-0.134	0.286
-1.060	-0.363	-1.244	-3.544	0.355	-0.691	-2.785	-0.222	-1.197	-0.101
-0.701	1.870	0.026	-0.384	0.879	-0.294	Colorectal	2.024	-1.171	-0.551
1.048	0.608	-0.565	-2.518	1.507	0.076	-0.684	-1.937	1.418	0.851
1.665	0.804	1.216	-1.946	-0.104	-0.104	-1.679	Colorectal	-1.852	-1.011
-0.996	0.283	-0.558	-0.282	-1.902	-1.118				

Table36.txt

-1.367	0.112	-0.730	-0.692	0.380	-1.035	0.316	
-0.501	0.962	1.482	-0.592	-1.101	Colorectal		
2.883	1.675	0.300	-0.355	0.761	0.668	-0.672	-0.192
3.260	-1.071	-0.049	0.223	0.856	0.702	0.389	
0.172	2.114	1.056	-1.741	0.177	Colorectal		
-2.471	-0.041	0.945	-0.973	-1.041	-1.189	-0.743	-0.959
-1.933	-1.465	-0.451	-0.522	1.301	-0.947	-1.127	
0.383	0.152	1.219	-1.315	-1.176	Colorectal		
-1.448	0.457	-1.031	-0.410	1.403	-2.570	-1.742	0.905
0.496	-2.494	-2.775	0.445	1.132	-1.568	-0.109	
-0.960	1.718	-0.862	-0.667	-0.279	Liver		
-0.544	-0.122	-0.503	1.195	-1.050	0.990	-0.525	-0.701
1.172	-1.353	2.339	-0.846	0.820	-0.772	1.016	
-0.657	-0.176	0.099	0.260	-1.622	Colorectal		
1.585	-0.513	0.488	2.188	1.068	-0.297	0.103	2.167
-1.641	-0.542	-1.885	0.038	1.155	0.774	-0.365	
-0.375	1.285	-0.351	2.311	2.166	Liver		
-0.092	-2.858	0.102	1.781	-0.932	-0.480	-0.217	-0.968
0.669	-0.003	0.555	1.405	-0.387	0.700	-0.855	
-1.977	2.415	0.697	-1.369	-1.272	Liver		
2.000	2.809	3.607	3.589	3.126	3.496	3.193	3.488
3.632	3.573	4.493	0.818	0.126	1.705	2.903	
2.790	1.520	0.313	2.594	0.834	Colorectal		
-1.695	0.036	0.529	-0.266	-0.471	-0.059	-1.460	-0.243
-0.422	0.169	-3.361	1.859	2.341	-0.738	1.287	
-2.891	-0.899	-2.743	0.099	-1.448	Liver		
-1.245	-1.040	0.607	1.635	0.925	1.078	3.783	-1.429
-0.023	-0.086	0.215	2.043	3.192	0.051	0.211	
-1.652	0.140	-0.773	-0.880	-0.042	Lung		
-2.129	-0.645	-1.045	0.200	-1.057	0.295	-2.158	-1.530
-0.121	-1.454	-0.523	-0.928	-0.544	1.903	-0.147	
0.338	0.518	0.282	0.574	1.201	Lung		
1.105	-0.336	-0.990	-0.031	-1.591	0.458	0.945	-2.100
-0.162	-0.095	0.323	-1.110	1.510	1.043	0.268	
-0.850	-0.063	-0.632	0.038	-0.324	Lung		
0.961	-1.347	-1.724	-0.852	-0.071	-1.286	0.093	-1.934
0.107	-3.344	-1.059	0.932	0.256	-0.474	0.986	
-0.423	-2.355	-1.928	0.020	-1.576	Lung		
0.266	0.194	-0.207	-0.459	-0.418	-0.621	-1.869	-0.825
-1.852	-0.442	-0.049	-1.444	-1.201	-0.077	-0.286	
0.532	0.616	-0.053	0.581	0.188	Lung		
0.647	1.873	-0.414	1.721	2.028	2.406	0.204	0.782
-0.997	3.174	-0.395	0.535	1.724	0.931	1.129	
1.805	1.239	1.553	0.927	1.323	Lung		
0.627	-1.763	-0.710	-0.174	-0.957	-0.551	-0.332	-0.369
-1.073	-2.546	-2.075	0.242	0.892	0.737	-1.047	
-0.303	-0.721	-1.305	0.005	0.574	Liver		
0.215	-0.274	-0.977	-0.870	-1.573	-0.083	-1.101	-1.587

Table36.txt

1.055	-0.417	0.374	-1.358	0.463	0.021	0.847	
0.018	1.216	-0.298	-0.870	-0.222	Colorectal		
-0.222	0.270	-0.299	0.820	-0.831	-2.512	-0.307	-1.433
-0.916	-1.815	0.100	-0.591	0.560	-1.323	-0.224	
-1.586	-0.683	-0.272	-1.138	-1.293	Colorectal		
4.700	3.983	1.448	-0.257	3.867	3.399	5.418	2.649
-0.542	2.816	2.482	3.070	0.902	-0.280	2.042	
0.076	3.606	0.403	1.068	0.642	Colorectal		
0.943	2.012	0.975	0.030	-0.433	0.269	-1.164	-0.396
0.785	0.642	-0.276	1.242	-0.288	-1.398	2.212	
-0.787	0.773	-0.875	-1.151	-0.003	Colorectal		
-0.418	-0.552	-0.165	-2.349	0.990	-0.853	-0.405	-0.051
-1.166	-0.469	0.296	-1.019	-0.520	-1.440	-1.091	
-0.466	-0.065	-1.339	0.058	-0.234	Colorectal		
-0.295	-0.250	-0.012	1.334	-1.562	-0.130	-1.047	-0.177
-0.365	0.226	-0.784	-0.211	-0.309	0.237	1.602	
-1.391	1.296	-2.528	-0.864	-1.427	Colorectal		
-0.037	0.351	0.078	0.342	0.467	0.301	-0.947	-0.360
0.265	-0.783	0.091	-1.595	1.130	-1.051	1.047	
0.734	-0.449	-0.223	0.006	-0.868	Colorectal		
-2.647	0.876	-0.407	0.596	-1.158	-0.825	-0.756	0.305
-0.348	-0.700	0.699	0.597	1.301	-0.497	1.358	
0.817	0.789	-0.587	0.702	-1.543	Colorectal		
-1.652	-0.444	-0.975	-0.248	-1.972	-0.790	-2.363	-1.925
-0.730	-1.301	0.712	0.244	-0.859	-3.858	1.195	
-0.012	0.388	-0.537	-0.493	-1.671	Colorectal		
1.409	-0.452	0.316	-0.049	-0.305	-1.234	-2.487	0.001
-2.333	-1.168	0.857	1.044	-1.170	-0.663	-0.012	
-0.864	0.392	-1.857	0.981	0.196	Colorectal		
-0.079	-0.020	-1.140	-0.021	-0.145	-1.235	-0.910	1.200
-0.613	-0.903	-1.521	-0.809	0.583	0.302	1.286	
-0.878	0.399	-0.232	1.284	0.493	Colorectal		
-0.590	-1.647	-0.707	2.224	20.337	14.068	-1.624	2.632
-0.559	-1.361	4.589	3.008	6.557	14.672	0.550	
-1.056	8.239	7.568	0.173	0.596	Colorectal		
0.343	-1.196	-1.947	3.605	-1.034	-2.097	-0.842	-0.500
0.089	-1.467	-2.305	-0.895	1.616	-0.243	0.473	
-1.062	-2.424	-0.971	-0.890	-0.478	Colorectal		
1.288	0.699	-0.798	-0.106	0.944	-1.382	0.013	-0.657
-0.901	0.551	-0.140	-0.586	1.363	0.748	-0.762	
1.564	-0.428	0.942	-0.086	-0.091	Colorectal		
-0.676	-1.333	-1.336	-0.148	1.936	-1.594	-1.120	-0.568
0.096	2.341	-0.408	0.267	0.306	-2.721	1.938	
0.331	-0.137	-0.358	-1.385	-0.638	Colorectal		
0.028	-2.314	3.474	0.379	-1.402	-1.297	-1.283	-2.086
-0.281	-0.845	-3.806	0.858	0.817	-1.214	0.285	
0.418	1.101	-0.998	-2.297	-1.315	Colorectal		
-1.192	-2.097	-1.043	0.027	-1.554	-1.231	0.561	-1.049

Table36.txt

0.807	0.247	-0.932	-0.263	1.377	-0.448	-1.378		
-0.209	-0.297	-1.254	-0.385	1.553	Liver			
-0.297	-2.133	-0.391	-0.721	-0.947	-0.741	1.030	-1.841	
-0.203	-2.686	-0.266	-1.951	-0.619	0.020	-0.277		
-0.182	0.283	-0.087	-0.316	-0.481	Colorectal			
-1.127	-0.270	-1.363	0.089	0.797	0.454	-1.810	-0.804	
0.126	-0.652	-1.795	1.213	0.947	-0.504	0.175		
-2.175	0.107	0.000	-1.726	-0.017	Colorectal			
-0.955	-1.520	-0.881	1.126	-0.830	-2.681	0.830	0.771	
-0.188	-0.706	2.515	-2.685	2.112	0.631	0.112		
0.945	2.445	1.358	0.165	-0.921	Colorectal			
0.610	-0.367	-1.519	2.186	-0.163	-0.475	-1.161	-0.116	
-0.144	0.742	-0.809	2.426	0.269	-1.654	1.013		
0.668	-1.131	-1.182	-3.513	1.866	Colorectal			
-1.770	-1.197	-0.578	-0.667	-1.768	-2.588	-0.250	0.489	
-0.875	-1.257	0.220	0.124	0.104	-0.247	0.830		
-1.558	0.430	-0.057	1.220	0.404	Colorectal			
-0.175	-0.040	-1.684	-0.729	1.513	-1.549	1.328	-1.601	
-2.909	-1.007	-0.185	-0.438	-0.476	-1.969	-1.696		
0.905	1.297	-0.239	-0.013	0.316	Colorectal			
0.844	-2.282	-0.202	0.682	-0.489	-0.706	-0.167	-1.100	
-0.300	0.239	-0.309	-0.333	1.772	0.050	-0.032		
-0.545	-0.183	-2.188	0.127	-0.633	Colorectal			
0.321	-2.046	-0.097	-0.367	-1.291	-1.412	-0.853	0.385	
0.058	-0.865	-2.377	0.232	-0.315	-1.356	-1.126		
0.485	0.223	-0.614	0.500	-0.001	Colorectal			
-0.093	-1.100	-1.264	-1.768	0.378	-0.339	-2.361	-1.111	
-0.429	-1.637	-0.640	0.211	-0.025	-1.926	1.047		
-1.016	1.046	0.692	-0.449	-1.055	Colorectal			
0.087	0.280	-0.391	1.425	-0.327	-0.897	-1.251	1.990	
-1.152	-0.562	-0.340	0.522	-1.655	-0.153	0.576		
0.005	0.559	-0.182	-0.455	-0.081	Colorectal			
-0.524	-1.057	-1.426	1.316	0.502	-2.977	-0.276	-0.148	
0.447	-2.079	0.782	-0.346	-0.613	0.829	-0.375		
-1.656	-0.230	-0.042	-0.253	-0.020	Colorectal			
-1.461	-2.569	-2.871	-0.752	-1.021	-0.334	-0.316	-0.313	
-1.293	-0.215	-0.183	-0.162	-0.524	-0.553	0.225		
-0.595	0.637	-2.193	0.750	-0.077	Colorectal			
-1.076	-1.244	-1.678	0.544	-0.110	-1.468	-0.629	-1.263	
0.782	0.038	-0.070	-0.151	0.495	-2.265	-0.890		
0.094	-1.169	-3.299	-1.388	-1.274	Colorectal			
0.990	-0.451	-0.294	1.532	0.468	-0.292	-0.744	-0.555	
0.213	0.327	-2.039	1.496	1.150	1.450	0.701		
-0.856	0.381	-1.403	0.297	0.458	Colorectal			
-0.823	-0.537	-1.421	-1.828	-1.568	-1.398	0.175	-0.988	
0.442	-0.554	0.024	0.640	-0.079	-0.090	1.026		
-1.591	-0.315	2.158	-1.091	-0.441	Colorectal			
-2.047	-1.174	-0.869	0.414	-1.305	-0.594	-1.777	-0.969	

Table36.txt

-1.082	0.884	-0.403	-1.619	-1.016	-0.656	0.870		
-0.724	0.858	1.363	-0.709	0.409	Colorectal			
1.527	-1.728	0.074	1.131	1.834	-1.509	0.300	-0.714	
0.835	-0.749	1.699	1.071	-0.569	-1.116	-2.081		
-0.680	1.489	0.895	0.350	-1.469	Colorectal			
-1.360	-1.500	-0.186	-1.290	-0.435	-0.858	-3.013	-0.642	
-1.388	0.373	-0.362	-0.655	0.138	-1.044	-1.034		
0.237	-2.337	-1.628	-1.492	-0.801	Colorectal			
-1.143	-0.662	-0.194	-0.488	-1.104	-0.453	0.569	-0.784	
-0.565	0.525	1.173	1.027	1.673	0.103	-2.209		
-1.821	-0.766	0.170	-0.052	-0.137	Colorectal			
2.256	-0.201	-0.041	0.495	0.403	-1.227	-0.208	2.003	
-0.381	-1.964	-0.824	0.936	0.723	-1.666	-0.135		
-1.076	1.244	1.148	1.108	1.642	Liver			
-0.491	-1.143	1.017	1.448	1.397	-0.779	0.240	-0.013	
1.232	-1.718	-1.207	0.317	-0.930	-0.310	1.807		
-0.134	0.936	1.430	1.740	0.122	Liver			
-1.562	-0.132	0.850	-0.110	2.131	-0.909	-1.066	-1.085	
-1.265	-0.436	-0.298	-0.652	0.336	-0.289	-0.658		
0.470	-0.311	0.523	-1.551	1.155	Liver			
1.653	1.280	1.712	2.523	0.005	2.403	1.540	0.909	
2.518	-0.217	-0.196	-0.621	-1.227	0.910	0.020		
0.392	-0.187	1.262	1.184	0.659	Liver			
0.544	-2.173	-0.097	0.266	-1.249	-0.250	-0.899	-1.967	
-1.303	-2.827	-1.750	1.450	-0.533	-0.730	0.082		
1.591	-0.829	-0.514	-0.813	0.139	Lung			
-0.169	0.381	-1.911	-0.306	-0.164	-0.905	-1.209	-0.693	
-0.610	-0.778	-0.951	0.304	-0.215	0.808	-0.194		
-0.704	0.142	-2.879	-2.067	-1.463	Lung			
-0.106	-0.049	0.406	-1.357	-0.515	-0.129	0.227	-2.017	
0.181	-0.193	-1.669	-0.415	0.299	0.984	-1.908		
-0.097	0.715	-0.629	1.885	-1.226	Liver			
1.323	0.032	1.027	1.009	0.219	-0.567	-0.543	1.012	
-2.363	0.208	-0.546	0.844	1.255	-0.005	1.490		
-0.659	1.443	0.290	2.087	-0.814	Liver			
-1.226	-0.124	0.035	0.674	0.138	-1.138	-2.240	-0.715	
0.138	-0.679	0.626	0.640	1.483	-0.105	-0.117		
-0.392	0.984	-1.592	0.729	-0.663	Lung			
-0.736	-0.187	-1.401	-0.299	-0.506	-0.654	-1.918	-0.225	
-0.842	0.221	-1.428	-0.748	-1.584	-1.215	-0.523		
-0.963	-1.185	0.493	-0.810	-2.094	Lung			
-0.073	-2.817	-0.134	-1.183	-1.407	-0.558	-0.271	-1.150	
0.251	-0.864	0.044	0.006	0.240	-0.323	-0.474		
-0.759	0.440	0.390	0.806	-0.440	Lung			
-1.479	0.667	-1.863	-2.827	0.075	-0.615	-1.713	0.164	
-0.353	-0.453	-1.563	-0.984	-1.095	-0.375	-0.010		
-2.874	-0.989	-1.124	-1.141	-1.071	Lung			
-1.134	1.491	-3.405	-3.299	0.063	-1.424	0.261	-0.111	

Table36.txt

-0.096	-0.805	1.212	-2.757	-0.253	-0.842	0.608	
-1.159	0.139	-2.002	-1.128	-1.985	Liver		
0.725	0.407	-0.322	-0.051	-1.209	-0.752	-2.167	-0.276
-0.408	-0.134	0.403	2.831	2.859	0.326	-0.778	
0.249	0.879	-0.408	0.532	1.623	Lung		
0.242	0.956	0.136	0.035	-0.470	-1.873	0.206	-1.655
-0.396	-0.671	-0.293	0.413	-2.356	-3.220	-1.526	
-1.250	-0.397	-2.123	-1.033	0.162	Lung		
-0.169	-2.163	-0.036	1.049	-1.721	-1.707	-0.667	-1.742
0.392	-3.089	-1.328	-1.822	-0.211	-0.032	1.117	
-0.727	-0.673	0.281	0.199	-1.158	Lung		
9.176	0.888	5.451	1.272	-1.290	16.885	11.116	-0.163
6.481	7.978	4.626	1.659	-0.616	6.054	3.486	
3.207	-1.006	-0.408	1.554	6.065	Lung		
-0.873	-0.307	-1.433	-1.106	-2.092	1.166	-0.942	-0.257
1.653	-0.716	0.399	1.956	1.700	-0.942	1.473	
-0.481	-0.112	-1.004	-1.806	-1.253	Lung		
0.927	0.179	-2.552	0.249	-1.573	-1.524	-1.024	-1.335
-0.929	1.311	-1.592	1.562	-1.561	-1.319	-2.027	
-0.782	1.583	-0.088	-0.083	2.048	Lung		
-2.132	-0.645	0.807	-1.219	-1.674	0.019	-0.707	-0.701
-0.494	0.248	0.099	-0.423	1.164	0.229	-1.482	
0.647	-1.066	-1.151	0.604	-0.492	Lung		
0.160	-1.036	-0.928	0.916	-1.505	-1.088	0.373	-1.511
-0.564	0.190	-1.126	-0.390	1.883	-0.690	0.870	
-0.683	1.436	-0.376	-0.929	0.267	Liver		
2.986	-0.667	1.871	1.525	6.772	4.133	0.968	-1.469
0.468	-0.750	0.448	0.070	2.716	-0.357	1.730	
3.650	-0.246	-0.509	2.739	0.615	Liver		
0.466	0.338	-1.014	-0.164	0.379	0.783	-0.658	-1.193
3.137	-0.775	-1.559	-0.945	0.876	-0.152	2.069	
-0.232	1.382	0.679	-1.017	-0.070	Liver		
13.528	15.931	18.822	12.142	20.477	19.160	19.003	15.071
9.166	13.789	7.099	9.797	9.963	16.129	6.226	
9.675	8.899	5.615	11.490	7.735	Liver		
-0.171	0.547	0.114	0.575	-0.014	-0.242	-0.448	-0.579
-1.411	-1.175	-1.913	-0.523	1.597	-0.839	1.371	
0.129	1.614	2.916	0.797	0.312	Liver		
-0.187	0.628	-2.369	0.144	-0.876	-1.410	-1.818	-0.308
-0.873	0.419	-0.849	0.622	1.144	-0.675	-0.587	
-1.102	-0.396	-1.901	-1.641	-0.859	Colorectal		
-0.068	-0.631	-0.742	-0.157	-1.384	1.561	-0.987	-0.514
0.633	-0.766	0.251	-1.226	-1.124	-1.460	0.643	
0.118	0.261	0.483	-1.921	-0.811	Liver		
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	Colorectal		
-1.634	0.172	-1.669	0.114	0.206	-0.777	-1.539	0.885

Table36.txt

1.086	0.195	1.477	-0.684	-0.691	1.419	0.423	
1.070	-0.163	-0.520	-1.099	-1.591	Colorectal		
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	Colorectal		
0.709	-1.099	-0.641	0.006	-0.051	-1.180	-1.378	0.929
0.820	-1.812	0.145	2.331	1.645	1.427	0.966	
-0.520	-0.561	-0.531	0.993	-0.068	Colorectal		
-0.924	-0.439	0.722	-1.887	0.169	-0.786	-0.929	0.172
0.501	0.589	0.588	0.304	0.891	-0.248	1.368	
-1.292	-1.659	0.827	2.081	-0.732	Liver		
1.524	-0.615	-1.761	0.081	-1.512	-0.518	-1.146	1.156
-2.385	-0.116	0.878	0.470	-1.532	-1.148	-0.432	
0.782	1.048	0.791	-1.022	0.260	Liver		
-1.177	-1.633	0.885	0.356	-0.528	0.090	-0.458	0.346
-1.625	-0.401	0.673	2.570	1.351	-1.355	1.980	
0.176	1.663	3.390	-0.402	0.410	Liver		
-1.103	0.427	-1.094	0.356	-1.038	-1.916	-1.139	-2.094
-0.371	0.150	0.242	-0.014	-0.158	0.113	-0.371	
-0.005	0.454	-0.842	1.057	-2.446	Liver		
1.440	-0.868	0.388	-0.828	0.081	-1.909	0.019	-0.783
-0.104	-0.628	0.710	-1.135	0.157	1.756	0.445	
0.324	0.190	-0.146	-1.173	0.156	Liver		
-0.511	0.903	1.058	-1.387	1.674	3.530	0.945	-0.421
1.257	0.690	0.421	0.536	1.927	2.722	0.931	
0.869	1.698	-0.830	1.306	0.727	Ovarian		
-0.659	-0.454	1.169	0.234	-0.316	-0.308	-1.256	0.850
-0.783	0.540	-1.023	-1.251	-2.929	-1.736	0.178	
-1.365	-0.572	-1.861	-0.173	0.001	Colorectal		
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	Colorectal		
-0.873	-0.677	-0.932	0.637	-1.293	-1.134	-0.583	-2.371
0.749	1.669	0.404	-0.346	-0.542	-0.714	-1.305	
0.575	-0.219	0.796	1.132	0.668	Colorectal		
-0.043	0.413	-0.987	0.398	-1.406	-0.412	-0.924	0.863
-1.106	0.092	-1.368	0.192	0.663	-1.004	-0.789	
-2.255	1.515	-1.633	-1.908	0.018	Colorectal		
0.771	-0.108	-1.004	0.997	-2.380	-0.431	-1.628	-2.050
-0.987	0.116	0.510	-1.572	-0.560	-0.429	-0.524	
-0.148	0.303	-0.588	-2.089	-0.787	Colorectal		
-0.757	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	Colorectal		
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	Colorectal		
-0.170	-0.953	-3.776	0.646	-0.772	-2.045	-1.462	-3.094

Table36.txt

-2.021	-0.270	0.278	-1.028	-3.592	-1.254	1.168		
0.922	0.488	-1.163	-0.688	-0.203	Colorectal			
0.574	-0.041	0.892	0.622	-1.471	0.704	1.347	1.387	
2.613	-0.020	-0.214	4.000	3.413	1.044	0.271		
1.531	1.602	2.954	0.270	1.399	Ovarian			
-0.016	-0.665	-0.050	-0.428	-1.519	-0.838	-1.912	-2.132	
-1.788	-1.087	-1.228	-0.896	-0.073	-1.029	0.825		
0.403	-1.995	-0.325	-1.517	-0.016	Colorectal			
-1.180	-2.630	-0.747	-0.102	-0.843	-1.102	-3.386	-1.268	
-1.807	-1.154	-0.041	0.070	2.174	1.536	-1.560		
-0.261	-1.685	-0.284	0.087	-1.017	Colorectal			
0.470	0.465	0.029	-0.068	-2.421	-1.228	0.101	-0.473	
0.596	-1.735	-0.117	-1.048	-0.848	1.426	-1.572		
-0.087	-0.557	-0.858	-1.138	-0.279	Colorectal			
-0.135	0.381	-0.410	-0.324	-0.866	-1.360	-1.173	0.944	
-1.862	-0.336	-2.150	-0.979	-0.435	-0.229	-1.395		
-0.202	-1.392	-0.335	-0.642	-0.994	Pancreas			
3.363	3.812	-0.892	0.822	0.604	3.257	-1.438	0.790	
-0.167	2.442	3.802	4.869	-1.236	-0.237	-0.341		
0.643	-1.146	-0.236	-1.514	3.555	Ovarian			
-0.282	-0.045	-0.927	0.397	0.160	-1.613	-2.315	-0.710	
-0.768	-0.139	-0.253	-0.453	-0.973	-2.319	-1.778		
-1.319	-1.150	0.970	-0.065	-0.098	Ovarian			
-1.399	-1.430	-0.186	1.158	-1.552	-2.520	-0.727	-0.075	
-0.691	0.298	-3.045	0.073	1.569	0.460	-0.936		
0.312	-0.552	-0.861	-2.060	-0.008	Pancreas			
0.000	0.000	-0.378	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0.000	0.000	0.000	0.000	0.000	Lung			
-1.410	-0.052	-2.684	-1.927	-1.223	1.969	0.158	-0.397	
-0.116	1.184	-0.775	-1.975	1.577	-0.419	-0.001		
0.631	-0.147	-0.205	-0.118	-0.690	Lung			
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0.000	0.000	0.000	0.000	0.000	Lung			
0.689	-0.322	-1.510	0.085	0.304	-1.365	0.035	-1.464	
-1.946	-1.527	0.007	-0.193	0.669	0.233	0.679		
-1.920	-1.001	-2.161	0.120	-0.974	Lung			
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0.000	0.000	0.000	0.000	0.000	Pancreas			
-1.402	0.242	-0.831	-1.382	0.159	-0.337	-2.070	-1.200	
-1.266	-2.095	-0.174	-0.429	-1.948	-1.669	1.334		
0.140	-1.726	-0.358	-0.851	0.466	Lung			
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0.000	0.000	0.000	0.000	0.000	Pancreas			
-2.145	-0.838	-0.517	-1.017	-1.625	-2.061	-3.051	-0.564	

Table36.txt

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    -0.400     -2.408     0.000      -1.607     0.000      0.233      -0.321
-1.169     -1.329     -0.144     -3.366     -2.967     Pancreas
0.707      0.488      0.664      -0.378     -0.498     -0.272     -0.567     -1.489
    0.450      -0.804     -1.200     1.313      -1.985     -0.248     0.162
-0.024     0.697      0.523      -0.691     0.632      Breast
0.000      0.000      0.000      0.000      0.000      0.000      0.000      0.000
    0.000      0.000      0.000      0.000      0.000      0.000      0.000
0.000      0.000      0.000      0.000      0.000      Pancreas
0.000      0.000      -1.616     0.000      -1.003     0.000      0.338      0.000
    0.000      0.218      0.000      0.000      0.000      -1.169     0.000
0.000      0.000      0.000      0.000      0.000      Pancreas
0.760      0.941      -0.791     -0.302     -0.299     0.121      -0.084     -0.929
    0.254      -0.869     -0.081     -0.302     0.240      -1.627     0.239
1.211      0.895      -0.053     -2.003     -0.899     Lung
0.162      1.213      0.695      -0.302     0.423      -0.445     0.361      0.743
    -0.071     -0.249     -0.740     0.130      0.923      2.563      -0.109
0.546      -0.899     0.173      -1.805     0.311      Breast
-0.995     0.679      -1.516     1.113      -0.757     -1.479     -1.059     1.387
    0.821      -2.527     -2.171     -0.765     1.751      1.791      1.512
0.334      2.131      -0.189     -0.709     -3.682     NA
-0.413     -1.037     0.648      -1.106     -3.304     -3.572     0.788      0.284
    0.446      -1.006     1.350      -0.490     0.395      -0.003     2.298
-0.112     -1.959     0.226      -0.758     1.138      NA
-1.345     -1.372     -0.882     -1.780     2.292      -1.849     -0.659     -1.656
    -1.566     -1.145     0.482      0.130      0.302      -0.517     -0.112
-0.233     -0.318     -1.990     -2.885     -0.627     NA
-0.759     -0.885     -1.874     -0.613     0.175      -0.504     -2.781     -0.909
    -2.761     -0.695     -0.334     -3.009     0.047      -0.876     -0.415
-0.665     -2.228     -0.142     0.139      0.793      NA
-1.085     -1.417     -0.285     -0.334     -2.032     -2.171     -1.128     -0.285
    -0.663     -0.177     -1.452     -1.351     -1.972     -1.309     -1.797
-0.974     -0.708     -0.493     0.728      0.741      NA
-2.036     0.591      0.907      0.645      -1.651     0.830      -1.209     -1.225
    -0.283     -1.495     -2.555     -1.361     -0.908     -1.900     -0.287
-0.688     -1.405     -1.472     -1.584     0.564      NA
0.590      -2.473     -1.641     -2.035     -1.483     0.019      -0.216     -0.889
    1.536      0.011      -0.521     -1.118     -0.720     -1.121     -0.015
-0.804     0.359      -1.262     0.466      -2.154     NA
-1.912     -1.598     0.027      0.071      -1.536     -1.803     -0.157     -1.172
    -2.217     0.081      -0.160     0.204      -0.506     -1.158     -0.254
-2.342     0.560      -0.879     -0.552     -1.428     NA
0.323      -1.216     -2.475     0.123      -1.186     -2.404     -1.266     0.434
    0.856      -2.288     -1.782     0.211      -0.672     -2.152     -1.068
-0.572     0.186      0.153      -1.582     -0.563     NA
-0.200     0.505      -1.121     0.598      -1.248     0.060      -2.902     -1.763
    -0.527     -0.869     -0.382     -1.566     0.211      0.558      -0.124
0.343      0.473      0.078      -0.007     -1.159     NA
0.535      -0.320     -1.896     0.576      -2.404     -2.234     -0.898     -2.646
```

Table36.txt

-1.045	-1.349	0.318	0.041	-1.288	0.482	-0.700	
-1.766	-0.440	0.362	-0.278	-1.916	NA		
0.341	-0.287	-2.735	-1.084	-1.896	-2.116	-1.087	-0.464
0.052	0.386	0.868	-0.933	-0.520	-0.227	0.228	
-0.831	1.586	-1.699	-0.257	0.714	NA		
2.327	-1.115	-0.713	0.118	-0.526	-0.060	-1.414	-0.879
-0.378	0.023	-1.012	-0.605	-0.933	-0.530	-0.061	
0.266	-0.918	-1.269	-0.061	-0.590	NA		
-0.206	-0.393	-1.926	-1.307	-1.010	-1.760	-0.162	-1.344
-1.870	-0.660	-0.391	-0.355	-0.637	-0.317	0.757	
-3.019	-0.807	0.006	0.604	-0.154	NA		
-3.491	0.636	-1.053	0.204	-1.775	0.153	-1.569	-1.993
-1.285	0.411	1.664	-1.038	-1.442	-0.475	0.697	
0.250	-0.884	-0.065	-0.895	-3.552	NA		
-1.554	1.806	-2.401	-1.829	-0.706	-1.950	-0.495	-0.930
0.431	-0.249	0.733	0.346	0.447	0.003	-0.416	
1.386	1.064	-2.763	0.019	-1.187	NA		
-1.272	0.312	-0.510	-2.067	-0.978	-1.256	-1.394	0.744
-0.527	-2.362	0.712	-0.272	0.272	0.233	-1.011	
-0.337	0.267	1.637	0.160	-0.513	NA		
-2.690	-0.601	0.012	-1.092	-0.012	-1.049	-0.241	-1.098
-0.645	0.074	-0.224	-1.527	-1.064	0.053	-0.803	
-2.051	-0.053	-1.339	-0.826	0.346	NA		
0.291	0.629	0.730	-0.228	-0.333	-0.632	-1.041	-0.204
-0.251	-0.844	-0.179	-0.156	-0.662	1.732	0.472	
-1.481	-1.189	-0.639	0.039	0.423	NA		
-1.331	0.714	-0.325	0.512	-2.361	0.075	-1.840	-2.466
-2.574	0.955	-0.928	-0.013	0.147	-1.493	-2.204	
0.078	-1.481	-0.667	0.213	-0.826	NA		
-0.376	-2.530	-1.939	-1.621	-0.264	-1.671	0.772	-0.983
0.607	-0.883	1.043	-0.322	0.755	-2.048	-1.445	
-1.004	-1.584	-0.885	-0.186	-0.669	NA		
-0.230	-0.760	-0.105	1.103	-0.714	-0.320	-0.472	-0.259
-1.934	-0.227	-0.917	0.226	-1.444	-0.245	0.591	
-0.535	0.073	-0.744	-1.112	-0.396	NA		
-0.390	0.473	-2.419	-1.208	-2.835	-0.938	-0.223	-1.270
0.588	0.975	-1.973	-0.392	0.895	-1.856	-0.900	
1.681	-0.557	-0.712	-0.757	-0.717	NA		
-0.319	-1.380	-0.792	-0.444	-0.781	-0.856	-1.762	-2.915
-0.055	0.353	1.367	-0.198	-0.542	-0.572	0.806	
-0.078	-0.593	0.267	-2.423	0.428	NA		
-0.290	-0.041	-0.914	-0.949	-0.531	0.330	-2.124	-2.263
-1.466	-0.502	-2.640	-1.359	-1.146	-1.998	-1.287	
-0.635	-1.297	-0.024	-2.514	-1.050	NA		
0.863	-0.653	-0.718	-0.694	-0.638	0.462	-0.442	1.654
-0.317	0.889	-3.512	-1.104	1.236	0.104	-1.716	
0.214	-1.738	-1.413	-0.736	-2.013	NA		
-0.757	-2.907	0.622	-0.225	0.623	-3.877	-2.575	-0.276

Table36.txt

-0.647	-1.608	-0.988	-0.317	0.203	-1.360	-1.187		
-1.396	0.061	-0.859	-0.468	1.189	NA			
-0.187	-0.243	-0.623	-1.152	0.772	-1.592	0.753	-2.760	
0.240	-1.048	-0.179	-1.919	-0.708	-1.364	-1.592		
-0.067	-0.149	-1.497	-0.820	0.176	NA			
-0.971	-0.330	-2.739	-2.184	2.654	-0.817	-0.053	0.778	
-0.522	-0.614	-0.452	1.835	0.699	-1.602	0.515		
-1.343	-2.999	-1.783	-1.552	-1.538	NA			
-0.923	-1.888	-0.349	1.081	-2.462	0.226	0.089	-0.971	
0.114	-1.533	1.477	-0.469	0.387	-1.587	-1.771		
-0.535	-0.671	0.775	-1.577	-0.844	NA			
-0.690	-0.751	-0.718	-0.972	-0.704	-1.383	-0.643	-0.685	
-0.508	-1.237	-0.781	-1.073	-0.483	-1.974	-0.145		
-1.327	0.442	0.724	-1.100	-1.023	NA			
-0.781	0.267	-2.634	-1.484	0.460	-1.644	-1.981	-0.631	
-0.447	1.081	-1.431	-0.468	-0.779	-0.842	-1.358		
-1.226	0.038	-2.258	-0.001	-0.580	NA			
0.281	-0.205	-2.018	-2.278	-1.750	-3.365	-3.532	-0.791	
0.414	-1.914	1.325	-1.082	-2.402	-1.063	-2.204		
-1.865	-1.818	-1.326	-4.003	-1.842	NA			
-1.487	-2.403	-1.452	-0.317	-0.878	-4.605	-1.849	0.939	
0.581	-0.811	-0.490	-1.285	-1.448	-0.488	-0.090		
-1.964	-2.645	0.374	-1.040	-1.547	NA			
-2.203	-1.841	-1.389	-1.692	-2.166	0.236	1.121	-1.314	
0.208	1.089	-2.996	-2.214	-0.381	-0.077	-2.072		
-0.536	-1.190	-2.209	-1.295	-1.136	NA			
-1.469	-0.047	-1.844	1.127	-0.393	-1.812	-1.220	-1.408	
-0.710	-0.723	-1.701	-1.234	-0.731	-0.891	-0.348		
1.136	-0.454	-1.566	-0.733	-0.398	NA			
-0.403	-0.537	-1.816	-0.645	-2.947	-1.180	-1.146	-1.532	
-0.135	-0.654	-2.209	-0.227	-0.150	-1.230	1.212		
-2.205	0.022	0.063	-0.086	0.047	NA			
-0.983	-2.516	-1.679	0.512	-2.084	-0.264	-1.886	-0.646	
-0.043	0.969	-0.721	0.695	0.261	0.337	-3.106		
-0.824	-0.282	-2.162	-1.149	1.365	NA			
-0.047	-1.036	-3.003	-1.135	-2.838	-3.759	-0.585	0.899	
-1.697	-0.864	0.381	-0.411	0.171	-2.063	2.135		
-1.388	-0.453	0.098	-0.864	-0.607	NA			
2.423	-1.263	-0.569	0.130	-2.032	-0.624	-0.969	-0.962	
1.797	-1.046	-1.123	-0.669	-0.562	-1.583	-0.249		
0.711	-0.721	-0.912	-0.823	0.539	NA			
-0.929	-2.126	-3.031	-2.217	-0.833	-1.186	-1.147	0.411	
-0.080	-0.432	-0.925	-0.957	0.082	-1.569	0.144		
-0.806	-0.380	-1.459	-1.425	0.029	NA			
-2.052	-0.053	-1.236	0.301	-1.186	-0.560	0.883	-1.961	
-1.564	-2.705	0.167	-1.896	-1.028	-0.401	-2.845		
-0.256	0.161	0.239	-0.533	-0.516	NA			
-1.846	-0.375	-2.470	0.156	-1.083	-1.787	-2.083	-2.308	

Table36.txt

1.429	-2.009	-0.960	-0.128	-0.062	-3.236	0.472		
-0.373	-2.022	-0.521	0.760	-0.733	NA			
-0.619	-0.662	-1.800	-2.312	-1.605	-2.748	-1.499	-0.454	
-0.937	0.412	-1.408	0.728	0.700	-1.495	0.138		
-3.945	-0.443	-0.318	-0.391	0.716	NA			
-1.201	-1.870	-0.911	1.060	-1.256	-1.631	-1.398	-2.665	
0.293	-2.049	-0.361	-0.141	-0.977	-1.081	-1.201		
0.839	0.600	-1.019	-0.306	1.065	NA			
-0.605	1.361	-0.608	-1.645	-1.993	-1.804	-2.083	-0.205	
-1.120	-1.635	-1.541	-1.270	0.653	-1.024	0.492		
-0.099	-0.057	-3.175	0.144	-1.102	NA			
0.984	-1.963	-2.266	-1.371	-1.645	-0.963	-1.366	-0.641	
-0.307	-0.588	0.100	-0.129	1.581	-0.482	0.369		
-1.353	0.166	-0.829	-1.544	-0.074	NA			
-0.685	0.162	-4.021	-1.558	-1.755	-0.961	-2.058	2.053	
-0.884	-1.906	-0.677	-0.157	0.016	0.528	-0.578		
-0.414	-0.285	0.036	-1.481	-1.093	NA			
-1.686	1.003	-0.444	-0.818	-3.273	-2.184	1.511	-0.720	
-1.222	-1.331	-1.049	0.545	-0.997	-1.673	0.181		
-0.414	-0.451	0.288	0.341	-0.378	NA			
-1.379	-0.284	-1.858	-1.760	-2.463	-0.674	-0.369	-1.252	
-0.898	-2.242	-0.789	0.250	0.611	0.397	-0.527		
-0.768	0.998	-1.009	-0.273	-0.931	NA			
-1.458	-0.245	0.071	-0.143	-0.090	0.333	-0.520	-0.494	
-0.147	0.101	0.795	-1.002	0.927	-0.765	0.028		
-1.286	1.051	1.225	0.516	-2.656	NA			
-0.082	-2.180	-2.717	0.251	-1.850	-4.124	-1.359	-1.168	
0.918	0.038	-1.805	0.045	-0.538	-0.819	1.400		
-1.962	-2.209	0.104	-0.127	0.608	NA			
-0.708	-0.630	-2.395	-0.828	0.911	0.562	-0.362	-0.165	
0.061	-0.862	0.172	-1.586	-2.724	1.088	-0.232		
-2.428	0.287	-0.801	0.715	-1.712	NA			
0.246	-0.357	-1.297	-1.176	-1.300	-0.973	-0.745	0.096	
-1.150	-0.404	0.468	-0.649	0.109	-1.652	1.315		
-1.509	0.247	-0.886	-0.211	-1.630	NA			
-1.024	-0.334	-0.897	-1.032	-0.418	-0.825	-2.369	-0.317	
-1.140	-1.484	-0.426	-0.636	0.038	1.870	-0.942		
1.326	-0.711	-3.017	-0.001	-0.237	NA			
1.996	-1.206	-1.362	0.590	-0.271	-0.394	-0.766	-0.280	
0.278	-0.702	-0.191	0.200	0.156	-0.513	0.416		
-0.693	-0.267	-1.126	-0.028	0.784	NA			
-0.801	1.168	-1.124	-2.012	-2.162	1.231	-0.454	-1.851	
-1.797	-1.396	-1.280	0.550	0.936	-1.387	-1.268		
0.027	-1.723	-2.653	-2.039	-1.184	NA			
-2.351	-1.117	-1.279	-0.277	-2.072	-0.742	-0.815	-2.758	
-0.756	-3.515	0.668	-3.417	1.594	-2.038	-0.386		
-2.991	0.516	-0.855	-1.577	-0.707	NA			
-1.331	-0.854	-0.902	-0.258	-2.677	-1.014	0.510	-0.358	

Table36.txt

-0.044	-1.642	-2.712	0.584	-0.911	-1.691	-0.998	
-2.596	-1.198	-0.652	-0.740	-1.745	NA		
-1.067	-2.277	-0.500	-2.529	-2.444	-2.163	-0.696	-1.448
-0.134	-0.496	1.424	-0.913	-0.258	-0.048	-1.627	
-0.594	-1.727	-1.038	-1.134	-0.405	NA		
0.803	-2.479	-1.135	-0.499	0.010	-0.373	-1.849	-1.506
0.233	-1.915	0.284	-0.757	0.556	0.103	-0.670	
-1.002	0.662	-0.817	0.671	0.499	NA		
-1.701	-1.010	-1.602	-0.257	-1.457	0.583	-0.833	-0.293
0.505	1.400	1.025	0.179	-0.609	0.113	1.737	
0.289	-1.228	-0.950	0.215	-3.138	NA		
-0.518	-1.576	-2.827	-0.775	-0.749	-1.103	-1.390	0.251
-0.324	-0.571	-0.370	0.563	-0.581	-1.021	-0.437	
-1.454	0.013	-0.783	-0.771	1.414	NA		
0.699	0.064	-1.664	-0.182	-2.212	-0.446	-3.163	-0.087
-0.247	-0.302	-0.495	-0.911	-0.054	-0.068	1.069	
-0.735	-0.997	0.691	1.057	0.306	NA		
0.091	0.088	0.794	-0.838	0.375	-0.632	-1.483	-2.110
-1.497	0.277	-0.049	-0.741	0.160	-1.856	-4.174	
1.257	-1.768	-0.841	0.918	-0.384	NA		
-0.270	-0.857	0.215	0.947	-0.367	-1.887	0.037	0.037
0.720	-0.609	0.077	-1.051	1.089	1.028	-1.558	
-0.027	1.989	-1.231	-0.391	0.320	NA		
-1.678	-0.997	-0.924	-0.384	-0.803	-2.480	-1.245	0.222
2.400	-1.738	0.503	0.578	-0.939	-1.240	-1.391	
-0.479	-0.001	0.324	-1.672	0.759	NA		
1.707	0.373	-0.045	-2.921	-2.343	-2.253	-0.511	0.588
0.071	-1.425	-1.502	2.377	0.705	-1.386	-1.458	
-1.277	1.659	-1.539	0.083	-0.335	NA		
-0.078	1.022	-1.070	-1.946	0.129	-0.176	-0.364	1.367
-0.767	0.747	-0.328	0.071	0.680	-0.277	0.994	
0.321	1.674	-0.906	0.778	1.017	NA		
-3.175	-1.461	-2.408	-1.131	1.052	-1.937	0.524	-2.118
-1.533	-0.766	-0.347	-0.945	-0.636	-1.898	-0.150	
-0.114	0.848	1.254	-1.134	-1.638	NA		
-1.781	-3.200	-1.225	-2.337	-1.640	-2.441	-1.815	-0.593
-0.651	-2.236	-0.826	-0.725	-0.986	-1.233	0.056	
0.979	0.534	0.669	-1.277	0.151	NA		
-1.430	-1.698	-1.099	0.390	0.797	-1.261	-2.114	-0.164
-1.391	0.387	-2.408	-0.839	-0.249	-1.890	0.335	
-0.609	-1.545	-0.057	-1.032	-0.055	NA		
0.313	-2.054	-0.972	-1.978	-0.251	0.453	0.243	-1.001
-0.504	0.259	-1.042	-1.999	-1.523	-1.574	0.632	
0.071	-1.554	0.119	0.114	0.951	NA		
-0.427	1.943	-2.223	0.364	0.090	-1.875	-1.609	0.215
2.540	0.299	-0.797	-2.133	-1.213	-1.771	-1.510	
0.763	-0.531	-1.628	0.201	-2.310	NA		
-2.055	0.047	-1.762	-0.335	-1.289	-2.515	-0.528	0.074

Table36.txt

0.435	-0.766	1.047	-2.770	-0.485	-2.027	-0.818	
-0.009	-1.213	1.446	0.650	-1.677	NA		
-1.775	-0.387	-0.824	0.327	-3.972	-2.668	0.013	0.639
-1.878	-1.413	1.785	-1.201	-1.290	-0.607	-1.242	
-0.685	-0.882	-2.091	-2.710	0.559	NA		
-1.570	0.366	-1.719	-0.797	-2.507	-1.583	-1.559	0.097
-1.233	-0.806	-1.273	-1.063	-2.671	-2.992	0.660	
-1.373	-1.423	0.804	-0.288	0.266	NA		
-2.544	0.170	2.080	-0.062	-0.419	-1.949	-0.136	-2.068
1.259	-0.963	-1.141	0.631	0.265	-1.088	0.217	
-0.064	1.113	-0.262	1.295	-2.764	NA		
2.045	-1.334	-3.548	-0.408	-1.909	-1.722	1.229	-2.797
-1.598	-0.366	-0.199	-1.481	0.803	-0.809	-0.300	
-1.675	-1.271	-0.590	0.030	-1.672	NA		
0.315	-0.841	0.754	-1.449	-1.893	-0.696	-1.312	0.191
-1.126	-0.425	-1.783	0.209	0.304	-1.648	-0.432	
-0.283	0.451	0.013	-0.128	-0.788	NA		
-1.720	-1.469	0.259	-0.479	-3.524	-0.028	-1.100	-1.533
-0.115	-1.479	-0.874	-1.437	-0.715	-1.313	-0.789	
-0.225	-0.178	-0.142	1.443	-1.093	NA		
-1.013	-0.747	-1.121	0.374	-0.457	-3.617	-1.072	-0.081
1.081	-1.893	-0.723	-0.209	-1.051	-0.885	-0.670	
-1.387	-0.044	0.820	0.635	0.196	NA		
-1.400	-2.635	-0.560	0.054	-1.314	-1.514	-0.855	-0.664
1.154	-1.089	-1.932	-2.120	0.097	-3.089	0.056	
-0.665	-0.919	-0.716	-0.057	-0.803	NA		
-0.301	0.490	-2.347	2.726	-3.136	-2.175	-1.720	-2.337
1.594	-1.396	-1.109	-0.410	-0.410	-1.948	-0.410	
-1.702	-0.621	0.452	-1.865	-0.951	NA		
0.475	-0.408	-1.751	-0.320	0.106	-1.532	0.052	-0.262
-0.603	0.416	0.728	-0.853	-2.492	0.282	-1.214	
0.077	-1.594	0.990	-2.205	-0.489	NA		
-0.702	-2.230	-1.392	-1.350	-0.883	-2.299	-1.929	-0.535
1.326	-0.108	-0.130	-0.710	-0.093	-1.022	0.668	
0.060	-3.138	-1.711	1.043	-1.079	NA		
-1.257	-2.281	-0.519	-1.719	-0.763	-2.239	-1.126	-1.526
1.533	-0.959	0.576	-0.514	-1.986	0.101	-0.009	
-2.170	1.186	-1.644	0.190	-1.721	NA		
-0.579	0.635	-1.529	0.118	-2.112	-1.211	-2.419	0.341
-0.275	-0.504	-1.521	-0.555	0.455	-0.154	-0.304	
0.266	-0.590	0.839	-1.086	-1.824	NA		
-1.959	-0.377	-1.038	-0.801	-0.849	-0.773	-2.814	0.370
-1.718	-0.673	0.979	0.445	1.142	-0.247	-1.009	
-0.108	-2.901	-0.907	-1.110	-2.272	NA		
-1.046	1.623	-1.918	-0.236	0.413	-0.715	-0.414	0.364
-2.216	-1.366	-0.499	-0.656	-1.177	-1.223	-0.452	
0.304	-1.639	-2.373	0.963	-1.876	NA		
3.459	0.859	1.661	2.170	4.374	6.048	1.503	2.209

Table36.txt

3.127	2.933	1.316	4.226	1.082	3.683	3.522	
0.269	3.175	2.180	1.894	0.862	Pancreas		
1.201	1.677	-0.890	-2.374	-0.017	0.354	-0.852	-1.125
0.130	-1.164	0.124	0.922	-0.773	0.048	-1.718	
-0.623	-0.169	-1.059	-1.804	-0.116	Colorectal		
0.257	-0.194	2.072	-1.990	-1.314	0.195	-1.912	0.267
0.675	-2.196	-1.378	-1.754	-0.650	-0.098	1.607	
-1.376	-0.788	0.411	0.615	-0.825	Lung		
-1.208	-1.389	0.277	-0.376	0.343	0.394	-0.008	-0.826
-0.461	0.078	0.264	1.331	-1.311	-0.747	0.078	
-0.492	-1.394	-0.690	-1.438	0.975	Lung		
0.385	-1.179	-1.260	-0.748	-1.814	-1.012	-1.193	-1.255
-0.632	-0.021	0.433	0.682	-1.102	0.634	-1.288	
-0.722	-0.961	-1.010	0.071	0.094	Lung		
0.374	0.066	-0.898	0.047	-0.897	-1.267	-1.496	0.260
-0.826	0.106	0.449	-0.134	1.617	-1.070	-0.304	
-0.157	1.250	-0.258	0.231	1.301	Lung		
-0.920	0.747	-1.471	-1.768	-0.238	-2.125	-0.660	-0.472
0.546	-1.010	0.909	0.643	0.935	-0.259	0.523	
0.847	-1.318	1.377	-0.522	-0.184	Lung		
-0.779	0.795	-0.802	0.550	-1.237	-1.787	-0.309	0.612
-1.197	-2.219	-0.730	-0.939	0.341	-1.010	-0.267	
-0.842	0.686	0.316	-0.664	-0.303	Lung		
-0.613	0.072	-0.198	0.066	-0.694	0.840	1.134	-0.851
0.645	-1.123	-0.630	-1.289	0.124	-0.864	-0.400	
-0.182	0.145	0.127	1.004	-0.040	Lung		
-0.848	-1.114	-1.821	1.433	-0.021	-1.586	0.684	-3.057
-0.587	-2.299	-2.299	0.901	0.870	-1.412	-0.168	
-0.362	-1.107	-0.211	-1.184	-1.512	Lung		
-1.505	-0.026	-0.381	0.309	-1.179	-1.400	0.419	-0.262
-0.466	-2.043	0.261	-1.272	2.077	-0.079	-1.893	
-1.583	0.412	-0.413	-1.497	-2.065	Lung		
-1.361	-1.310	-0.906	-0.162	0.588	-0.957	0.346	-1.290
-2.489	-1.127	-0.731	-0.186	-0.053	-0.596	0.496	
1.794	1.071	0.332	-0.517	-0.547	Lung		
-0.057	0.748	-1.371	-0.783	-0.554	-1.303	-1.161	0.019
1.098	-0.629	-1.103	-0.159	-0.880	-0.727	0.294	
-0.243	0.632	-2.773	-0.062	-0.207	Lung		
-0.307	-1.447	-2.994	-0.264	-1.138	-0.074	0.137	0.393
0.059	1.040	-0.189	1.854	0.862	-2.637	-0.733	
0.115	-0.093	-0.525	-2.552	1.228	Lung		
-0.537	0.339	-0.359	0.422	-1.824	-0.965	0.054	-1.747
-1.521	-2.614	-1.906	0.264	-0.371	-0.672	-0.951	
-0.968	-0.933	-1.767	-0.051	-0.535	Lung		
0.974	-0.863	-1.182	-0.094	-1.700	-2.077	-1.186	-1.609
0.172	0.115	0.862	-1.221	0.324	-0.511	-2.582	
-0.376	0.736	-0.250	-0.483	0.180	Lung		
0.413	-1.849	-1.133	1.073	-0.740	-0.534	0.516	0.263

Table36.txt

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    0.496      -1.244     0.287      0.571      -0.621     -0.575     -1.291
0.799      2.576      -1.181     -0.481     -1.284     Lung
-2.067     0.739      1.784      -0.167     -2.137     -0.251     0.991      -3.787
    -0.824     -1.127     0.734      -1.226     0.473      0.265      0.739
-1.896     -0.881     -0.611     -0.779     0.407      Lung
-1.382     -0.650     0.126      -1.227     -0.014     -1.741     -1.812     -0.963
    -0.216     0.094      -0.748     0.703      0.820      -3.266     -2.617
-0.158     -0.470     -1.057     0.917      -0.539     Lung
-1.538     -0.703     -1.112     -1.176     2.133      -0.300     -1.088     -0.409
    0.775      -0.373     0.350      -0.949     -1.235     0.227      -0.420
-0.893     2.373      -0.529     -0.834     -0.254     Lung
-0.997     -1.024     -1.317     -0.704     -2.634     -1.261     -1.936     -2.044
    1.930      0.018      -1.197     -1.097     -2.298     -0.187     -0.404
-0.428     0.825      0.289      1.925      -0.327     Lung
-0.392     -0.830     -0.372     -3.673     -0.843     -2.059     -0.997     -0.486
    1.075      -0.451     0.482      -0.384     -0.792     -4.610     0.498
-1.241     -0.325     0.412      -1.249     -1.284     Lung
2.316      -1.532     -1.939     -0.762     0.051      0.012      0.986      -0.671
    -0.486     -1.404     -1.801     -1.073     0.905      0.925      0.381
-0.819     -0.455     -0.311     -0.255     -0.653     Lung
1.385      -0.908     -1.922     -0.309     -1.337     -2.238     -1.033     -0.229
    -1.719     -0.525     -0.967     -0.461     0.297      -0.642     1.191
-0.566     1.763      1.749      -1.338     -0.294     Lung
-0.835     0.321      -0.650     0.509      -1.329     -0.298     -1.959     -3.352
    -0.585     -1.534     -0.151     0.240      -2.058     0.134      1.218
-0.069     2.214      -0.170     0.575      -1.343     Lung
-0.589     -1.024     -1.015     -0.789     -0.203     -1.214     -1.319     -1.732
    -0.330     0.048      0.028      1.002      -0.799     0.472      1.134
-1.080     -0.146     0.532      -0.834     -0.447     Lung
0.680      0.133      -0.879     -0.988     -0.116     -1.052     -1.166     -2.531
    0.353      -0.456     0.010      0.213      1.022      1.312      -0.549
0.381      -0.873     -0.620     -0.677     -0.125     Colorectal
-0.411     -0.851     -0.127     0.814      -1.637     -1.357     -1.005     -2.970
    -0.946     -1.452     -0.218     -2.136     -1.769     0.342      1.444
-0.407     0.007      -1.255     -0.290     -1.049     Colorectal
-0.471     -1.195     0.112      0.988      -0.219     0.012      -1.003     -1.379
    0.419      -1.772     0.676      -0.118     -0.159     -1.830     1.730
-0.066     -0.017     -0.619     0.029      -1.226     Colorectal
0.263      -0.452     0.273      0.542      0.391      -2.009     0.634      -0.283
    -0.438     0.212      -0.508     0.804      -0.733     0.512      -2.222
-0.497     0.799      -1.173     -0.205     0.285      Colorectal
-1.846     0.985      -1.885     -1.341     -2.015     -2.504     0.373      1.022
    0.004      -1.064     1.454      0.427      1.305      -0.494     0.650
0.615      1.284      0.205      0.738      -0.810     Colorectal
12.493     12.695     16.586     11.239     14.970     18.293     10.041     13.265
    7.477      8.582      5.958      6.203      8.739      14.321     4.804
7.800      8.933      4.293      9.531      7.697      Colorectal
0.947      -1.163     -1.127     8.895      -1.622     15.664     12.430     3.431
```

Table36.txt

-0.499	-1.554	5.922	6.190	4.657	8.183	3.334		
6.664	4.518	1.380	-0.099	5.996	Colorectal			
-0.123	-1.581	0.207	0.901	0.657	-0.732	-0.698	0.901	
-0.506	-0.067	0.142	0.048	1.317	-2.652	1.456		
1.507	-1.446	1.774	-0.254	0.302	Colorectal			
-0.382	1.018	-0.840	0.219	-0.727	-0.697	-2.239	-1.402	
0.743	-2.279	-0.109	-0.693	0.683	-0.642	-0.077		
-0.211	-2.457	-3.384	-1.592	-2.207	Colorectal			
-0.565	-1.107	-0.739	-0.830	-0.201	0.318	-1.528	-0.478	
-0.824	-0.199	-0.066	2.152	0.661	-0.314	0.372		
-1.430	0.733	-1.306	-0.846	0.571	Colorectal			
-2.386	-1.768	-1.936	-1.237	1.068	-0.861	-1.753	-0.854	
-0.955	-0.894	0.068	-0.399	-0.285	-0.657	0.460		
-0.879	2.561	-0.616	-0.506	-1.527	Colorectal			
-0.939	-1.507	-1.016	-2.135	-0.960	-0.270	-1.076	1.160	
0.397	-0.109	-0.974	-0.179	-1.895	-1.254	-0.036		
-0.248	0.107	0.411	-1.142	-0.858	Colorectal			
6.979	8.408	12.097	3.998	12.192	14.978	6.714	8.125	
4.125	6.473	3.027	3.883	4.610	10.593	3.961		
3.195	3.665	0.156	5.110	4.823	Colorectal			
1.814	0.333	4.031	0.757	2.050	3.357	0.128	1.320	
-0.570	1.703	1.529	2.739	4.565	3.787	3.282		
-1.668	3.951	-0.068	-0.007	0.781	Colorectal			
0.780	-2.304	-2.639	-0.367	-1.960	0.065	1.112	-0.307	
-0.900	0.324	-0.251	0.184	1.568	-0.397	-0.481		
0.907	0.382	-0.594	1.997	-0.143	Colorectal			
0.295	-1.822	-1.633	0.506	-1.033	-0.336	0.343	-1.558	
0.420	0.148	-1.114	-0.773	1.138	-0.698	0.940		
0.316	0.563	-0.532	-1.092	0.881	Colorectal			
-1.383	-1.097	-0.312	-0.092	0.877	0.930	-0.716	-1.227	
-1.243	0.235	-0.345	-0.558	-1.295	0.154	-0.060		
-0.823	-0.135	-0.514	-0.943	0.249	Colorectal			
-0.646	-0.016	-0.485	0.563	0.949	-1.001	-0.694	-0.178	
0.876	0.822	-1.277	-0.551	0.647	0.355	1.738		
-1.477	2.517	1.423	0.523	-0.422	Colorectal			
-0.690	-2.193	0.956	-1.324	-1.798	0.545	0.700	-1.464	
0.706	0.324	0.433	0.488	-0.487	-0.220	1.109		
-0.748	-0.819	-0.047	-1.994	-1.713	Breast			
-1.003	-0.555	-1.158	1.784	-1.635	-1.422	0.401	-2.153	
0.283	-1.815	-1.292	-0.658	0.626	-0.294	0.718		
1.112	0.044	1.424	-0.893	-0.531	Breast			
0.001	-2.784	-0.899	-0.104	-0.762	-0.678	-0.357	0.066	
0.855	-2.859	-0.689	0.666	0.940	0.117	2.355		
0.642	-0.460	-1.302	-1.261	-1.675	Ovarian			
-0.873	-1.108	-0.565	2.133	-0.502	-1.666	-1.241	-0.295	
0.724	0.653	0.575	-0.463	0.087	0.450	-1.671		
1.606	-0.129	-0.046	-0.263	-1.148	Colorectal			
-2.830	0.590	-0.537	-0.615	-1.350	-1.556	-1.868	-0.311	

Table36.txt

-0.842	0.121	-0.705	0.698	-0.593	-1.307	-0.848	0.070	-0.306	-0.197
0.010	-0.838	Colorectal	-2.005	-0.625	0.363	-0.468	-1.163	1.843	-0.269
-0.927	-2.169	-2.092	-0.562	0.110	-1.142	0.914	-0.328	0.893	1.306
-0.949	1.171	-3.034	Colorectal	2.225	7.877	1.400	7.427	12.038	-0.380
0.418	-1.489	3.725	3.853	7.440	7.557	1.369	2.431	4.064	-0.246
8.983	7.008	0.776	0.036	Colorectal	-0.590	-0.318	-0.699	-1.236	-2.826
-2.048	-0.571	-1.028	-0.198	-0.253	0.217	-0.736	-0.674	0.452	1.022
-1.438	0.594	-0.222	-0.859	-0.222	Colorectal	-1.028	-0.346	-0.262	-0.443
-1.805	0.242	-0.991	-0.087	-0.831	0.046	0.325	0.129	-0.531	0.231
-0.734	-0.320	0.146	0.148	-0.337	-1.540	Pancreas	0.362	-0.268	-0.657
-0.377	0.605	-1.539	0.326	-0.581	1.188	-1.643	-0.016	1.141	0.971
0.588	0.168	0.080	4.110	-1.045	-0.757	0.053	Pancreas	-0.678	-1.406
-0.151	0.394	0.137	-2.047	0.103	-3.070	0.515	-0.426	0.703	-1.137
1.712	0.223	0.148	-0.461	0.087	-1.546	2.448	-0.576	Pancreas	-0.511
-1.120	-1.254	-0.101	-0.855	-2.432	-0.642	-0.830	0.295	-1.117	-1.452
-0.732	-0.554	0.200	-0.251	-1.499	0.176	-0.230	-0.502	-1.330	Colorectal
-2.693	-1.372	-1.994	-0.502	-0.526	-1.025	-1.377	1.103	-0.007	-1.448
-1.186	-0.594	0.242	-0.847	0.260	-0.854	1.076	0.181	-1.944	-0.709
Colorectal	-0.694	-0.579	0.289	-0.635	-0.865	-2.115	-0.358	-0.721	-2.738
-0.909	1.006	-0.806	-1.308	-1.206	0.587	-0.963	1.532	-0.134	0.560
-0.032	Colorectal	0.474	-1.794	-0.733	0.855	-2.310	-0.502	-1.439	-1.735
-0.352	0.355	-1.430	-0.354	-0.008	0.670	1.769	-0.728	0.201	0.644
-0.924	-1.604	Colorectal	0.059	0.380	0.478	-0.957	0.651	-1.673	-2.875
-0.848	-1.187	-1.279	-0.060	0.094	-0.559	-1.848	0.170	0.040	-1.051
0.681	0.812	0.593	Colorectal	-3.959	-1.898	-0.958	-0.959	-2.285	0.175
-1.462	-1.028	0.083	0.477	1.282	-1.950	-0.144	-0.597	0.742	0.316
1.284	-0.303	-3.502	0.098	Colorectal	-0.744	-1.203	-0.758	-1.691	-0.547
-1.323	-2.374	-0.485	-2.035	0.279	-1.143	-0.609	-0.003	0.709	0.709
-0.729	-0.609	-0.539	-1.906	-0.303	Colorectal	-0.709	-0.813	-0.532	-1.484
-1.794	-1.917	-1.344	-2.570	0.008	-0.600	-0.746	0.314	-1.872	-4.107
-0.470	-0.421	-1.936	-0.899	-2.374	-1.092	Colorectal	-0.844	0.143	-0.233
1.320	1.938	-1.677	0.914	0.791	-0.751	-0.372	0.318	1.595	0.598
-1.746	-1.033	0.100	0.395	0.740	1.068	-0.789	Colorectal	0.276	-0.462
-0.864	-0.017	0.581	0.209	0.407	-1.787				

Table36.txt

0.718	-0.931	-1.753	1.503	-0.392	0.177	-0.779	
-0.207	0.214	0.971	-0.626	-0.804	Colorectal		
-0.774	-0.429	-1.264	1.667	1.432	-1.229	-0.667	0.227
0.775	-2.214	-0.714	0.647	2.764	-0.797	-0.554	
-0.808	0.534	-1.740	-0.746	-0.343	Colorectal		
0.016	-1.631	0.398	1.299	0.891	-0.505	-0.103	0.868
-0.971	0.638	1.319	0.694	1.415	-0.256	1.902	
1.220	1.788	-1.690	-0.030	0.094	Colorectal		
-0.683	0.656	-0.594	-0.971	-1.449	-3.006	-1.968	-1.857
-0.412	-1.738	-2.116	0.296	0.239	-1.972	-0.729	
-0.571	0.140	-0.658	-1.529	0.251	Colorectal		
0.216	-0.901	-2.695	1.162	-0.204	0.274	-2.500	-1.082
0.354	-0.437	-1.015	0.686	-0.331	0.941	2.373	
-0.420	0.017	0.395	-1.423	-0.759	Colorectal		
-2.427	-1.755	-1.925	-2.036	-0.926	-1.141	-1.220	-2.245
-0.096	-0.619	-1.241	-0.134	1.664	-0.909	-0.174	
-0.626	1.084	-0.740	-0.247	-0.657	Colorectal		
-1.037	-1.526	-0.447	0.893	2.282	-0.437	-1.190	0.017
-2.684	0.827	0.483	0.068	-0.484	0.002	-0.530	
-1.284	-0.197	-0.687	-1.273	2.483	Colorectal		
-1.478	-0.410	-0.473	-1.512	-0.331	0.532	-1.116	0.303
0.679	-0.234	-1.328	-1.318	-0.103	-1.269	-0.109	
0.442	0.429	0.885	-0.204	-0.168	Colorectal		
-0.097	-1.304	0.473	-1.224	0.069	-0.624	0.046	-2.190
0.088	0.165	-1.256	0.393	1.154	2.345	0.059	
-0.688	0.353	-0.752	0.739	0.761	Colorectal		
-0.835	-1.925	-1.865	1.190	0.503	0.000	0.473	-1.471
-0.028	-0.952	-0.087	-0.437	-1.792	-0.638	-0.414	
-0.092	-1.549	-0.311	-0.378	-1.191	Colorectal		
1.753	1.024	-0.797	0.870	1.205	-0.603	-1.080	-1.237
-0.572	-2.064	-0.279	1.422	-1.254	-1.903	1.072	
0.209	2.585	0.421	-0.988	1.653	Colorectal		
-0.274	0.777	0.145	0.515	1.346	-0.266	-0.828	-0.123
0.124	0.709	0.089	-0.809	-0.738	-0.227	0.301	
-0.220	-0.063	-0.899	1.487	0.742	Colorectal		
-0.708	-0.940	-1.782	-0.264	-1.091	-0.950	-1.110	0.095
0.566	0.745	-0.853	-0.712	-0.237	-0.428	0.927	
0.255	-1.525	0.675	-2.734	-0.736	Colorectal		
-0.547	-0.859	0.500	-0.858	-1.155	1.166	-1.091	-0.119
0.869	-1.623	-0.112	-0.598	-0.360	-0.501	0.684	
1.787	0.189	-0.480	0.870	0.395	Colorectal		
1.366	-2.718	-0.004	2.036	-1.239	-0.853	-0.615	-1.267
1.606	-1.285	-1.405	0.487	1.685	0.103	-0.152	
-0.639	2.096	-0.584	-1.191	-0.201	Colorectal		
-0.854	-1.271	-0.979	-1.645	0.117	-0.958	0.928	-0.269
-0.628	-0.387	-3.026	-0.776	0.734	-0.400	-0.321	
-0.909	0.812	-1.129	-1.714	0.000	Colorectal		
-0.228	-0.237	-0.217	-0.409	0.458	-0.773	-1.005	-0.968

Table36.txt

0.686	-0.185	0.658	0.055	-0.736	-1.206	-0.965		
-1.195	-0.790	-0.418	0.623	-0.773	Colorectal			
-1.189	0.494	-1.593	-1.996	-0.601	0.201	0.420	-1.602	
-0.183	-2.727	0.254	0.594	-0.876	-1.258	2.150		
-0.575	-0.962	-0.401	-0.862	0.364	Breast			
-0.597	-0.599	-4.426	-1.351	-1.950	-0.775	-1.846	-1.212	
-0.903	-1.835	-0.884	0.891	0.077	-1.617	-0.356		
-0.327	-1.916	-0.709	-0.895	-0.561	Colorectal			
-2.418	-0.385	0.303	-1.479	0.736	-2.389	0.014	-0.430	
-0.664	0.304	-1.417	0.579	-2.190	-0.975	-0.324		
-2.027	0.417	-1.551	-1.514	-2.169	Breast			
-1.572	-0.813	1.061	0.299	-2.345	0.269	-0.426	-3.626	
-0.547	-0.842	-0.122	-0.114	-0.071	-2.105	-2.687		
1.132	0.507	-1.522	-0.240	-0.547	Breast			
-1.105	-0.744	-2.080	-0.755	-1.604	-0.908	0.231	-0.756	
-0.808	-0.912	-2.360	-1.630	-0.070	-1.253	-1.014		
-0.737	-1.609	1.185	-0.353	0.943	Breast			
-1.429	-1.529	1.625	-1.037	0.636	-1.368	0.032	-1.169	
-0.057	0.068	-0.400	0.927	-0.481	-0.866	0.251		
0.420	0.979	-0.829	-1.017	-0.999	Breast			
1.609	-0.359	-0.227	-0.481	0.538	1.191	-0.481	-0.361	
-1.192	-0.995	-1.071	-0.567	-0.798	0.877	-0.056		
0.177	1.021	-0.953	-0.371	-0.710	Breast			
-1.661	-0.358	-1.676	-0.308	-1.677	-2.335	-1.824	0.482	
-0.774	0.470	-1.587	-0.426	0.223	-1.198	1.214		
0.080	-0.412	-0.224	0.188	-0.405	Breast			
2.748	0.014	4.162	2.469	0.122	3.407	-1.517	-0.790	
0.508	1.886	1.485	3.583	0.673	1.993	1.128		
0.601	1.757	0.876	-0.247	-0.102	Ovarian			
-0.901	0.637	-0.142	1.209	0.683	0.229	0.027	-0.964	
0.130	-1.325	-1.018	-0.991	-0.296	0.429	1.141		
0.896	0.839	0.622	1.044	0.041	Pancreas			
9.472	6.656	11.315	-1.415	-1.762	8.913	-0.591	11.694	
1.448	2.513	8.215	0.995	7.675	12.990	3.005		
4.233	8.206	7.349	3.566	1.204	Colorectal			
0.305	-2.043	-0.114	-0.770	-0.730	-0.679	-1.787	-0.447	
-1.766	-0.618	0.808	0.248	-1.888	-2.310	1.592		
-0.635	1.135	0.909	0.234	1.192	Colorectal			
-0.343	0.511	-1.232	-1.873	-3.774	-0.625	-0.900	-2.383	
1.351	0.498	-1.458	-0.037	0.234	-0.848	0.269		
0.442	-0.467	0.724	-0.293	-0.568	Colorectal			
1.813	-0.817	-0.378	1.386	-0.718	-2.158	-2.629	-0.218	
-0.258	-1.113	-1.014	0.557	2.554	-1.491	-0.690		
-0.131	-2.073	-0.322	0.930	-0.247	Colorectal			
-1.449	-2.781	-1.392	-0.477	-1.331	0.564	-1.754	-1.747	
-1.104	-0.790	0.624	-1.125	-1.431	-1.186	-0.934		
1.905	0.546	-1.723	0.861	0.702	Colorectal			
-1.580	-0.616	-1.219	-0.476	0.198	-1.622	-0.693	-0.016	

Table36.txt

-3.255	-1.445	-0.440	-0.366	-0.235	-2.229	0.603	
-0.260	-0.841	-0.130	-0.601	-2.244	Colorectal		
-0.009	-1.171	0.189	0.058	-0.025	-0.120	0.033	0.121
-1.554	-1.665	-0.199	-0.744	-0.418	-2.272	-1.010	
-0.902	-0.712	0.957	0.098	-0.276	Colorectal		
0.416	-1.293	-0.583	-0.265	-1.538	1.334	-2.654	0.912
-0.036	-1.643	0.403	-1.406	-0.107	-0.149	-0.053	
-1.260	0.413	1.603	-1.617	-0.272	Ovarian		
-1.543	-0.621	-1.472	-0.765	-0.731	-0.383	-1.643	-2.321
-0.243	0.409	-0.594	-0.426	-1.558	-1.007	-0.914	
0.294	-0.203	-1.282	-2.392	-0.499	Colorectal		
-0.717	-1.644	-0.688	0.599	-1.919	-3.212	-1.264	0.154
1.000	-0.795	0.788	0.591	0.910	-0.530	-1.190	
0.135	-0.457	-1.792	-0.435	-0.442	Colorectal		
0.637	-2.174	-0.584	0.858	-0.551	-0.283	0.022	0.618
0.633	-1.373	-1.019	3.148	-1.205	-0.322	2.572	
-0.592	-0.886	-1.372	-0.385	-0.957	Ovarian		
-3.005	-0.180	-1.156	-0.337	0.106	-1.483	-2.241	0.563
-0.922	1.009	0.745	0.501	-0.206	0.235	0.012	
1.420	-0.263	-3.845	-1.697	-0.364	Breast		
1.783	0.456	1.490	0.842	2.473	13.886	6.374	0.701
0.743	2.328	4.462	3.806	1.261	1.569	-0.439	
2.250	6.711	4.054	4.000	2.451	Colorectal		
-3.678	-1.316	-1.600	-2.041	-2.099	-0.575	-1.875	-1.462
0.001	1.029	-0.697	-0.939	-0.499	-0.202	0.037	
-0.284	-1.381	0.592	0.355	-0.299	Colorectal		
-2.052	-1.549	-0.928	-2.862	-0.894	-1.512	0.532	-1.537
0.626	-0.885	-2.078	-0.705	2.042	1.417	-1.979	
-0.307	-2.957	-0.348	0.606	0.190	Breast		
1.191	-0.047	-1.015	-1.341	-2.023	0.168	-4.535	-0.948
-0.643	-1.745	-0.712	0.829	1.053	0.013	0.255	
-0.087	0.064	-1.138	0.213	-1.301	Colorectal		
-2.058	-0.692	-2.785	0.161	-1.809	-2.346	0.629	0.099
-0.503	-0.051	-0.871	-0.949	1.676	-0.013	1.955	
1.555	0.418	0.721	0.035	-0.970	Colorectal		
-1.112	0.758	-0.815	-1.530	-1.487	-2.578	-0.401	-1.904
-1.097	-2.392	-0.415	-0.885	-1.381	-1.332	-0.119	
-0.342	-0.452	-1.817	-1.269	0.076	Colorectal		
-3.358	-0.572	-1.475	1.005	0.037	-0.860	-0.297	-0.636
0.353	-2.391	-0.782	1.421	-2.179	-1.510	0.938	
-1.777	1.644	0.663	-0.903	-1.599	Breast		
-1.332	0.131	-0.452	-0.548	-1.747	-1.395	0.027	-0.708
-0.489	-1.626	-0.035	-2.221	-0.934	-1.522	1.357	
-1.825	-0.700	-0.997	-1.379	-1.371	Colorectal		
-0.352	-1.337	0.108	-0.275	0.656	-1.422	-1.017	-0.522
-0.876	-1.676	0.373	-0.333	1.683	-0.334	0.636	
-1.060	-0.601	-0.390	-1.284	1.106	Breast		
0.684	-0.961	-2.820	-1.271	-0.078	-0.699	-1.339	-0.252

Table36.txt

-0.102	-1.185	0.389	0.370	-0.319	-0.502	1.931			
-2.449	-0.104	-1.876	-2.555	0.341	Breast				
-0.583	-0.900	-1.840	-1.064	-2.243	-1.021	-2.226	0.088		
-1.368	-1.192	-0.995	-1.437	0.255	-1.707	1.845			
-0.642	-1.015	-1.508	0.263	0.387	Breast				
-2.018	0.683	-1.578	-2.664	-0.967	-0.922	0.373	0.208		
0.132	-1.406	-0.421	-0.191	0.394	-1.023	0.010			
-1.560	-1.618	-0.726	-0.826	-0.048	Breast				
-1.299	-1.450	-2.091	-2.223	-2.994	-2.323	-0.459	0.311		
-1.594	-0.586	-1.106	-1.043	-0.222	-0.365	1.849			
0.828	0.282	0.734	-1.681	0.641	Ovarian				
-1.989	-0.568	-0.355	-1.688	-1.684	-1.393	-0.948	-2.159		
-0.556	-0.289	0.759	0.669	-2.146	-1.492	1.600			
-1.264	-0.412	-0.436	-1.751	0.104	Colorectal				
-1.037	-1.197	-0.193	-1.971	0.334	-0.974	-0.255	-1.051		
0.612	-1.229	0.206	-0.025	0.577	-0.207	-2.602			
-0.779	0.017	-0.148	1.782	-0.223	Colorectal				
-1.055	-0.673	-0.911	-1.370	-1.094	-1.297	0.469	-2.131		
0.782	-1.387	-1.533	-3.252	-1.091	-3.411	-0.481			
-1.859	0.342	-0.565	-0.035	-0.146	Colorectal				
0.718	-2.443	-0.612	-0.934	-0.958	-1.843	-0.930	0.731		
-0.563	-1.581	-0.413	-0.709	1.171	0.334	0.879			
-0.045	0.408	-0.989	-1.761	-0.296	Breast				
-1.121	0.697	-0.895	-1.187	0.063	-0.067	-1.453	0.501		
-0.166	-1.876	-0.753	1.338	0.228	-0.657	0.489			
1.494	-0.874	-1.390	0.562	-0.425	Breast				
-0.511	-1.498	-0.824	0.643	-0.923	-0.413	-1.229	-0.639		
-0.141	-0.245	-0.208	0.080	-1.418	-0.102	0.305			
0.628	0.110	-0.431	-1.025	1.393	Colorectal				
0.044	-1.348	-0.668	2.469	-0.247	-1.871	0.177	-1.302		
0.769	-0.543	-0.507	0.165	-0.832	-0.058	-1.188			
-0.437	0.130	0.923	-0.219	-1.135	Breast				
-0.069	-0.850	-1.363	1.473	-1.041	-2.210	-1.446	-1.274		
-0.170	0.000	-1.021	-0.996	0.592	-0.825	-0.100			
-0.814	-0.321	-0.272	0.538	0.269	Colorectal				
-1.046	0.824	-1.306	1.349	-1.753	-1.343	-0.891	0.262		
-1.555	-2.269	-0.465	-2.693	0.462	-0.854	-1.440			
0.486	-0.368	0.653	-0.137	-1.153	Pancreas				
0.786	-0.188	-0.067	-1.118	-0.271	-0.786	-0.240	-1.072		
-1.637	0.308	1.719	-1.014	1.300	-1.056	1.615			
0.120	-0.235	1.439	-1.061	1.123	Esophagus				
1.081	-0.759	-0.547	-0.137	0.941	-0.993	1.746	-0.746		
-1.379	-0.302	-0.888	0.534	2.509	0.819	1.378			
-0.500	-0.700	-0.440	-0.920	-0.152	Esophagus				
7.727	10.075	10.718	3.038	10.015	10.673	9.340	10.225		
3.664	3.637	4.201	3.059	4.754	8.331	2.481			
6.716	6.135	3.438	7.873	3.095	Pancreas				
-0.353	2.928	0.818	2.910	2.896	1.258	1.066	0.150		

Table36.txt

0.626	3.322	0.789	0.230	0.405	1.652	0.746	
0.850	2.795	-0.841	1.481	-1.021	Esophagus		
-0.372	-1.306	1.342	-0.226	1.441	-0.673	-0.955	0.140
-1.001	-1.920	-1.306	0.477	-0.333	0.653	0.267	
-0.749	1.242	-1.245	-0.992	-0.486	Esophagus		
0.102	-1.603	-1.239	-0.833	-0.253	0.146	0.059	-1.772
-0.579	1.615	0.315	0.662	0.600	-0.380	-0.549	
0.905	0.564	-0.109	-0.742	0.317	Esophagus		
10.132	11.433	15.458	8.475	15.669	16.932	9.556	11.107
6.894	10.047	4.751	7.934	6.203	9.875	7.121	
5.147	6.809	6.934	10.075	5.567	Esophagus		
0.212	-0.917	0.461	-0.130	1.651	-1.252	-0.594	-1.595
0.021	0.226	2.517	0.706	0.665	-1.248	1.848	
-1.942	-1.222	-0.820	-0.762	0.165	Esophagus		
15.383	19.193	20.956	13.289	22.332	20.818	20.241	17.440
9.205	13.055	7.213	9.130	10.561	18.408	8.320	
9.088	11.542	8.507	15.472	8.767	Esophagus		
-0.160	-0.056	-0.688	-1.170	-0.716	1.183	0.017	0.803
0.217	-0.966	-0.440	0.058	0.540	1.785	0.589	
0.985	1.762	0.309	-0.287	-0.209	Esophagus		
1.452	0.288	-0.012	-0.537	-0.235	-0.222	-0.286	-1.440
1.002	-0.743	0.450	1.351	0.114	-0.865	-1.217	
-2.517	-0.026	0.331	0.008	0.421	Esophagus		
0.039	0.302	-0.805	0.162	-0.600	-1.398	-1.048	-0.829
-2.318	-0.841	0.611	-0.095	0.215	-2.506	-0.536	
0.728	-0.254	-0.722	0.434	0.310	NA		
-0.202	1.532	-0.647	-0.947	-0.942	-2.342	-1.453	-0.821
0.042	-0.772	0.944	-0.877	0.136	-0.002	-0.332	
-0.283	-0.013	-0.862	-2.516	-0.181	NA		
-1.623	-1.314	-0.821	-1.775	-0.491	-0.803	-0.413	-0.881
2.134	-1.634	-1.501	-0.344	0.239	0.364	-0.017	
-1.995	0.573	-1.007	1.146	-0.142	NA		
0.252	-1.810	-1.984	-2.921	-1.218	1.610	-0.880	-0.536
1.767	-0.368	-0.884	0.276	-1.180	-0.635	1.652	
0.122	-0.184	-0.406	-1.063	0.381	NA		
-1.125	-0.177	-0.653	0.783	1.860	-1.512	-2.259	0.221
-1.367	0.176	-0.709	0.441	0.392	0.516	-1.214	
-0.264	-2.390	-1.096	-1.086	-0.348	NA		
-1.605	-1.437	-1.036	0.045	3.034	-0.558	0.036	-0.409
-1.145	-2.232	-1.127	-1.598	-0.421	-1.497	0.109	
0.916	-0.459	-1.594	2.200	1.300	NA		
-0.884	-1.639	-1.037	-1.808	-0.189	-1.072	1.279	-1.460
-0.572	0.115	-0.576	-1.110	-0.685	0.675	-0.845	
1.059	0.966	-0.605	-2.177	-1.222	NA		
0.180	-2.561	-0.385	-1.455	0.428	-2.180	-0.210	0.628
-2.177	-1.405	1.155	-0.479	0.214	0.215	-0.386	
1.793	0.856	0.527	-0.655	-0.769	NA		
-2.902	-0.395	-0.531	1.396	-0.467	-1.007	-0.768	-0.774

Table36.txt

0.921	0.519	-1.019	-2.001	0.334	0.988	-0.094	-1.504	0.038
-0.360	-2.607	-0.191	NA	0.187	1.053	-0.117	1.236	0.399
-1.838	-1.559	0.521	-0.513	-1.268	0.051	0.651	0.549	0.911
-1.203	-1.634	1.272	-0.528	0.358	-0.042	NA	-0.975	-0.625
-1.815	-0.125	-0.350	-1.586	0.363	-1.728	-0.814	-0.101	0.235
-0.618	0.393	-1.699	-3.896	-0.505	-0.567	-0.776	-1.082	-1.052
NA	-0.145	-0.236	-1.393	-0.608	0.345	0.748	-2.278	-2.217
-1.192	-0.110	0.226	0.341	0.006	0.935	0.381	-1.582	0.773
-0.243	-0.406	0.071	NA	-1.939	-1.923	-0.913	-0.848	-0.587
0.471	-1.984	-1.363	0.606	2.024	-0.107	0.563	1.336	-0.227
0.000	-1.502	-1.948	0.392	1.057	-2.281	NA	-1.572	0.178
-0.508	-0.045	-2.407	-0.837	-1.630	-0.277	-1.048	-2.320	-0.530
-1.244	-0.259	-1.227	-0.697	0.025	0.386	-1.184	-0.077	0.410
NA	-1.390	-0.650	-1.304	-0.807	-2.408	-1.139	-1.748	-2.185
-0.416	-0.144	-2.784	0.854	0.323	-3.537	-0.189	0.175	1.160
1.083	-0.533	-0.249	NA	-1.292	0.055	-2.479	0.422	-0.626
0.340	0.446	-2.164	-1.334	0.360	-1.286	-0.607	0.112	-1.148
0.579	-0.500	0.006	0.798	-1.636	-0.667	NA	-0.745	0.453
-1.321	-0.580	-0.628	-1.493	-0.486	-1.705	-1.030	-0.509	-1.462
-1.814	-1.773	-1.385	-0.832	-1.023	-0.934	0.815	-0.226	0.559
NA	-1.886	-0.867	-2.513	0.914	-3.058	-0.775	-0.987	-2.825
0.196	-2.016	0.469	-2.604	-1.732	-1.018	-1.174	-0.559	-1.411
0.650	-0.838	-0.233	NA	0.559	0.116	-2.405	-0.228	-1.023
-0.699	-0.724	-0.386	-1.349	0.120	-0.685	-1.700	-1.071	-0.462
0.462	-0.295	-0.612	-1.792	0.064	-1.202	NA	0.262	-2.621
0.752	-0.143	-1.939	0.426	-0.532	-1.711	-0.071	-0.379	-0.378
-2.217	-0.508	-0.948	-2.493	0.629	-1.466	-0.805	-0.048	-0.155
NA	-0.393	-1.805	-0.021	0.600	-0.905	0.473	1.108	-2.738
-1.077	-0.570	-1.870	-1.937	1.380	-0.105	1.639	-0.760	-0.983
-0.012	-0.976	-0.349	NA	-1.565	0.599	-1.058	0.663	-0.630
-0.803	-0.488	-0.841	-1.001	-1.736	-1.129	-0.723	0.891	0.658
1.825	-0.264	-0.652	0.871	-1.304	0.856	NA	0.602	-0.400
-1.352	-0.076	-0.301	-0.204	-3.237	-0.815	-1.782	0.069	-0.449
-0.188	0.497	-0.409	-0.899	-0.950	0.320	-2.295	-1.350	-1.105
NA	-0.243	-0.252	-0.852	0.090	-1.180	-0.005	-2.519	-0.613
-2.186	-1.472	-0.215	-0.443	-0.513	-0.706	-0.127	0.461	-1.574
-1.155	-1.384	0.038	NA	0.368	-2.173	0.034	0.160	-1.411
-3.029	-1.446	-0.119						

Table36.txt

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    -0.119     -0.409     1.301      -0.237     0.543      -1.419     -0.115
0.548      0.748      0.646      0.174      -0.873     NA
1.212      -1.800     -1.516     -0.625     -0.388     -0.600     -1.687     0.883
    0.793      0.562      1.079      1.191      -0.483     0.375      -1.108
-0.487     -0.259     1.459      -1.000     -0.507     NA
-0.520     -1.265     -2.105     -1.116     -2.322     -0.547     -1.800     -0.312
    -0.021     -0.570     0.588      -0.402     -0.132     0.406      -2.241
-0.760     -0.871     -0.815     0.366      -0.498     NA
-1.251     -1.003     0.131      -1.217     -3.191     -2.400     -1.603     -1.914
    -0.936     0.070      -0.962     -1.659     1.001      0.348      0.811
1.561      -1.677     0.818      -0.788     -0.097     NA
-1.195     -0.481     -2.058     -0.719     0.055      -0.789     -1.172     -0.125
    1.657      -1.086     -0.386     -0.900     0.551      -0.957     1.150
-1.272     -0.969     -1.665     0.025      -1.308     Pancreas
-1.583     0.079      0.048      1.483      1.620      -0.983     -0.524     0.800
    -0.153     -0.040     1.164      -2.238     0.539      -1.333     1.094
-1.764     0.453      -0.498     -1.417     0.324      Pancreas
-0.559     -1.969     -2.343     0.369      -1.865     -0.198     -1.191     -0.326
    -0.632     0.001      -0.782     0.338      -0.655     -0.985     0.739
-0.322     -1.296     2.755      0.727      -0.410     Pancreas
0.062      -1.991     0.183      -0.574     -2.453     -0.240     -0.768     1.137
    -1.178     -0.325     0.328      0.550      -0.775     -1.260     -3.309
0.442      -0.500     1.613      -1.579     -0.742     Pancreas
-0.899     -1.011     -1.819     -0.471     -0.318     -1.719     -2.212     0.143
    2.149      -1.487     -0.846     0.064      0.577      0.838      0.496
-0.067     -0.693     0.128      0.546      0.637      Pancreas
-1.387     -0.432     -0.375     -0.838     -0.650     -1.201     -0.836     -0.591
    -1.666     -0.778     -0.231     0.660      0.538      -0.522     0.150
0.257      -0.073     -1.015     0.865      -1.558     Pancreas
-1.788     1.375      0.450      0.072      0.838      0.199      -2.157     -0.629
    -2.232     1.659      -0.532     -0.232     -0.792     -0.408     -0.062
-0.334     0.061      -1.285     -1.336     0.117      Pancreas
-1.880     0.056      -2.408     0.398      -0.419     0.422      0.542      1.934
    0.127      -1.933     2.142      -1.930     1.050      -1.112     -0.088
-1.975     0.590      -0.327     0.157      -0.327     Pancreas
-1.845     -0.456     -0.994     0.269      -2.199     -1.925     -0.593     1.419
    -1.554     0.621      1.076      -0.561     -0.795     0.180      -0.190
-2.512     0.076      -0.046     -1.258     0.966      Pancreas
-1.457     -2.093     -0.740     1.425      -1.853     -1.480     -0.823     0.407
    0.549      -1.647     -1.706     -0.519     -2.297     -2.018     0.662
1.522      -1.695     0.398      -1.335     -1.411     Pancreas
0.165      -0.285     0.710      -1.812     -2.277     -1.228     -0.697     0.946
    1.204      -0.548     -0.187     0.573      1.513      0.800      -0.869
-0.126     0.418      0.265      -0.081     -0.094     Pancreas
-0.070     -1.018     -0.539     -0.019     -1.277     -0.570     -1.028     -0.254
    -0.926     0.764      1.066      0.272      0.768      -1.453     1.238
-0.671     0.961      -0.673     -0.587     -0.548     Pancreas
-1.131     -0.531     -0.594     -2.223     -1.556     -0.685     -0.580     0.883
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Table36.txt

1.980	-0.084	-1.964	0.202	1.233	-0.568	0.437		
1.447	-0.291	-0.438	-1.191	-0.746	Pancreas			
0.950	-1.743	-0.728	-1.458	-2.094	-2.424	-2.223	-1.072	
-1.459	-0.579	-2.040	0.402	0.407	-1.297	0.789		
-0.665	-0.857	-0.321	-1.132	-1.616	Pancreas			
1.215	-0.534	-0.976	0.358	-1.124	-0.645	-1.411	-1.264	
0.258	-0.615	0.017	-0.437	-1.854	-0.913	-0.756		
0.836	-0.407	1.031	-0.413	-0.365	Pancreas			
-1.433	-0.746	-0.851	-0.031	-3.218	-0.080	-1.441	-2.026	
0.192	0.508	-0.871	-2.064	0.258	-1.767	-0.694		
-1.439	-1.470	0.572	-1.766	-1.695	Pancreas			
0.004	0.370	-1.793	-0.744	-2.550	-0.875	-0.835	-1.191	
0.481	-1.312	-0.096	-1.780	-1.664	-0.659	-1.802		
-1.193	0.201	-2.620	1.106	0.352	Pancreas			
-0.547	0.778	-1.134	-0.721	-1.480	1.823	1.455	-0.578	
1.086	-0.558	-0.340	-0.320	-0.538	-0.820	1.381		
-0.624	-1.885	-1.172	-0.898	-2.259	Pancreas			
0.454	-1.516	-2.925	-1.545	-2.361	-0.802	-1.868	-1.088	
0.547	-3.152	-0.281	-1.977	0.114	-1.321	0.020		
0.149	0.047	-1.132	-2.701	-1.224	Pancreas			
-0.540	-0.882	-2.446	-0.695	-1.233	-3.041	-1.490	0.412	
-0.526	1.426	-0.032	-0.545	0.861	-3.214	-0.117		
0.643	1.145	-1.438	0.095	0.623	Pancreas			
0.439	-0.479	-2.175	0.458	-0.804	-1.986	-0.359	-0.431	
1.105	-0.923	-0.328	-1.208	1.475	-0.481	-0.990		
-0.006	0.297	0.490	-0.048	-2.103	Pancreas			
-0.256	-0.562	-0.044	-0.960	-1.358	0.029	-0.768	-1.168	
-1.188	-1.064	-1.289	0.663	-1.142	-0.800	0.116		
0.277	0.172	-0.361	-1.487	-0.553	Pancreas			
0.215	-0.365	1.449	-0.934	-0.596	0.549	-1.271	-0.585	
0.340	-0.912	1.574	-1.116	0.398	-1.462	-2.603		
0.093	-2.175	1.903	-0.636	0.011	Pancreas			
-1.747	-0.907	-2.017	-0.594	-0.669	-1.741	-1.469	-1.515	
-1.023	-1.861	-0.709	1.926	0.990	-0.043	0.965		
-1.109	-0.155	-0.818	0.573	-2.594	Pancreas			
-2.377	-2.779	-0.501	-0.167	0.392	-0.810	0.153	-1.545	
0.318	0.473	-1.159	0.144	0.322	-1.469	-0.645		
-0.352	-0.576	-0.112	0.463	-1.345	Pancreas			
-0.587	-0.688	1.208	1.076	-3.424	-1.574	0.182	-0.558	
0.078	-0.218	0.357	-2.335	0.925	-0.938	0.202		
-0.397	-1.469	-1.340	-0.471	-1.349	Pancreas			
1.080	-0.153	-1.501	1.402	-2.185	-0.576	-1.247	-2.057	
1.037	-0.197	0.766	-1.134	2.574	-0.429	-0.136		
-1.650	-1.307	-1.402	-0.530	1.088	Pancreas			
-1.525	0.956	-0.374	0.326	-0.105	-1.944	0.084	-0.319	
-1.271	0.047	0.215	1.409	-0.704	-0.764	-1.435		
0.769	0.552	-0.081	0.392	0.918	Pancreas			
-0.260	-0.508	-0.875	-0.185	-2.600	-0.460	-1.340	-0.633	

Table36.txt

1.897	-1.549	0.506	-0.268	0.008	-0.428	0.513		
0.554	0.213	0.345	0.144	0.661	Pancreas			
-1.498	-1.226	-0.882	-0.586	0.002	-0.299	-0.553	-1.135	
-1.104	0.308	-0.875	0.205	0.625	0.037	1.399		
1.453	-0.165	0.109	-1.011	-0.386	Pancreas			
0.494	-0.771	0.234	-1.957	0.258	-1.054	-0.068	-0.232	
0.625	-0.058	-1.654	1.018	1.244	-2.098	1.551		
-0.158	-1.830	-1.903	0.105	0.615	Pancreas			
0.072	-0.509	-1.410	-0.862	-0.420	-0.637	-0.819	-1.062	
-1.188	-0.708	-1.202	0.010	-0.618	-2.750	1.672		
-0.381	-1.262	0.354	-0.334	0.071	Pancreas			
0.827	-0.168	-0.887	-0.372	-1.743	-1.124	-1.394	0.732	
-1.578	-0.842	-1.918	-0.991	1.009	-0.329	1.307		
-1.260	-3.119	-0.605	-0.620	-0.828	Pancreas			
-1.456	-0.530	-2.706	-0.336	-2.804	-2.151	-0.561	0.289	
-1.687	-0.188	-1.299	0.408	-0.275	-0.192	-0.844		
1.447	-0.390	-1.400	0.164	0.178	Pancreas			
-0.437	1.515	-2.530	-1.362	-1.263	-2.264	0.040	-1.298	
-0.874	-0.776	-0.183	1.224	-1.229	-1.362	-1.001		
0.807	-2.465	1.847	0.871	2.102	Pancreas			
-0.494	-1.213	-0.938	-1.850	-1.208	1.118	-0.339	-1.562	
-0.708	-0.961	0.241	0.590	-0.042	-0.444	-0.236		
-0.638	0.598	0.834	-0.624	-1.258	Pancreas			
-0.780	-1.527	1.305	0.537	-2.129	-1.796	-1.629	-1.879	
-0.011	-0.663	0.354	1.275	0.182	-0.985	0.521		
-0.454	0.483	0.327	-0.891	-1.067	Pancreas			
0.284	-0.652	-1.044	-0.630	-0.591	-1.270	-1.495	-0.139	
-1.731	-0.750	-0.515	0.876	1.647	-1.540	-0.378		
-0.154	0.540	-2.451	0.453	-0.792	Pancreas			
-1.885	-2.363	-0.850	0.025	-0.795	-1.121	-2.093	0.540	
-0.278	-3.689	-0.580	-0.870	0.865	-0.069	-1.257		
-0.688	0.353	0.390	-1.552	-0.042	Pancreas			
-0.447	-0.135	0.133	-0.323	-1.710	-1.993	0.349	-0.280	
0.924	0.641	-0.006	-2.165	-1.426	-0.181	1.380		
0.498	2.759	-0.082	1.593	0.191	Pancreas			
-0.367	-1.246	-0.105	-0.047	-0.822	-1.395	-1.266	0.911	
-0.540	-0.370	-0.090	-0.329	2.043	0.793	-0.010		
-0.625	0.118	-0.981	-0.235	-2.942	Pancreas			
-0.652	-0.742	-1.639	-0.026	-0.463	-0.996	-1.187	1.520	
-0.418	-1.407	-1.111	-0.472	1.130	-1.537	-0.828		
0.120	0.347	-0.743	-0.336	-2.084	Pancreas			
-1.617	-1.525	0.738	-0.340	-1.825	-1.303	-1.006	-0.484	
0.585	-0.262	0.219	0.205	1.592	-1.045	-0.203		
0.734	-0.463	-0.562	0.549	-0.781	Pancreas			
-2.224	-2.124	1.240	0.414	-0.933	0.888	-0.556	0.597	
1.019	-1.290	-1.807	2.081	-1.132	-1.481	1.265		
-1.417	0.084	0.145	-1.856	1.016	Pancreas			
-1.748	-0.336	0.515	0.140	-0.394	-0.628	-1.036	-1.167	

Table36.txt

-0.842	-0.414	-0.626	0.272	0.259	0.386	0.850	0.600
-1.788	0.419	0.508	-0.248	Pancreas			
-2.051	-1.002	-0.890	-0.569	-1.714	-0.497	-0.215	-0.241
-0.257	-0.314	-1.393	0.437	-0.830	-0.532	-1.925	-0.365
-2.029	-0.305	-0.117	-0.613	Pancreas			
-0.522	-0.429	-0.130	-2.544	0.128	-1.943	-0.990	0.712
-0.322	-1.317	1.036	0.320	-0.093	-0.542	1.888	0.101
-0.708	-0.058	-1.175	-0.266	Pancreas			
0.326	-0.588	-0.809	1.126	-1.203	-0.816	-1.418	-0.976
0.507	-0.830	-0.794	-0.347	-0.495	-1.560	0.941	-2.640
-0.846	0.605	-2.385	-0.407	Pancreas			
-0.677	0.447	-0.889	-0.335	-1.255	-3.488	-0.800	0.241
-0.368	0.973	-0.889	-1.094	-0.023	-2.221	0.281	-0.205
-0.983	-1.819	0.171	-0.214	Pancreas			
-0.780	-1.439	0.766	-0.118	-0.482	-1.814	-0.240	-0.653
0.282	-0.928	-2.574	-0.055	-0.300	-0.494	-0.743	-2.037
0.708	-0.481	-2.559	-2.646	Pancreas			
-0.297	-1.261	-1.221	-0.312	0.654	-2.079	-1.102	0.206
-0.287	0.412	-1.782	0.633	-1.304	0.317	1.381	-0.800
0.555	-1.163	1.337	-0.496	Pancreas			
-0.999	-4.657	-1.089	-0.355	1.561	-0.938	-0.612	1.254
0.592	-0.967	0.774	-0.289	-1.225	0.990	1.913	0.340
3.435	0.619	-0.117	-0.140	Pancreas			
-1.364	-0.251	-1.294	-0.422	-0.197	-1.382	-0.904	-0.108
0.121	-1.344	-0.506	-1.693	-1.042	-0.821	-0.637	-0.767
1.289	-1.680	-1.337	-0.489	Pancreas			
-0.407	0.303	0.390	-1.688	-0.304	-1.733	-0.346	-2.342
-0.877	-0.030	-0.433	0.072	0.581	-1.136	-0.064	-0.324
1.945	-0.009	-0.041	-0.334	Pancreas			
0.990	0.631	-1.353	0.773	-1.495	-0.601	0.080	-0.848
-0.138	-0.942	0.615	-1.461	-1.258	-0.665	0.142	-0.565
0.536	-0.851	-3.351	-0.938	Pancreas			
-0.675	-0.885	-0.291	-0.573	-0.462	-0.106	-2.022	-0.537
0.889	-1.143	-0.022	1.890	1.563	-1.919	0.179	-0.440
2.048	-0.209	0.032	-0.420	Pancreas			
0.259	1.051	-2.401	1.156	-0.477	-2.725	-1.228	1.871
0.088	-1.133	0.822	-0.696	0.461	-0.110	0.139	-1.034
-0.035	-1.496	-2.235	-2.457	Pancreas			
-0.896	-0.036	-0.787	-0.744	-1.330	-2.439	-1.171	-0.507
-0.439	0.844	-0.167	-1.091	-1.481	-1.287	0.348	-0.392
0.206	-0.874	-0.572	0.466	Pancreas			
0.863	-0.284	-0.561	-2.319	-0.655	0.474	-1.071	-1.506
0.788	-0.880	-0.374	0.816	-1.996	0.375	0.729	-0.247
-0.759	0.383	-0.860	1.120	Pancreas			
-1.713	-0.936	-3.085	0.169	-0.817	-1.300	-0.925	-0.953
-1.215	-0.966	-0.368	-0.470	-1.392	-1.133	0.671	-0.215
-3.131	2.249	0.158	-0.470	Pancreas			
-1.323	-3.276	-0.112	-0.459	-1.752	-1.139	-1.430	-1.661

Table36.txt

-1.290	1.126	-0.824	-1.366	-1.956	1.466	-0.517		
-1.791	-0.042	-0.588	0.386	-1.882	Pancreas			
-2.188	0.419	-1.839	1.404	-0.882	-2.805	-0.100	1.058	
-0.751	0.041	-0.993	-1.377	0.776	-0.734	0.371		
0.001	-0.498	-0.704	0.723	-0.913	Pancreas			
-0.103	0.082	-0.503	1.056	-1.848	-1.563	-1.617	-0.235	
0.235	-2.127	-2.433	1.070	-2.081	0.099	-1.121		
-1.219	-1.240	-1.498	-0.356	0.276	Pancreas			
0.823	-0.474	-0.752	-1.660	0.795	-0.904	-0.822	-0.150	
0.725	-1.001	-2.433	-0.821	-1.299	-1.278	0.749		
-1.578	-0.986	-0.307	-1.250	0.005	Pancreas			
-2.791	-1.373	0.043	-1.197	-0.461	-0.790	0.221	-0.335	
1.653	-2.442	-0.851	0.100	-0.147	-1.667	-2.582		
-0.411	0.790	0.382	0.578	-0.862	Pancreas			
-0.401	0.305	-0.819	0.358	-0.545	-0.277	-3.640	0.078	
-0.791	0.066	-1.087	0.298	0.432	-0.302	-0.802		
-0.405	1.195	1.692	-2.500	-0.443	Pancreas			
-0.453	-1.521	0.218	0.640	-1.170	-2.088	-1.187	1.148	
0.538	-1.542	0.028	0.090	0.462	-1.626	-0.738		
-1.188	1.555	0.170	0.514	0.547	Pancreas			
-1.212	-0.866	0.014	-0.370	-0.643	-1.487	-0.324	-0.201	
-0.513	-1.089	-1.530	-0.332	-0.492	0.960	0.075		
-1.493	-0.146	0.034	-0.047	-0.295	Pancreas			
0.228	-0.390	1.006	-1.417	0.069	-1.397	-1.638	-0.321	
-0.202	-0.565	0.499	-0.012	0.115	0.813	-0.004		
-0.226	-0.253	-0.350	-1.334	-0.544	Pancreas			
-0.853	-1.070	-0.353	1.136	-1.415	-2.138	-0.972	0.473	
-0.712	0.168	-0.223	-0.177	-0.026	-0.194	-0.421		
0.915	0.345	0.252	-1.086	-0.349	Pancreas			
-0.586	-1.117	-1.861	0.648	-1.140	-3.001	-2.129	0.422	
1.419	-0.878	-0.003	-0.106	1.963	0.168	-0.418		
0.812	1.190	-1.364	0.430	-0.891	Pancreas			
-0.169	-1.907	-1.438	-0.609	-0.435	-1.331	0.257	0.384	
-0.749	-0.269	-0.977	-1.765	-0.901	-0.291	0.365		
-0.607	-0.051	-1.230	0.045	-0.530	Pancreas			
-1.190	-0.913	-1.020	-0.536	0.583	0.047	-2.598	-1.646	
-1.775	-0.038	0.377	0.716	-0.169	-2.525	1.120		
-0.601	-2.864	-0.335	-1.568	-2.689	Pancreas			
-2.642	-3.580	-1.622	-1.085	-0.851	-0.666	-1.077	0.176	
0.287	-0.956	-2.880	-0.599	0.470	-1.380	-1.141		
-1.093	-0.389	-3.101	-1.578	0.450	Pancreas			
-0.973	-1.523	-0.398	-0.657	-0.929	-1.736	-1.062	-2.667	
0.136	-0.141	-1.201	-2.200	2.350	-2.707	-1.602		
0.383	0.885	-0.763	-0.580	-0.649	Pancreas			
0.268	-1.811	-0.603	1.106	-0.799	0.125	2.128	-1.761	
-1.494	0.093	0.942	-1.026	1.331	-1.078	0.806		
0.231	-0.836	-0.132	-2.026	-0.080	Pancreas			
-0.198	0.162	-0.009	-0.163	1.334	-0.505	-0.645	-1.651	

Table36.txt

1.779	0.493	-0.705	-0.375	0.050	-0.193	-0.187	-0.222	0.633
0.528	-2.066	-0.967	Pancreas					
-0.150	0.806	0.064	-1.321	-1.618	-0.506	-0.315	-3.828	-1.398
-0.780	0.653	-1.220	-1.511	-1.479	-0.089	-1.592	0.460	-1.395
0.166	-0.203	Pancreas						
-0.672	-0.523	-0.022	-0.788	-1.299	-2.177	-2.445	-1.043	-0.474
-0.908	0.617	-0.916	0.978	-2.678	0.882	0.325	0.932	-1.357
-0.880	-3.285	Pancreas						
0.178	0.337	-1.472	-0.912	0.073	-1.063	-0.653	0.137	0.530
-1.469	-0.841	0.036	2.269	0.478	0.373	-1.434	-0.344	0.752
-0.642	0.882	Pancreas						
0.426	-1.800	0.541	0.057	-2.933	-0.853	-1.523	-0.562	0.281
-1.699	-0.991	1.770	1.109	-0.982	0.754	0.193	0.920	-0.258
-2.295	0.097	Pancreas						
0.019	-0.208	-1.495	-0.273	-1.619	-1.964	-1.792	-0.939	-1.392
0.666	-1.853	-0.732	-0.420	-1.224	0.181	-0.244	-0.469	-1.171
-0.922	-2.740	Pancreas						
-1.610	-0.751	0.213	-0.812	-0.892	-3.267	-0.057	-0.140	-0.132
-2.012	-0.928	-1.704	0.411	-0.781	0.054	0.838	1.768	0.996
0.116	-1.067	Pancreas						
-1.163	-0.780	-0.459	-0.609	-1.417	-0.849	-0.495	-1.236	0.493
-0.306	-0.666	-1.846	-0.537	-2.348	0.017	-1.135	0.106	-0.359
-0.763	0.077	Pancreas						
0.291	-0.791	-0.518	-0.960	-1.799	-2.133	-1.585	-1.030	-0.706
-0.552	-0.661	-2.900	0.529	-2.077	-0.769	0.334	-0.813	-1.188
-0.212	-0.691	Pancreas						
-1.045	0.096	-1.650	-1.419	-0.469	-1.679	-0.902	-2.969	-0.034
-2.073	1.223	-2.256	0.686	-0.718	0.449	-0.719	0.949	-1.509
0.829	1.563	Pancreas						
-0.130	-0.819	-1.213	-0.760	-3.302	-0.181	-1.552	0.042	-3.304
0.535	-2.795	-0.249	-0.017	-1.542	-0.218	-1.055	-1.490	-0.213
-0.210	0.240	Pancreas						
0.011	-1.749	0.531	-1.689	0.612	-1.227	-0.239	-0.552	0.237
0.051	1.134	-0.172	1.572	-0.842	-0.290	0.433	1.866	-1.217
0.480	0.095	Pancreas						
-1.652	-0.048	-2.099	-1.356	-1.784	-2.396	-1.513	-1.527	0.381
-2.534	-0.338	-1.736	-0.846	-1.524	0.998	0.570	-3.374	-0.825
-0.301	0.047	Pancreas						
-2.537	-0.095	0.278	1.764	-1.787	-1.381	-1.602	-0.773	1.311
-0.663	-0.362	1.339	1.779	-0.385	1.342	0.391	-0.625	0.494
-2.016	0.198	Pancreas						
-0.723	-2.091	0.160	-0.410	-2.532	-2.413	-0.204	-0.821	0.587
-1.366	-0.616	0.643	1.531	-0.124	-0.413	-0.206	0.779	0.389
-0.776	-1.112	Pancreas						
0.977	-1.671	-0.702	-0.182	-3.092	-1.769	-1.552	0.692	-0.521
-0.849	-0.339	0.321	-0.978	0.608	-0.591	-0.698	-1.654	-0.872
-1.385	-0.613	Pancreas						
1.110	-1.182	0.291	-0.562	0.582	-1.303	-0.479	-0.295	

Table36.txt

-0.577	-0.291	-1.904	-0.162	0.345	-0.137	1.183	
-1.369	-0.120	-0.586	-0.623	-1.681	Pancreas		
-1.697	-1.981	-1.096	-1.620	-0.356	0.218	-1.028	-0.337
-2.397	-2.080	-2.943	-1.440	0.156	-3.262	1.033	
0.424	0.342	0.708	-1.874	0.301	Pancreas		
-0.329	1.723	-3.243	-1.835	-2.021	-2.007	-0.970	-2.895
-0.416	-0.148	-0.601	-2.465	-0.401	-2.149	0.283	
-0.994	-2.040	0.323	-0.398	-0.830	Pancreas		
0.417	-0.268	-1.817	-2.715	-1.259	0.439	-2.261	0.216
-1.311	0.027	-1.431	0.909	-2.609	-1.626	0.197	
-0.319	-0.569	-0.838	0.559	-0.386	Pancreas		
-0.430	-1.863	0.632	-0.078	-1.593	-0.272	-2.354	-1.706
-1.279	0.253	0.363	0.428	1.025	0.621	0.077	
1.088	-0.705	-3.838	-0.499	-2.177	Pancreas		
0.408	-1.569	-0.183	0.399	-0.466	0.074	-1.413	-1.261
0.046	0.212	-1.241	-0.176	-0.039	-0.093	-0.537	
-2.743	0.109	-1.113	0.481	-0.809	Pancreas		
-0.419	-1.119	-2.042	0.520	-1.755	0.137	-1.623	-1.477
-1.260	-1.699	-1.287	-1.386	-1.212	-0.298	0.018	
-1.427	0.017	-0.146	-1.242	0.062	Pancreas		
0.588	0.125	-1.794	-0.743	-1.959	-0.713	-1.114	-1.039
-1.336	-0.435	1.252	1.445	-2.068	0.015	0.656	
-0.558	1.778	-0.128	-1.246	-0.661	Pancreas		
-2.394	-0.372	0.982	0.190	-1.588	-0.677	-1.484	0.093
-1.326	-1.129	-0.967	-1.174	-0.766	-0.575	1.187	
-0.416	-1.978	-0.194	0.280	-1.279	Pancreas		
-0.825	0.101	-0.637	-0.008	-1.288	-0.825	-1.370	-2.088
0.190	-0.890	-0.949	0.053	0.401	-2.151	2.631	
0.140	-0.342	-0.844	-0.906	-1.108	Pancreas		
0.297	-1.709	-0.465	-1.593	-0.716	-0.827	-0.931	0.243
-0.990	-0.348	-0.229	-1.311	-0.255	-2.138	0.259	
-0.627	0.489	-0.275	-1.035	-0.279	Pancreas		
0.627	0.228	-0.769	-0.126	-2.520	-0.519	-0.456	-0.706
-1.593	-0.221	-0.313	-1.773	0.869	-1.906	0.911	
-1.788	1.354	0.591	-1.806	-1.307	Pancreas		
-2.507	0.381	-0.527	0.088	-0.554	-2.841	-1.444	-1.258
-0.566	0.145	0.065	-1.337	1.330	0.256	0.380	
-0.522	0.701	0.666	0.101	-1.286	Pancreas		
-0.984	-0.814	0.462	-0.442	-1.114	-2.054	-0.138	-1.791
-0.696	-1.529	2.210	0.502	0.150	-1.507	-1.682	
-1.309	1.109	-0.322	-0.012	-0.070	Pancreas		
-0.197	-0.705	-1.738	-0.397	-1.953	-0.215	-0.692	0.030
-2.656	-1.534	-1.278	0.038	-0.804	-1.287	1.371	
-0.365	-0.328	-2.568	0.478	-1.970	Pancreas		
-1.073	-0.728	-0.584	-1.865	-1.622	-4.054	-2.002	-0.915
-1.928	0.445	0.405	-1.408	-0.582	-1.784	-0.057	
-2.623	-0.378	-1.766	-0.957	-1.923	Pancreas		
0.792	-1.004	-1.241	-2.089	-0.823	-3.572	0.338	-0.594

Table36.txt

0.958	-0.870	0.316	0.350	-0.274	-2.070	-0.500		
-0.867	0.493	-1.414	-0.741	-1.400	Pancreas			
0.242	-0.913	-2.629	-1.543	0.117	-1.754	-4.188	-1.817	
-0.052	-0.203	-0.830	0.402	0.296	-0.301	-1.770		
-0.419	-0.373	0.804	-1.913	-0.669	Pancreas			
-2.922	-0.485	-1.826	-2.896	-1.438	-1.725	-1.477	-0.021	
0.217	-2.446	0.650	-0.914	-0.778	-1.265	0.971		
-2.543	-0.802	-0.718	0.439	-2.026	Pancreas			
-1.047	-2.426	0.983	-0.321	-0.574	-2.199	-0.657	-1.279	
0.315	-1.365	0.154	-0.599	0.520	-1.481	-0.820		
-0.703	-0.251	-0.455	-0.306	-1.092	Pancreas			
-0.619	-1.274	-1.366	-1.364	-0.666	-0.686	-0.570	0.409	
-1.491	0.003	1.167	-0.398	-1.014	-0.466	0.218		
0.093	0.518	-0.299	-2.197	-1.016	Pancreas			
-0.023	-0.953	-1.745	-1.857	0.243	-0.371	-0.035	-0.298	
-0.931	-1.684	0.062	0.387	-1.159	-1.437	1.700		
-2.087	-0.154	-0.437	-1.417	-0.216	Pancreas			
-1.508	-0.328	-1.012	-1.366	-1.420	0.357	-2.348	0.928	
-0.524	-0.540	0.890	-0.201	-2.162	0.214	0.632		
-1.375	-1.426	2.222	-0.401	0.811	Pancreas			
-0.563	-0.554	-2.112	0.499	-1.322	-0.760	-2.844	0.871	
-0.385	-1.263	0.766	-1.231	0.083	-0.435	0.581		
1.209	-0.825	-0.974	-1.574	-0.530	Pancreas			
-0.849	-1.545	-1.494	-0.579	-1.195	-0.974	-1.977	-1.015	
-0.931	-0.699	-0.164	-0.249	-1.543	-0.211	-2.589		
-1.573	1.019	0.162	-0.282	0.815	Pancreas			
-2.416	-0.635	-1.308	-0.109	-0.721	-1.021	-2.671	-2.035	
-0.715	-1.410	-0.016	-0.309	-3.118	0.117	-1.389		
-0.640	-2.279	-0.463	0.236	-0.907	Pancreas			
-0.899	-1.118	-1.971	-0.506	-2.463	-2.716	-1.763	-2.670	
-1.667	-2.493	-2.508	-2.047	-0.581	-1.185	0.842		
-1.505	0.500	0.050	-1.558	-1.268	Pancreas			
-1.565	0.228	-2.701	-1.274	-1.955	-1.127	0.641	-2.802	
-0.674	-2.712	0.658	-2.126	-0.953	-1.583	-0.908		
-2.604	-0.069	-0.904	1.403	-0.250	Pancreas			
0.256	-0.517	-1.696	0.259	0.047	-0.942	9.009	-1.301	
-0.014	0.872	-0.261	0.102	1.734	-1.665	-0.682		
0.261	1.273	-0.594	-1.095	-1.810	Pancreas			
0.029	-0.760	-1.739	-0.939	1.048	-1.069	0.092	-0.337	
-1.335	0.079	-0.282	0.506	-0.097	-0.903	1.511		
-0.691	-0.922	-0.362	-1.317	0.581	Pancreas			
-1.277	-0.934	-0.620	-2.674	-1.430	-1.267	-0.411	-1.090	
-2.108	-0.295	0.541	-1.616	-1.107	-0.168	-0.046		
-2.143	-0.783	1.472	-1.349	-0.309	Pancreas			
-1.098	-1.015	-0.708	0.741	1.799	-2.605	-1.177	-1.476	
0.736	-0.934	-1.182	-1.688	0.319	-0.309	0.173		
-1.076	1.486	-0.669	-0.541	-1.136	Pancreas			
-0.982	-1.124	0.183	-0.728	-2.389	-0.174	-2.768	-0.537	

Table36.txt

-1.910	0.009	0.069	-0.322	-0.729	-1.835	-0.583		
-1.149	-2.245	-0.828	-1.179	0.015	Pancreas			
-0.817	-2.378	-0.807	-1.384	-1.839	-0.906	-1.620	-0.696	
-0.275	0.298	0.730	-1.691	0.869	-1.681	2.123		
-0.012	0.466	0.953	-1.073	0.148	Pancreas			
-1.845	-1.664	-0.482	-0.533	-2.645	-0.808	-4.864	-0.603	
0.585	-3.286	0.458	-0.179	-0.372	0.555	-0.317		
-0.333	1.409	-1.236	-1.580	-0.846	Pancreas			
-0.700	-1.597	-0.482	-0.024	-0.627	-2.428	0.878	-0.225	
-0.580	-1.238	1.515	0.061	0.317	-0.947	-0.317		
-0.577	-1.681	-1.028	-1.149	-2.110	Pancreas			
-2.218	-0.948	-2.108	-1.779	-0.893	-1.575	-1.531	0.222	
-1.137	-1.632	-0.719	-1.093	0.259	-1.798	0.158		
0.314	-0.800	-0.142	-1.606	0.864	Pancreas			
0.059	0.764	-0.666	-0.101	-1.610	-0.322	-0.785	1.087	
-0.156	-0.630	-2.234	0.319	-0.877	-0.965	-0.309		
-1.179	-0.244	-1.159	0.047	-0.800	Pancreas			
-0.586	-0.491	-1.078	-2.221	0.359	-1.722	-0.368	-0.151	
-0.151	0.129	0.520	-0.009	-0.072	-1.935	0.328		
0.195	-2.001	-1.463	-0.407	-0.810	Pancreas			
-1.228	-1.864	0.092	-1.081	-1.394	-1.016	-1.997	-0.046	
-1.692	-0.445	0.690	-0.712	0.054	-0.603	-0.256		
0.091	-1.064	0.190	0.467	-1.716	Pancreas			
-1.492	-0.004	0.341	-0.336	-2.507	-2.413	-1.032	-1.043	
-1.488	-0.008	-1.032	-2.386	-0.924	-2.486	-0.541		
-1.436	-1.331	-1.922	-0.004	-1.241	Pancreas			
-0.991	-0.307	-2.907	-1.309	0.452	-1.296	-0.584	0.320	
0.305	0.467	1.243	-1.033	-0.012	-1.418	-1.367		
-2.159	-0.775	-0.383	0.937	0.136	Pancreas			
-2.014	-0.702	-0.635	-0.599	-0.148	-0.895	-1.467	-0.595	
0.960	-1.719	-0.284	0.858	0.489	-1.243	0.312		
-0.795	-2.066	-0.016	-0.129	-1.665	Pancreas			
-0.486	-0.580	-0.020	-0.012	-1.476	-0.865	-0.975	0.156	
0.451	-0.708	1.089	-0.561	0.585	-1.632	-1.115		
-0.553	-1.683	-1.698	-0.668	0.007	Pancreas			
-1.871	-0.592	-1.269	-0.517	-0.704	-0.617	-1.157	1.120	
-1.423	0.457	-3.803	-0.549	0.574	-0.855	3.161		
-0.390	-1.617	0.666	-0.841	-1.454	Pancreas			
1.682	0.283	-2.200	-2.165	-1.477	-1.111	0.537	0.119	
-0.717	0.887	0.906	-0.347	-1.052	-1.370	-0.134		
-2.261	-0.803	-0.510	-1.419	-0.665	Pancreas			
-0.770	-0.356	0.121	0.511	-1.439	-2.034	-0.990	-1.397	
-0.511	1.343	-0.062	-1.361	0.115	-0.172	0.073		
-1.558	-1.480	-1.662	-1.238	0.529	Pancreas			
0.730	-1.001	-0.271	0.451	-1.491	-1.949	-2.497	0.834	
0.060	-1.175	-0.221	-0.698	0.995	-1.623	-0.018		
-1.485	-0.686	-0.079	-0.361	-0.494	Pancreas			
-0.217	0.313	-0.424	-0.968	0.091	0.596	-1.189	-1.061	

Table36.txt

-2.494	-1.099	-0.694	-2.821	0.396	-1.896	0.217	0.099	0.586
-0.375	-1.898	0.206	Pancreas					
0.000	0.258	0.529	-1.702	-1.078	-3.608	-1.836	-1.816	-0.874
1.022	-0.568	-0.709	-0.253	0.374	1.228	-1.139	-2.745	0.460
-1.667	0.253	Pancreas						
-0.717	-0.852	0.009	-0.308	-2.395	-1.989	-1.432	-0.912	0.189
-0.998	-0.461	-0.709	0.803	-3.278	0.022	-1.982	-0.386	-0.144
-0.540	0.380	Pancreas						
0.815	-1.027	0.514	0.204	-0.106	-1.696	-1.115	-2.303	0.043
-1.496	-0.086	-1.964	-1.927	-1.852	-2.532	-2.510	-1.707	0.939
-0.600	-0.793	Breast						
0.085	-0.486	-2.169	-1.721	0.290	-2.481	-0.542	-1.820	-3.017
-0.871	-1.339	0.577	0.282	-2.032	0.274	-1.686	-0.877	1.414
0.258	0.041	Liver						
-1.012	-1.638	-1.521	2.268	-0.939	5.121	-2.561	0.200	-0.494
2.600	2.061	2.163	-0.578	-1.471	0.823	-0.032	0.441	1.169
-1.548	-1.621	Liver						
-0.597	-0.574	-1.796	-0.660	-0.297	-1.862	-1.112	-1.170	-0.173
-0.797	0.135	0.922	0.248	-1.831	-0.560	-1.641	-0.064	-2.833
-0.995	-0.062	Stomach						
-2.840	0.558	-1.171	1.224	0.806	-0.477	-0.977	-1.561	-1.674
-0.762	-2.435	-1.346	0.348	-0.086	-1.544	-0.345	-0.037	-2.113
-0.907	-1.060	Breast						
-1.025	-2.204	1.009	0.553	-1.286	-0.215	-2.245	-1.710	-0.945
-0.681	-0.874	-0.904	-0.608	0.497	0.460	-0.554	0.380	-0.016
0.408	0.019	Ovarian						
-1.146	-2.204	-0.806	0.562	-0.174	-3.504	-1.032	-2.058	-0.002
-1.470	0.044	-1.648	2.932	-1.173	1.670	1.219	-0.674	1.284
0.172	-2.367	Breast						
-0.679	-2.975	-0.278	-0.183	-2.393	-0.570	-1.614	-2.568	-0.129
-0.591	-1.631	1.245	-0.972	1.337	-0.233	-0.290	-1.292	-1.101
-1.537	-3.053	Breast						
1.186	-2.725	-2.076	-1.556	-1.797	-1.582	-3.914	-0.509	-0.020
-0.462	-0.558	-1.433	-0.127	-2.182	-1.891	0.508	0.803	-0.134
-2.353	1.087	Esophagus						
-1.516	-1.703	-1.611	0.425	-1.928	0.080	-2.235	-0.449	-1.528
-0.588	-1.631	-1.468	-0.963	0.116	0.040	-1.977	0.984	-1.024
-0.638	-1.329	Breast						
0.347	-0.397	0.292	0.524	-0.245	-1.221	-1.325	-0.311	0.983
-0.539	0.661	0.803	0.671	-0.809	0.506	1.534	1.661	1.936
-0.205	0.082	Stomach						
-1.907	-1.150	-1.726	-2.165	-0.010	-1.299	-1.249	-1.103	-0.563
-2.606	-0.282	-0.779	-0.212	-1.012	-1.314	-0.713	1.116	0.496
-1.405	-1.312	Breast						
0.019	-1.666	-1.300	-0.220	-1.526	-2.043	-1.386	0.051	-0.522
-0.829	-0.829	-0.812	-1.979	-0.201	-0.035	-0.999	-3.103	-0.983
-0.567	0.542	Breast						
0.982	-0.520	-0.960	-1.646	-0.461	-1.383	-0.811	-0.555	

Table36.txt

-1.924	-1.061	0.515	1.769	1.724	-1.051	0.704		
0.210	0.399	-0.690	-2.761	-0.547	Stomach			
-2.633	-2.786	0.107	-1.780	-0.762	-1.729	-0.125	-1.153	
-1.225	-0.802	-0.548	-0.248	-1.961	1.201	-1.159		
-1.623	-1.423	-0.594	0.700	-2.277	Stomach			
-1.698	-0.539	-2.528	-1.655	-0.520	-2.358	0.213	-0.554	
-1.179	0.196	-0.386	-1.466	-0.256	-0.997	0.036		
-0.561	-1.831	0.263	-1.318	-0.643	Stomach			
-0.167	-0.300	-2.493	-0.110	-1.422	-0.998	-0.058	-2.690	
-1.355	-1.248	-0.655	-1.677	0.277	-0.607	-1.144		
0.460	1.474	0.118	0.755	-0.698	Ovarian			
0.107	0.362	4.035	0.778	-2.253	1.763	1.014	-0.470	
-0.460	-2.125	2.886	3.576	-1.184	0.793	2.067		
1.726	-0.293	-0.136	0.676	1.430	Ovarian			
-1.962	0.218	-1.989	-0.381	-0.977	-0.737	-0.156	-1.135	
-0.748	-1.391	-0.254	-0.327	0.142	-0.913	0.776		
-0.298	-2.211	0.611	-1.203	-0.564	Esophagus			
-0.921	-1.088	-0.194	-0.423	-0.565	-0.970	-0.800	0.008	
0.644	-0.842	-0.134	-2.007	-0.535	-0.895	0.743		
0.382	-0.917	-0.745	-2.837	-1.706	Ovarian			
-1.976	-1.352	-1.084	-0.716	-1.536	-1.425	-1.270	-2.483	
0.189	-1.095	-0.690	0.126	-1.197	-0.145	-0.109		
-1.239	-0.335	-1.956	-0.806	-0.109	Esophagus			
-1.543	-0.851	-0.416	-0.107	-2.305	-2.854	-1.667	-2.005	
-1.217	-1.389	-0.896	1.734	-0.493	-0.990	-1.227		
-0.823	-0.072	-0.315	-1.096	-0.722	Ovarian			
-2.969	-0.443	-1.945	0.386	-1.513	-0.964	-0.220	-1.322	
0.780	-1.018	-0.244	-0.444	-0.321	-1.008	-0.241		
-0.164	-1.583	0.942	-0.124	0.151	Esophagus			
-0.943	-0.660	-2.802	-1.594	-3.769	-2.842	-3.635	-1.832	
-0.959	-0.949	-0.570	-2.348	-0.660	-1.123	-0.919		
-1.738	-0.341	0.895	-1.541	-1.879	NA			
-2.046	-0.278	-2.577	0.337	-0.565	-1.672	-1.929	-0.390	
0.864	-0.553	-0.982	-1.213	-1.619	-0.844	-1.688		
-0.776	-0.185	-3.169	-1.149	0.066	NA			
-1.503	-0.531	-2.344	1.059	-0.798	-2.151	-2.968	-0.498	
-1.096	-2.787	-1.464	-0.096	-2.507	-3.195	1.147		
-1.048	0.365	-0.489	-2.243	-0.739	NA			
-0.827	-2.348	-3.416	-1.970	-3.828	-2.727	-1.140	-1.502	
-2.449	-0.056	-0.741	0.084	-1.483	-1.468	-1.391		
-1.426	0.849	-0.584	-1.589	-2.156	NA			
-1.299	-0.554	-2.477	-2.785	-1.665	-0.976	-1.141	-2.064	
0.284	-1.735	-1.490	-0.201	-0.059	-1.930	0.000		
0.183	0.029	-1.349	-1.253	-1.215	NA			
-2.894	-1.046	-1.996	0.947	-2.627	-1.830	-2.688	-3.005	
-1.667	-0.929	0.462	-1.572	-2.138	-2.090	-1.479		
-1.860	-1.235	-0.489	-1.045	-1.106	NA			
-3.039	-1.214	-2.650	0.134	-0.845	-4.462	-1.492	-2.355	

Table36.txt

-0.031	-0.775	-2.849	-1.674	-2.452	-0.997	-0.342	
-0.528	-1.087	0.141	-0.222	-0.294	NA		
-4.158	-0.914	-2.830	-1.376	-1.651	-2.760	-1.737	-2.692
-1.335	-1.704	-1.038	-0.195	-0.484	-2.735	0.804	
0.814	-2.014	-1.205	-0.971	-1.926	NA		
-3.736	-1.319	-3.336	-0.372	-1.860	-2.714	-1.569	-2.101
-2.086	-1.107	-0.527	-1.039	-0.971	-2.420	-0.034	
-1.367	-2.079	0.031	-1.036	-1.811	NA		
-0.984	-1.366	-1.675	-1.588	-2.638	-1.722	-1.608	-2.123
-1.903	0.223	0.628	-1.048	0.044	-2.537	-1.294	
-0.921	-0.620	-0.437	-1.030	-0.376	NA		
-2.232	-1.140	-1.640	-0.513	-1.929	-2.782	-2.210	-2.524
-1.485	-2.996	-2.779	-1.893	-1.056	-1.815	-0.965	
-1.848	0.024	-0.971	-1.786	-2.141	NA		
-2.567	-2.450	-1.506	-1.429	-3.857	-3.004	-2.615	0.398
-1.456	-1.324	-1.574	0.160	-1.601	-2.288	-1.756	
-1.938	-2.202	-0.905	0.309	-0.302	NA		
-1.766	0.849	-0.847	-2.061	-2.989	-1.460	-0.024	-0.718
-0.918	-2.716	-1.228	-0.593	-0.833	-1.041	-0.552	
-0.263	-0.804	-1.651	-2.378	1.161	NA		
-1.538	-4.001	-3.149	-0.771	-2.186	-1.262	-1.236	-0.777
-1.731	-0.611	-1.532	0.277	0.350	-2.942	1.849	
0.348	-2.010	-0.543	-2.294	0.550	NA		
-0.946	-0.676	-1.809	-1.194	-0.089	-2.344	-1.030	-1.428
1.386	-2.088	0.205	-0.041	-0.197	-2.030	0.179	
-0.535	-0.380	-0.945	-1.019	-1.406	NA		
-1.202	-1.644	-3.961	-0.903	-1.362	-1.336	-2.661	-1.534
-2.766	-1.585	-2.882	-0.447	-0.870	-2.292	0.441	
-1.283	-1.091	0.083	-0.026	-0.228	NA		
-2.347	-0.766	-5.046	-1.011	-3.487	-2.324	-1.571	-1.938
-1.480	0.139	-0.656	0.183	0.020	-0.198	-0.547	
-1.750	-1.133	-1.850	-1.442	0.834	NA		
-1.101	-2.530	-1.855	-1.558	-1.516	-1.497	-2.064	-1.536
-0.365	-1.195	-1.117	-2.289	-1.364	-1.058	-1.170	
-0.059	0.660	-1.726	-2.114	-0.378	NA		
-1.107	-2.202	-2.354	-0.818	-2.369	-2.046	-2.369	-1.297
-3.881	-3.145	-0.329	-1.962	-0.219	-1.721	-1.273	
0.325	-2.813	-2.517	-1.388	-1.201	NA		
-2.138	0.743	-3.547	-1.850	-0.381	-2.434	-1.174	1.070
-1.792	-0.228	-0.919	0.623	-2.132	-2.495	-1.281	
-2.066	-1.715	0.421	-1.416	1.006	NA		
-1.740	-1.046	-1.228	-1.617	-2.765	-1.750	-1.288	0.056
-1.427	-2.087	-2.657	-2.150	-0.335	-2.807	-0.580	
-1.776	-1.553	0.138	-2.034	-1.846	NA		
-1.728	-2.867	-1.455	-4.106	-2.671	-2.675	-2.127	-1.371
-2.064	-1.737	-1.110	-2.479	-2.291	-1.596	-0.556	
-3.303	-0.529	-0.433	0.450	0.167	NA		
-2.152	-2.330	-2.650	-1.065	-3.377	-1.441	-2.199	-0.854

Table36.txt

0.080	-0.892	-1.746	-1.010	-1.237	-1.002	0.120		
-0.458	-0.412	-1.306	-1.628	-0.655	NA			
-2.159	-1.456	-2.664	-1.105	-1.668	-1.759	-1.472	-1.573	
-1.741	-2.142	-0.787	0.691	-1.147	-2.934	-0.729		
-3.734	-2.015	0.000	-1.003	-0.384	NA			
-3.709	0.083	-2.607	-2.127	-1.189	-2.136	-1.466	-1.948	
1.027	-1.620	0.891	-0.292	-1.938	-3.305	-2.417		
-2.580	-0.571	-1.392	0.482	0.078	NA			
-2.274	-2.200	-2.092	-0.887	-2.752	-4.603	-3.448	-1.447	
-1.432	-1.228	0.810	-0.715	-1.195	-2.689	-0.828		
-2.206	-0.643	-0.049	0.241	-0.637	NA			
-2.097	-1.109	-1.382	-1.999	-1.758	-2.313	-1.651	-1.433	
-1.588	-1.939	-0.906	-2.779	-0.892	-0.582	-1.264		
0.379	-1.813	0.766	-0.494	-2.792	NA			
-0.160	-1.419	-1.084	-1.283	-1.499	-1.312	-0.015	-1.755	
-1.130	-1.006	-1.917	-0.423	-2.214	-1.902	0.807		
-2.175	0.644	-1.843	-0.607	-2.396	NA			
-1.346	-1.526	-1.140	-0.064	-1.987	-1.376	-1.105	-1.527	
-0.912	-2.318	-0.930	0.567	-1.768	-1.064	-0.910		
-2.001	-0.368	-1.096	-1.167	-0.217	NA			
-3.243	-2.419	-1.261	-2.053	-1.394	-1.917	-0.775	-2.481	
-0.711	-2.299	0.604	-1.574	-2.297	-0.210	0.066		
-2.601	0.240	-1.054	-0.325	0.402	NA			
-2.201	-0.092	-0.488	0.717	-2.998	-0.222	-0.863	-2.893	
-0.445	-0.378	0.000	0.309	0.000	0.050	0.000		
0.000	0.050	0.000	0.000	-0.144	NA			
-1.330	-0.048	-1.512	-1.731	-2.350	-1.415	-1.071	-1.115	
0.171	-0.418	-0.825	-0.084	-1.388	-1.424	-0.027		
-0.423	-1.132	0.000	-0.094	-0.421	NA			
-2.127	-0.308	-1.977	-1.646	-4.976	-3.001	0.429	0.237	
-1.128	-0.924	-0.174	-2.466	-1.741	-1.630	-0.212		
0.309	-0.227	0.602	-0.273	-0.505	NA			
-1.864	-2.489	-1.381	0.752	-0.727	-1.240	-1.682	1.060	
-1.608	-0.968	0.115	-2.215	-0.071	-0.485	0.437		
-1.676	-1.732	-1.017	0.155	-2.163	NA			
-2.189	-1.073	-0.949	-0.682	-1.809	-2.748	-1.203	-2.501	
-1.120	-2.327	-0.720	-1.388	-1.657	-1.193	-0.579		
1.137	-1.459	-1.821	-1.839	0.055	NA			
-2.048	-1.031	0.540	-2.502	-0.559	-1.999	-2.107	-0.553	
-0.912	-1.152	-0.953	-2.444	-1.101	-1.267	-0.137		
0.396	-3.212	1.525	-1.033	0.072	NA			
-1.642	-2.695	-1.326	0.033	-1.028	-2.934	-2.888	-2.861	
1.168	-1.040	-1.586	-1.581	-1.456	-2.795	-0.562		
-0.302	-2.095	-1.463	-1.013	0.059	NA			
-3.549	0.352	-2.921	-0.786	-1.312	-1.923	-2.575	-3.728	
-0.071	-1.574	-0.480	-0.362	-1.256	-1.372	-0.293		
-1.887	2.252	-1.868	0.811	-1.546	NA			
-1.127	-0.612	-1.017	-2.386	-1.233	-1.073	-1.542	-1.684	

Table36.txt

-1.665	0.033	-0.137	0.048	-1.577	-3.041	-0.910		
0.251	0.284	-0.983	-0.407	-0.869	NA			
-3.585	-1.877	-1.808	-2.364	-0.433	-0.137	-1.928	0.129	
-0.026	-2.123	-1.461	-1.366	-1.229	-1.858	1.876		
-2.050	-0.610	-3.092	-2.397	-0.060	NA			
-2.027	-1.756	-1.451	0.574	-2.648	-1.609	-1.459	-1.909	
-1.401	0.770	0.389	-0.213	-1.619	-3.216	-2.808		
-0.142	0.301	-1.021	-0.984	-0.958	NA			
-0.286	-1.406	-1.503	-1.562	-0.536	-3.148	-0.025	-1.193	
-1.602	-0.412	-0.301	-1.145	0.531	-1.899	-0.992		
-0.732	-1.681	-1.391	-0.907	-3.005	NA			
-2.506	-0.677	-3.170	-1.061	-2.736	-3.049	-1.962	-0.764	
-1.596	-0.683	-1.190	-1.440	-1.057	-0.656	-4.385		
-2.545	-1.300	-1.326	-0.865	-0.094	NA			
-2.012	0.000	-1.920	0.000	-2.351	0.149	-1.923	-0.541	
-0.445	-3.090	0.000	-1.050	0.000	-1.235	0.000		
-0.486	0.000	-0.414	0.415	0.000	NA			
-0.824	0.501	-2.051	0.016	-2.079	-3.364	1.036	-0.874	
-0.541	1.168	0.529	-0.437	0.000	-0.729	0.139		
-1.905	-1.400	0.351	-1.284	0.204	NA			
-0.875	-1.217	-1.283	-1.351	-2.672	-1.430	-1.694	-0.285	
-1.145	-0.445	-1.281	0.644	0.739	-0.469	-1.169		
0.000	-3.090	0.000	-0.105	0.370	NA			
-0.420	-3.090	0.000	0.000	-1.256	0.338	0.000	-0.294	
0.000	0.000	-0.790	0.163	0.137	-1.214	0.000		
0.000	1.153	0.000	0.000	0.000	NA			
-1.389	-1.073	-1.813	-2.201	-2.041	-1.789	-1.053	-0.695	
-1.784	-0.472	0.199	-1.947	-0.342	-1.857	0.000		
-0.261	-1.110	-0.265	-0.143	-0.391	NA			
-1.427	-1.214	0.137	-0.414	-0.335	-1.128	0.050	-1.192	
0.000	0.000	0.000	0.000	0.000	0.218	0.000		
0.000	0.000	-3.090	0.000	0.000	NA			
-2.406	-0.212	-1.131	-0.405	-0.450	-1.305	0.331	-0.208	
-0.531	0.192	0.000	-0.790	-3.090	-1.917	-1.169		
0.137	-1.169	1.153	0.000	-0.510	NA			
-0.405	-0.968	-0.551	-1.599	-3.347	-2.039	-2.507	-0.882	
-1.439	-1.027	-0.632	-1.573	-1.636	-2.538	-0.302		
0.409	-2.190	-2.085	-0.231	-1.301	NA			
-0.894	-1.355	-0.409	-0.375	1.655	-2.313	0.651	-0.621	
0.000	-1.545	0.000	-1.169	-1.425	-0.619	0.000		
0.000	0.595	0.038	-0.545	-0.442	NA			
-1.186	-2.093	-1.514	-0.448	-1.578	-2.352	-2.493	-1.227	
0.595	-0.016	-2.559	-1.791	-0.479	0.687	-1.444		
-2.311	-0.969	-1.748	-1.669	-0.624	NA			
-1.282	-3.247	-2.744	-0.079	-0.760	-2.409	0.137	-0.435	
-0.317	-0.944	-0.861	-0.231	-0.054	-0.795	0.033		
-0.700	-0.658	-2.499	0.391	-1.766	NA			
-3.054	-1.843	-0.828	-1.885	-0.865	-2.958	-0.049	-0.248	

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-2.808	-1.773	-0.858	0.706	0.024	-2.424	-0.540		
-1.613	-0.162	-0.866	-2.978	-0.479	NA			
0.188	-0.603	-0.827	-1.153	-1.989	-1.474	-1.354	-0.658	
-1.140	-0.630	0.926	-1.210	-0.076	-1.051	0.366		
0.533	-1.693	-2.362	-0.803	-0.823	NA			
-2.114	-1.593	-0.657	-1.751	-2.610	-1.325	-1.577	-2.969	
-4.090	-3.000	-0.717	0.314	-0.310	-0.844	-1.329		
-0.534	-1.765	-1.279	-1.440	0.843	NA			
-0.534	-1.836	-2.577	-0.032	-1.051	-2.388	-1.912	-2.234	
-2.219	-1.453	0.000	-0.027	-0.221	-1.535	0.000		
-0.739	-1.371	-0.584	-1.061	0.660	NA			
-1.320	-0.532	-0.472	-1.399	-0.618	-0.111	-3.033	-1.086	
0.137	0.000	-0.949	-0.251	0.278	-1.509	0.000		
0.595	-0.261	-1.214	0.000	0.865	NA			
-3.747	-0.249	-1.672	-0.901	-2.762	-1.745	-1.601	-3.615	
-1.269	-0.175	-0.478	-1.012	-1.807	-1.425	-1.510		
-0.739	-0.827	-2.260	-2.116	-1.224	NA			
-1.209	-2.431	-0.405	-0.505	-0.672	-1.971	-0.071	0.060	
-0.578	0.000	0.000	0.000	-0.949	0.378	0.000		
0.000	0.000	0.000	-0.736	0.000	NA			
0.000	0.231	0.000	0.139	-1.214	0.000	-3.090	0.000	
0.000	0.000	0.000	0.000	0.000	0.000	0.000		
0.000	0.000	0.000	0.000	0.000	NA			
-0.760	0.366	-0.713	-1.322	0.610	0.312	0.481	0.137	
-0.161	0.000	-0.217	-2.817	0.050	-0.144	0.137		
0.000	0.137	-3.090	1.395	0.000	NA			
-1.407	0.492	-1.862	0.160	-0.073	-1.335	-2.674	-0.780	
-0.065	-0.386	-0.378	-1.214	-1.214	0.362	-0.082		
-0.168	-1.685	0.000	0.081	-0.161	NA			
-2.714	-0.250	-1.090	-0.419	0.544	-2.131	-0.174	-2.311	
-2.196	-2.185	-2.314	1.289	-2.278	-1.687	1.095		
-2.166	-0.797	-0.950	-0.939	-2.008	NA			
-2.202	0.496	-2.179	0.630	-2.460	-0.068	-1.014	-1.341	
0.163	-0.064	0.000	-1.004	-1.283	-1.082	0.000		
-1.389	-1.006	-0.378	-1.277	-0.378	NA			
-1.483	-1.015	-0.779	-1.747	-3.189	-1.569	0.798	-0.977	
-0.627	-1.239	-1.018	1.041	-0.253	-1.182	-2.126		
0.861	-1.956	-1.503	0.671	-0.730	NA			
-0.825	-2.329	-1.106	-0.942	-1.179	-1.248	-2.849	-2.230	
-0.970	-0.417	-0.850	0.127	-0.244	-1.190	0.000		
-0.238	-1.013	0.678	-1.276	0.000	NA			
-0.590	-1.752	-2.045	-0.081	-1.549	-2.621	0.417	-3.610	
-0.574	-0.616	-0.653	-1.257	-0.319	0.386	0.226		
-1.183	-1.024	-1.049	-2.359	-0.737	NA			
-1.153	0.000	-0.015	0.309	-0.344	-0.216	0.000	0.137	
0.000	0.000	0.050	0.717	0.218	0.000	0.000		
0.000	0.000	0.000	0.000	-0.505	NA			
-0.762	-2.655	-2.159	-1.574	-2.533	-1.576	-0.783	-1.523	

Table36.txt

-0.676	-0.446	0.717	-0.153	-1.034	-0.725	1.059		
0.000	-3.090	1.194	-0.793	-0.967	NA			
-0.909	-0.841	-0.109	-0.648	0.717	-2.465	-0.949	-0.103	
0.000	-0.660	0.000	-0.217	-1.136	-2.713	0.309		
0.000	-0.610	0.137	-0.682	0.000	NA			
-1.380	-0.085	-0.044	-0.576	-2.005	-0.195	-0.053	0.059	
0.308	0.098	0.137	-0.870	-0.505	0.000	-0.395		
0.000	-2.052	-0.082	-3.090	0.000	NA			
-1.120	0.000	-0.144	0.000	-1.169	-1.104	-0.700	-0.378	
0.366	-0.378	0.000	0.000	0.000	0.000	0.163		
0.000	0.000	0.000	0.000	0.000	NA			
-1.511	-0.280	-1.202	-0.740	-1.883	-2.992	-0.581	-0.794	
-1.415	0.608	-2.606	0.023	-1.558	-3.134	0.126		
0.062	-0.926	-1.024	-1.840	-1.247	NA			
-1.135	-0.798	-1.514	0.618	-0.852	-1.272	-0.330	0.076	
0.000	-1.301	0.000	0.715	-0.815	-0.027	-0.790		
0.000	-1.214	0.000	-0.794	-0.510	NA			
-2.382	-0.296	-2.742	-0.451	-1.294	0.374	-1.792	-1.027	
-1.646	-0.368	-0.770	-1.367	-0.592	-1.378	1.607		
-0.584	-0.867	-1.506	0.099	0.460	NA			
-2.140	-2.948	-0.753	-0.675	-0.692	-0.693	-2.252	-0.013	
-0.123	-0.275	-0.378	0.354	-0.396	-1.483	-0.404		
0.426	-0.256	0.395	0.494	-1.175	NA			
-2.194	0.766	-2.555	0.000	0.661	-1.511	0.309	-0.988	
-0.592	1.037	0.000	0.000	0.000	0.000	0.000		
0.000	0.670	0.000	0.762	0.000	NA			
-1.662	-0.928	0.130	-0.273	-2.784	-2.914	-2.134	-0.903	
-2.242	0.513	-0.614	0.396	0.328	-3.633	-2.626		
-0.466	-1.795	-1.214	0.197	0.581	NA			
-2.005	-1.526	-1.286	-0.353	-3.706	-1.140	-0.786	-0.845	
-0.170	-2.098	-0.811	-0.690	0.425	-0.460	-0.790		
-0.660	0.366	0.218	-1.996	-2.713	NA			
-0.779	-0.646	-2.316	-0.819	-2.702	-1.446	-0.699	-0.867	
0.027	-1.585	-1.774	-0.058	-0.507	-0.711	0.000		
0.843	-1.773	-1.367	-1.190	-1.137	NA			
-2.806	-1.065	-4.282	0.323	-2.324	-2.174	-2.041	-1.247	
-0.971	-2.465	-1.467	-1.321	0.372	-1.990	-0.542		
-1.317	0.022	0.163	-1.214	0.302	NA			
-2.153	0.113	-0.086	-2.089	-1.750	-1.324	-0.224	-1.825	
0.779	-1.049	-0.573	-0.733	-0.293	-1.686	0.197		
0.712	-0.187	-1.715	-0.874	-1.586	NA			
-0.166	-1.674	-2.515	-0.060	-2.277	-3.346	-2.123	-1.103	
-1.023	-1.438	-1.001	0.618	-0.216	-2.045	-1.099		
-1.231	-1.178	-0.233	-1.470	0.214	NA			
-0.368	-0.428	-0.759	-0.782	-3.529	-2.079	-1.730	0.124	
0.588	-1.043	-0.299	-2.085	-1.908	-1.511	-0.435		
-1.906	-1.328	-1.309	-0.928	-0.257	NA			
-1.234	-0.039	-0.588	0.000	-0.583	0.229	0.429	0.460	

Table36.txt

-0.823	0.000	0.000	0.000	-0.378	-5.332	-0.790	
0.218	-0.623	0.000	0.309	-1.214	NA		
-2.370	-1.078	-1.141	-1.609	-1.905	-1.364	0.220	-1.218
-1.388	-1.268	0.081	-1.217	1.090	-1.975	0.653	
0.186	-2.064	-1.074	-0.205	-1.113	NA		
-1.841	-0.636	-1.126	-1.781	-2.120	-1.912	-4.340	-1.067
1.053	1.298	-0.124	0.232	0.260	0.328	0.984	
-2.159	-2.906	-1.708	-1.116	-0.639	NA		
-0.808	-2.518	-0.995	-0.671	-0.457	-3.692	-1.058	-1.123
0.462	-1.852	-0.182	-1.003	0.390	-0.314	-0.246	
-1.872	-0.078	0.852	-0.845	-1.145	NA		
-0.286	-1.578	-0.927	-1.121	-2.248	-1.640	-1.736	-0.187
-0.264	-0.592	-0.986	-0.645	-2.650	0.154	0.037	
1.087	-1.411	-2.061	-1.416	-1.407	NA		
-2.510	-0.598	-0.973	-1.402	-2.193	-1.871	-0.007	-2.248
-2.364	-2.191	0.162	-1.163	-2.908	-1.045	0.037	
0.685	0.392	-1.465	0.607	-0.237	NA		
-1.113	-1.397	-2.868	-0.065	-0.774	-1.777	-2.131	-0.507
-1.773	-2.880	-0.259	-1.140	-0.820	-2.595	-2.639	
-1.760	1.427	-2.418	-1.032	-1.423	NA		
-0.505	-0.445	-0.321	0.651	-1.169	0.000	0.000	-0.445
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.460	0.137	0.000	0.050	NA		
-2.127	-3.506	0.693	-0.306	-1.087	-0.861	-1.631	0.441
-1.028	-1.542	-2.594	-1.129	0.191	-1.669	-1.281	
-4.367	-0.161	-1.329	-1.067	-0.716	NA		
-0.995	-3.090	-0.986	-0.330	1.184	-1.224	-2.053	-1.169
0.000	-0.802	-0.445	-0.592	-2.401	-0.493	-0.378	
-0.623	0.366	0.460	-1.169	0.163	NA		
-0.981	-1.319	-1.961	0.143	-1.889	-2.930	-1.631	-2.234
-0.483	-0.382	-2.287	-0.779	-0.220	-1.857	-0.418	
0.000	-1.481	-0.244	0.706	-0.261	NA		
-1.338	-3.756	-1.926	-3.840	-1.387	-1.676	-1.894	-0.126
-0.941	-2.172	-1.797	-2.437	-1.903	-0.559	-1.968	
-1.436	-0.628	-1.333	0.173	-0.579	NA		
-1.741	-2.495	-1.056	-1.602	-3.702	-1.420	-0.806	-1.851
-2.422	-2.421	-1.049	-1.427	-3.149	-3.494	-2.052	
-0.291	-2.377	-0.923	-0.981	-1.121	NA		
-1.108	-0.002	-2.004	-0.415	-1.686	-2.017	0.548	-1.617
-1.865	-0.955	-0.264	-3.277	-0.124	-2.933	-0.223	
-1.223	-0.445	-0.903	0.844	-0.855	NA		
-2.458	-2.911	0.422	-0.258	-2.277	-0.754	-1.333	-0.893
0.899	-0.371	-1.119	-1.671	-0.390	0.260	-1.936	
0.749	-0.816	-0.280	-1.614	-3.222	NA		
0.000	-0.505	0.309	-2.706	0.000	-0.829	0.137	0.000
-0.027	-0.217	0.000	0.000	-0.505	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	NA		
-1.036	-1.253	-1.342	0.088	0.130	-2.353	0.269	0.139

Table36.txt

0.945	-1.245	0.201	-0.742	-0.505	-2.098	-1.174	
-1.297	0.315	-1.041	1.266	-0.595	NA		
0.028	-1.429	-0.441	-1.232	-0.670	-0.116	-0.692	-2.486
0.646	0.946	0.000	0.981	0.362	-1.944	0.000	
0.460	-0.542	0.204	0.366	0.000	NA		
0.000	0.000	-1.214	0.000	0.137	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.000	0.000	NA		
-1.832	-1.166	-2.732	0.779	-3.350	-0.847	-0.955	-0.154
-0.084	-1.324	0.000	-1.854	-3.090	-1.012	-2.139	
-0.546	-1.910	-0.616	1.534	-0.094	NA		
-0.539	-1.259	-1.688	0.330	-1.535	-2.551	0.062	-0.978
-0.662	-0.953	-1.575	0.050	0.071	-2.032	0.000	
-1.852	0.236	1.080	0.138	0.633	NA		
0.000	0.309	0.014	0.000	0.000	0.000	0.529	-3.090
-0.204	0.000	0.000	0.000	0.000	0.000	0.000	
0.000	0.000	0.000	0.137	0.000	NA		
0.093	-1.923	-0.274	-0.480	0.961	-2.213	-1.939	-0.055
0.309	-0.752	0.000	-1.045	0.000	-0.953	0.000	
0.000	0.000	0.000	-1.763	0.000	NA		
0.000	0.000	-0.736	0.000	-1.169	0.176	-0.736	-0.675
0.000	0.000	0.000	0.000	0.000	-0.378	0.000	
0.000	0.000	0.000	0.000	0.000	NA		
-0.758	-1.412	0.002	0.586	-1.154	-1.024	0.249	-0.962
0.000	-3.506	0.000	0.000	-0.289	-0.044	0.000	
0.000	-1.412	-0.532	-0.059	0.670	NA		
-0.716	-1.101	-0.070	-1.704	-0.937	-1.635	-1.049	-2.320
-1.123	-0.594	-2.095	0.620	-1.666	-2.916	-0.693	
-1.016	-2.836	-1.151	-0.577	0.817	NA		
-2.900	-2.255	-1.622	0.503	-0.047	-2.486	-1.300	-0.834
-1.396	-0.678	-0.705	-0.340	-0.495	-1.340	0.327	
0.591	-2.092	-1.787	-0.632	-0.627	NA		
0.438	-1.747	-1.203	0.810	-0.055	-1.358	-3.031	-0.501
-0.734	-0.702	0.249	-1.891	-1.449	-0.352	-0.134	
-0.569	-0.248	-1.239	-1.527	-0.331	NA		
-1.851	-0.647	-1.551	-1.580	-1.761	-2.349	-0.146	-1.292
0.382	-2.186	1.149	-2.654	-0.672	-1.058	-2.160	
0.010	-1.490	-2.645	-2.830	-0.912	NA		
0.613	-2.112	-1.269	-0.554	-1.705	-1.577	-1.063	-3.078
-0.323	-2.469	0.196	1.459	-0.987	-1.506	-1.931	
-0.268	1.044	0.681	-1.313	0.627	NA		
-1.497	-1.302	-3.263	-0.951	-1.930	-4.017	-0.915	-3.054
-0.944	-0.692	0.966	-1.407	-1.599	-0.790	-0.161	
-2.225	0.565	-1.571	-1.456	-0.042	NA		
-0.002	-0.788	-1.639	-1.732	-0.924	-1.559	-1.429	-1.481
1.158	-2.753	-0.656	-2.752	-1.896	-0.905	-0.185	
-0.583	-1.329	-1.825	-2.107	0.549	NA		
-0.689	-2.296	-1.977	-1.663	-2.446	-3.891	-3.630	-2.206

Table36.txt

0.163	-1.835	-2.334	-2.294	0.560	-1.650	-0.439	
0.118	-1.037	-0.123	-1.857	-0.551	NA		
-1.490	-1.707	-1.819	0.658	-1.185	-1.391	-3.273	-1.333
0.181	-2.971	-2.096	-2.110	0.887	-0.437	-1.120	
-1.005	-1.283	-0.842	-1.619	0.344	NA		
-1.545	-0.510	-0.923	-0.211	-2.327	-1.410	0.059	-1.198
-3.571	-1.905	0.768	-0.715	0.740	-1.355	-0.162	
-1.444	0.345	-0.938	-1.195	-1.032	NA		
-2.509	-1.921	-1.293	-0.020	-0.798	-0.287	-0.316	0.121
0.883	-0.628	0.420	-0.310	-0.602	0.128	-1.321	
0.002	-1.814	-3.149	-0.139	-0.862	NA		
-0.444	-0.055	-1.332	-1.967	-1.597	-1.754	-1.314	-0.463
-0.306	0.243	-2.278	-0.620	-0.645	-1.667	-0.311	
0.015	-1.023	-1.265	-2.888	0.033	NA		
-2.047	0.892	-2.184	-0.823	-0.795	-0.811	-2.600	-1.938
-1.865	-0.334	-1.692	-2.083	0.139	-2.026	-0.533	
-1.226	-0.486	0.397	-1.713	0.064	NA		
0.052	-1.982	-2.116	0.297	-1.085	-0.859	-1.244	-0.510
-0.915	0.239	-1.592	-0.377	0.345	0.710	0.111	
-2.001	1.566	-0.798	-0.488	-0.944	NA		
-1.557	-2.269	-1.055	0.478	-1.254	0.138	0.471	-1.961
-0.862	0.536	-1.581	-0.384	0.527	-0.584	0.956	
0.115	-1.343	0.189	1.561	0.098	NA		
-1.793	-1.769	-0.614	-0.094	-2.170	-0.257	-2.089	-2.874
-0.339	-1.805	-1.222	-1.121	-0.472	-2.853	-0.978	
0.984	-0.241	-1.052	0.164	-0.139	NA		
0.247	-0.299	-0.219	-1.329	-1.970	-0.486	-0.734	-0.908
0.181	-1.184	-0.598	-1.767	-0.366	0.494	0.753	
-0.096	-0.333	2.061	0.115	1.172	NA		
-1.469	0.270	-0.630	0.323	-0.010	-1.280	-1.132	-2.595
0.863	-1.511	-0.487	-1.540	-0.088	-1.908	0.200	
-1.124	-1.470	0.932	-1.516	0.200	NA		
-0.855	-1.033	-1.857	0.230	-1.236	-1.294	-1.270	-1.075
-2.142	-1.279	0.638	0.087	-0.926	-1.182	0.181	
-0.559	-0.738	-0.550	0.384	-0.075	NA		
0.567	-1.215	-1.146	-1.219	-1.740	-0.690	-0.475	-1.068
-1.507	-0.761	-0.091	-0.970	-1.146	-0.485	-2.264	
0.490	-2.053	-0.465	-1.008	0.167	NA		
-3.195	-1.005	-1.698	-1.448	-1.363	-1.408	-1.476	-1.905
-0.913	-2.261	-0.165	-1.141	-1.094	-1.078	0.367	
-0.873	-0.404	0.214	-0.867	0.449	NA		
0.131	-0.383	-1.208	-1.367	-1.345	-2.453	-1.782	-1.398
-2.447	-1.991	0.059	-0.110	-0.341	-2.715	-0.135	
-2.371	-0.451	-0.444	0.032	1.067	NA		
-1.645	-1.018	-0.033	-0.582	-2.087	-0.455	-1.580	-0.385
-0.393	-1.294	0.385	-0.596	0.314	-1.547	-0.367	
0.848	0.747	-1.164	-1.447	-0.105	NA		
-0.568	-0.595	-1.230	0.838	-0.679	-0.388	-1.354	-1.601

Table36.txt

-1.039	-0.864	-1.202	0.079	-0.445	-0.025	-0.395	
-1.122	-1.929	-0.388	-2.372	-0.365	NA		
-0.781	-1.392	0.461	-1.631	-1.566	-2.394	-2.500	-0.379
-0.987	1.747	-0.323	0.454	-1.746	-1.874	-1.555	
0.856	-1.779	-0.761	-1.096	-2.114	NA		
-2.023	-2.202	-0.893	-1.575	-1.683	-4.301	-1.429	-1.198
0.401	-0.591	-0.359	0.941	-0.634	0.803	-0.127	
0.456	0.656	-3.215	0.396	1.093	NA		
-0.604	-1.106	-1.039	0.626	-0.823	-0.693	-1.543	-0.029
0.185	-1.974	-1.158	-0.427	-0.567	0.390	-1.456	
-0.042	-0.045	0.476	0.210	-0.046	NA		
-1.742	-0.578	-0.618	-0.600	0.399	-1.574	-1.618	-1.463
1.686	-1.012	-0.105	0.194	-0.309	-2.610	1.245	
-1.379	0.686	-0.728	-1.435	0.541	NA		
-0.942	-0.743	-1.738	-1.552	1.189	-1.171	-0.291	-0.278
-1.548	0.170	1.061	-1.753	0.616	0.236	-0.217	
-0.363	0.608	-0.428	-0.964	-0.777	NA		
-1.178	-1.860	-0.228	-1.470	-1.576	-2.527	-2.623	-2.395
-2.071	-0.857	0.463	-1.089	0.726	-0.411	0.868	
1.009	0.382	-0.875	-1.486	-0.926	NA		
-0.437	-1.981	-0.217	0.509	-2.997	-2.626	-1.877	0.580
-0.372	-0.096	-1.774	-2.179	-0.491	-0.589	-0.204	
-0.147	0.858	-1.833	-0.291	-0.338	NA		
-0.059	-1.593	-1.418	-0.134	-1.429	-2.939	-0.408	-0.500
-0.553	-2.106	-2.744	-0.933	-2.250	-1.580	-0.369	
-0.081	-1.285	-3.218	0.234	-0.725	NA		
-1.868	-1.296	-1.033	1.714	-0.187	-1.219	-1.696	-2.081
-1.664	-0.613	0.224	1.029	-1.477	-1.178	-0.445	
0.095	-0.132	-0.469	-1.108	-0.333	NA		
-2.822	-2.098	-1.621	-0.221	-3.077	-2.321	-1.609	0.192
-0.590	-0.639	-0.485	-0.427	-1.873	-1.463	-0.321	
-2.816	-0.028	-0.216	-1.696	-1.145	NA		
-1.286	-0.609	-0.652	-1.791	-0.705	-1.029	-0.927	-0.408
0.622	-2.585	0.651	-2.734	-0.622	-1.560	-1.149	
-2.013	0.274	-1.217	-0.454	-1.370	NA		
-2.623	-0.923	-1.611	-0.408	-2.043	-2.026	-1.771	-2.673
0.174	-0.885	-1.783	0.814	0.205	-1.405	0.371	
-2.360	-0.361	-2.560	-0.056	-1.222	NA		
-4.623	-2.185	-1.503	-1.422	-2.370	-1.199	-2.629	-1.401
-0.842	-0.445	0.388	0.363	-0.502	-1.026	0.263	
0.001	-0.721	-0.224	-1.062	0.953	NA		
-1.954	-2.838	-0.899	-1.527	-1.893	-3.849	-2.613	-0.757
-0.745	-0.431	-1.730	1.149	0.367	0.056	-2.335	
-0.945	-1.485	0.207	-0.478	-0.789	NA		
-2.309	-1.437	-0.872	-0.490	-1.205	-0.120	-0.201	-0.243
-1.664	-0.210	0.625	-2.334	-0.863	-0.338	-0.766	
-2.064	0.456	-2.122	-1.244	-0.716	NA		
1.024	-2.424	-0.591	0.790	-1.848	-0.072	-2.437	-0.582

Table36.txt

-0.379	0.342	-3.378	-0.815	0.795	-0.321	-0.663		
-0.472	-1.114	-0.081	-2.577	-1.332	NA			
-1.870	-0.149	-0.794	-1.725	-2.050	-5.309	-1.687	-0.951	
-0.267	-1.159	-0.029	-3.049	-4.054	-1.163	0.180		
-2.999	-0.552	-0.205	-1.093	-2.429	NA			
-1.191	-0.756	-0.949	-2.574	-3.094	-3.101	-2.551	-1.363	
0.169	-0.470	-1.137	-2.637	-0.812	-1.147	-0.040		
-0.610	0.591	-1.558	-2.187	-0.136	NA			
-2.754	-1.010	-0.835	-0.794	-3.556	-1.384	-1.569	-1.329	
0.218	-1.803	0.962	-0.605	1.137	-0.018	-1.184		
-1.374	-2.787	-1.017	-0.401	-0.985	NA			
-2.873	-3.269	-0.137	-1.867	-0.937	-2.239	-2.366	-0.418	
-0.945	-0.547	-2.697	-0.128	-3.035	-1.442	-1.491		
-0.305	-0.626	-0.261	0.599	-0.868	NA			
-1.127	-2.288	-2.295	-1.758	-3.613	-3.024	-1.837	-0.375	
-2.510	-1.412	0.022	-0.234	-0.737	-2.742	0.345		
-0.695	0.531	-1.368	-1.196	-0.563	NA			
-1.098	-0.940	-1.029	-0.935	-1.273	-2.697	-1.973	-2.183	
-1.658	-2.066	-1.868	-2.296	-0.145	-0.680	0.181		
0.526	-1.285	-2.614	-1.518	-1.714	NA			
-0.610	-0.857	-1.311	-0.447	-2.442	-1.849	-0.420	-1.572	
1.339	-2.532	-0.784	-1.089	-0.695	-1.382	1.338		
-1.949	-1.164	-0.866	-0.198	0.273	NA			
-2.217	-1.254	-2.812	-2.573	-1.477	-3.389	-1.707	-2.073	
-2.307	-0.630	-0.811	0.426	-0.874	-1.475	-2.198		
1.862	-0.689	-0.016	-1.689	-0.804	NA			
-2.379	-0.115	-1.380	-0.894	-1.341	-3.277	-1.264	2.809	
-0.416	-1.019	-1.336	-2.928	-1.603	-2.301	1.846		
1.226	-0.901	-0.842	-1.822	-1.128	NA			
-0.878	-1.406	-2.319	-1.875	-0.908	-0.867	-2.691	-0.791	
0.495	-0.432	-2.086	-1.035	0.740	-1.388	0.274		
0.614	-1.356	0.304	0.432	0.428	NA			
-1.437	-0.345	-2.374	-0.600	-2.300	-2.047	-1.861	-1.742	
-1.768	-0.088	0.899	-1.627	-0.780	-1.729	-0.325		
-0.115	0.306	-1.210	-1.753	-2.762	NA			
-2.372	-1.632	-1.666	-1.435	-0.077	-2.693	-3.026	-0.880	
-0.195	-1.739	0.816	0.299	-0.532	-0.700	-0.298		
0.407	-0.402	-1.257	-0.525	-1.338	NA			
-2.106	-3.348	-0.834	-1.602	-2.534	-0.798	-3.924	-2.428	
-0.020	-0.346	-2.220	-3.087	-0.692	-1.374	-3.440		
-0.562	-1.288	-1.337	-2.757	-1.674	NA			
-1.949	-1.328	-0.901	-1.166	-2.594	-1.349	0.295	-0.635	
0.381	0.745	-1.578	-1.350	-0.962	-0.974	-1.123		
-0.510	-0.269	0.274	-0.717	-0.246	NA			
-1.939	-0.557	-0.310	0.177	-0.665	-2.689	-0.797	0.577	
-3.069	-1.387	-0.395	-1.589	-0.841	-2.537	1.198		
-1.560	-1.358	-1.029	-0.470	-1.198	NA			
-0.354	-0.420	-1.969	-1.352	-0.214	-4.491	-0.440	-0.490	

Table36.txt

-0.290	-2.255	-0.326	0.696	-1.508	-3.518	-0.729	
-0.489	-0.208	1.145	0.319	-1.659	NA		
-1.766	-0.164	-3.131	-0.518	-2.113	-3.676	-2.363	-1.905
0.511	-1.714	-0.463	-0.332	-1.167	-3.166	-0.005	
-1.150	-1.171	-1.462	-1.261	-1.170	NA		
-0.081	-2.442	-1.708	-0.383	-0.993	-2.225	-0.943	0.256
-1.867	-0.947	0.093	-0.066	1.797	-2.213	-3.764	
0.003	-2.255	0.087	-1.435	-2.685	NA		
0.428	-2.089	-1.922	0.118	-1.138	-2.821	-0.759	-2.960
-0.201	-0.747	-0.712	0.111	0.620	-1.422	-0.145	
0.176	-0.538	0.052	-0.455	-1.061	NA		
-2.634	-1.550	-2.353	0.015	-2.407	-1.393	-2.464	-2.660
-2.363	-1.406	-0.589	-1.106	-0.417	-1.284	0.199	
-0.771	1.879	-0.779	0.071	-0.581	NA		
-1.073	-0.537	-0.895	1.635	-0.985	-0.030	-0.882	-0.708
0.986	0.392	-1.490	0.831	0.393	-0.666	-1.689	
-0.551	-0.177	0.082	-1.949	-0.509	NA		
-1.525	0.421	-0.088	1.536	-1.472	-0.998	-2.153	-1.471
-0.763	-1.088	-0.611	-0.278	0.853	-0.327	-0.133	
-0.643	-0.886	-1.053	-0.112	-1.547	NA		
-2.677	-0.805	-1.461	-0.467	-0.945	-2.257	-0.996	-2.965
-0.345	-0.152	-0.154	-1.423	-0.141	-3.132	1.716	
-2.647	0.972	-0.106	-1.046	-0.953	NA		
-0.369	-2.375	-2.104	0.687	-1.644	-2.100	-0.738	-1.554
-2.729	-1.700	-1.531	-1.952	-1.535	-0.855	-2.898	
-0.411	-0.740	-1.030	-0.977	-0.779	NA		
-0.650	-1.687	-1.435	-1.190	-0.790	-1.867	-3.304	0.027
0.671	-1.901	-1.091	0.217	-0.168	-1.333	0.515	
-2.625	-0.027	-2.441	-0.472	-0.648	NA		
-0.022	-1.727	-1.801	-0.809	-1.232	-1.591	-2.209	-1.038
0.053	-0.778	-1.748	-1.378	-2.392	-2.068	-2.113	
-1.278	-0.727	0.167	-2.225	0.305	NA		
-0.764	-1.753	-1.681	-1.078	-1.907	-1.057	-0.858	-1.411
-2.597	-1.445	-0.795	-0.925	-0.448	-2.811	-0.514	
-0.250	-2.791	0.851	-2.514	-0.164	NA		
-0.648	-1.298	-1.892	-0.548	-2.673	-1.440	-1.912	-0.135
0.472	-0.793	-1.669	-1.462	-0.681	-2.247	0.331	
-2.594	-1.945	0.062	-1.314	-0.746	NA		
0.503	1.110	-3.017	-0.201	-1.389	0.245	-0.278	-0.270
-1.461	-0.601	-0.997	-1.614	0.557	-2.676	0.098	
-0.879	-0.467	-1.551	1.004	0.100	NA		
0.066	-1.219	-2.446	-1.268	-1.154	-0.693	-1.041	-0.142
1.449	-1.010	-1.193	-1.090	-2.171	-1.553	-0.659	
-1.184	0.070	-0.678	-0.212	0.095	NA		
-0.983	-1.536	-2.640	-0.183	-1.353	-3.205	-0.513	-0.250
-0.142	-1.747	0.122	0.503	-0.257	-1.627	-1.711	
-1.039	-0.188	-2.809	0.572	-1.216	NA		
-2.598	-1.840	-2.077	-1.096	-1.652	-0.626	-3.485	-2.693

Table36.txt

0.894	-1.714	-2.292	-1.271	-0.257	-0.828	-0.863		
-3.496	-1.560	-1.541	1.054	-0.440	NA			
-0.740	-1.222	-1.656	0.330	-1.489	-2.084	-2.076	-1.836	
-1.875	-0.835	-0.329	-1.967	0.241	-3.187	-1.149		
-1.384	-0.471	-1.908	0.189	-0.780	NA			
-3.169	-0.481	-2.035	0.130	-1.369	-1.589	-2.913	-0.626	
0.271	-1.325	-1.603	-1.534	-1.691	-1.063	0.056		
-0.457	-1.592	-0.315	-2.406	0.505	NA			
-3.699	-1.101	-0.972	-1.621	-4.496	-0.444	-2.207	-1.104	
0.176	-0.592	1.016	-1.582	0.570	-2.425	0.937		
-0.531	0.118	-1.693	-1.369	-1.084	NA			
-0.180	-2.407	0.455	-1.119	0.374	-0.578	-2.109	-0.460	
-0.211	-1.889	-0.759	-0.672	-2.084	-1.776	1.339		
-1.889	-0.262	-1.635	0.687	-1.565	NA			
-3.930	0.110	-0.526	-0.321	-2.257	-0.540	-0.730	0.434	
0.000	0.000	-0.378	-0.541	0.000	-0.790	0.000		
0.254	0.000	0.000	-3.090	0.000	NA			
-1.139	-1.396	-2.842	-2.206	-1.392	-0.878	-1.458	-0.286	
-1.132	-1.644	-1.506	-0.426	-0.303	-0.445	-0.502		
-0.924	0.004	-0.664	-0.764	-0.487	NA			
-0.861	-0.820	1.045	1.204	-0.214	-1.574	0.155	-0.724	
1.169	0.028	-0.371	-1.108	-1.089	-1.194	1.212		
-2.630	-0.558	-1.892	-1.539	-0.409	NA			
-0.319	-0.725	-2.120	-0.230	-0.159	0.019	-2.046	-0.903	
0.493	-1.843	-3.807	-1.262	0.633	-1.140	-0.571		
-1.807	0.372	-1.582	-1.860	-1.604	NA			
-0.302	0.088	-1.237	0.707	-2.240	-0.993	0.290	-0.619	
-1.402	-0.612	-2.573	-2.423	0.078	-2.966	0.380		
-0.375	0.017	-1.330	-0.515	-1.205	NA			
-2.277	-1.222	-0.764	-0.672	-1.156	0.519	0.114	0.039	
-0.911	-0.784	-0.714	-1.551	-2.210	-3.503	-1.556		
-2.908	-1.045	-0.962	-0.320	-0.335	NA			
-2.302	-0.789	-3.095	0.690	-0.398	-2.677	-1.180	-1.047	
-1.591	-0.620	0.030	-1.202	-0.451	-1.248	-0.260		
0.573	1.156	-2.397	-1.814	0.370	NA			
-2.596	-1.675	-0.001	-0.047	-0.569	-1.741	-1.047	-1.756	
-0.887	0.187	-0.335	0.014	-0.122	-1.186	-0.201		
-2.193	-0.507	-1.072	-1.524	-0.296	NA			
-0.752	-1.019	0.069	-2.664	-0.981	-1.449	-0.727	0.494	
-1.203	-0.548	0.967	0.236	-1.049	-1.797	-3.090		
0.106	-1.933	-1.452	-0.894	0.884	NA			
-1.335	-1.423	-0.246	-1.101	-3.714	-1.318	-0.285	0.459	
0.005	-1.888	-2.280	-1.233	1.233	-1.423	0.000		
0.487	0.080	-1.335	0.398	-0.529	NA			
0.416	-0.535	-1.177	-0.134	-1.995	-3.320	-4.160	-0.934	
-1.057	-1.588	0.222	-0.800	0.012	-0.899	-0.457		
-0.380	0.772	-1.523	-1.813	0.064	NA			
-1.924	-2.073	-2.638	1.504	-1.728	-2.847	-3.480	-0.043	

Table36.txt

-1.603	-1.490	-0.685	-0.632	0.132	-1.330	0.399		
0.451	-1.095	-0.870	-1.977	-1.235	NA			
-2.263	-0.930	-1.280	-0.184	-3.399	-2.285	-0.119	-1.039	
-0.540	-1.685	0.474	1.498	1.381	-1.664	-3.005		
0.054	-0.958	0.950	0.597	-0.716	NA			
-0.665	-1.094	-1.061	-0.534	-1.909	-1.943	0.000	-3.016	
0.592	-0.586	-1.863	0.187	-2.490	-2.625	-1.507		
-2.588	-2.065	-0.978	0.913	0.005	NA			
-0.981	-1.208	-2.799	-1.242	-2.303	-3.513	-0.557	-0.601	
2.086	-2.001	-0.322	-2.117	-1.897	0.389	-1.168		
0.158	-1.939	0.734	0.126	0.661	NA			
-1.088	-0.610	-1.806	-0.524	-0.493	0.603	0.390	-0.822	
0.327	-0.898	-1.744	-0.041	0.155	-2.212	-1.021		
-0.753	-1.148	0.102	-0.607	0.031	NA			
-0.546	-1.548	-1.974	-0.051	-3.066	-2.584	-0.165	-0.660	
0.683	-1.143	-1.839	-0.074	-0.970	-0.944	-0.427		
2.171	1.160	-1.243	0.220	0.030	NA			
-2.177	-0.464	-0.942	-1.310	-0.412	0.384	-1.185	-0.436	
-0.501	-0.172	-0.399	-1.499	-0.629	-0.119	0.247		
-0.898	0.109	0.081	-0.446	-0.428	NA			
-0.091	0.016	-1.100	-0.815	-1.924	-0.705	-0.470	-0.343	
0.597	-0.531	0.345	-1.882	-0.761	-1.104	0.725		
-1.039	0.212	-2.998	-1.235	-1.088	NA			
-0.126	-1.424	-1.633	-0.447	0.212	-0.943	-0.075	0.429	
0.157	-1.662	-0.517	-0.964	-1.049	1.137	-0.192		
-0.488	-0.805	-0.587	-2.330	-1.544	NA			
-0.892	-0.661	-2.417	0.218	-0.901	-0.584	-0.217	-0.385	
1.120	-1.422	-0.366	1.068	1.941	-1.292	0.104		
0.128	-1.249	-0.682	-1.678	0.040	NA			
0.415	-0.317	-0.681	-0.713	1.664	1.257	1.316	1.074	
1.298	1.290	-1.553	1.584	-0.672	-0.367	0.762		
2.536	-0.173	-2.123	1.857	-0.798	NA			
-1.975	0.813	-2.004	-0.056	-0.749	-2.480	-0.499	-1.037	
-0.303	-1.085	1.176	-0.172	1.337	0.360	-3.473		
1.191	-0.685	-0.153	-1.116	-0.398	NA			
0.937	0.854	-0.215	-0.549	0.212	-1.975	-0.691	-1.192	
1.259	0.388	1.121	-0.362	0.194	-0.944	-1.322		
-1.070	-0.465	-1.732	1.236	-0.811	NA			
-2.659	0.863	-2.419	-0.857	-0.995	-5.098	-0.162	-0.791	
-0.762	-0.431	0.848	-1.098	0.258	-0.031	0.236		
-1.661	0.620	-0.845	1.481	0.545	NA			
-0.771	-1.758	-0.877	1.006	-0.470	-0.143	0.185	0.683	
-0.468	-0.102	0.056	-0.227	0.552	-0.473	0.227		
0.164	0.115	-0.574	-0.140	-1.794	NA			
-0.362	-1.782	-0.639	-1.965	-1.857	-1.910	-0.448	-0.209	
0.739	-0.230	0.341	-0.786	-1.262	0.128	-1.036		
-0.440	-0.953	0.321	-1.941	-2.226	NA			
-0.223	0.490	-3.549	0.612	-0.956	-0.652	-0.397	-1.000	

Table36.txt

0.300	-1.436	0.063	-0.345	-0.184	1.092	-1.827	-2.768	-0.098
-0.010	-0.033	1.114	NA	-1.293	-1.273	-1.197	-0.406	-0.286
-0.182	-0.980	0.738	0.834	0.315	-0.883	-0.935	-0.566	-0.086
-0.530	-1.052	-0.290	-0.239	-2.539	0.540	NA	-0.570	-1.734
-0.957	-0.849	-1.112	-0.543	-0.675	-1.201	-1.835	-1.468	-0.591
-1.538	0.608	-1.545	0.127	-0.534	0.049	-0.230	-0.155	-1.783
NA	-1.286	-1.451	-0.273	-0.214	-1.514	-1.708	-2.364	-0.797
-2.069	-2.150	0.317	0.914	-0.571	-0.258	-0.232	-0.895	0.133
-2.938	-1.385	-0.519	NA	0.563	-2.139	-0.245	-0.107	-0.025
-1.916	-1.027	0.280	-1.809	-2.394	-1.124	0.741	1.475	-0.267
0.081	-2.882	0.338	-0.858	-2.720	-0.632	NA	-1.968	0.702
-1.922	-0.972	-0.907	-1.368	-1.358	-0.183	0.651	-0.062	-1.160
-0.079	-0.438	-0.838	0.925	-1.235	-0.320	-0.965	0.359	-1.224
NA	-1.262	-2.012	-1.785	-0.301	-0.801	-1.895	-0.187	-1.138
1.383	-1.446	0.470	0.040	-1.002	-1.293	-0.405	-1.673	0.289
-2.964	0.417	-0.449	NA	-1.981	-1.745	-0.701	-1.172	-2.347
-2.792	-0.115	1.562	-0.300	-0.662	-2.090	-0.982	-2.234	-0.889
0.366	-2.170	0.308	1.084	-0.998	-0.675	NA	-1.287	-0.338
-2.383	0.238	-2.462	-1.809	-1.845	-0.173	-0.256	-2.867	-4.482
-0.141	0.098	-1.059	-0.215	0.517	-1.868	-0.035	-2.367	-1.395
NA	-1.195	-1.122	-1.608	-0.331	-0.499	-1.254	-1.406	-0.959
-1.251	-1.250	-0.525	-2.001	0.255	-1.592	-0.391	0.446	0.813
-0.344	-1.082	-0.159	NA	-0.848	0.010	-1.843	-0.815	-2.535
-3.423	-0.664	-3.477	-1.660	-1.036	-1.338	-2.103	-0.997	-0.552
-1.171	-0.276	0.477	0.238	-1.413	-0.883	NA	-4.078	-0.219
-2.318	0.809	-1.534	-3.348	-0.206	0.856	0.265	-0.624	-0.294
-0.799	0.115	-0.557	1.053	-0.462	-1.367	-0.923	0.933	-1.683
NA	-4.428	-0.075	-2.189	-0.926	-1.446	-0.831	-2.614	-0.015
0.800	-0.960	-1.126	0.004	1.091	-0.356	-0.093	-0.185	-2.277
-1.372	0.640	-0.054	NA	-3.053	-0.589	-0.966	-0.900	-2.828
-3.090	-2.202	-3.594	-1.248	-2.303	-0.066	-0.066	0.647	-2.917
-2.844	-1.156	0.193	0.561	-0.160	-0.574	NA	0.557	0.496
-1.391	-0.785	-2.405	-0.747	-1.635	-0.218	-1.690	-1.988	1.612
0.948	0.228	-2.108	0.522	1.011	-0.129	-1.261	1.581	-0.535
NA	-1.464	-1.397	-2.554	0.032	-2.123	0.085	-2.704	-0.763
-1.244	0.188	-1.161	-0.380	0.450	-1.419	-2.131	-0.757	0.670
-0.488	-1.432	-0.346	NA	-1.514	-0.406	-2.034	-0.812	-1.596
-2.277	-1.777	-0.072						

Table36.txt

-0.241	-2.146	-1.167	-2.319	0.873	-2.399	-0.750		
-0.516	-0.692	-0.730	-1.409	-0.781	NA			
-1.493	-0.776	-2.845	-1.199	-2.589	-1.337	-1.528	-1.585	
-0.481	1.467	0.577	-0.613	-0.340	-1.384	0.344		
-0.100	-0.581	-2.168	-1.414	0.264	NA			
-2.031	-2.283	-2.290	-3.324	-1.922	-2.399	-0.922	-1.152	
-2.474	-3.423	-0.829	-0.626	-0.086	-0.929	-1.227		
-1.963	-0.602	-0.865	-0.768	-1.100	NA			
-0.583	-0.981	-0.960	0.138	-2.533	-2.361	-0.913	-1.769	
-1.766	-2.067	1.004	-0.891	-1.419	-1.789	-0.945		
-1.094	-2.100	0.556	0.673	-1.265	NA			
0.862	-2.859	-1.485	-0.411	-1.999	-3.754	-2.577	-1.611	
-1.282	-1.170	-1.031	-0.507	-0.482	-1.388	-0.909		
-0.511	-2.735	1.248	-2.314	-0.616	NA			
-1.772	-0.601	-1.580	0.458	-1.258	-3.329	-1.830	-1.590	
-0.756	0.794	0.069	-1.768	-0.969	-1.040	-0.360		
-0.519	-0.465	-0.217	-1.634	-1.149	NA			
-1.296	-0.708	-1.504	-0.508	-2.721	-2.166	-2.308	-0.223	
-1.095	-1.399	0.239	-2.705	0.178	-1.762	-0.548		
-1.031	-0.516	-1.666	-1.574	-0.390	NA			
-3.041	-1.000	-0.706	-0.779	-2.607	-0.418	-3.614	-1.238	
-0.479	0.578	-1.075	-0.973	0.836	-0.881	-0.699		
-1.661	0.062	0.176	-1.097	-0.327	NA			
-1.394	-3.308	-2.485	-1.897	-2.322	-2.447	-2.693	-0.803	
-1.331	-0.793	-1.534	-2.640	-1.998	-0.720	0.056		
-0.964	-0.137	0.105	-1.704	-1.804	NA			
-1.681	-2.280	-0.500	-1.136	-2.166	-0.551	-2.928	-1.755	
-0.033	-2.407	-1.663	-1.731	-0.338	-2.054	0.429		
-1.135	-1.625	-1.129	0.602	0.359	NA			
-1.813	-0.914	-2.654	-1.781	-1.816	-2.488	0.457	-2.450	
-0.557	-2.171	-1.658	-1.433	-1.185	-0.614	-0.837		
-1.328	-0.549	-3.184	-1.007	-0.426	NA			
-2.269	-1.675	-3.761	-2.164	-2.361	-2.641	-2.759	-2.961	
-0.591	-1.818	-1.004	-2.643	1.269	-0.655	-1.827		
-2.392	-1.128	-0.604	-0.834	-0.496	NA			
0.004	-2.461	-1.977	-1.838	-0.150	-0.992	-3.674	-0.671	
-1.189	-0.327	-1.477	-0.773	-0.950	-2.406	-0.989		
-0.406	1.050	-1.658	-1.575	0.972	NA			
-0.434	-0.729	0.493	-1.135	-1.593	-4.022	-0.798	-1.676	
0.996	-0.237	-0.891	1.117	-0.073	-0.394	0.599		
-1.380	0.123	-0.655	-1.070	-1.145	NA			
-2.924	0.245	-2.015	-1.413	0.041	-3.504	-1.900	-1.030	
-0.857	-1.785	-0.187	0.932	-1.855	-2.001	1.428		
-0.687	-1.102	-1.992	-1.818	-0.766	NA			
-0.191	-1.242	0.792	-1.078	-4.002	-2.366	-0.774	-0.076	
-1.336	-2.099	-0.273	-0.092	0.024	-0.420	-3.681		
-0.470	0.263	0.449	0.446	0.460	NA			
-3.260	-0.621	-1.922	-0.974	-0.862	-2.244	-1.494	-0.737	

Table36.txt

-1.953 -1.002 -4.132 0.537 -1.205 -0.803 0.151
-1.127 0.003 -1.516 -0.769 -2.228 NA
-1.324 -1.826 -1.310 -2.165 -0.975 -3.297 -2.500 -2.576
-0.727 -0.515 0.526 -1.257 0.940 0.319 -0.499
-0.756 -0.964 -1.103 -1.645 -1.136 NA
-0.137 -3.066 -3.990 -0.770 -1.875 -3.056 -2.223 -0.545
-0.951 -1.155 -1.512 -0.259 -0.790 -1.004 -0.172
-1.334 0.354 -1.471 -0.630 -1.384 NA
-0.889 -1.699 -2.914 -1.526 -1.317 -1.675 -2.175 -1.328
-0.551 -0.621 -1.446 -1.901 -0.895 -1.704 -0.740
-0.427 -0.065 -1.058 0.500 -0.002 NA
-2.636 -0.865 -1.330 -1.466 -1.376 -1.900 -0.519 -1.290
0.678 -1.650 -3.469 0.014 -1.908 -0.165 -0.932
-0.934 -1.306 -0.361 -1.934 -0.968 NA
-3.703 -0.355 -3.352 -0.308 -2.172 -1.992 -1.662 -0.181
-0.059 -1.692 -0.503 -0.517 0.879 -1.656 0.295
-1.070 -0.869 -0.183 1.175 0.372 NA
-1.968 -1.100 -3.502 -1.199 -1.442 -1.141 -1.376 -1.387
-1.396 -1.060 -1.914 0.860 -0.605 -2.152 -1.151
1.478 -1.936 0.350 -0.419 -2.133 NA
0.334 0.365 1.831 -0.244 -1.907 -1.865 -1.748 -0.896
-0.594 -0.140 -0.606 -0.557 0.240 -2.229 -0.916
-0.238 -0.480 1.122 -0.990 -0.755 NA
-0.339 -0.952 -0.431 1.376 -2.128 -1.691 -0.251 -0.219
-0.816 -0.751 -0.153 -2.412 -1.874 -1.873 -0.952
1.893 -0.248 -2.184 -1.539 0.790 NA
1.368 -2.400 -0.862 0.083 -1.823 -2.634 -0.834 -2.136
-1.361 -4.065 0.356 -2.814 -0.565 -3.371 -0.770
0.127 -1.966 -3.318 -2.035 -1.468 NA
-1.116 -0.945 -2.407 -1.543 -1.717 -3.325 -0.580 0.380
-1.077 0.019 -0.975 -0.037 1.368 -1.485 0.095
-0.611 0.817 -1.185 -1.055 -0.730 NA
-0.542 -2.152 -0.648 -2.267 -1.990 -0.618 -2.003 -0.558
-1.777 -1.227 -0.071 -0.550 -0.309 0.503 -0.777
-0.072 -2.756 -2.817 -0.840 -0.697 NA
-1.265 -1.596 -2.328 -0.710 -1.962 -3.502 -2.981 0.099
1.035 -0.089 -0.862 -1.039 -3.667 -0.608 -0.287
-1.991 -0.904 -1.645 -2.027 0.017 NA
-3.048 -2.655 -3.463 -0.687 -2.535 -1.738 -0.620 -3.136
-0.876 -1.278 -1.616 -2.109 0.741 -1.390 -0.305
0.151 0.402 -0.169 -1.221 0.330 NA
-1.229 -2.372 -2.122 -2.494 -1.042 -1.306 -2.601 -1.197
-1.163 -0.716 -0.812 -0.792 -0.439 -2.227 -0.656
-1.235 -2.412 0.043 -1.616 -2.894 NA
0.066 -0.957 -0.049 -1.857 -1.871 -1.830 1.202 -0.583
-1.614 -0.908 -0.868 -0.185 -0.173 -2.100 0.652
-0.334 0.896 1.866 -1.480 0.451 NA
-1.818 1.470 -0.813 -1.161 -1.788 0.243 -0.676 -0.548

Table36.txt

0.569	-0.896	-0.626	-1.281	0.821	-0.965	-0.584		
-1.096	0.503	-0.205	-1.820	-1.615	NA			
-3.073	-3.129	-2.746	-0.451	-0.914	0.273	-2.427	-2.492	
-0.687	0.826	-0.404	-1.290	-0.454	-2.137	-1.019		
-1.529	-0.328	-0.644	-0.386	-0.503	NA			
0.480	0.029	-1.301	-2.458	-2.095	-1.102	-2.754	0.113	
0.110	-0.505	-0.417	-1.931	-1.694	-0.603	-0.014		
1.055	-0.693	-0.289	-0.192	-0.603	NA			
-0.529	-3.020	-1.377	-1.066	-0.331	-2.228	-0.466	-1.277	
-0.380	0.231	-1.856	-0.431	-1.607	-0.550	-0.889		
0.345	-1.404	-2.415	-2.009	0.623	NA			
-1.668	-1.332	-1.941	-0.460	-3.076	-2.411	-1.975	-1.706	
0.313	-2.002	-1.801	-1.606	-0.444	-2.666	-0.580		
-1.063	-0.139	0.407	-0.934	0.767	NA			
-3.036	-1.706	-0.878	0.068	-0.512	-2.184	-1.352	-4.193	
-2.438	-0.909	-0.265	-0.909	0.178	-1.207	-0.096		
-0.451	-1.100	-0.080	-0.617	0.741	NA			
-1.356	1.368	-1.214	0.380	-1.714	-2.382	-1.666	-0.365	
-0.874	-1.588	-0.358	1.698	0.785	-1.836	0.491		
-0.628	-0.704	-0.203	0.436	-0.073	NA			
-0.505	-0.101	-0.208	0.125	-1.297	-2.237	-0.032	-0.398	
0.404	-2.315	-0.606	-0.283	-0.159	-1.613	-0.260		
0.522	-0.436	-0.026	-0.489	-2.681	NA			
-3.287	-0.815	-1.185	-0.159	-0.107	0.053	-0.855	0.110	
-0.063	-0.470	0.679	-2.479	-1.487	-0.808	-1.654		
-0.652	-0.147	-0.271	-1.673	-1.079	NA			
-0.586	0.800	1.258	0.048	-0.178	-3.935	-1.463	-0.722	
-0.627	0.993	-0.518	-0.497	-0.510	-1.608	-0.168		
-1.255	-0.743	-1.486	-1.025	-0.297	NA			
0.356	-2.756	0.025	-1.959	-1.395	-1.895	-3.591	0.139	
0.977	-0.894	-1.103	0.005	-0.715	-1.182	-0.191		
-0.439	-1.351	-2.311	0.579	0.528	NA			
-3.414	-1.058	0.042	-1.282	0.265	-2.433	-1.831	-0.710	
-1.454	0.322	-0.233	0.709	-0.868	-1.347	-0.848		
2.438	0.312	-2.198	1.396	-1.704	NA			
-2.484	-0.294	-1.680	-1.065	-0.608	-0.092	-0.733	-0.481	
-0.430	-0.478	-0.020	-1.722	-1.528	-0.894	0.909		
1.383	1.007	0.070	1.348	1.207	NA			
0.281	-0.667	-1.191	-0.031	-0.578	-0.821	0.682	0.126	
-1.546	-1.120	-0.139	-0.142	-0.819	-0.516	-1.043		
-0.150	2.001	-0.083	-0.274	-0.687	NA			
0.169	0.104	-1.160	0.410	-1.512	-0.754	0.570	-0.941	
0.120	-1.356	0.411	-0.235	0.867	-1.485	-0.363		
-0.376	-2.644	-0.035	1.657	-0.227	NA			
-1.965	0.730	-0.116	-0.274	-1.217	-0.248	-1.958	-2.120	
-0.492	-0.984	0.066	0.050	0.134	0.798	-0.176		
-0.148	-0.784	-2.665	1.378	-1.143	NA			
-0.979	0.861	-0.939	0.654	-2.412	-1.832	-2.487	-0.112	

Table36.txt

-1.789 0.230 0.202 0.038 -1.003 0.115 -1.151
-0.538 -2.830 1.145 1.609 1.043 NA
0.266 -0.352 -0.209 1.366 -0.732 0.001 -0.236 -1.698
-0.059 -3.469 -0.018 -1.620 -0.741 -3.223 -0.364
-0.083 -1.449 -0.861 -0.150 -0.730 NA
-0.157 1.335 0.397 -0.226 0.636 5.774 -0.459 -1.417
-0.521 -1.108 0.345 1.500 2.794 2.181 0.672
-0.460 -0.421 0.540 -0.613 0.872 Liver

Mutant

Allele Fraction	Mutation	Gene	Estimated Stage	Grade Fraction	Subtype
0.020	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.040	NA	NA
0.005	TP53_0272_0283.chr17.7577120.C>A	TP53	0.009	NA	NA
0.001	TP53_219_224.chr17.7578191.A>G	TP53	0.001	NA	NA
0.001	TP53_262_267.chr17.7577141.C>A	TP53	0.002	NA	NA
0.000	TP53_219_224.chr17.7578190.T>C	TP53	0.001	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	NA	NA
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA	NA
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	NA
0.013	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.026	NA	NA
0.009	TP53_262_267.chr17.7577141.C>T	TP53	0.019	NA	NA
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.015	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	NA	NA
0.001	TP53_151_163.chr17.7578466.G>T	TP53	0.001	NA	NA
0.016	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.033	NA	NA

Table36.txt

0.000	GNAS_201.chr20.57484420.C>T	GNAS	0.001	NA	
			NA	NA	
0.001	TP53_098_109.chr17.7579389.G>A	TP53	0.002	NA	
			NA	NA	
0.000	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	NA	
			NA	NA	
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	NA	
			NA	NA	
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.002	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	NA	
			NA	NA	
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.014	NA	
			NA	NA	
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA	
			NA	NA	
0.001	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	NA	
			NA	NA	
0.214	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.427	NA	
			NA	NA	
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA	
			NA	NA	
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577111.G>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.003	NA	
			NA	NA	
0.001	TP53_151_163.chr17.7578461.C>T	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	NA	
			NA	NA	

Table36.txt

0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	NA	NA
0.004	TP53_0196_0205.chr17.7578263.G>A	TP53	0.007	NA	NA
0.001	TP53_172A.chr17.7578389.G>A	TP53	0.001	NA	NA
0.000	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	NA
0.001	TP53_0248_0261.chr17.7577536.T>A	TP53	0.001	NA	NA
0.003	TP53_167_177.chr17.7578406.C>T	TP53	0.007	NA	NA
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	NA	NA
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA	NA
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA	NA
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.003	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	NA
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.005	NA	NA
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	NA
0.001	TP53_167_177.chr17.7578401.G>A	TP53	0.002	NA	NA
0.002	TP53_167_177.chr17.7578421.G>A	TP53	0.003	NA	NA
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.016	NA	NA
0.004	TP53_0272_0283.chr17.7577124.C>T	TP53	0.009	NA	NA
0.004	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.008	NA	NA
0.008	TP53_0248_0261.chr17.7577536.T>A	TP53	0.016	NA	NA
0.000	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA	NA
0.000	TP53_262_267.chr17.7577153.C>A	TP53	0.001	NA	NA
0.000	TP53_132_142.chr17.7578527.A>C	TP53	0.001	NA	NA
0.002	TP53_172A.chr17.7578400.G>A	TP53	0.004	NA	NA

Table36.txt

0.001	PTEN_91_98.chr10.89692791.A>G	PTEN	0.002	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	NA	
			NA	NA	
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	
			NA	NA	
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	
			NA	NA	
0.001	TP53_172A.chr17.7578396.G>T	TP53	0.003	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA	
			NA	NA	
0.001	TP53_151_163.chr17.7578463.C>G	TP53	0.001	NA	
			NA	NA	
0.001	KRAS_144_147A.chr12.25378562.C>T	KRAS	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	NA	
			NA	NA	
0.000	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	
			NA	NA	
0.046	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.092	NA	
			NA	NA	
0.001	PTEN_136.chr10.89692923.G>A	PTEN	0.001	NA	
			NA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.001	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.001	NA	
			NA	NA	
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	
			NA	NA	
0.001	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.001	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.001	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	

Table36.txt

NA NA NA

Table36.txt

	NA	NA			NA		NA		
NA						NA		NA	

Table36.txt

	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
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	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	0.001	TP53_0272_0283.chr17.7577093.C>T			TP53		0.002		
NA						NA		NA	
	0.001	TP53_113_125.chr17.7579350.A>C			TP53		0.001		
NA						NA		NA	
	0.001	KRAS_012_+13_-4.chr12.25398279.C>T			KRAS		0.001		
NA						NA		NA	

Table36.txt

0.000	KRAS_0057_0064.chr12.25380276.T>C	KRAS	0.001	NA	
NA		NA	NA		
0.047	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.094	NA	
NA		NA	NA		
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	NA	
NA		NA	NA		
0.001	TP53_151_163.chr17.7578464.G>A	TP53	0.002	NA	
NA		NA	NA		
0.001	PIK3CA_0345.chr3.178921548.G>A	PIK3CA	0.002	NA	
NA		NA	NA		
0.002	GNAS_201.chr20.57484420.C>T	GNAS	0.004	NA	
NA		NA	NA		
0.005	TP53_188_195.chr17.7578265.A>G	TP53	0.009	NA	
NA		NA	NA		
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	NA	
NA		NA	NA		
0.000	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	
NA		NA	NA		
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	
NA		NA	NA		
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	
NA		NA	NA		
0.001	TP53_151_163.chr17.7578461.C>A	TP53	0.001	NA	
NA		NA	NA		
0.000	TP53_0227_0236.chr17.7577580.T>C	TP53	0.001	NA	
NA		NA	NA		
0.001	TP53_172A.chr17.7578407.G>A	TP53	0.001	NA	
NA		NA	NA		
0.001	TP53_167_177.chr17.7578431.G>A	TP53	0.001	NA	
NA		NA	NA		
0.003	TP53_0227_0236.chr17.7577571.A>T	TP53	0.006	NA	
NA		NA	NA		
0.000	TP53_151_163.chr17.7578475.G>A	TP53	0.001	NA	
NA		NA	NA		
0.000	TP53_208_218.chr17.7578204.A>T	TP53	0.001	NA	
NA		NA	NA		
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	NA	
NA		NA	NA		
0.001	TP53_233_245.chr17.7577548.C>T	TP53	0.003	NA	
NA		NA	NA		
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	
NA		NA	NA		
0.000	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.001	NA	
NA		NA	NA		
0.000	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	NA	
NA		NA	NA		
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.003	NA	
NA		NA	NA		

Table36.txt

0.001	GNAS_201.chr20.57484420.C>T	GNAS	0.001	NA	
			NA	NA	
0.001	PTEN_136.chr10.89692923.G>A	PTEN	0.002	NA	
			NA	NA	
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	
			NA	NA	
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.016	NA	
			NA	NA	
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	NA	
			NA	NA	
0.000	TP53_167_177.chr17.7578408.C>A	TP53	0.001	NA	
			NA	NA	
0.000	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	NA	
			NA	NA	
0.022	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.044	NA	
			NA	NA	
0.000	TP53_167_177.chr17.7578410.T>C	TP53	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	NA	
			NA	NA	
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.002	NA	
			NA	NA	
0.000	TP53_172A.chr17.7578389.G>A	TP53	0.001	NA	
			NA	NA	
0.008	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.015	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.003	NA	
			NA	NA	
0.001	TP53_219_224.chr17.7578191.A>G	TP53	0.001	NA	
			NA	NA	
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.003	NA	
			NA	NA	
0.002	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.003	NA	
			NA	NA	
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA	
			NA	NA	
0.001	TP53_126_131.chr17.7578538.T>C	TP53	0.001	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.001	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	NA	
			NA	NA	

Table36.txt

0.000	TP53_233_245.chr17.7577550.C>T	TP53	0.001	NA	NA
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	NA
0.000	TP53_342.chr17.7574018.G>A	TP53	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	NA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.000	TP53_132_142.chr17.7578530.A>C	TP53	0.001	NA	NA
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	NA
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	NA
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	NA
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	NA
0.001	TP53_151_163.chr17.7578464.G>A	TP53	0.002	NA	NA
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.000	NA	NA
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.003	NA	NA
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	NA	NA
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	NA
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	NA
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	NA
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.001	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.005	NA	NA
0.005	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.009	NA	NA
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA	NA
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	NA

Table36.txt

0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.002	NA	
			NA	NA	
0.000	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.001	NA	
			NA	NA	
0.000	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA	
			NA	NA	
0.013	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.026	NA	
			NA	NA	
0.001	TP53_342.chr17.7574018.G>A	TP53	0.003	NA	
			NA	NA	
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	NA	
			NA	NA	
0.000	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.002	NA	
			NA	NA	
0.002	TP53_0248_0261.chr17.7577538.C>T	TP53	0.003	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.003	NA	
			NA	NA	
0.003	TP53_233_245.chr17.7577559.G>T	TP53	0.007	NA	
			NA	NA	
0.000	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	
			NA	NA	
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	
			NA	NA	
0.000	TP53_298_306.chr17.7577022.G>A	TP53	0.001	NA	
			NA	NA	
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA	
			NA	NA	
0.002	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA	
			NA	NA	
0.002	TP53_0280_0289.chr17.7577094.G>A	TP53	0.003	NA	
			NA	NA	
0.002	TP53_0280_0289.chr17.7577094.G>A	TP53	0.003	NA	
			NA	NA	
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	NA	
			NA	NA	
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.004	NA	
			NA	NA	
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA	
			NA	NA	

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0.001	TP53_126_131.chr17.7578541.A>C	TP53	0.002	NA	
			NA	NA	
0.000	TP53_126_131.chr17.7578541.A>C	TP53	0.001	NA	
			NA	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	
			NA	NA	
0.003	TP53_113_125.chr17.7579315.G>T	TP53	0.006	NA	
			NA	NA	
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_172A.chr17.7578393.A>C	TP53	0.001	NA	
			NA	NA	
0.000	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	
			NA	NA	
0.000	GNAS_201.chr20.57484420.C>T	GNAS	0.001	NA	
			NA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	NA	
			NA	NA	
0.000	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	NA	
			NA	NA	
0.000	TP53_219_224.chr17.7578190.T>C	TP53	0.001	NA	
			NA	NA	
0.000	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.001	NA	
			NA	NA	
0.000	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	NA	
			NA	NA	
0.010	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.021	NA	
			NA	NA	
0.001	PIK3CA_1039_1050.chr3.178952085.A>T	PIK3CA	0.003	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.002	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.003	NA	
			NA	NA	
0.003	TP53_151_163.chr17.7578475.G>A	TP53	0.006	NA	
			NA	NA	
0.001	TP53_342.chr17.7574021.C>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_167_177.chr17.7578403.C>A	TP53	0.002	NA	
			NA	NA	
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	NA	
			NA	NA	
0.001	TP53_0227_0236.chr17.7577580.T>C	TP53	0.001	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	
			NA	NA	

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0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	NA
0.001	CDKN2A_7_88.chr9.21971099.G>A	CDKN2A	0.002	NA	NA
0.001	TP53_151_163.chr17.7578457.C>T	TP53	0.002	NA	NA
0.000	TP53_172A.chr17.7578407.G>C	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	NA	NA
0.000	TP53_342.chr17.7574003.G>A	TP53	0.001	NA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA	NA
0.001	TP53_113_125.chr17.7579350.A>C	TP53	0.002	NA	NA
0.002	TP53_219_224.chr17.7578191.A>G	TP53	0.003	NA	NA
0.002	TP53_219_224.chr17.7578191.A>G	TP53	0.004	NA	NA
0.003	TP53_219_224.chr17.7578191.A>G	TP53	0.006	NA	NA
0.007	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.014	NA	NA
0.005	TP53_298_306.chr17.7577022.G>A	TP53	0.009	NA	NA
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	NA	NA
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	NA
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.000	TP53_233_245.chr17.7577548.C>T	TP53	0.001	NA	NA
0.001	KRAS_144_147A.chr12.25378561.G>A	KRAS	0.001	NA	NA
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.006	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.011	NA	NA
0.001	TP53_172A.chr17.7578407.G>A	TP53	0.001	NA	NA
0.000	TP53_262_267.chr17.7577139.G>A	TP53	0.001	NA	NA
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	NA	NA
0.231	TP53_0248_0261.chr17.7577505.T>A	TP53	0.461	NA	NA

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0.002	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.004	NA	
			NA	NA	
0.000	TP53_0196_0205.chr17.7578253.C>A	TP53	0.001	NA	
			NA	NA	
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.002	NA	
			NA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	
			NA	NA	
0.003	NRAS_4_14.chr1.115258747.C>T	NRAS	0.006	NA	
			NA	NA	
0.000	BRAF_594_602.chr7.140453145.A>T	BRAF	0.001	NA	
			NA	NA	
0.001	TP53_0196_0205.chr17.7578235.T>C	TP53	0.002	NA	
			NA	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	
			NA	NA	
0.002	TP53_172A.chr17.7578403.C>T	TP53	0.004	NA	
			NA	NA	
0.000	TP53_172A.chr17.7578407.G>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.003	NA	
			NA	NA	
0.000	CDKN2A_7_88.chr9.21971098.C>T	CDKN2A	0.001	NA	
			NA	NA	
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA	
			NA	NA	
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.004	NA	
			NA	NA	
0.006	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.011	NA	
			NA	NA	
0.002	TP53_0272_0283.chr17.7577093.C>T	TP53	0.004	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	NA	
			NA	NA	
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	
			NA	NA	
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.005	NA	
			NA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577568.C>T	TP53	0.002	NA	
			NA	NA	
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	
			NA	NA	
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.001	NA	
			NA	NA	
0.001	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.002	NA	
			NA	NA	

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0.000	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.001	NA	NA
0.001	TP53_0227_0236.chr17.7577571.A>T	TP53	0.001	NA	NA
0.001	PTEN_130.chr10.89692905.G>A	PTEN	0.001	NA	NA
0.000	PTEN_130.chr10.89692905.G>A	PTEN	0.001	NA	NA
0.000	TP53_122.chr17.7579313.G>A	TP53	0.001	NA	NA
0.000	TP53_0227_0236.chr17.7577604.C>A	TP53	0.001	NA	NA
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	NA
0.001	TP53_342.chr17.7574018.G>A	TP53	0.001	NA	NA
0.004	TP53_167_177.chr17.7578403.C>T	TP53	0.007	NA	NA
0.007	TP53_172A.chr17.7578403.C>T	TP53	0.014	NA	NA
0.029	TP53_233_245.chr17.7577559.G>A	TP53	0.057	NA	NA
0.034	TP53_233_245.chr17.7577559.G>A	TP53	0.068	NA	NA
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	NA	NA
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	NA
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	NA	NA
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.007	NA	NA
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.005	NA	NA
0.000	TP53_172A.chr17.7578407.G>A	TP53	0.001	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.004	NA	NA
0.001	TP53_098_109.chr17.7579358.C>G	TP53	0.002	NA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.001	NA	NA
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.002	NA	NA

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0.001	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.003	NA	NA
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	NA	NA
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005	NA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.000	TP53_172A.chr17.7578407.G>A	TP53	0.001	NA	NA
0.001	TP53_132_142.chr17.7578524.G>C	TP53	0.001	NA	NA
0.001	TP53_0272_0283.chr17.7577117.A>G	TP53	0.002	NA	NA
0.040	TP53_0280_0289.chr17.7577096.T>C	TP53	0.080	NA	NA
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.003	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA	NA
0.006	TP53_342.chr17.7574021.C>A	TP53	0.013	NA	NA
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003	NA	NA
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	NA
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA	NA
0.003	TP53_0280_0289.chr17.7577094.G>A	TP53	0.005	NA	NA
0.000	PTEN_91_98.chr10.89692803.C>T	PTEN	0.001	NA	NA
0.001	TP53_132_142.chr17.7578513.C>A	TP53	0.002	NA	NA
0.002	TP53_151_163.chr17.7578461.C>T	TP53	0.003	NA	NA
0.133	GNAS_201.chr20.57484421.G>A	GNAS	0.266	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.003	NA	NA
0.012	GNAS_201.chr20.57484421.G>A	GNAS	0.025	NA	NA

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0.001	TP53_172A.chr17.7578407.G>A	TP53	0.002	NA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA	NA
0.003	TP53_167_177.chr17.7578406.C>T	TP53	0.005	NA	NA
0.001	TP53_151_163.chr17.7578457.C>T	TP53	0.001	NA	NA
0.002	TP53_233_245.chr17.7577580.T>C	TP53	0.004	NA	NA
0.002	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA	NA
0.002	TP53_0280_0289.chr17.7577070.G>A	TP53	0.004	NA	NA
0.005	TP53_113_125.chr17.7579313.G>A	TP53	0.010	NA	NA
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	NA	NA
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	NA
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.003	NA	NA
0.018	TP53_188_195.chr17.7578266.T>A	TP53	0.036	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA

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	NA	NA		NA		NA	
NA					NA		NA
	NA	NA		NA		NA	
NA					NA		NA
	NA	NA		NA		NA	
NA					NA		NA
	0.004	KRAS_012_+13_-4.chr12.25398284.C>A		KRAS		0.008	
NA					NA		NA
	0.004	KRAS_012_+13_-4.chr12.25398284.C>A		KRAS		0.008	
NA					NA		NA
	0.001	KRAS_012_+13_-4.chr12.25398284.C>T		KRAS		0.002	
NA					NA		NA
	0.002	KRAS_012_+13_-4.chr12.25398284.C>T		KRAS		0.004	
NA					NA		NA
	0.001	TP53_0272_0283.chr17.7577124.C>T		TP53		0.002	
NA					NA		NA
	0.001	PTEN_91_98.chr10.89692802.C>G		PTEN		0.002	
NA					NA		NA
	0.001	CTNNB1_0032_0039.chr3.41266104.G>A		CTNNB1		0.002	
NA					NA		NA
	0.001	TP53_342.chr17.7574003.G>A		TP53		0.002	
NA					NA		NA
	0.001	CDKN2A_051_057.chr9.21971186.G>A		CDKN2A		0.001	
NA					NA		NA
	0.002	TP53_167_177.chr17.7578406.C>T		TP53		0.004	
NA					NA		NA
	0.001	PTEN_91_98.chr10.89692802.C>G		PTEN		0.003	
NA					NA		NA
	0.001	TP53_208_218.chr17.7578211.C>T		TP53		0.002	
NA					NA		NA
	0.007	TP53_167_177.chr17.7578406.C>T		TP53		0.013	
NA					NA		NA
	0.001	TP53_167_177.chr17.7578406.C>T		TP53		0.001	
NA					NA		NA
	0.001	TP53_208_218.chr17.7578211.C>T		TP53		0.003	
NA					NA		NA
	0.001	TP53_208_218.chr17.7578212.G>A		TP53		0.001	
NA					NA		NA
	0.000	TP53_167_177.chr17.7578407.G>A		TP53		0.001	
NA					NA		NA
	0.001	PPP2R1A_176_187.chr19.52715979.C>T		PPP2R1A		0.001	
NA					NA		NA
	0.002	TP53_208_218.chr17.7578208.T>C		TP53		0.004	
NA					NA		NA
	0.000	TP53_132_142.chr17.7578518.C>T		TP53		0.001	
NA					NA		NA

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0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.002	NA	NA
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA	NA
0.004	GNAS_201.chr20.57484421.G>A	GNAS	0.007	NA	NA
0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.003	NA	NA
0.003	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.005	NA	NA
0.004	TP53_219_224.chr17.7578190.T>C	TP53	0.008	NA	NA
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA	NA
0.001	TP53_083_94.chr17.7579414.C>T	TP53	0.002	NA	NA
0.002	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.002	NA	NA
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	NA
0.001	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.001	NA	NA
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA	NA
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	NA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA	NA
0.000	TP53_098_109.chr17.7579378.G>C	TP53	0.001	NA	NA
0.002	FBXW7_505.chr4.153247288.C>T	FBXW7	0.003	NA	NA
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	NA	NA
0.005	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.010	NA	NA
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.001	TP53_0272_0283.chr17.7577103.C>T	TP53	0.002	NA	NA
0.002	TP53_0248_0261.chr17.7577539.G>A	TP53	0.004	NA	NA

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0.012	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.025	NA	NA
0.001	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	NA	NA
0.002	TP53_0272_0283.chr17.7577114.C>T	TP53	0.005	NA	NA
0.002	FBXW7_505.chr4.153247289.G>A	FBXW7	0.004	NA	NA
0.001	TP53_026.chr17.7579717.G>A	TP53	0.002	NA	NA
0.002	TP53_122.chr17.7579313.G>A	TP53	0.003	NA	NA
0.002	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.004	NA	NA
0.001	TP53_219_224.chr17.7578190.T>C	TP53	0.002	NA	NA
0.001	APC_1450_1458.chr5.112175639.C>T	APC	0.002	NA	NA
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA	NA
0.000	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	NA	NA
0.003	TP53_167_177.chr17.7578407.G>A	TP53	0.006	NA	NA
0.002	TP53_208_218.chr17.7578212.G>A	TP53	0.004	NA	NA
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	NA	NA
0.004	TP53_0227_0236.chr17.7577580.T>C	TP53	0.007	NA	NA
0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.002	NA	NA
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	NA	NA
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.000	TP53_122.chr17.7579315.G>T	TP53	0.001	NA	NA
0.000	TP53_0272_0283.chr17.7577111.G>A	TP53	0.001	NA	NA
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA	NA
0.001	TP53_122.chr17.7579315.G>T	TP53	0.001	NA	NA

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0.487	CDKN2A_051_057.chr9.21971188.G>A	CDKN2A	0.974	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	NA	
			NA	NA	
0.001	TP53_0227_0236.chr17.7577586.A>T	TP53	0.002	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.002	NA	
			NA	NA	
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.002	NA	
			NA	NA	
0.001	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.003	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.006	NA	
			NA	NA	
0.003	TP53_233_245.chr17.7577581.A>G	TP53	0.006	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577106.G>T	TP53	0.002	NA	
			NA	NA	
0.158	TP53_233_245.chr17.7577568.C>T	TP53	0.317	NA	
			NA	NA	
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.017	NA	
			NA	NA	
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	Squamous cell carcinoma	
			IIB	NA	
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	Adenocarcinoma	
			IIA	NA	
0.001	APC_1450_1458.chr5.112175639.C>T	APC	0.002	Adenocarcinoma	
			IIIA	NA	
0.001	PTEN_130.chr10.89692907.A>G	PTEN	0.002	Squamous cell carcinoma	
			IA	NA	
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.002	Adenocarcinoma	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.002	neuro-endocrine carcinoma	
			IV	NA	
0.001	TP53_098_109.chr17.7579377.G>A	TP53	0.002	Adenocarcinoma	
			IIA	NA	
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001	Squamous cell carcinoma	
			IIIB	NA	
0.017	FBXW7_474_482.chr4.153247367.G>C	FBXW7	0.034	Squamous cell carcinoma	
			IIA	NA	
0.013	TP53_167_177.chr17.7578403.C>A	TP53	0.025	Adenocarcinoma	
			IIB	NA	
0.003	TP53_0272_0283.chr17.7577121.G>A	TP53	0.006	Squamous cell carcinoma	
			IB	NA	
0.001	PTEN_136.chr10.89692925.G>A	PTEN	0.001	Squamous cell carcinoma	
			IB	NA	

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0.001	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.003		
Squamous cell carcinoma			IIIA	NA	
0.001	TP53_188_195.chr17.7578265.A>G	TP53	0.001		
Adenocarcinoma			IIA	NA	
0.014	TP53_298_306.chr17.7577046.C>A	TP53	0.027		
Adenocarcinoma			IB	NA	
0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.001		
Adenocarcinoma			IIIA	NA	
0.002	TP53_0248_0261.chr17.7577535.C>A	TP53	0.003		
Squamous cell carcinoma			IB	NA	
0.001	TP53_098_109.chr17.7579368.A>C	TP53	0.002		
Adenocarcinoma			IIIB	NA	
0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.001		
neuro-endocrine carcinoma			IIIA	NA	
0.006	TP53_151_163.chr17.7578457.C>A	TP53	0.011		
pleomorh carcinoma			IV	NA	
0.002	TP53_151_163.chr17.7578469.C>A	TP53	0.004		
Squamous cell carcinoma			IV	NA	
0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.002		
pleomorh carcinoma			IIIA	NA	
0.001	PIK3CA_1039_1050.chr3.178952082.C>T	PIK3CA	0.002		
Squamous cell carcinoma			IIB	NA	
0.009	TP53_262_267.chr17.7577141.C>A	TP53	0.018		
Adenocarcinoma			NA	NA	
0.001	TP53_041_052.chr17.7579542.C>T	TP53	0.002		
adenosquam□ses Karzinom			IB	NA	
0.002	TP53_151_163.chr17.7578479.G>C	TP53	0.003		
Adenocarcinoma			IB	NA	
0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.002		
squamous cell carcinoma			IB	NA	
0.002	TP53_0272_0283.chr17.7577121.G>A	TP53	0.003		
non-keratinizing squamous cell carcinoma			IIIA	NA	
0.007	TP53_0248_0261.chr17.7577539.G>A	TP53	0.014		
Squamous cell carcinoma			IIA	NA	
0.001	TP53_151_163.chr17.7578449.C>A	TP53	0.003		
Adenocarcinoma			IIIA	NA	
0.094	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.189		
carcinoid tumor			IA	NA	
0.001	TP53_233_245.chr17.7577581.A>G	TP53	0.002		
adenosquamous carcinoma			IIIA	NA	
0.001	TP53_0272_0283.chr17.7577094.G>C	TP53	0.002		
Adenocarcinoma			IV	NA	
0.002	TP53_208_218.chr17.7578208.T>C	TP53	0.004		
mucinous adenocarcinoma			IIB	NA	
0.004	TP53_0272_0283.chr17.7577099.C>T	TP53	0.009		
Adenocarcinoma			IA	NA	
0.003	TP53_208_218.chr17.7578203.C>T	TP53	0.005		
squamous cell carcinoma			IIB	NA	

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0.000	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	adenocarcinoma - mixed type	
			IIIA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	adenocarcinoma - mixed type	
			IIIA	NA	
0.001	FBXW7_361_371.chr4.153251907.G>A	FBXW7	0.003	squamous cell carcinoma	
			IA	NA	
0.000	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	Squamous cell carcinoma	
			IIIA	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	squamous cell carcinoma	
			IB	NA	
0.003	TP53_262_267.chr17.7577142.C>A	TP53	0.006	adenocarcinoma - mixed type	
			IB	NA	
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	adenocarcinoma - mixed type	
			IIA	NA	
0.013	TP53_342.chr17.7574012.C>A	TP53	0.026	Adenocarcinoma	
			IIIB	NA	
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.001	Adenocarcinoma	
			IB	NA	
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	Adenosquamous carcinoma	
			IIIB	NA	
0.002	TP53_122.chr17.7579315.G>T	TP53	0.004	adenocarcinoma	
			IA	NA	
0.001	TP53_188_195.chr17.7578268.A>T	TP53	0.002	adenocarcinoma	
			IA	NA	
0.001	FBXW7_361_371.chr4.153251907.G>A	FBXW7	0.003	adenocarcinoma	
			IB	NA	
0.000	PIK3CA_0345.chr3.178921546.A>G	PIK3CA	0.001	squamous cell carcinoma	
			IIA	NA	
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.002	adenocarcinoma	
			NA	NA	
0.014	GNAS_201.chr20.57484420.C>T	GNAS	0.028	squamous cell carcinoma	
			IA	NA	
0.004	TP53_342.chr17.7574026.C>A	TP53	0.007	adenocarcinoma	
			IA	NA	
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	squamous cell carcinoma	
			IB	NA	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	adenocarcinoma	
			IIIA	NA	
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.002	adenocarcinoma	
			IB	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	squamous cell carcinoma	
			IIIA	NA	
0.003	KRAS_012_+13_-4.chr12.25398282.C>A	KRAS	0.006	neuroendocrine and small cell carcinoma	
			IIA	NA	
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.004	adenocarcinoma	
			IB	NA	
0.001	PIK3CA_0345.chr3.178921548.G>A	PIK3CA	0.002	squamous cell carcinoma	
			IB	NA	

Table36.txt

0.001	TP53_0227_0236.chr17.7577604.C>T	TP53	0.001		
NA			IIa	G3	
0.003	TP53_188_195.chr17.7578268.A>C	TP53	0.006		
NA			IIa	G3	
0.006	TP53_0272_0283.chr17.7577120.C>T	TP53	0.012		
NA			IA	G1	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
NA			IA	G3	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
NA			NA	NA	
NA	NA	NA	NA		
NA			NA	NA	
NA	NA	NA	NA		
Hepatocellular Carcinoma, Acinar Type			II	NA	
0.046	TP53_132_142.chr17.7578535.T>C	TP53	0.092		
Hepatocellular Carcinoma, Solid Type			II	NA	
0.000	NRAS_4_14.chr1.115258744.C>A	NRAS	0.001		
Hepatocellular Carcinoma, Pleomorphic Type			II	NA	
0.001	TP53_167_177.chr17.7578403.C>A	TP53	0.002		
Hepatocellular Carcinoma			NA	NA	
0.001	TP53_0272_0283.chr17.7577121.G>A	TP53	0.002		
Adenocarcinoma			IIB	NA	
0.002	TP53_053.chr17.7579529.C>T	TP53	0.005		
Hepatocellular carcinoma, Trabecular			II	NA	
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.000		
Tubulo-papillary Adenocarcinoma			II	NA	
0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001		
Low Grade Gastro-Intestinal Stromal Tumor, (GIST), Spindle Cell			IB	NA	
0.000	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001		
Diffuse Poorly Differentiated Adenocarcinoma with Signet Ring C			II	NA	
0.005	TP53_219_224.chr17.7578190.T>C	TP53	0.009		
Mucinous Adenocarcinoma			II	NA	
0.000	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.000		
Cholangiocarcinoma			IV	NA	
0.000	TP53_298_306.chr17.7577022.G>A	TP53	0.001		
Adenocarcinoma, diffuse type			II	NA	
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001		
Adenocarcinoma, diffuse type			II	NA	
0.000	PTEN_136.chr10.89692941.G>A	PTEN	0.001		
Adenocarcinoma, intestinal type			IIIA	NA	
0.000	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001		
Adenocarcinoma, diffuse type			II	NA	
0.032	TP53_0248_0261.chr17.7577538.C>T	TP53	0.064		
Adenocarcinoma, intestinal type			IB	NA	
0.000	TP53_298_306.chr17.7577022.G>A	TP53	0.001		
Signet ring cell adenocarcinoma			II	NA	
0.000	TP53_298_306.chr17.7577022.G>A	TP53	0.001		
Hepatocellular carcinoma, clear cell type			IIIA	NA	

Table36.txt

0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	Hepatocellular carcinoma, Trabecular	IIIA NA
0.002	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.003	Hepatocellular carcinoma, pleomorphic type	IIIA NA
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	Hepatocellular Carcinoma, Trabecular Type	IIIA NA
0.000	CTNNB1_0039_0046.chr3.41266137.C>T	CTNNB1	0.001	Hepatocellular Carcinoma, Trabecular Type	II NA
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	Mucinous Adenocarcinoma	IIA NA
0.002	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.004	Hepatocellular Carcinoma	II NA
0.004	TP53_0196_0205.chr17.7578263.G>A	TP53	0.009	Hepatocellular Carcinoma, Solid Type	IIIA NA
0.005	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.010	hepatocellular carcinoma	II NA
0.010	TP53_0248_0261.chr17.7577534.C>A	TP53	0.019	hepatocellular carcinoma	NA NA
0.004	FBXW7_505.chr4.153247289.G>A	FBXW7	0.008	cholangiocarcinoma	IVB NA
0.087	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.174	Adenocarcinoma, NOS	II NA
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.004	Adenocarcinoma, NOS	IIB NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	Adenocarcinoma, NOS	I NA
0.001	BRAF_594_602.chr7.140453139.G>A	BRAF	0.001	Adenocarcinoma, NOS	I NA
0.000	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.000	Adenocarcinoma, NOS	I NA
0.001	TP53_233_245.chr17.7577556.C>T	TP53	0.002	Mucinous adenocarcinoma	I NA
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.001	Adenocarcinoma, NOS	I NA
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	Adenocarcinoma, NOS	IIB NA
0.123	APC_1450_1458.chr5.112175639.C>T	APC	0.246	Adenocarcinoma, NOS	IIIB NA
0.462	TP53_172A.chr17.7578406.C>T	TP53	0.924	Adenocarcinoma, NOS	IIIB NA
0.000	TP53_233_245.chr17.7577548.C>T	TP53	0.000	Hepatocellular carcinoma, Trabecular	II NA
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	Mucinous adenocarcinoma (8480/3)	IIA NA
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.000	Adenocarcinoma, NOS	IIA NA
0.007	PIK3CA_0542_0551.chr3.178936092.A>C	PIK3CA	0.014	Adenocarcinoma, NOS	III NA

Table36.txt

0.000	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001		
Adenocarcinoma, NOS			I	NA	
0.000	TP53_122.chr17.7579312.C>T	TP53	0.001		
cholangiocarcinoma			II	NA	
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.003		
hepatocellular carcinoma			NA	NA	
0.003	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.006		
hepatocellular carcinoma			I	NA	
0.003	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.007		
hepatocellular carcinoma			NA	NA	
0.005	TP53_188_195.chr17.7578265.A>G	TP53	0.010		
cholangiocarcinoma			II	NA	
0.002	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.005		
hepatocellular carcinoma			NA	NA	
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001		
hepatocellular carcinoma			NA	NA	
0.044	CTNNB1_0032_0039.chr3.41266097.G>T	CTNNB1	0.087		
hepatocellular carcinoma			NA	NA	
0.001	TP53_323.chr17.7576853.C>A	TP53	0.001		
Adenocarcinoma			I	NA	
0.006	TP53_113_125.chr17.7579329.T>C	TP53	0.013		
Papillary adenocarcinoma			I	NA	
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001		
Adenocarcinoma, NOS			IIB	NA	
0.125	TP53_151_163.chr17.7578449.C>T	TP53	0.249		
Tubular adenocarcinoma			IIB	NA	
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001		
Adenocarcinoma			IIB	NA	
0.000	TP53_172A.chr17.7578403.C>T	TP53	0.001		
Adenocarcinoma			IIB	NA	
0.000	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001		
Adenocarcinoma			IIB	NA	
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001		
Adenocarcinoma			IIIB	NA	
0.000	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001		
Adenocarcinoma			IIA	NA	
0.000	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001		
Adenocarcinoma			IVA	NA	
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001		
Tubular adenocarcinoma			IIA	NA	
0.037	TP53_0272_0283.chr17.7577117.A>C	TP53	0.075		
Adenocarcinoma			IVA	NA	
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.001		
Papillary adenocarcinoma			IIB	NA	
0.000	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001		
Adenocarcinoma			IIB	NA	
0.001	TP53_208_218.chr17.7578208.T>C	TP53	0.002		
Adenocarcinoma			IVA	NA	

Table36.txt

0.007	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.014		
Mucinous carcinoma			IIIB	NA	
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001		
Adenocarcinoma			I	NA	
0.000	TP53_113_125.chr17.7579313.G>A	TP53	0.001		
Adenocarcinoma			IIA	NA	
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.002		
Mucinous carcinoma			IIIA	NA	
0.010	TP53_0196_0205.chr17.7578263.G>A	TP53	0.020		
Keratinizing Squamous Cell Carcinoma			II	NA	
0.001	TP53_233_245.chr17.7577578.T>C	TP53	0.003		
Adenocarcinoma			II	NA	
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001		
Keratinizing Squamous Cell Carcinoma			II	NA	
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.003		
Keratinizing Squamous Cell Carcinoma			IIB	NA	
0.478	TP53_026.chr17.7579705.C>T	TP53	0.955		
Adenocarcinoma			II	NA	
0.002	TP53_233_245.chr17.7577581.A>T	TP53	0.004		
Adenocarcinoma			IIA	NA	
0.000	TP53_0248_0261.chr17.7577498.C>A	TP53	0.001		
Adenocarcinoma			III A	NA	
0.003	TP53_167_177.chr17.7578416.C>A	TP53	0.007		
Adenocarcinoma			II A	NA	
0.023	TP53_0272_0283.chr17.7577121.G>A	TP53	0.047		
Hepato-Cholangiocarcinoma			III A	NA	
0.004	TP53_126_131.chr17.7578536.T>A	TP53	0.008		
Papillary Adenocarcinoma			II A	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006		
Adenocarcinoma			II A	NA	
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001		
Adenocarcinoma			II A	NA	
0.000	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001		
Adenocarcinoma			III A	NA	
0.003	TP53_098_109.chr17.7579389.G>A	TP53	0.006		
Papillary Adenocarcinoma			II A	NA	
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001		
Hepatocellular Carcinoma, Solid Type			III A	NA	
0.001	PTEN_91_98.chr10.89692791.A>G	PTEN	0.001		
Adenocarcinoma			III A	NA	
0.000	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001		
Cholangiocarcinoma			IV	NA	
0.002	TP53_233_245.chr17.7577578.T>C	TP53	0.004		
Hepatocellular Carcinoma			II	NA	
0.002	TP53_262_267.chr17.7577144.A>G	TP53	0.004		
Adenocarcinoma			II A	NA	
0.001	TP53_298_306.chr17.7577022.G>A	TP53	0.001		
hepatocellular carcinoma			NA	NA	

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0.000	TP53_151_163.chr17.7578458.G>A	TP53	0.001	neuroendocrine carcinoma	IIA NA
0.030	TP53_098_109.chr17.7579373.C>G	TP53	0.060	adenocarcinoma	IA NA
0.001	FBXW7_505.chr4.153247289.G>A	FBXW7	0.001	adenocarcinoma	IIB NA
0.001	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	squamous cell carcinoma	IIIA NA
0.005	TP53_0196_0205.chr17.7578263.G>A	TP53	0.009	adenoid-cystic carcinoma	IIIA NA
0.000	TP53_151_163.chr17.7578464.G>A	TP53	0.001	large cell neuroendocrine carcinoma	IIA NA
0.060	TP53_233_245.chr17.7577568.C>A	TP53	0.121	cholangiocarcinoma	NA NA
0.032	TP53_0227_0236.chr17.7577574.T>C	TP53	0.064	Adenocarcinoma	I NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	Adenocarcinoma	I NA
0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.002	Adenocarcinoma	I NA
0.000	TP53_113_125.chr17.7579337.C>T	TP53	0.001	Adenocarcinoma	I NA
0.001	TP53_0196_0205.chr17.7578263.G>A	TP53	0.001	Adenocarcinoma	I NA
0.001	PTEN_130.chr10.89692893.C>A	PTEN	0.002	Adenocarcinoma	II B NA
0.026	TP53_172A.chr17.7578406.C>T	TP53	0.053	Adenocarcinoma	II B NA
0.001	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.002	Papillary Adenocarcinoma	II B NA
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.002	Papillary Adenocarcinoma	I NA
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	Adenocarcinoma	III B NA
0.002	TP53_233_245.chr17.7577548.C>T	TP53	0.003	Adenocarcinoma	I NA
0.024	TP53_151_163.chr17.7578479.G>A	TP53	0.048	Adenocarcinoma	IV NA
0.291	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.583	Adenocarcinoma	II A NA
0.034	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.068	Mucinous Adenocarcinoma	II A NA
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	Mucinous Adenocarcinoma	II A NA
0.000	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	Adenocarcinoma	II A NA
0.001	FBXW7_474_482.chr4.153247384.C>A	FBXW7	0.001	Clear Cell Hepatocellular Carcinoma	III A NA

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0.003	TP53_233_245.chr17.7577578.T>C	TP53	0.005		
Adenocarcinoma			II A	NA	
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.001		
Adenocarcinoma			IV	NA	
0.003	TP53_0272_0283.chr17.7577117.A>T	TP53	0.007		
Adenocarcinoma with Signet Ring Cell			II A	NA	
0.001	TP53_233_245.chr17.7577556.C>T	TP53	0.002		
Adenocarcinoma			III A	NA	
0.000	TP53_151_163.chr17.7578461.C>T	TP53	0.001		
Adnocarcinoma with Mucinous Production			II A	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001		
Infiltrating Ductal Carcinoma, NOS			II A	NA	
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002		
Adenocarcinoma			II A	NA	
0.016	GNAS_201.chr20.57484421.G>A	GNAS	0.033		
Poorly Differentiated Adenocarcinoma with Signet Ring Cells			II A	NA	
0.004	TP53_0196_0205.chr17.7578239.C>A	TP53	0.007		
Adenocarcinoma with Mucin Production			II A	NA	
0.000	TP53_298_306.chr17.7577022.G>A	TP53	0.001		
Adenocarcinoma			II B	NA	
0.000	TP53_167_177.chr17.7578407.G>A	TP53	0.001		
Adenocarcinoma			II B	NA	
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001		
Adenocarcinoma			II B	NA	
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001		
Adenocarcinoma			II B	NA	
0.000	TP53_233_245.chr17.7577581.A>G	TP53	0.001		
Adenocarcinoma			II A	NA	
0.001	NRAS_4_14.chr1.115258747.C>T	NRAS	0.002		
Adenocarcinoma			II A	NA	
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001		
Signet ring cell adenocarcinoma			NA	COAD;COADREAD	
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.002		
mucinous adenocarcinoma			NA	COAD;COADREAD	
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001		
NA			IIA	COAD;COADREAD	
0.001	PTEN_91_98.chr10.89692794.A>G	PTEN	0.002		
Adenocarcinoma			NA	COAD;COADREAD	
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.003		
Hepatocellular carcinoma, pleomorphic type			0	NA	
0.002	TP53_262_267.chr17.7577144.A>G	TP53	0.005		
Hepatocellular Carcinoma			III A	NA	
0.045	CTNNB1_0039_0046.chr3.41266124.A>G	CTNNB1	0.091		
Hepatocellular Carcinoma, Adenoid Type			II	NA	
0.002	TP53_151_163.chr17.7578457.C>A	TP53	0.004		
Hepatocellular carcinoma, Trabecular Type			III A	NA	
0.079	TP53_0248_0261.chr17.7577534.C>A	TP53	0.157		
Solid Predominant with Mucin Production Adenocarcinoma			I B	NA	

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0.000	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	Micropapillary Predominant Adenocarcinoma	II B	NA
0.002	TP53_126_131.chr17.7578553.T>C	TP53	0.004	Cholangiocarcinoma	III A	NA
0.001	TP53_0280_0289.chr17.7577097.C>A	TP53	0.001	Hepatocellular Carcinoma	III A	NA
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	adenocarcinoma	IB	NA
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002	adenocarcinoma with acinar type	IA	NA
0.001	PIK3CA_0542_0551.chr3.178936092.A>C	PIK3CA	0.001	carcinoid tumor	IA	NA
0.001	BRAF_594_602.chr7.140453134.T>C	BRAF	0.002	adenocarcinoma	IIA	NA
0.001	TP53_0272_0283.chr17.7577106.G>T	TP53	0.001	hepatocellular carcinoma	III A	NA
0.000	TP53_208_218.chr17.7578211.C>T	TP53	0.001	adenocarcinoma	III A	NA
0.052	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.104	squamous cell carcinoma	III A	NA
0.000	TP53_151_163.chr17.7578454.G>A	TP53	0.001	non-keratinizing squamous cell carcinoma	IB	NA
0.000	KRAS_0057_0064.chr12.25380275.T>G	KRAS	0.001	NA	IIIA	G3
0.223	TP53_188_195.chr17.7578272.G>A	TP53	0.446	NA	IA	G3
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	NA	IIA	G3
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.008	adenocarcinoma	III A	NA
0.002	TP53_0280_0289.chr17.7577082.C>A	TP53	0.004	NA	NA	NA
0.001	CDKN2A_7_88.chr9.21971120.G>A	CDKN2A	0.003	Hepatocellular carcinoma, Trabecular	IIIA	NA
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	Hepatocellular carcinoma, Solid Type	II	NA
0.000	TP53_0196_0205.chr17.7578263.G>A	TP53	0.001	Hepatocellular carcinoma, Solid Type	II	NA
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	Hepatocellular carcinoma, Trabecular	II	NA
0.001	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.002	Papillary adenocarcinoma	IIA	NA
0.001	TP53_208_218.chr17.7578204.A>C	TP53	0.002	Hepatocellular carcinoma	IIIA	NA
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	Tubular adenocarcinoma	IIA	NA
0.002	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.004	Adenocarcinoma	IIA	NA

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0.001	TP53_208_218.chr17.7578204.A>T	TP53	0.002	Mucinous adenocarcinoma	
		IIA	NA		
0.002	TP53_233_245.chr17.7577580.T>C	TP53	0.005	Adenocarcinoma	
		IIA	NA		
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	Hepatocellular carcinoma, Acinar Type	
		II	NA		
0.000	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	Hepatocellular carcinoma	
		IIIA	NA		
0.000	TP53_0280_0289.chr17.7577097.C>A	TP53	0.001	Hepatocellular carcinoma, Trabecular	
		IIIA	NA		
0.001	KRAS_144_147A.chr12.25378561.G>A	KRAS	0.001	Hepatocellular carcinoma	
		NA	NA		
0.001	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.001	Adenocarcinoma	
		NA	NA		
0.011	TP53_0272_0283.chr17.7577099.C>T	TP53	0.023	carcinoma	
		IIIC	NA		
0.085	TP53_219_224.chr17.7578190.T>C	TP53	0.169	Adenocarcinoma	
		IIIC	NA		
0.007	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.013	Adenocarcinoma	
		IIIB	NA		
0.012	KRAS_0057_0064.chr12.25380277.G>T	KRAS	0.024	Adenocarcinoma	
		IIA	NA		
0.002	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.004	Adenocarcinoma	
		IIA	NA		
0.003	TP53_0280_0289.chr17.7577082.C>T	TP53	0.006	Adenocarcinoma	
		IIIB	NA		
0.040	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.080	Adenocarcinoma	
		I	NA		
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	Adenocarcinoma	
		IVB	NA		
0.513	TP53_0280_0289.chr17.7577097.C>T	TP53	0.513	Adenocarcinoma	
		IIIA	NA		
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	ovarian carcinoma - serous type	
		IIIC	NA		
0.118	TP53_0272_0283.chr17.7577120.C>T	TP53	0.235	mucinous adenocarcinoma	
		IIA	NA		
0.000	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	Adenocarcinoma	
		I	NA		
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	Adenocarcinoma	
		IIC	NA		
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	adenocarcinoma	
		IIB	NA		
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	ovarian carcinoma - serous papillary type	
		IV	NA		
0.241	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.483	ovarian carcinoma - serous papillary type	
		IA	NA		
0.001	TP53_188_195.chr17.7578280.G>A	TP53	0.002	mucinous adenocarcinoma	
		IIB	NA		

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0.004	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.008	squamous cell carcinoma	
			IIA	NA	
0.004	TP53_0272_0283.chr17.7577124.C>A	TP53	0.008	squamous cell carcinoma	
			IB	NA	
0.001	PTEN_136.chr10.89692941.G>A	PTEN	0.001	adenocarcinoma with acinar type	
			IA	NA	
0.001	TP53_262_267.chr17.7577138.C>T	TP53	0.002	adenocarcinoma	
			IV	NA	
0.002	TP53_262_267.chr17.7577139.G>A	TP53	0.003	ductal adenocarcinoma	
			IV	NA	
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	keratinizing squamous cell carcinoma	
			III A	NA	
0.003	TP53_0272_0283.chr17.7577106.G>T	TP53	0.007	ductal adenocarcinoma	
			IIB	NA	
0.000	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	ductal adenocarcinoma	
			III	NA	
0.000	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	ductal carcinoma	
			IIA	NA	
0.001	PPP2R1A_176_187.chr19.52715986.C>T	PPP2R1A	0.001	Adenocarcinoma	
			IIB	NA	
0.000	TP53_167_177.chr17.7578406.C>T	TP53	0.001	Adenocarcinoma	
			IV	NA	
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.013	Squamous cell carcinoma	
			NA	NA	
0.022	TP53_342.chr17.7574017.C>A	TP53	0.044	ductal carcinoma	
			IA	NA	
0.002	PIK3CA_1039_1050.chr3.178952077.T>G	PIK3CA	0.003	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
NA	NA	NA	NA	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	NA	
			NA	NA	
0.001	TP53_026.chr17.7579705.C>T	TP53	0.003	NA	
			NA	NA	
0.000	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	NA	
			NA	NA	
0.002	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.004	NA	
			NA	NA	

Table36.txt

	0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.002	
NA			NA	NA	
	0.001	TP53_132_142.chr17.7578524.G>C	TP53	0.002	
NA			NA	NA	
	0.001	TP53_0280_0289.chr17.7577102.C>T	TP53	0.001	
NA			NA	NA	
	0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.001	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.002	
NA			NA	NA	
	0.000	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	
NA			NA	NA	
	0.002	PIK3CA_0542_0551.chr3.178936093.G>T	PIK3CA	0.003	
NA			NA	NA	
	0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.002	
NA			NA	NA	
	0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	
NA			NA	NA	
	0.001	TP53_172A.chr17.7578389.G>A	TP53	0.003	
NA			NA	NA	
	0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	
NA			NA	NA	
	0.001	FBXW7_505.chr4.153247289.G>A	FBXW7	0.002	
NA			NA	NA	
	0.001	TP53_172A.chr17.7578374.C>T	TP53	0.002	
NA			NA	NA	
	0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	
NA			NA	NA	
	0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	
NA			NA	NA	
	0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.002	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	
	NA	NA	NA	NA	
NA			NA	NA	

	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	0.002	TP53_172A.chr17.7578406.C>T			TP53		0.004		
NA						NA		NA	
	0.001	TP53_0272_0283.chr17.7577120.C>T			TP53		0.002		
NA						NA		NA	
	NA	NA			NA		NA

Table36.txt

NA NA NA NA
NA NA NA
NA NA NA NA
NA NA NA
NA NA NA NA
NA NA NA

Table36.txt

	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
NA						NA	NA	
	NA	NA			NA		NA	
Mixed cell adenocarcinoma						NA	NA	
	0.001	TP53_219_224.chr17.7578191.A>G			TP53		0.002	
Adenocarcinoma						IIA	NA	
	0.011	APC_1450_1458.chr5.112175639.C>T			APC		0.023	
adenocarcinoma						IIIA	NA	
	0.109	KRAS_012_+13_-4.chr12.25398285.C>A			KRAS		0.218	
squamous cell carcinoma						IIB	NA	
	0.020	TP53_0248_0261.chr17.7577539.G>A			TP53		0.039	
adenocarcinoma						IB	NA	
	0.001	TP53_026.chr17.7579705.C>T			TP53		0.002	
squamous cell carcinoma						IIIA	NA	
	0.000	PTEN_145_153.chr10.89692961.C>T			PTEN		0.001	
adenocarcinoma						IIIA	NA	
	0.002	FBXW7_474_482.chr4.153247366.C>T			FBXW7		0.005	
adenocarcinoma						IA	NA	
	0.003	TP53_172A.chr17.7578403.C>A			TP53		0.007	
large cell carcinoma						IIA	NA	
	0.002	TP53_132_142.chr17.7578534.C>A			TP53		0.005	
adenocarcinoma						IB	NA	
	0.003	GNAS_201.chr20.57484421.G>A			GNAS		0.005	
large cell carcinoma						IB	NA	
	0.006	FBXW7_474_482.chr4.153247367.G>A			FBXW7		0.012	
large cell carcinoma						IIA	NA	
	0.001	KRAS_012_+13_-4.chr12.25398285.C>A			KRAS		0.002	
carcinoma						IIB	NA	
	0.006	TP53_342.chr17.7574021.C>A			TP53		0.012	
adenocarcinoma with acinar type						IB	NA	
	0.002	TP53_233_245.chr17.7577565.T>C			TP53		0.005	
squamous cell carcinoma						IB	NA	
	0.013	TP53_126_131.chr17.7578553.T>C			TP53		0.026	
adenocarcinoma						IIIA	NA	
	0.077	KRAS_012_+13_-4.chr12.25398284.C>A			KRAS		0.155	
adenocarcinoma						IIA	NA	

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0.000	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001	squamous cell carcinoma	
		IB	NA		
0.001	TP53_233_245.chr17.7577548.C>T	TP53	0.002	squamous cell carcinoma	
		IIIA	NA		
0.020	PIK3CA_1039_1050.chr3.178952085.A>T	PIK3CA	0.041	squamous cell carcinoma	
		IIIB	NA		
0.001	TP53_0196_0205.chr17.7578235.T>C	TP53	0.003	adenocarcinoma	
		IIIA	NA		
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.005	squamous cell carcinoma	
		IB	NA		
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	squamous cell carcinoma	
		IIA	NA		
0.001	PIK3CA_0542_0551.chr3.178936082.G>A	PIK3CA	0.002	squamous cell carcinoma	
		IB	NA		
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.002	squamous cell carcinoma	
		IIIA	NA		
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	adenocarcinoma	
		IB	NA		
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	Adenocarcinoma	
		II A	NA		
0.004	TP53_172A.chr17.7578403.C>T	TP53	0.008	Adenocarcinoma	
		II A	NA		
0.005	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.009	Adenocarcinoma	
		II B	NA		
0.007	TP53_132_142.chr17.7578508.C>T	TP53	0.013	Adenocarcinoma	
		II B	NA		
0.003	TP53_233_245.chr17.7577548.C>T	TP53	0.006	Papillary Adenocarcinoma	
		I A	NA		
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	Mucin-producing adenocarcinoma	
		IIIA	NA		
0.047	TP53_0248_0261.chr17.7577538.C>A	TP53	0.094	Mucinous adenocarcinoma	
		IIIB	NA		
0.292	TP53_0248_0261.chr17.7577508.T>C	TP53	0.584	Signet ring cell carcinoma	
		IIIB	NA		
0.006	TP53_208_218.chr17.7578208.T>C	TP53	0.013	Adenocarcinoma	
		IIIB	NA		
0.002	TP53_0227_0236.chr17.7577575.A>G	TP53	0.004	Adenocarcinoma	
		IIIA	NA		
0.004	TP53_0248_0261.chr17.7577538.C>A	TP53	0.007	Adenocarcinoma with Mucinous Differentiation	
		II A	NA		
0.005	PTEN_136.chr10.89692923.G>A	PTEN	0.010	Mucinous Adenocarcinoma	
		II A	NA		
0.001	TP53_298_306.chr17.7577022.G>A	TP53	0.002	Adenocarcinoma	
		II	NA		
0.020	TP53_151_163.chr17.7578457.C>T	TP53	0.040	Papillary Adenocarcinoma	
		I	NA		
0.002	TP53_113_125.chr17.7579313.G>A	TP53	0.003	Papillary Adenocarcinoma	
		II A	NA		

Table36.txt

0.030	GNAS_201.chr20.57484421.G>A	GNAS	0.060	adenocarcinoma	III B	NA
0.003	BRAF_594_602.chr7.140453145.A>C	BRAF	0.007	adenocarcinoma	IIA	NA
0.000	TP53_151_163.chr17.7578458.G>A	TP53	0.001	mucinous adenocarcinoma	III B	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	ductal carcinoma	IIA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	ductal carcinoma	IA	NA
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001	ovarian carcinoma - serous papillary type	III C	NA
0.007	TP53_208_218.chr17.7578205.C>A	TP53	0.014	adenocarcinoma	IIA	NA
0.000	TP53_122.chr17.7579313.G>A	TP53	0.001	adenocarcinoma	IIA	NA
0.001	PIK3CA_0542_0551.chr3.178936095.A>C	PIK3CA	0.002	adenocarcinoma	I	NA
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	adenocarcinoma	IVA	NA
0.000	TP53_122.chr17.7579313.G>A	TP53	0.001	adenocarcinoma	IIA	NA
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003	ductal adenocarcinoma	IIA	NA
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.001	ductal adenocarcinoma	IV	NA
0.000	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	ductal adenocarcinoma	IIB	NA
0.000	TP53_208_218.chr17.7578211.C>T	TP53	0.001	Adenocarcinoma	IIIA	NA
0.000	TP53_188_195.chr17.7578275.G>A	TP53	0.001	Adenocarcinoma	IIIA	NA
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.002	Adenocarcinoma	IV	NA
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	Adenocarcinoma	IIIC	NA
0.000	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	Adenocarcinoma	IIIB	NA
0.002	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.003	Adenocarcinoma	IIIB	NA
0.084	PIK3CA_0345.chr3.178921553.T>A	PIK3CA	0.169	Adenocarcinoma	IIIB	NA
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.013	Mucinous adenocarcinoma	IIA	NA
0.000	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	Adenocarcinoma	IIA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	Adenocarcinoma	I	NA

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0.001	PIK3CA_1039_1050.chr3.178952082.C>T	PIK3CA	0.002		
Adenocarcinoma			IIA	NA	
0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001		
Papillary adenocarcinoma			IB	NA	
0.000	TP53_0272_0283.chr17.7577090.C>T	TP53	0.001		
Adenocarcinoma			IIA	NA	
0.004	APC_1450_1458.chr5.112175639.C>T	APC	0.008		
Adenocarcinoma			IIB	NA	
0.000	TP53_167_177.chr17.7578406.C>T	TP53	0.001		
Adenocarcinoma			IIB	NA	
0.002	TP53_151_163.chr17.7578442.T>C	TP53	0.005		
Adenocarcinoma			IIA	NA	
0.002	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.004		
Papillary adenocarcinoma			IIA	NA	
0.001	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.001		
Adenocarcinoma			IIB	NA	
0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.002		
Adenocarcinoma			I	NA	
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003		
Adenocarcinoma			IIA	NA	
0.000	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.000		
Adenocarcinoma			IIB	NA	
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002		
Mucinous adenocarcinoma			II	NA	
0.003	TP53_0272_0283.chr17.7577121.G>A	TP53	0.005		
Adenocarcinoma			IIA	NA	
0.006	BRAF_594_602.chr7.140453154.T>C	BRAF	0.012		
adenocarcinoma			III C	NA	
0.029	BRAF_594_602.chr7.140453136.A>T	BRAF	0.058		
adenocarcinoma			III B	NA	
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.004		
adenocarcinoma			I	NA	
0.000	TP53_151_163.chr17.7578458.G>A	TP53	0.001		
ductal carcinoma			IIA	NA	
0.001	TP53_151_163.chr17.7578461.C>T	TP53	0.001		
signet-ring cells carcinoma			IIA	NA	
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.002		
ductal carcinoma			IIA	NA	
0.001	PTEN_91_98.chr10.89692790.G>T	PTEN	0.002		
lobular carcinoma			IIB	NA	
0.001	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.003		
ductal carcinoma			III A	NA	
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.001		
ductal carcinoma			IIB	NA	
0.000	TP53_0272_0283.chr17.7577124.C>T	TP53	0.001		
ductal carcinoma			IIB	NA	
0.001	PTEN_91_98.chr10.89692794.A>G	PTEN	0.002		
ductal carcinoma			IIB	NA	

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0.001	TP53_233_245.chr17.7577568.C>T	TP53	0.002		
ovarian carcinoma - endometrioid type			IIC	NA	
0.073	TP53_151_163.chr17.7578442.T>C	TP53	0.147		
ductal adenocarcinoma			IIA	NA	
0.001	PTEN_91_98.chr10.89692802.C>T	PTEN	0.003		
adenocarcinoma			IVA	NA	
0.303	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.606		
adenocarcinoma			IIA	NA	
0.001	NRAS_0055_0062.chr1.115256528.T>G	NRAS	0.002		
adenocarcinoma			IIA	NA	
0.001	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001		
adenocarcinoma			III	A	NA
0.001	TP53_342.chr17.7574018.G>A	TP53	0.001		
adenocarcinoma			III	A	NA
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002		
signet-ring cells carcinoma			IVA	NA	
0.001	GNAS_201.chr20.57484420.C>A	GNAS	0.002		
adenocarcinoma			III	B	NA
0.000	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001		
ovarian carcinoma - endometrioid type			IIA	NA	
0.035	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.070		
mucinous adenocarcinoma			IIA	NA	
0.002	BRAF_594_602.chr7.140453136.A>T	BRAF	0.004		
adenocarcinoma			IIA	NA	
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.002		
adenocarcinoma			III	B	NA
0.000	TP53_122.chr17.7579313.G>A	TP53	0.001		
lobular carcinoma			III	C	NA
0.061	AKT1_0016_0017.chr14.105246551.C>T	AKT1	0.122		
Adenocarcinoma			NA	NA	
0.246	TP53_172A.chr17.7578382.G>C	TP53	0.492		
adenocarcinoma			III	A	NA
0.006	TP53_0272_0283.chr17.7577124.C>T	TP53	0.011		
ductal carcinoma			IIA	NA	
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002		
adenocarcinoma			III	B	NA
0.001	PPP2R1A_176_187.chr19.52715986.C>T	PPP2R1A	0.001		
adenocarcinoma			IIA	NA	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003		
adenocarcinoma			III	B	NA
0.004	TP53_172A.chr17.7578406.C>T	TP53	0.007		
mucinous carcinoma			IIA	NA	
0.001	TP53_098_109.chr17.7579378.G>C	TP53	0.001		
adenocarcinoma			III	B	NA
0.000	APC_1450_1458.chr5.112175639.C>T	APC	0.001		
ductal carcinoma			IIA	NA	
0.001	FBXW7_505.chr4.153247289.G>A	FBXW7	0.001		
ductal carcinoma			IA	NA	

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0.000	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	lobular carcinoma	IIA	NA
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.002	ductal carcinoma	IA	NA
0.001	TP53_167_177.chr17.7578410.T>A	TP53	0.002	ovarian carcinoma - serous papillary type	IV	NA
0.002	TP53_151_163.chr17.7578479.G>A	TP53	0.005	adenocarcinoma	III B	NA
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	adenocarcinoma	IIA	NA
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	adenocarcinoma	III B	NA
0.001	APC_1304_1310.chr5.112175207.G>T	APC	0.002	lobular carcinoma	IIA	NA
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	ductal carcinoma	IIA	NA
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	adenocarcinoma	III C	NA
0.010	TP53_0248_0261.chr17.7577539.G>A	TP53	0.020	ductal carcinoma	IA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	adenocarcinoma	IVA	NA
0.007	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.014	Ductal carcinoma	IIA	NA
0.001	TP53_0227_0236.chr17.7577580.T>C	TP53	0.002	Neuroendocrine carcinoma	IIA	NA
0.003	TP53_132_142.chr17.7578508.C>T	TP53	0.006	Squamous cell carcinoma, keratinizing	IIA	NA
0.006	TP53_132_142.chr17.7578535.T>C	TP53	0.013	Intraductal papillary carcinoma	III	NA
0.003	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.005	Squamous cell carcinoma	IIA	NA
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	Squamous cell carcinoma, keratinizing	IIA	NA
0.000	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	Squamous cell carcinoma	IIB	NA
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	Squamous cell carcinoma, keratinizing	III	NA
0.001	TP53_188_195.chr17.7578271.T>A	TP53	0.002	Squamous cell carcinoma, keratinizing	IIA	NA
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	Squamous cell carcinoma, keratinizing	IIB	NA
0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	Squamous cell carcinoma, nonkeratinizing,	III	NA
0.000	TP53_172A.chr17.7578407.G>A	TP53	0.001	Squamous cell carcinoma, nonkeratinizing,	III	NA
0.022	TP53_233_245.chr17.7577547.C>T	TP53	0.044	NA	NA	NA

Table36.txt

NA NA NA

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	NA	NA		NA		NA	
NA					NA		NA
	NA	NA		NA		NA	
NA					NA		NA
	NA	NA		NA		NA	
NA					NA		NA
	NA	NA		NA		NA	
NA					NA		NA
	0.001	TP53_172A.chr17.7578406.C>T		TP53		0.001	
NA					NA		NA
	0.003	TP53_0272_0283.chr17.7577120.C>T		TP53		0.007	
NA					NA		NA
	0.001	TP53_0272_0283.chr17.7577108.C>A		TP53		0.002	
NA					NA		NA
	0.001	TP53_208_218.chr17.7578212.G>A		TP53		0.002	
NA					NA		NA
	0.001	TP53_098_109.chr17.7579389.G>A		TP53		0.002	
NA					NA		NA
	0.001	TP53_151_163.chr17.7578458.G>A		TP53		0.002	
NA					NA		NA
	0.001	GNAS_201.chr20.57484421.G>A		GNAS		0.001	
NA					NA		NA
	0.001	TP53_233_245.chr17.7577556.C>A		TP53		0.001	
NA					NA		NA
	0.001	TP53_0248_0261.chr17.7577539.G>A		TP53		0.002	
NA					NA		NA
	0.000	KRAS_012_+13_-4.chr12.25398279.C>T		KRAS		0.001	
NA					NA		NA
	0.000	TP53_172A.chr17.7578406.C>T		TP53		0.001	
NA					NA		NA
	0.004	KRAS_012_+13_-4.chr12.25398284.C>A		KRAS		0.009	
NA					NA		NA
	0.001	TP53_208_218.chr17.7578211.C>T		TP53		0.002	
NA					NA		NA
	0.003	TP53_167_177.chr17.7578413.C>G		TP53		0.006	
NA					NA		NA
	0.001	CDKN2A_7_88.chr9.21971132.C>T		CDKN2A		0.001	
NA					NA		NA
	0.001	KRAS_012_+13_-4.chr12.25398284.C>T		KRAS		0.003	
NA					NA		NA
	0.001	TP53_172A.chr17.7578407.G>C		TP53		0.002	
NA					NA		NA
	0.001	TP53_132_142.chr17.7578518.C>T		TP53		0.001	
NA					NA		NA
	0.001	CDKN2A_7_88.chr9.21971098.C>T		CDKN2A		0.002	
NA					NA		NA
	0.000	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A		0.001	
NA					NA		NA

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0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.003	NA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	NA	NA
0.001	TP53_132_142.chr17.7578526.C>T	TP53	0.002	NA	NA
0.001	TP53_219_224.chr17.7578190.T>C	TP53	0.002	NA	NA
0.000	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA	NA
0.001	TP53_233_245.chr17.7577551.C>T	TP53	0.002	NA	NA
0.000	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	NA	NA
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002	NA	NA
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA	NA
0.001	TP53_167_177.chr17.7578413.C>T	TP53	0.002	NA	NA
0.000	TP53_233_245.chr17.7577548.C>T	TP53	0.001	NA	NA
0.001	TP53_172A.chr17.7578400.G>C	TP53	0.003	NA	NA
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	NA	NA
0.000	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA	NA
0.001	TP53_026.chr17.7579705.C>T	TP53	0.002	NA	NA
0.000	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	NA
0.000	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	NA	NA
0.003	TP53_233_245.chr17.7577551.C>T	TP53	0.006	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	NA	NA
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	NA	NA
0.020	TP53_233_245.chr17.7577551.C>A	TP53	0.040	NA	NA
0.004	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.007	NA	NA
0.001	TP53_262_267.chr17.7577138.C>T	TP53	0.002	NA	NA
0.000	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	NA

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0.000	TP53_0248_0261.chr17.7577535.C>G	TP53	0.001	NA	NA
0.001	TP53_0280_0289.chr17.7577070.G>A	TP53	0.002	NA	NA
0.004	TP53_233_245.chr17.7577581.A>T	TP53	0.008	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	NA
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.003	NA	NA
0.008	TP53_167_177.chr17.7578413.C>A	TP53	0.017	NA	NA
0.002	TP53_113_125.chr17.7579313.G>A	TP53	0.003	NA	NA
0.000	PTEN_136.chr10.89692923.G>A	PTEN	0.001	NA	NA
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	NA	NA
0.001	TP53_0227_0236.chr17.7577574.T>C	TP53	0.002	NA	NA
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	NA	NA
0.000	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	NA
0.001	TP53_233_245.chr17.7577580.T>C	TP53	0.001	NA	NA
0.001	GNAS_201.chr20.57484420.C>T	GNAS	0.001	NA	NA
0.000	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA	NA
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA	NA
0.000	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	NA	NA
0.018	TP53_172A.chr17.7578393.A>C	TP53	0.035	NA	NA
0.004	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.007	NA	NA
0.002	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.003	NA	NA
0.000	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA	NA
0.001	TP53_172A.chr17.7578389.G>A	TP53	0.002	NA	NA
0.001	PTEN_91_98.chr10.89692802.C>T	PTEN	0.002	NA	NA
0.002	TP53_098_109.chr17.7579377.G>A	TP53	0.004	NA	NA

Table36.txt

0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.002	NA	NA
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA	NA
0.001	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.003	NA	NA
0.001	CDKN2A_7_88.chr9.21971120.G>A	CDKN2A	0.002	NA	NA
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA	NA
0.000	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA	NA
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.001	NA	NA
0.001	TP53_172A.chr17.7578394.T>A	TP53	0.001	NA	NA
0.002	TP53_262_267.chr17.7577138.C>T	TP53	0.005	NA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA	NA
0.001	TP53_233_245.chr17.7577556.C>G	TP53	0.002	NA	NA
0.000	TP53_122.chr17.7579315.G>T	TP53	0.001	NA	NA
0.000	TP53_208_218.chr17.7578205.C>A	TP53	0.001	NA	NA
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.003	NA	NA
0.000	TP53_262_267.chr17.7577138.C>T	TP53	0.001	NA	NA
0.001	HRAS_007_018.chr11.534289.C>T	HRAS	0.001	NA	NA
0.000	TP53_219_224.chr17.7578191.A>G	TP53	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.002	NA	NA
0.004	TP53_233_245.chr17.7577568.C>T	TP53	0.008	NA	NA
0.005	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.009	NA	NA
0.000	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	NA	NA
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.003	NA	NA
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA	NA

Table36.txt

0.000	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA	
			NA	NA	
0.001	BRAF_594_602.chr7.140453155.C>T	BRAF	0.002	NA	
			NA	NA	
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	NA	
			NA	NA	
0.001	TP53_208_218.chr17.7578205.C>A	TP53	0.003	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA	
			NA	NA	
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	NA	
			NA	NA	
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA	
			NA	NA	
0.000	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA	
			NA	NA	
0.025	PIK3CA_0542_0551.chr3.178936092.A>G	PIK3CA	0.051	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	NA	
			NA	NA	
0.031	TP53_219_224.chr17.7578190.T>C	TP53	0.063	NA	
			NA	NA	
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	NA	
			NA	NA	
0.001	PIK3CA_0542_0551.chr3.178936091.G>C	PIK3CA	0.002	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA	
			NA	NA	
0.001	PTEN_136.chr10.89692925.G>A	PTEN	0.001	NA	
			NA	NA	
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.003	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	NA	
			NA	NA	
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.001	NA	
			NA	NA	
0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	
			NA	NA	
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	NA	
			NA	NA	
0.001	TP53_233_245.chr17.7577557.A>C	TP53	0.001	NA	
			NA	NA	
0.001	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.001	NA	
			NA	NA	
0.003	TP53_233_245.chr17.7577547.C>A	TP53	0.006	NA	
			NA	NA	
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA	
			NA	NA	

Table36.txt

0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA	NA
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.005	NA	NA
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.002	NA	NA
0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	NA
0.001	TP53_132_142.chr17.7578526.C>T	TP53	0.002	NA	NA
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.004	NA	NA
0.002	TP53_0248_0261.chr17.7577538.C>A	TP53	0.003	NA	NA
0.000	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	NA
0.001	TP53_233_245.chr17.7577557.A>G	TP53	0.001	NA	NA
0.001	TP53_122.chr17.7579313.G>A	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.001	NA	NA
0.003	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.007	NA	NA
0.000	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	NA	NA
0.000	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	NA	NA
0.000	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	NA
0.000	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA	NA
0.002	TP53_151_163.chr17.7578457.C>T	TP53	0.004	NA	NA
0.000	TP53_033_040.chr17.7579575.G>A	TP53	0.001	NA	NA
0.022	TP53_098_109.chr17.7579362.A>C	TP53	0.043	NA	NA
0.001	TP53_0272_0283.chr17.7577120.C>A	TP53	0.001	NA	NA
0.006	TP53_233_245.chr17.7577568.C>T	TP53	0.012	NA	NA

Table36.txt

0.000	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001		
NA			NA	NA	
0.001	TP53_233_245.chr17.7577575.A>T	TP53	0.001		
NA			NA	NA	
0.000	CDKN2A_7_88.chr9.21971108.C>T	CDKN2A	0.001		
ductal carcinoma			IIA	G2	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
hepatocellular carcinoma			II	G2	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003		
NA			IIIA	G2	
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.004		
NA			IV	G3	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005		
NA			IIA	G2	
0.006	TP53_151_163.chr17.7578475.G>A	TP53	0.013		
NA			IIIC	NA	
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005		
ductal carcinoma			IIA	G2	
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.006		
NA			IIB	G3	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003		
NA			IB	G2	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002		
NA			IIIA	G2	
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.006		
adenocarcinoma, partially of signet ring cell-type - diffuse ty			IV	G3	
0.181	TP53_0196_0205.chr17.7578263.G>A	TP53	0.362		
NA			IV	G3	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
NA			IIA	G2	
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.008		
adenocarcinoma - intestinal type			IIB	G2	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
adenocarcinoma			IIB	G3	
0.005	TP53_0272_0283.chr17.7577120.C>T	TP53	0.010		
adenocarcinoma			IIB	G3	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
NA			IIIB	NA	
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005		
carcinoma - serous papillary type			III C	G3	
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.007		
adenocarcinoma - intestinal type			III B	G2	
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004		
carcinoma - serous type			IV	G3	
0.004	TP53_298_306.chr17.7577022.G>A	TP53	0.009		
NA			IA	G1	
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003		
NA			IC	G3	

Table36.txt

	0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003					
adenocarcinoma					III	C	G2		
	0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003					
NA					NA		NA		
	0.001	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.001					
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	NA	NA	NA		NA				
NA					NA		NA		
	0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.001					
NA					NA		NA		
	0.000	TP53_233_245.chr17.7577547.C>T	TP53	0.001					
NA					NA		NA		
	0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.002					
NA					NA		NA		
	0.001	TP53_233_245.chr17.7577568.C>T	TP53	0.001					
NA					NA		NA		
	0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001					
NA					NA		NA		
	0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001					
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	0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.001					
NA					NA		NA		
	0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.001					
NA					NA		NA		
	0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001					
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	0.001	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001					
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	0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.001					
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	0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.001					
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NA					NA		NA		
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NA					NA		NA		
	NA	NA	NA		NA				
NA					NA		NA		
	NA	NA	NA		NA				
NA					NA		NA		
	NA	NA	NA		NA				
NA					NA		NA		
	NA	NA	NA		NA				
NA					NA		NA		
	NA	NA	NA		NA				
NA					NA		NA		

Table36.txt

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NA	NA		NA	NA	NA	NA	NA
NA	NA		NA	NA	NA	NA	NA
0.001	TP53_122.chr17.7579313.G>A		TP53	0.001	NA	NA	NA
0.001	TP53_342.chr17.7574003.G>A		TP53	0.001	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715979.C>T		PPP2R1A	0.002	NA	NA	NA
0.000	TP53_151_163.chr17.7578461.C>T		TP53	0.001	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A	0.001	NA	NA	NA
0.001	TP53_167_177.chr17.7578406.C>T		TP53	0.002	NA	NA	NA
0.001	TP53_0272_0283.chr17.7577120.C>T		TP53	0.001	NA	NA	NA
0.001	PTEN_145_153.chr10.89692958.G>A		PTEN	0.001	NA	NA	NA
0.001	PTEN_91_98.chr10.89692794.A>G		PTEN	0.002	NA	NA	NA
0.001	TP53_0272_0283.chr17.7577111.G>A		TP53	0.002	NA	NA	NA
0.001	TP53_0196_0205.chr17.7578263.G>A		TP53	0.003	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A	0.002	NA	NA	NA
0.000	TP53_0272_0283.chr17.7577118.C>A		TP53	0.001	NA	NA	NA
0.001	TP53_262_267.chr17.7577138.C>T		TP53	0.001	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A	0.002	NA	NA	NA
0.001	TP53_0272_0283.chr17.7577094.G>A		TP53	0.002	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A	0.001	NA	NA	NA
0.001	TP53_0248_0261.chr17.7577538.C>T		TP53	0.001	NA	NA	NA
0.001	FBXW7_505.chr4.153247288.C>A		FBXW7	0.001	NA	NA	NA
0.002	TP53_0248_0261.chr17.7577539.G>A		TP53	0.003	NA	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T		PPP2R1A	0.001	NA	NA	NA

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	0.001	CDKN2A_7_88.chr9.21971099.G>A	CDKN2A	0.002	
NA			NA	NA	
	0.000	GNAS_201.chr20.57484421.G>A	GNAS	0.001	
NA			NA	NA	
	0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.002	
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	NA	NA	NA	NA

Table36.txt

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NA						NA		NA	
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NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	0.003	TP53_0272_0283.chr17.7577120.C>T			TP53		0.007		
NA						NA		NA	
	0.001	TP53_0272_0283.chr17.7577094.G>A			TP53		0.002		
NA						NA		NA	
	0.002	TP53_0272_0283.chr17.7577120.C>T			TP53		0.004		
NA						NA		NA	
	0.003	TP53_0272_0283.chr17.7577120.C>T			TP53		0.006		
NA						NA		NA	

Table36.txt

	0.007	TP53_0272_0283.chr17.7577120.C>T	TP53		0.013				
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	0.001	TP53_0272_0283.chr17.7577120.C>T	TP53		0.002				
NA				NA	NA				
	0.003	TP53_0272_0283.chr17.7577120.C>T	TP53		0.006				
NA				NA	NA				
	NA	NA	NA		NA

Table36.txt

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	NA	NA			NA		NA		
NA						NA		NA	
	NA	NA			NA		NA		
NA						NA		NA	
	0.003	TP53_0272_0283.chr17.7577120.C>T			TP53		0.006		
NA						NA		NA	
	0.003	TP53_0272_0283.chr17.7577120.C>T			TP53		0.006		
NA						NA		NA	
	0.002	TP53_0272_0283.chr17.7577120.C>T			TP53		0.003		
NA						NA		NA	
	0.005	TP53_0272_0283.chr17.7577120.C>T			TP53		0.009		
NA						NA		NA	
	NA	NA			NA		NA

Table36.txt

NA NA NA

Table36.txt

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NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
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    NA          NA                                                  NA          NA
NA                                                                  NA      NA
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NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
NA                                                                  NA      NA
    NA          NA                                                  NA          NA
combined hepatocellular carcinoma and cholangiocarcinoma            NA      NA
    0.061       TP53_151_163.chr17.7578461.C>A                      TP53        0.122
```

Table37.txt

Table 37. Primer sequences for multiplex PCR assays.

Amplicon Name	Amplicon-specific forward primer	SEQ ID NO:	Gene	Amplicon-specific reverse primer	SEQ ID NO:	Genomic coordinates of amplified region*	Region of interest length (bp)	Amplicon length (bp)
NRAS_0055_0062	TGGTCTCTCATGGCACTGTACT	1	NRAS	ATGGTGAAACCTGTTTGTTGG	2	chr1:115256502-115256571	27	70
NRAS_4_14	TTGCTGGTGTGAAATGACTGA	3	NRAS	GATTGTCAGTGCGCTTTTCC	4	chr1:115258719-115258794	35	76
CTNNB1_0032_0039	ACTGGCAGCAACAGTCTTACCT	5	CTNNB1	ACTCAGAGAAGGAGCTGTGGTAGT	6	chr3:41266074-41266144	25	71
CTNNB1_0039_0046	CTGGACTCTGGAATCCATTCTG	7	CTNNB1	TTCCTCAGGATTGCCTTTACC	8	chr3:41266094-41266165	29	72
PIK3CA_80_89	TTGAAAAAGCCGAAGGTCAC	9	PIK3CA	GTAAGTGTTACTCAAGAAGCAGAAAGG	10	chr3:178916824-178916901	31	78
PIK3CA_0345	CAGAATAAAAATTCTTTGTGCAACC	11	PIK3CA	TGACTTTACCTTATCAATGTCTCGAA	12	chr3:178921520-178921586	16	67
PIK3CA_0542_0551	TTTTAGCACTTACCTGTGACTCCA	13	PIK3CA	CAATTTCTACACGAGATCCTCTCTC	14	chr3:178936056-178936135	31	80
PIK3CA_1039_1050	CCAATCCATTTTTGTTGTCCA	15	PIK3CA	TGAGCAAGAGGCTTTGGAGT	16	chr3:178952038-178952116	38	79
FBXW7_505	ACCCTCCTGCCATCATATTG	17	FBXW7	GGCCAGTGTTTACATGTTTTGA	18	chr4:153247261-153247331	29	71
FBXW7_474_482	TGTCTCAATATCCCAAACCCTAA	19	FBXW7	TTGTTTTTCTGTTTCTCCCTCTG	20	chr4:153247332-153247409	32	78
FBXW7_464_472A	CCATGACAAGATTTTCCCTTACC	21	FBXW7	CACCTTATATGGGCATACTTCCACT	22	chr4:153249338-153249413	28	76
FBXW7_361_371	TGCAGAGTTCAGTTACCTTAGGAGA	23	FBXW7	TGCATACATCAGACAGCACAGA	24	chr4:153251868-153251947	33	80
APC_1304_1310	GATCTTCAGCTGACCTAGTTCCAA	25						

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CAGATTCTGCTAATACCCTGCAA			26	APC
chr5:112175178-112175246	22	69		
APC_1450_1458	GTCCACTCTCTCTCTTTTCAGCA			27
CCTCAAACAGCTCAAACCAAG			28	APC
chr5:112175618-112175690	29	73		
EGFR_856_867	GCAGCATGTCAAGATCACAGAT			29
TGCCTCCTTCTGCATGGTAT			30	EGFR
chr7:55259486-55259565	38	80		
BRAF_594_602	TGGGACCCACTCCATCG			31
ATATTTCTTCATGAAGACCTCACAGTAA			32	BRAF
chr7:140453112-140453191	35	80		
CDKN2A_7_88	CAACTGCGCCGACCCC			33
CAGCGTGTCCAGGAAGCC			34	CDKN2A
chr9:21971076-21971148	39	73		
CDKN2A_051_057	ACCCTGGCTCTGACCATTC			35
CAGCAGCTCCGCCACTC			36	CDKN2A
chr9:21971169-21971241	37	73		
PTEN_91_98	ACCACAGTTGCACAATATCCTTT			37
TCTTCACAAAAGGGTTTGATAAGTTC			38	PTEN
chr10:89692763-89692836	25	74		
PTEN_130	CATGTTGCAGCAATTCACTGT			39
CCGATGTAATAAATATGCACATATCATTAC			40	PTEN
chr10:89692868-89692942	24	75		
PTEN_136	GGAAAGGGACGAACTGGTG			41
TAGGGCCTCTTGTGCCTTTA			42	PTEN
chr10:89692895-89692972	39	78		
PTEN_145_153	CTCTGGTCCTTACTTCCCCATAG			43
CATATTTATTACATCGGGGCAAA			44	PTEN
chr10:89692926-89693000	29	75		
FGFR2_252	AGTCCGGCTTGGAGGATG			45
TCCCCACTCCTCCTTTCTTC			46	FGFR2
chr10:123279647-123279717	33	71		
HRAS_007_018	GCGATGACGGAATATAAGCTG			47
CTGGATCAGCTGGATGGTCA			48	HRAS
chr11:534248-534325	37	78		
KRAS_144_147A	CAAGAAGTTATGGAATTCCTTTTATTGA			49
TTTATTTCAGTGTTACTTACCTGTCTTG			50	KRAS
chr12:25378528-25378597	14	70		
KRAS_0057_0064	GAGAAACCTGTCTCTTGGATATTCTC			51
TGTACTGGTCCCTCATTGCAC			52	KRAS
chr12:25380244-25380315	25	72		
KRAS_012_+13_-4	CGTCAAGGCACTCTTGCC			53
TGCTGAAAATGACTGAATATAAACTTGT			54	KRAS
chr12:25398259-25398326	22	68		
AKT1_0016_0017	GCCGCCAGGTCTTGATGT			55
GGGTCTGACGGGTAGAGTGTG			56	AKT1
chr14:105246530-105246603	35	74		
TP53_374_385	TGAGTCAGGCCCTTCTGTCT			57

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GCCACCTGAAGTCCAAAAAG 58 TP53
chr17:7572933-7573009 37 77
TP53_368_to_374 TTTTATGGCGGGAGGTAGACT 59
TCATCTCTCCTCCCTGCTTCT 60 TP53
chr17:7572965-7573040 34 76
TP53_345 CCCTGGCTCCTTCCCAG 61
CTTCGAGATGTTCCGAGAGC 62 TP53
chr17:7573947-7574016 33 70
TP53_342 TCCTCTGTTGCTGCAGATCC 63
TGAGTTCCAAGGCCTCATTC 64 TP53
chr17:7573976-7574049 34 74
TP53_323 CACTTGATAAGAGGTCCCAAGACTTA 65
CCCAGCCAAAGAAGAAACCA 66 TP53
chr17:7576823-7576899 31 77
TP53_307 TCTTCTTTGGCTGGGGAGA 67
TTTTATCACCTTTCCTTGCCTCT 68 TP53
chr17:7576885-7576956 30 72
TP53_298_306 AAAGGGGAGCCTCACCAC 69
ACCGCTTCTTGTCCTGCTT 70 TP53
chr17:7576994-7577064 34 71
TP53_0280_0289 GTGAGGCTCCCCTTTCTTG 71
CGTGTTTGTGCCTGTCCTG 72 TP53
chr17:7577050-7577121 34 72
TP53_0272_0283 GGGACGGAACAGCTTTGAG 73
GCGGAGATTCTCTTCCTCTGT 74 TP53
chr17:7577068-7577143 36 76
TP53_262_267 AACACGCACCTCAAAGCTG 75
TGCCTCTTGCTTCTCTTTTCCT 76 TP53
chr17:7577116-7577188 32 73
TP53_0248_0261 GTGGCAAGTGGCTCCTGA 77
CATGGGCGGCATGAAC 78 TP53
chr17:7577480-7577555 42 76
TP53_233_245 TGGCTCTGACTGTACCACCA 79
ATGGGCCTCCGGTTCAT 80 TP53
chr17:7577529-7577606 41 78
TP53_0227_0236 CCCATGCAGGAACTGTTACAC 81
GGCCTGTGTTATCTCCTAGGTTG 82 TP53
chr17:7577550-7577627 34 78
TP53_219_224 TAACCCCTCCTCCCAGAGAC 83
TTTTCGACATAGTGTGGTGGTG 84 TP53
chr17:7578139-7578216 36 78
TP53_208_218 TTGCGTGTGGAGTATTTGGA 85
AGACCTCAGGCGGCTCATAG 86 TP53
chr17:7578173-7578248 36 76
TP53_0196_0205 CGAAAAGTGTTTCTGTCATCCA 87
GCCCCTCCTCAGCATCTTAT 88 TP53
chr17:7578211-7578284 32 74
TP53_188_195 CGCAAATTTCCTTCCACTCG 89

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CTGATTCCTCACTGATTGCTCTT 90 TP53
chr17:7578244-7578314 28 71
TP53_172A AGCCCCAGCTGCTCACC 91
ACATGACGGAGGTTGTGAGG 92 TP53
chr17:7578355-7578427 36 73
TP53_167_177 TGGCCATCTACAAGCAGTCA 93
GAGCAGCGCTCATGGTG 94 TP53
chr17:7578382-7578451 33 70
TP53_151_163 CGTCATGTGCTGTGACTGCTT 95
CAGCTGTGGGTTGATTCCA 96 TP53
chr17:7578420-7578500 41 81
TP53_132_142 GAATCAACCCACAGCTGCAC 97
AGTACTCCCCTGCCCTCAAC 98 TP53
chr17:7578484-7578556 33 73
TP53_126_131 GGCCAGTTGGCAAAACATCT 99
GCCCTGACTTTCAACTCTGTCT 100 TP53
chr17:7578516-7578593 36 78
TP53_122 ATACGGCCAGGCATTGAAGT 101
GGGACAGCCAAGTCTGTGA 102 TP53
chr17:7579260-7579338 40 79
TP53_113_125 CCCCTCAGGGCAACTGAC 103
AGCTACGGTTTCCGTCTGG 104 TP53
chr17:7579294-7579371 41 78
TP53_098_109 GGCCCCTGTCATCTTCTGT 105
CAGAATGCAAGAAGCCCAGA 106 TP53
chr17:7579338-7579415 39 78
TP53_083_94 TTCTGGGAAGGGACAGAAGA 107
TGCACCAGCAGCTCCTACAC 108 TP53
chr17:7579385-7579462 38 78
TP53_053 GAGCAGCCTCTGGCATTCT 109
GTCCCCGGACGATATTGAAC 110 TP53
chr17:7579476-7579552 38 77
TP53_041_052 CCTGGGTCTTCAGTGAACCA 111
CTTGCCGTCCCAAGCAAT 112 TP53
chr17:7579511-7579585 37 75
TP53_033_040 GGGGACAGCATCAAATCATC 113
TGACTGCTCTTTTCACCCATC 114 TP53
chr17:7579547-7579616 29 70
TP53_026 AGCCCAACCCTTGTCCTTAC 115
CCATGGGACTGACTTTCTGC 116 TP53
chr17:7579680-7579754 35 75
TP53_010_022 TGGATCCACTCACAGTTTCCA 117
GCCGCAGTCAGATCCTAGC 118 TP53
chr17:7579826-7579904 39 79
PPP2R1A_176_187 TACTTCCGGAACCTGTGCTC 119
GGCAAACTCCCCCAGCTT 120 PPP2R1A
chr19:52715940-52716014 37 75
GNAS_201 TGTTTCAGGACCTGCTTCG 121

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TCCACCTGGAACTTGGTCTC 122 GNAS
chr20:57484397-57484463 28 67

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

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Table 38. Primer sequences for multiplex PCR assays

Amplicon-specific forward primer	SEQ ID NO	Amplicon-specific reverse primer	SEQ ID NO	Region of interest	Gene	hg19 coordinates	Amplicon length (bp)
KRAS_0057_0064	123	TGTACTGGTCCCTCATTGCAC	124	KRAS	chr12:25,380,244-25,380,315	72	25
KRAS_012_+13_-4	125	TGCTGAAAATGACTGAATATAAACTTGT	126	KRAS	chr12:25,398,259-25,398,326	68	22
TP53_342	127	TGAGTTCCAAGGCCTCATTC	128	TP53	chr17:7,573,976-7,574,049	74	34
TP53_298_306	129	ACCGCTTCTTGTCCTGCTT	130	TP53	chr17:7,576,994-7,577,064	71	34
TP53_0280_0289	131	CGTGTTTGTGCCTGTCCTG	132	TP53	chr17:7,577,050-7,577,121	72	34
TP53_0272_0283	133	GCGGAGATTCTCTTCCTCTGT	134	TP53	chr17:7,577,068-7,577,143	76	36
TP53_262_267	135	TGCCTCTTGCTTCTCTTTTCCT	136	TP53	chr17:7,577,116-7,577,188	73	32
TP53_0248_0261	137	CATGGGCGGCATGAAC	138	TP53	chr17:7,577,480-7,577,555	76	42
TP53_233_245	139	ATGGGCCTCCGGTTCAT	140	TP53	chr17:7,577,529-7,577,606	78	41
TP53_0227_0236	141	GGCCTGTGTTATCTCCTAGGTTG	142	TP53	chr17:7,577,550-7,577,627	78	34
TP53_219_224	143	TTTTCGACATAGTGTGGTGGTG	144	TP53	chr17:7,578,139-7,578,216	78	36
TP53_208_218	145	AGACCTCAGGCGGCTCATAG	146	TP53	chr17:7,578,173-7,578,248	76	36
TP53_0196_0205	147	CGAAAAGTGTTTCTGTCATCCA					

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GCCCCTCCTCAGCATCTTAT		148	TP53	
chr17:7,578,211–7,578,284	32	74		
TP53_188_195	CGCAAATTTCCTTCCACTCG			149
CTGATTCCTCACTGATTGCTCTT		150	TP53	
chr17:7,578,244–7,578,314	28	71		
TP53_172A	AGCCCCAGCTGCTCACC			151
ACATGACGGAGGTTGTGAGG		152	TP53	
chr17:7,578,355–7,578,427	36	73		
TP53_167_177	TGGCCATCTACAAGCAGTCA			153
GAGCAGCGCTCATGGTG		154	TP53	
chr17:7,578,382–7,578,451	33	70		
TP53_151_163	CGTCATGTGCTGTGACTGCTT			155
CAGCTGTGGGTTGATTCCA		156	TP53	
chr17:7,578,420–7,578,500	41	81		
TP53_126_131	GGCCAGTTGGCAAAACATCT			157
GCCCTGACTTTCAACTCTGTCT		158	TP53	
chr17:7,578,516–7,578,593	36	78		

Table39.txt

Table S3: Genomic regions covered in multiplex assays for Pap and intrauterine samples.

Gene	Genomic coordinates of amplified region*	SEQ ID NO: Forward primer	SEQ ID NO: Reverse primer**
NRAS	chr1:115256505-115256588		
CACACAGGAAACAGCTATGACCATGACACCCCCAGGATTCTTACAG		159	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGCCTGTCCTCATGTATTGG			160
NRAS	chr1:115258739-115258820		
CACACAGGAAACAGCTATGACCATGGATGTGGCTCGCCAATTAAC		161	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGATTGTCAGTGCGCTTTTCC			162
PTEN	chr10:89624227-89624322		
CACACAGGAAACAGCTATGACCATGAGCCACAGGCTCCCAGAC		163	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGACAGAAAGGTAAAGAGGAGCA			164
PTEN	chr10:89653765-89653832		
CACACAGGAAACAGCTATGACCATGGCTGCATATTTCAGATATTTCTTTCC		165	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCATCATCAATATTGTTCCTGTATACGC			166
PTEN	chr10:89653830-89653910		
CACACAGGAAACAGCTATGACCATGGGATTTCCTGCAGAAAGACTTG		167	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCTTTTCTAAATGAAAACACAACATGA			168
PTEN	chr10:89685256-89685338		
CACACAGGAAACAGCTATGACCATGAATAGTTGTTTTAGAAGATATTTGCAAGC		169	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTAATGGTGGCTTTTTGTTTGTT			170
PTEN	chr10:89690739-89690822		
CACACAGGAAACAGCTATGACCATGAAGATTCAGGCAATGTTTGTTAGTATT		171	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCAATTAAATTTGGCGGTGT			172
PTEN	chr10:89690812-89690878		
CACACAGGAAACAGCTATGACCATGCAGTAAGATACAGTCTATCGGGTTTAAGT		173	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTTTAAACTTTTCTTTTAGTTGTGCTGA			174
PTEN	chr10:89692767-89692847		
CACACAGGAAACAGCTATGACCATGTTTCTTATTCTGAGGTTATCTTTTTACCA		175	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCATGATTGTCATCTTCACTTAGCC			176
PTEN	chr10:89692813-89692901		
CACACAGGAAACAGCTATGACCATGCCATAACCCACCACAGCTAGA		177	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCACATATCATTACACCAGTTCGTC			178
PTEN	chr10:89692900-89692975		
CACACAGGAAACAGCTATGACCATGGCAATTCACTGTAAAGCTGGAAA		179	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGTCCTTACTTCCCCATAGAA			180
PTEN	chr10:89692976-89693060		
CACACAGGAAACAGCTATGACCATGAAACCCAAAATCTGTTTTCCAA		181	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGGCACAAGAGGCCCTAGAT			182
PTEN	chr10:89711865-89711928		
CACACAGGAAACAGCTATGACCATGTCAATTTGGCTTCTCTTTTTTTTC		183	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCACTGGTCTATAATCCAGATGATTCTT			184

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PTEN chr10:89711926-89711986
CACACAGGAAACAGCTATGACCATGGCGCTATGTGTATTATTATAGCTACCTG 185
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGCCACTGAACATTGGAATAG 186
PTEN chr10:89711943-89712020
CACACAGGAAACAGCTATGACCATGGCTACCTGTTAAAGAATCATCTGGA 187
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGAAGGATGAGAATTTCAAGCAC 188
PTEN chr10:89717590-89717670
CACACAGGAAACAGCTATGACCATGAGGCATTTCCTGTGAAATAATACTG 189
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGAACTTGTCTTCCCGTCGT 190
PTEN chr10:89717640-89717734
CACACAGGAAACAGCTATGACCATGTGTGGTCTGCCAGCTAAAGG 191
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGTTCTGTTTGTGGAAGAACTCTACTTT 192
PTEN chr10:89717717-89717788
CACACAGGAAACAGCTATGACCATGTTGAGTTCCCTCAGCCGTTA 193
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTTGGATATTTCTCCCAATGAAAG 194
PTEN chr10:89720666-89720754
CACACAGGAAACAGCTATGACCATGTTTTTTTTTTAGGACAAAATGTTTCAC 195
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGCACGCTCTATACTGCAAATG 196
PTEN chr10:89720757-89720836
CACACAGGAAACAGCTATGACCATGTCTATGTGATCAAGAAATCGATAGCA 197
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAAGTATCGGTTGGCTTTGTCTTT 198
PTEN chr10:89720833-89720895
CACACAGGAAACAGCTATGACCATGTTTAACAAAAAATGATCTTGACAAAGC 199
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACAAGTCAACAACCCCCACA 200
PTEN chr10:89725039-89725114
CACACAGGAAACAGCTATGACCATGTGGGTTTTCATTTTAAATTTTCTTTC 201
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGGTTCATTGTCACTAACATCTGGT 202
PTEN chr10:89725089-89725180
CACACAGGAAACAGCTATGACCATGTAGAGGAGCCGTCAAATCCA 203
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGATCTTCATCAAAAGGTTCATTC 204
PTEN chr10:89725178-89725266
CACACAGGAAACAGCTATGACCATGGGTCCATTTTCAGTTTATTCAAGTTTA 205
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGACACCACTGACTCTGATCC 206
FGFR2 chr10:123247510-123247588
CACACAGGAAACAGCTATGACCATGGCAGCCAGAAATGTTTTGGTA 207
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACTGCCATCGACTTACATTGG 208
FGFR2 chr10:123257989-123258069
CACACAGGAAACAGCTATGACCATGGCAGAGTATTTGGGCGAATG 209
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCTGGTGTCAGAGATGGAGATG 210
FGFR2 chr10:123279596-123279682
CACACAGGAAACAGCTATGACCATGGCTGGGCATCACTGTAAACC 211
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCTTCCCTCTCTCCACCAGA 212
KRAS chr12:25378560-25378631
CACACAGGAAACAGCTATGACCATGGGAAATAAATGTGATTTGCCTTCT 213
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTTCAGTGTTACTTACCTGTCTTGTCTT 214
KRAS chr12:25380265-25380337
CACACAGGAAACAGCTATGACCATGTTCTCCCTTCTCAGGATTCCTAC 215
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGTACTGGTCCCTCATTGCAC 216

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KRAS	chr12:25398230-25398289	
CACACAGGAAACAGCTATGACCATGTTTACCTCTATTGTTGGATCATATTCG	217	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGACTGAATATAAACTTGTGGTAGTTGG		218
POLE	chr12:133250276-133250363	
CACACAGGAAACAGCTATGACCATGGTCTGTGTGGTGCCCAGTTT	219	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGACTGCCCACAGGAAGGTAA		220
POLE	chr12:133253112-133253206	
CACACAGGAAACAGCTATGACCATGCCCATCCCAGGAGCTTACTT	221	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGCATTTGACATTGAGACG		222
AKT1	chr14:105246502-105246583	
CACACAGGAAACAGCTATGACCATGTCCTTGTAGCCAATGAAGGTG	223	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGGGTCTGACGGGTAGAGTGT		224
TP53	chr17:7572912-7572989	
CACACAGGAAACAGCTATGACCATGGCCACCTGAAGTCCAAAAAG	225	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGAGGCTGTCAGTGGGGAAC		226
TP53	chr17:7572950-7573022	
CACACAGGAAACAGCTATGACCATGATGTCATCTCTCCTCCCTGCT	227	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGTCTGAGTCAGGCCCTTCTG		228
TP53	chr17:7573901-7573987	
CACACAGGAAACAGCTATGACCATGGTTCCGAGAGCTGAATGAGG	229	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTAGGAAGGCAGGGGAGTAGG		230
TP53	chr17:7573964-7574039	
CACACAGGAAACAGCTATGACCATGCCCTGGCTCCTTCCCAG	231	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTTCTCCCCCTCCTCTGTTG		232
TP53	chr17:7576804-7576878	
CACACAGGAAACAGCTATGACCATGAAGAAGAAAACGGCATTTTGAG	233	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCAGCCAAAGAAGAAACCAC		234
TP53	chr17:7576865-7576933	
CACACAGGAAACAGCTATGACCATGTTTTATCACCTTTCCTTGCCTCT	235	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAAGACTTAGTACCTGAAGGGTGAA		236
TP53	chr17:7577017-7577102	
CACACAGGAAACAGCTATGACCATGCGTGTTTGTGCCTGTCCTG	237	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCTTCTTGTCCTGCTTGCTT		238
TP53	chr17:7577089-7577167	
CACACAGGAAACAGCTATGACCATGTGCCTCTTGCTTCTCTTTTCC	239	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCGGAGATTCTCTTCCTCTGT		240
TP53	chr17:7577498-7577584	
CACACAGGAAACAGCTATGACCATGTGGCTCTGACTGTACCACCATC	241	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGTGGCAAGTGGCTCCTGA		242
TP53	chr17:7577533-7577614	
CACACAGGAAACAGCTATGACCATGTGTGATGATGGTGAGGATGG	243	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCATCTTGGGCCTGTGTTATC		244
TP53	chr17:7578157-7578240	
CACACAGGAAACAGCTATGACCATGGTGGAAGGAAATTTGCGTGT	245	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTTAACCCCTCCTCCCAGAG		246
TP53	chr17:7578233-7578308	
CACACAGGAAACAGCTATGACCATGGTCCCCAGGCCTCTGATT	247	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGAAAAGTGTTTCTGTCATCCA		248

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TP53 chr17:7578354-7578436
CACACAGGAAACAGCTATGACCATGGCCATGGCCATCTACAAGC 249
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACCAGCCCTGTCGTCTCTC 250
TP53 chr17:7578437-7578518
CACACAGGAAACAGCTATGACCATGCTCCGTCATGTGCTGTGACT 251
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAACAAGATGTTTTGCCAACTG 252
TP53 chr17:7578493-7578571
CACACAGGAAACAGCTATGACCATGGCCCTGACTTTCAACTCTGTCT 253
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGGGGTGTGGAATCAACC 254
TP53 chr17:7579291-7579376
CACACAGGAAACAGCTATGACCATGGCATTGAAGTCTCATGGAAGC 255
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCCTTCCCAGAAAACCTACC 256
TP53 chr17:7579358-7579444
CACACAGGAAACAGCTATGACCATGCTGCACCAGCAGCTCCTAC 257
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAGAATGCAAGAAGCCCAGA 258
TP53 chr17:7579408-7579482
CACACAGGAAACAGCTATGACCATGAGCTCCCAGAATGCCAGAG 259
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGGAAGGGACAGAAGATGA 260
TP53 chr17:7579459-7579551
CACACAGGAAACAGCTATGACCATGGCAATGGATGATTTGATGCTG 261
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGGTGTAGGAGCTGCTGG 262
TP53 chr17:7579522-7579595
CACACAGGAAACAGCTATGACCATGTGACTGCTCTTTTCACCCATC 263
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCATCTGGACCTGGGTCTTC 264
TP53 chr17:7579698-7579770
CACACAGGAAACAGCTATGACCATGAGCCCCCTAGCAGAGACCT 265
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAGCCCAACCCTTGTCCTT 266
TP53 chr17:7579839-7579915
CACACAGGAAACAGCTATGACCATGCCTTCCAATGGATCCACTCAC 267
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACTGCCTTCCGGGTCACT 268
RNF43 chr17:56435078-56435169
CACACAGGAAACAGCTATGACCATGCGACACCCACAGAGGAAAAG 269
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGACCAAGGATATGCCACAC 270
RNF43 chr17:56448267-56448353
CACACAGGAAACAGCTATGACCATGAATGCCAGTGATGACGACAA 271
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGTGTAGGGCGAAGTGTGAG 272
PPP2R1A chr19:52715960-52716038
CACACAGGAAACAGCTATGACCATGACATGGGGATGATCTCACTCTT 273
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTACTTCCGGAACCTGTGCTC 274
PPP2R1A chr19:52716302-52716401
CACACAGGAAACAGCTATGACCATGTTCCCTTCTGAGAGTGTCAGTGT 275
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGTGATGCCCACTCTGC 276
MAPK1 chr22:22127141-22127224
CACACAGGAAACAGCTATGACCATGACATTCAACCCACACAAGAGG 277
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNATCTATGTCCCTGAAGCAGCA 278
CTNNB1 chr3:41266060-41266143
CACACAGGAAACAGCTATGACCATGGCCATGGAACCAGACAGAAA 279
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCTCAGGATTGCCTTTACCA 280

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PIK3CA chr3:178916801-178916879
CACACAGGAAACAGCTATGACCATGCCCCCTCCATCAACTTCTTC 281
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGAAAAAGCCGAAGGTCACAA 282
PIK3CA chr3:178921457-178921533
CACACAGGAAACAGCTATGACCATGTTATTCCAGACGCATTTCCAC 283
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACATTCACGTAGGTTGCACAAA 284
PIK3CA chr3:178936043-178936115
CACACAGGAAACAGCTATGACCATGCAATGAATTAAGGGAAAATGACAAA 285
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTCCATTTTAGCACTTACCTGTGAC 286
PIK3CA chr3:178951947-178952035
CACACAGGAAACAGCTATGACCATGGCATGCCAATCTCTTCATAAATC 287
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCCAAAGCCTCTTGCTCAGT 288
PIK3CA chr3:178952014-178952094
CACACAGGAAACAGCTATGACCATGTTTGATGACATTGCATACATTCG 289
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGATCCAATCCATTTTTGTTGTCCAG 290
FBXW7 chr4:153247231-153247316
CACACAGGAAACAGCTATGACCATGTTGAGACAGGCCAGTGTTTACAT 291
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAGTCTCTGGATCCCACACC 292
FBXW7 chr4:153247315-153247386
CACACAGGAAACAGCTATGACCATGTTGTTTTTCTGTTTCTCCCTCTG 293
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGCAACATGACCCATCAAA 294
FBXW7 chr4:153249349-153249437
CACACAGGAAACAGCTATGACCATGGAAGTCCCAACCATGACAAGA 295
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGGACACTCAAAGTGTGGAA 296
PIK3R1 chr5:67588915-67588976
CACACAGGAAACAGCTATGACCATGAAACCTTAAGATGAGCATTGTTTTG 297
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCATTTTAGTAGACGCATCTCGTACC 298
PIK3R1 chr5:67588948-67589025
CACACAGGAAACAGCTATGACCATGTCAGGGAAGAAGTGAATGAAAAA 299
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAGCTATATTCCCTGGCTTACCT 300
PIK3R1 chr5:67589078-67589162
CACACAGGAAACAGCTATGACCATGGGGTTTTGGGCTGATATTAAAAC 301
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCATATTTCCCATCTCGATGAA 302
PIK3R1 chr5:67589480-67589561
CACACAGGAAACAGCTATGACCATGTGTTTCCATGTCAGCTATTTTGTT 303
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGTAATTTTTTCCCTACAGCTTCAA 304
PIK3R1 chr5:67589557-67589642
CACACAGGAAACAGCTATGACCATGTCTAGGATCAAGTTGTCAAAGAAGA 305
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGGGATGTGCGGGTATATT 306
PIK3R1 chr5:67589582-67589651
CACACAGGAAACAGCTATGACCATGAGATAATATTGAAGCTGTAGGGAAAAAA 307
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAAAACTCACCTGGGATGTGC 308
PIK3R1 chr5:67590332-67590419
CACACAGGAAACAGCTATGACCATGTGCAGTAAGAGATTGTTCTATGAAAGG 309
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGGTCTGGCACTGTTCTTCA 310
PIK3R1 chr5:67590392-67590477
CACACAGGAAACAGCTATGACCATGCCAAATGAAAAGGACAGCTATTG 311
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTCTTTCTCATTGCCTTCACG 312

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PIK3R1 chr5:67590439-67590511
CACACAGGAAACAGCTATGACCATGTTTGAAGAACAGTGCCAGACC 313
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGCACAAGAACAAGGGAAACA 314
PIK3R1 chr5:67590980-67591053
CACACAGGAAACAGCTATGACCATGTTTCTTTTGCCTGCAGGATT 315
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTACTCAGCTGCCTGCTTCTTC 316
PIK3R1 chr5:67591049-67591122
CACACAGGAAACAGCTATGACCATGTTGACAGTAGAAGAAGATTGGAAGAA 317
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGTCTCTCGTCTTTCTCAGC 318
PIK3R1 chr5:67591114-67591187
CACACAGGAAACAGCTATGACCATGCCTGAATTGTAGCAATCACCAA 319
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACGTATGAACAGCATTAAACCAGA 320
PIK3R1 chr5:67592041-67592115
CACACAGGAAACAGCTATGACCATGGATGAAGATTTGCCCCATCA 321
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCTCCCGGACAAGAAAAGTG 322
APC chr5:112173652-112173733
CACACAGGAAACAGCTATGACCATGCCCAAGGCATCTCATCGTAG 323
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGGACAGTCATGTTGCCAGTATT 324
APC chr5:112173706-112173776
CACACAGGAAACAGCTATGACCATGTGATTATGTTTTTGACACCAATCG 325
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGAAGAGGAGCTGGGTAACACTG 326
APC chr5:112173764-112173851
CACACAGGAAACAGCTATGACCATGCAACATGACTGTCCTTTCACCA 327
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTAGACCAATTCCGCGTTCTC 328
APC chr5:112173802-112173885
CACACAGGAAACAGCTATGACCATGTGTTACCCAGCTCCTCTTCATC 329
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAAGTTCCTGGATTTTCTGTTGCT 330
APC chr5:112173872-112173945
CACACAGGAAACAGCTATGACCATGGAGAACGCGGAATTGGTCTA 331
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCATGACTTTGGCAATCTGG 332
APC chr5:112173892-112173980
CACACAGGAAACAGCTATGACCATGGGCAACTACCATCCAGCAAC 333
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTTCTGTCTTCCTGAGAGGTATGAA 334
APC chr5:112173974-112174062
CACACAGGAAACAGCTATGACCATGGCCAAAGTCATGGAAGAAGTG 335
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGTGTATGGGCAGCAGAGCTT 336
APC chr5:112174054-112174132
CACACAGGAAACAGCTATGACCATGGTATTCTAATTTGGCATAAGGCATAGA 337
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGTGTGACAGATGAGAGAAATGC 338
APC chr5:112174130-112174200
CACACAGGAAACAGCTATGACCATGAAGTCGGAAAATTCAAATAGGACA 339
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGACCTCTTTTACCATAACCATCA 340
APC chr5:112174156-112174226
CACACAGGAAACAGCTATGACCATGGTTCTATGCCTTATGCCAAATTAGA 341
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGATTCAATCGAGGGTTTCA 342
APC chr5:112174225-112174298
CACACAGGAAACAGCTATGACCATGTGATGGTTATGGTAAAAGAGGTCA 343
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGCACTATGTATTTTATGGGCTAGGT 344

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APC	chr5:112174281-112174335	
CACACAGGAAACAGCTATGACCATGAAGATGATGAAAGTAAGTTTTGCAGTT	345	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGTGTATCTAGTTCTCCATCATTATCA		346
APC	chr5:112174314-112174403	
CACACAGGAAACAGCTATGACCATGAGCCGACCTAGCCCATAAAA	347	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGAAGGACTTTGCCTTCCAG		348
APC	chr5:112174361-112174432	
CACACAGGAAACAGCTATGACCATGGGATGATAATGATGGAGAACTAGATACA	349	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGTTTGGGTCTTGCCCATCT		350
APC	chr5:112174410-112174475	
CACACAGGAAACAGCTATGACCATGAGATGAGCAGTTGAACTCTGGAA	351	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCTTGATTGTCTTTGCTCACTTT		352
APC	chr5:112174469-112174546	
CACACAGGAAACAGCTATGACCATGATGTGGTTGGAACTTGAGGTG	353	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGACCCAAACACATAATAGAAGATGAA		354
APC	chr5:112174543-112174611	
CACACAGGAAACAGCTATGACCATGTCGATTTGTTTCTGAACCATTG	355	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCTGTTTATACTGAGAGCACTGATGA		356
APC	chr5:112174587-112174663	
CACACAGGAAACAGCTATGACCATGATTTTGGACAGCAGGAATGTG	357	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTCTTGACACAAAGACTGGCTTAC		358
APC	chr5:112174633-112174712	
CACACAGGAAACAGCTATGACCATGCCAATGGTTCAGAAACAAATCG	359	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCTTCAGAGTAACGTTCACTATAATTGG		360
APC	chr5:112174681-112174748	
CACACAGGAAACAGCTATGACCATGTTTGTTGGTCTCTCTTCTTCTTCAT	361	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCAAAATGTAAGCCAGTCTTTGTG		362
APC	chr5:112174729-112174802	
CACACAGGAAACAGCTATGACCATGTCAATAGGCTGATCCACATGAC	363	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGATAAGCCTACCAATTATAGTGAACG		364
APC	chr5:112174782-112174852	
CACACAGGAAACAGCTATGACCATGAAGAAGAGAGACCAACAAATTATAGCA	365	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAAAATGACTGTTTCTGTGATGAAGG		366
APC	chr5:112174823-112174895	
CACACAGGAAACAGCTATGACCATGCGGTTTTACTGCTTTGTCCAG	367	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCGTCATGTGGATCAGCCTATT		368
APC	chr5:112174874-112174959	
CACACAGGAAACAGCTATGACCATGTTCCTTCATCACAGAAACAGTCA	369	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGATTCTGCCTCTTGGCATTA		370
APC	chr5:112174936-112175009	
CACACAGGAAACAGCTATGACCATGCCGAACATATGTCTTCAAGCAG	371	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGCCTTTTGAGGCTGACCAC		372
APC	chr5:112175006-112175077	
CACACAGGAAACAGCTATGACCATGGAAAAACATATTGGAGTATCTTCTACACA	373	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCATCCAAGTTCTGCACAGAGT		374
APC	chr5:112175061-112175137	
CACACAGGAAACAGCTATGACCATGCTTGCAAAGTTTCTTCTATTAACCAAG	375	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGATTACATCCTATTTCATCTTCAGC		376

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APC	chr5:112175138-112175213	
CACACAGGAAACAGCTATGACCATGGATGTAGTTCATTATCATCTTTGTCATCA	377	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCTGACCTAGTTCCAATCTTTTCTT		378
APC	chr5:112175182-112175258	
CACACAGGAAACAGCTATGACCATGGTGCTGTGACACTGCTGGAA	379	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCAGACGACACAGGAAGCAGA		380
APC	chr5:112175253-112175345	
CACACAGGAAACAGCTATGACCATGGGTCAGCTGAAGATCCTGTGA	381	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCGCTCCTGAAGAAAATTCAA		382
APC	chr5:112175343-112175422	
CACACAGGAAACAGCTATGACCATGAGAATCAGCCAGGCACAAAG	383	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAACATGAGTGGGGTCTCCTG		384
APC	chr5:112175404-112175479	
CACACAGGAAACAGCTATGACCATGGGTGCTCAGACACCCAAAAG	385	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGGCAATCGAACGACTCTC		386
APC	chr5:112175443-112175520	
CACACAGGAAACAGCTATGACCATGCAGGAGACCCCACTCATGTT	387	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNATGCCACTTACCATTCCACTG		388
APC	chr5:112175520-112175600	
CACACAGGAAACAGCTATGACCATGGCTCCGTTCAGAGTGAACCAT	389	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGGAGGTGGTGGAGGTGTTT		390
APC	chr5:112175601-112175682	
CACACAGGAAACAGCTATGACCATGCATGCCACCAAGCAGAAGTA	391	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCAGCTTGCTTAGGTCCACTC		392
APC	chr5:112175640-112175726	
CACACAGGAAACAGCTATGACCATGCTCAAACAGCTCAAACCAAGC	393	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAGCATCTGGAAGAACCTGGA		394
APC	chr5:112175709-112175795	
CACACAGGAAACAGCTATGACCATGAGCACTCAGGCTGGATGAAC	395	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGACCTAAGCAAGCTGCAGTAA		396
APC	chr5:112175782-112175870	
CACACAGGAAACAGCTATGACCATGTTTGCCACGGAAAGTACTCC	397	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCCATTGTCATTTTCCTGAACTG		398
APC	chr5:112175837-112175913	
CACACAGGAAACAGCTATGACCATGGAGCCTCGATGAGCCATTT	399	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTGGTTTTCATTTGATTCTTTAGGC		400
APC	chr5:112175913-112175981	
CACACAGGAAACAGCTATGACCATGGGGAATGAAACAGAATCAGAGC	401	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTCAATATCATCATCATCTGAATCATCTA		402
APC	chr5:112175954-112176022	
CACACAGGAAACAGCTATGACCATGAAAACCAAGAGAAAGAGGCAGAA	403	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTGGCATGGCAGAAATAATACA		404
APC	chr5:112176000-112176080	
CACACAGGAAACAGCTATGACCATGAGGACCTATTAGATGATTCAGATGATG	405	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGTGGAGGTAATTTTGAAGCAG		406
APC	chr5:112176056-112176139	
CACACAGGAAACAGCTATGACCATGCAACCTGTTTTGTGATGGTAGAAG	407	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCATGCCAACAAAGTCATCA		408

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EGFR	chr7:55241657-55241734	
CACACAGGAAACAGCTATGACCATGTGTGCCAGGGACCTTACCT	409	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGAGAAGCTCCCAACCAAG		410
EGFR	chr7:55242440-55242519	
CACACAGGAAACAGCTATGACCATGCTGGATCCCAGAAGGTGAGA	411	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCCCACACAGCAAAGCAGAA		412
EGFR	chr7:55249057-55249146	
CACACAGGAAACAGCTATGACCATGCGATCTGCACACACCAGTTG	413	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCATCTGCCTCACCTCCAC		414
EGFR	chr7:55259508-55259594	
CACACAGGAAACAGCTATGACCATGTCCCTGGTGTCAGGAAAATG	415	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCAGCATGTCAAGATCACAGAT		416
BRAF	chr7:140453119-140453192	
CACACAGGAAACAGCTATGACCATGTGTTTTCCTTTACTTACTACACCTCAGA	417	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNAACTGTTCAAACTGATGGGACC		418
CDKN2A	chr9:21968184-21968280	
CACACAGGAAACAGCTATGACCATGTGTGCCACACATCTTTGACC	419	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTGTAGGACCTTCGGTGACTG		420
CDKN2A	chr9:21970899-21970986	
CACACAGGAAACAGCTATGACCATGAGGAGCTGGGCCATCG	421	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNACAAATTCTCAGATCATCAGTCCTC		422
CDKN2A	chr9:21970985-21971073	
CACACAGGAAACAGCTATGACCATGCTTCCTGGACACGCTGGT	423	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCAGGTACCGTGCGACAT		424
CDKN2A	chr9:21971015-21971121	
CACACAGGAAACAGCTATGACCATGGACCCCGCCACTCTCAC	425	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGCTCCTCAGCCAGGTCCA		426
CDKN2A	chr9:21971092-21971171	
CACACAGGAAACAGCTATGACCATGCCGAGTGGCGGAGCTG	427	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCACCAGCGTGTCCAGGAAG		428
CDKN2A	chr9:21971132-21971216	
CACACAGGAAACAGCTATGACCATGTGGCTCTGACCATTCTGTTCT	429	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGGTCGGGTGAGAGTGG		430
CDKN2A	chr9:21974669-21974742	
CACACAGGAAACAGCTATGACCATGGGGTCGGGTAGAGGAGGTG	431	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCTCCCGCTGCAGACCCT		432
CDKN2A	chr9:21974704-21974781	
CACACAGGAAACAGCTATGACCATGAGCCTTCGGCTGACTGG	433	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNGGCCTCCGACCGTAACTATT		434
CDKN2A	chr9:21974762-21974843	
CACACAGGAAACAGCTATGACCATGGGGGAGAGCAGGCAGC	435	
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNCACCTCCTCTACCCGACCC		436

*Coordinates refer to the human reference genome hg19 release (Genome Reference Consortium GRCh37, Feb 2009).

** N = bases with an equal probability of A, C, T, and G

Table40.txt

Table 40. Primers used to detect mutations in the 10-gene multiplex panel and TERT.

Gene	Forward Primer	SEQ ID NO	Chr	Hg19 Start-End	SEQ ID NO	Reverse Primer
CDKN2A	CTGTAGGACCTTCGGTGACTG	437	chr9	21968163-21968300	438	TGTGCCACACATCTTTGACC
CDKN2A	ACAAATTCTCAGATCATCAGTCCTC	439	chr9	21970874-21971002	440	AGGAGCTGGGCCATCG
CDKN2A	GCAGGTACCGTGCGACAT	441	chr9	21970967-21971091	442	CTTCCTGGACACGCTGGT
CDKN2A	GCTCCTCAGCCAGGTCCA	443	chr9	21970997-21971138	444	GACCCCGCCACTCTCACCCG
CDKN2A	CACCAGCGTGTCCAGGAAG	445	chr9	21971073-21971187	446	CCGAGTGGCGGAGCTG
CDKN2A	GGGTCGGGTGAGAGTGG	447	chr9	21971115-21971237	448	TGGCTCTGACCATTCTGTTCT
CDKN2A	CTCCCGCTGCAGACCCT	449	chr9	21974652-21974761	450	GGGTCGGGTAGAGGAGGTG
CDKN2A	GGCCTCCGACCGTAACTATT	451	chr9	21974684-21974798	452	AGCCTTCGGCTGACTGG
CDKN2A	CACCTCCTCTACCCGACCC	453	chr9	21974743-21974859	454	GGGGAGAGCAGGCAGC
ERBB2	TGTTCCATCCTCTGCTGTCA	455	chr17	37868148-37868263	456	GGGTATGTGGCTACATGTTCCT
FGFR3	GTCATCTGCCCCCACAGA	457	chr4	1803545-1803665	458	TGCGTCACTGTACACCTTGC
FGFR3	ACCACCAGGATGAACAGGAA	459	chr4	1806034-1806150	460	CCTCAACGCCCATGTCTTT
FGFR3	AGGCGTCCTACTGGCATGA	461	chr4	1807817-1807951	462	ACCGAGGACAACGTGATGA
HRAS	GTGGTCATTGATGGGGAGAC	463	chr11	533804-533926	464	GATGGCAAACACACACAGGA
HRAS	GTTCTGGATCAGCTGGATGG	465	chr11	534245-534371	466	GGCAGGAGACCCTGTAGGAG
KRAS	TTTCAGTGTTACTTACCTGTCTTGTCTT	467	chr12	25378532-25378655	468	GGAAATAAATGTGATTTGCCTTCT
KRAS	TGTACTGGTCCCTCATTGCAC	469	chr12	25380244-25380360	470	TTCTCCCTTCTCAGGATTCCTAC
KRAS	TGACTGAATATAAACTTGTGGTAGTTGG	471	chr12	25398203-25398317	472	TTTACCTCTATTGTTGGATCATATTCG
MET	TTTTGAGTTTGCAGACTTTCCA	473	chr7	116423378-116423501	474	TCAAGGTTGCTGATTTTGGTC
MLL	GTTGCCTTCCACAAACGTG	475	chr11	118359341-118359461	476	CAAGTCTGTTGTGAGCCCTTC
PIK3CA	GAAAAAGCCGAAGGTCACAA	477	chr3	178916781-178916899	478	CCCCCTCCATCAACTTCTTC
PIK3CA	ACATTCACGTAGGTTGCACAAA	479	chr3	178921436-178921555	480	TTATTCCAGACGCATTTCCAC

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PIK3CA	CTCCATTTTAGCACTTACCTGTGAC	481					
CAATGAATTAAGGGAAAATGACAAA	482	chr3	178936018-178936140				
PIK3CA	TCCAAAGCCTCTTGCTCAGT	483					
GCATGCCAATCTCTTCATAAATC	484	chr3	178951924-178952055				
PIK3CA	GATCCAATCCATTTTTGTTGTCCAG	485					
TTTGATGACATTGCATACATTCG	486	chr3	178951991-178952119				
PLEKHS1	ATGAAGAAAGTGCCCATAACAGA	487				CTTCCAAGGCTGGGATGAT	
488	chr10	115511551-115511660					
TP53	GAGGCTGTCAGTGGGGAAC	489				GCCACCTGAAGTCCAAAAAG	
490	chr17	7572893-7573009					
TP53	AGTCTGAGTCAGGCCCTTCTG	491				ATGTCATCTCTCCTCCCTGCT	
492	chr17	7572929-7573043					
TP53	TAGGAAGGCAGGGGAGTAGG	493				GTTCCGAGAGCTGAATGAGG	
494	chr17	7573881-7574007					
TP53	CTTCTCCCCCTCCTCTGTTG	495				CCCTGGCTCCTTCCCAG	
496	chr17	7573947-7574059					
TP53	CCAGCCAAAGAAGAAACCAC	497				AAGAAGAAAACGGCATTTTGAG	
498	chr17	7576782-7576898					
TP53	CAAGACTTAGTACCTGAAGGGTGAA	499					
TTTTATCACCTTTCCTTGCCTCT	500	chr17	7576840-7576956				
TP53	GCTTCTTGTCCTGCTTGCTT	501				CGTGTTTGTGCCTGTCCTG	
502	chr17	7576997-7577121					
TP53	GCGGAGATTCTCTTCCTCTGT	503				TGCCTCTTGCTTCTCTTTTCC	
504	chr17	7577068-7577188					
TP53	GTGGCAAGTGGCTCCTGA	505				TGGCTCTGACTGTACCACCATC	
506	chr17	7577480-7577606					
TP53	TCATCTTGGGCCTGTGTTATC	507				TGTGATGATGGTGAGGATGG	
508	chr17	7577513-7577635					
TP53	CTTAACCCCTCCTCCCAGAG	509				GTGGAAGGAAATTTGCGTGT	
510	chr17	7578137-7578260					
TP53	CGAAAAGTGTTTCTGTCATCCA	511				GTCCCCAGGCCTCTGATT	
512	chr17	7578211-7578326					
TP53	ACCAGCCCTGTCGTCTCTC	513				GCCATGGCCATCTACAAGC	
514	chr17	7578335-7578455					
TP53	CAACAAGATGTTTTGCCAACTG	515				CTCCGTCATGTGCTGTGACT	
516	chr17	7578417-7578540					
TP53	GGGGGTGTGGAATCAACC	517				GCCCTGACTTTCAACTCTGTCT	
518	chr17	7578475-7578593					
TP53	CCCTTCCCAGAAAACCTACC	519				GCATTGAAGTCTCATGGAAGC	
520	chr17	7579270-7579396					
TP53	CAGAATGCAAGAAGCCCAGA	521				CTGCACCAGCAGCTCCTAC	
522	chr17	7579338-7579463					
TP53	TGGGAAGGGACAGAAGATGA	523				AGCTCCCAGAATGCCAGAG	
524	chr17	7579388-7579501					
TP53	CGGTGTAGGAGCTGCTGG	525				GCAATGGATGATTTGATGCTG	
526	chr17	7579441-7579572					
TP53	TCATCTGGACCTGGGTCTTC	527				TGACTGCTCTTTTCACCCATC	
528	chr17	7579502-7579616					

Table40.txt

TP53	CAGCCCAACCCTTGTCCTT		529		AGCCCCCTAGCAGAGACCT
	530	chr17	7579679-7579789		
TP53	ACTGCCTTCCGGGTCACT		531		CCTTCCAATGGATCCACTCAC
	532	chr17	7579818-7579933		
VHL	CCGCCGTCTTCTTCAGG		533		CCCGGGTGGTCTGGAT
	534	chr3	10183506-10183620		
VHL	CGGCCTCCATCTCCTCCT		535		AGGCAGGCGTCGAAGAGTA
	536	chr3	10183581-10183700		
VHL	GGACTGCGATTGCAGAAGAT		537		CGGCCCGGAAGAGTCC
	538	chr3	10183645-10183773		
VHL	CGGCAGCGTTGGGTAG		539		GCTGCGCTCGGTGAACT
	540	chr3	10183717-10183837		
VHL	CGTGCTATCGTCCCTGCT		541		CCGTATGGCTCAACTTCGAC
	542	chr3	10183788-10183917		
VHL	GCTGTCCGTCAACATTGAGA		543		CCGGTGTGGCTCTTTAACAA
	544	chr3	10188159-10188293		
VHL	CCAAACTGAATTATTTGTGCCATC		545		
TCTATCCTGTACTTACCACAACAACC		546	chr3	10188250-10188376	
VHL	GGTGGTCTTCCAGATCTTCGT		547		GATTTGGTTTTTGCCCTTCC
	548	chr3	10191449-10191581		
VHL	TCAATCTCCCATCCGTTGAT		549		CAGGAGACTGGACATCGTCA
	550	chr3	10191532-10191649		
VHL	TCATCAGTACCATCAAAAGCTGA		551		CCCAAATGTGCAGAAAGACC
	552	chr3	10191580-10191703		
TERT	GGCCGCGGAAAGGAAG		553		CGTCCTGCCCCTTCACC
	554	chr5	1295189-1295314		

Chr, chromsome; Hg19, human genome 19.
The sequences listed include only the gene-specific component. Common sequences to allow a second round of amplification were appended to

Table41.txt

Table 41. Primers used for identity matching

Chr	Forward Primer	SEQ ID NO	Reverse Primer	SEQ ID NO	Hg19 Start-End
chr10	CCGTCCATACTCTTTCATTTGC	555	AGGGAGAACTAAAGGGGAACC	556	79548243-79548321
chr10	GCGACTGAAAGTAGAAGTCTGTCC	557	GTGCTTCTGGGTCCTGGTT	558	79552059-79552130
chr10	AGCGGCTATCTCCAGAGCAG	559	GGATTTTCAGGGCTCCGAGT	560	79560752-79560823
chr10	AGAGAGAGCCACGGTGACAG	561	CTGCCTCGTGAGGTTCAGA	562	79590640-79590714
chr10	TGCCAAGTCCATAGTCAGTCC	563	TATGTCATTCTGCCCCCAAG	564	79653363-79653444
chr10	TATGGAAGCATGGCCCTTT	565	GTGTTTGTTCTGGCCCACTC	566	79754079-79754158
chr10	GGGATGCTCCCACTCTAAGAA	567	CAGAAGGGCCGTTTACACTC	568	79876320-79876395
chr10	TTGTCAAAGTGCCTTCACTGAC	569	CAGGGAGCTGTTTTCAGGTG	570	79945906-79945977
chr10	TTGGAAGCAGCAGACATCAC	571	AGCATTTCTGGCCTCCTGT	572	79948701-79948771
chr10	AACTAAGTCCTTATCTGTGGTGGTG	573	GTGGGAGAAAGTCAGTTTGAATAAA	574	79984769-79984838
chr20	TTTTGATTTTGCATTGTTTTGC	575	TTTCACCCTCACCTCCGTTA	576	3631922-79736933
chr20	CCTCAGAATGGGTCAGAGTCA	577	GCCCTAGTACCCTGCCATCT	578	3632306-3632451
chr20	ACTACTTGCTGTGCCCACCT	579	AAACCCAAGTCACATCATTGAAC	580	3701090-3701233
chr20	AGGTGAGGTCAGGTCCCTTT	581	CTGCCAGCCATGCTCAAG	582	3763830-3763969
chr20	CACTTTCTCAGGGGGTGCT	583	TGATGGCTTCCATCTCCACT	584	3799550-3799692
chr20	ACCCCAAAGTTCCAGGAGAG	585	CACTGAAGTGCCCCTTCTTC	586	3807498-3807632
chr20	GATCCGTCTGTGTTGGCTTC	587	GATTGGTTGTAGCAGGCTGAA	588	3868644-3868790
chr20	AGGTACGCTAGTGATAGGAGTTGG	589	CCCTAATTTTTCATACTAAAGGAGCA	590	3889053-3889173
chr20	CGCTGAGAAAGGGAGATGAC	591	CCAGATGAGGGACCACTAACA	592	3912268-3912409
chr20	GCCCAATCCTAGCAGAATGA	593	GAATGCTCTGCACTCTGCAC	594	3912326-3912455
chr20	TCACCTCTGTTATGGGGCTCT	595	CTGATGCACAGGGACAGAAA	596	3912615-3912755
chr20	TTTTCTGGAATCCAACCTCTGT	597	TTTCCAAACCGGATTCTGTC	598	3913096-3913218
chr20	CCACATTTCAGAGCCCAGAG	599	GCCAAGGCTACACATGGTTT		

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	600	39497583-39497723		
chr20	TTTTAACTACTCATACATCCCCATGTC		601	CCCTCTTCCATCCCGTATTT
	602	39513796-39513915		
chr20	GTCCAAGAACAGGCCAGATG		603	GGAGAAAAGCCAAGTCAGCA
	604	39754578-39754717		
chr20	TCTGGGAAGCAAGTGTGATG		605	AACCCATGGCCCTACTTGAG
	606	39774138-39774257		

Chr = Chromsome. Hg19 = Human genome 19

Table42.txt

Table 42. Primers used for 10 gene Multiplex assay

Gene	Forward Primer	SEQ ID NO	Reverse Primer	SEQ ID NO	Chr	Hg19 Start-End
CDKN2A	CTGTAGGACCTTCGGTGACTG	607	TGTGCCACACATCTTTGACC	608	chr9	21968163-21968300
CDKN2A	ACAAATTCTCAGATCATCAGTCCTC	609	AGGAGCTGGGCCATCG	610	chr9	21970874-21971002
CDKN2A	GCAGGTACCGTGCGACAT	611	CTTCCTGGACACGCTGGT	612	chr9	21970967-21971091
CDKN2A	GCTCCTCAGCCAGGTCCA	613	GACCCCGCCACTCTCACCCG	614	chr9	21970997-21971138
CDKN2A	CACCAGCGTGTCCAGGAAG	615	CCGAGTGGCGGAGCTG	616	chr9	21971073-21971187
CDKN2A	GGGTCGGGTGAGAGTGG	617	TGGCTCTGACCATTCTGTTCT	618	chr9	21971115-21971237
CDKN2A	CTCCCGCTGCAGACCCT	619	GGGTCGGGTAGAGGAGGTG	620	chr9	21974652-21974761
CDKN2A	GGCCTCCGACCGTAACTATT	621	AGCCTTCGGCTGACTGG	622	chr9	21974684-21974798
CDKN2A	CACCTCCTCTACCCGACCC	623	GGGGAGAGCAGGCAGC	624	chr9	21974743-21974859
ERBB2	TGTTCCATCCTCTGCTGTCA	625	GGGTATGTGGCTACATGTTCCT	626	chr17	37868148-37868263
FGFR3	GTCATCTGCCCCCACAGA	627	TGCGTCACTGTACACCTTGC	628	chr4	1803545-1803665
FGFR3	ACCACCAGGATGAACAGGAA	629	CCTCAACGCCCATGTCTTT	630	chr4	1806034-1806150
FGFR3	AGGCGTCCTACTGGCATGA	631	ACCGAGGACAACGTGATGA	632	chr4	1807817-1807951
HRAS	GTGGTCATTGATGGGGAGAC	633	GATGGCAAACACACACAGGA	634	chr11	533804-533926
HRAS	GTTCTGGATCAGCTGGATGG	635	GGCAGGAGACCCTGTAGGAG	636	chr11	534245-534371
KRAS	TTTCAGTGTTACTTACCTGTCTTGTCTT	637	GGAAATAAATGTGATTTGCCTTCT	638	chr12	25378532-25378655
KRAS	TGTACTGGTCCCTCATTGCAC	639	TTCTCCCTTCTCAGGATTCCTAC	640	chr12	25380244-25380360
KRAS	TGACTGAATATAAACTTGTGGTAGTTGG	641	TTTACCTCTATTGTTGGATCATATTCG	642	chr12	25398203-25398317
MET	TTTTGAGTTTGCAGACTTTCCA	643	TCAAGGTTGCTGATTTTGGTC	644	chr7	116423378-116423501
MLL	GTTGCCTTCCACAAACGTG	645	CAAGTCTGTTGTGAGCCCTTC	646	chr11	118359341-118359461
PIK3CA	GAAAAAGCCGAAGGTCACAA	647	CCCCCTCCATCAACTTCTTC	648	chr3	178916781-178916899
PIK3CA	ACATTCACGTAGGTTGCACAAA	649	TTATTCCAGACGCATTTCCAC	650	chr3	178921436-178921555
PIK3CA	CTCCATTTTAGCACTTACCTGTGAC	651	CAATGAATTAAGGGAAAATGACAAA			

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652	chr3	178936018-178936140			
PIK3CA	TCCAAAGCCTCTTGCTCAGT		653	GCATGCCAATCTCTTCATAAATC	
654	chr3	178951924-178952055			
PIK3CA	GATCCAATCCATTTTTGTTGTCCAG		655	TTTGATGACATTGCATACATTCG	
656	chr3	178951991-178952119			
PLEKHS1	ATGAAGAAAGTGCCCATAACAGA		657	CTTCCAAGGCTGGGATGAT	
658	chr10	115511551-115511660			
TP53	GAGGCTGTCAGTGGGGAAC		659	GCCACCTGAAGTCCAAAAAG	
660	chr17	7572893-7573009			
TP53	AGTCTGAGTCAGGCCCTTCTG		661	ATGTCATCTCTCCTCCCTGCT	
662	chr17	7572929-7573043			
TP53	TAGGAAGGCAGGGGAGTAGG		663	GTTCCGAGAGCTGAATGAGG	
664	chr17	7573881-7574007			
TP53	CTTCTCCCCCTCCTCTGTTG		665	CCCTGGCTCCTTCCCAG	
666	chr17	7573947-7574059			
TP53	CCAGCCAAAGAAGAAACCAC		667	AAGAAGAAAACGGCATTTTGAG	
668	chr17	7576782-7576898			
TP53	CAAGACTTAGTACCTGAAGGGTGAA		669	TTTTATCACCTTTCCTTGCCTCT	
670	chr17	7576840-7576956			
TP53	GCTTCTTGTCCTGCTTGCTT		671	CGTGTTTGTGCCTGTCCTG	
672	chr17	7576997-7577121			
TP53	GCGGAGATTCTCTTCCTCTGT		673	TGCCTCTTGCTTCTCTTTTCC	
674	chr17	7577068-7577188			
TP53	GTGGCAAGTGGCTCCTGA		675	TGGCTCTGACTGTACCACCATC	
676	chr17	7577480-7577606			
TP53	TCATCTTGGGCCTGTGTTATC		677	TGTGATGATGGTGAGGATGG	
678	chr17	7577513-7577635			
TP53	CTTAACCCCTCCTCCCAGAG		679	GTGGAAGGAAATTTGCGTGT	
680	chr17	7578137-7578260			
TP53	CGAAAAGTGTTTCTGTCATCCA		681	GTCCCCAGGCCTCTGATT	
682	chr17	7578211-7578326			
TP53	ACCAGCCCTGTCGTCTCTC		683	GCCATGGCCATCTACAAGC	
684	chr17	7578335-7578455			
TP53	CAACAAGATGTTTTGCCAACTG		685	CTCCGTCATGTGCTGTGACT	
686	chr17	7578417-7578540			
TP53	GGGGGTGTGGAATCAACC		687	GCCCTGACTTTCAACTCTGTCT	
688	chr17	7578475-7578593			
TP53	CCCTTCCCAGAAAACCTACC		689	GCATTGAAGTCTCATGGAAGC	
690	chr17	7579270-7579396			
TP53	CAGAATGCAAGAAGCCCAGA		691	CTGCACCAGCAGCTCCTAC	
692	chr17	7579338-7579463			
TP53	TGGGAAGGGACAGAAGATGA		693	AGCTCCCAGAATGCCAGAG	
694	chr17	7579388-7579501			
TP53	CGGTGTAGGAGCTGCTGG		695	GCAATGGATGATTTGATGCTG	
696	chr17	7579441-7579572			
TP53	TCATCTGGACCTGGGTCTTC		697	TGACTGCTCTTTTCACCCATC	
698	chr17	7579502-7579616			
TP53	CAGCCCAACCCTTGTCCTT		699	AGCCCCCTAGCAGAGACCT	

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	700	chr17	7579679-7579789		
TP53	ACTGCCTTCCGGGTCACT		701	CCTTCCAATGGATCCACTCAC	
	702	chr17	7579818-7579933		
VHL	CCGCCGTCTTCTTCAGG		703	CCCGGGTGGTCTGGAT	
	704	chr3	10183506-10183620		
VHL	CGGCCTCCATCTCCTCCT		705	AGGCAGGCGTCGAAGAGTA	
	706	chr3	10183581-10183700		
VHL	GGACTGCGATTGCAGAAGAT		707	CGGCCCGGAAGAGTCC	
	708	chr3	10183645-10183773		
VHL	CGGCAGCGTTGGGTAG		709	GCTGCGCTCGGTGAACT	
	710	chr3	10183717-10183837		
VHL	CGTGCTATCGTCCCTGCT		711	CCGTATGGCTCAACTTCGAC	
	712	chr3	10183788-10183917		
VHL	GCTGTCCGTCAACATTGAGA		713	CCGGTGTGGCTCTTTAACAA	
	714	chr3	10188159-10188293		
VHL	CCAAACTGAATTATTTGTGCCATC		715	TCTATCCTGTACTTACCACAACAACC	
	716	chr3	10188250-10188376		
VHL	GGTGGTCTTCCAGATCTTCGT		717	GATTTGGTTTTTGCCCTTCC	
	718	chr3	10191449-10191581		
VHL	TCAATCTCCCATCCGTTGAT		719	CAGGAGACTGGACATCGTCA	
	720	chr3	10191532-10191649		
VHL	TCATCAGTACCATCAAAAGCTGA		721	CCCAAATGTGCAGAAAGACC	
	722	chr3	10191580-10191703		
TERT	GGCCGCGGAAAGGAAG		723	CGTCCTGCCCCTTCACC	
	724	chr5	1295189-1295314		

Chr = Chromsome. Hg19 = Human genome 19

Table43.txt

Table 43. Human samples, bottleneck sequencing library preparation, and sequencing information

BotSeqS Library ID	Sample Name	Technical Replicate Performed (BotSeqS Library ID Replicate)	Biological Replicate Performed (Sample Name Replicate)
		Normal Human Tissue	Cohort
Bot01	AA_105	yes* (Bot23)	yes (AA_105, AA_124, AA_126)
		Kidney Cortex	Aristolochic acid-associated UTUC#
Bot02	AA_124	yes* (Bot24)	yes (AA_105, AA_124, AA_126)
		Kidney Cortex	Aristolochic acid-associated UTUC#
Bot03	AA_126	yes* (Bot25)	yes (AA_105, AA_124, AA_126)
		Kidney Cortex	Aristolochic acid-associated UTUC#
Bot04	SA_117	yes* (Bot26)	yes (SA_117, SA_118, AA_119)
		Kidney Cortex	Smoking-assocated UTUC#
Bot05	SA_118	yes* (Bot27)	yes (SA_117, SA_118, AA_119)
		Kidney Cortex	Smoking-assocated UTUC#
Bot06	SA_119	yes* (Bot28)	yes (SA_117, SA_118, AA_119)
		Kidney Cortex	Smoking-assocated UTUC#
Bot07	COL229	no	yes (COL229, COL231)
		Colon Epithelium, Splenic Flexure	Control, child colon
Bot08	COL231	no	yes (COL229, COL231)
		Colon Epithelium, Cecum	Control, child colon
Bot09	COL232	no	yes (COL232, COL233, COL234)
		Colon Epithelium, Cecum	Control, old adult colon
Bot10	COL233	no	yes (COL232, COL233, COL234)
		Colon Epithelium,Cecum	Control, old adult colon
Bot11	COL234	no	yes (COL232, COL233, COL234)
		Colon Epithelium, Cecum	Control, old adult colon
Bot12	COL235	yes (Bot18)	yes (COL235, COL236, COL237, COL373, COL374, COL375)
		Colon Epithelium, Sigmoid	Control, young adult colon
Bot13	COL236	yes (Bot19)	yes (COL235, COL236, COL237, COL373, COL374, COL375)
		Colon Epithelium, Sigmoid	Control, young adult colon
Bot14	COL237	no	yes (COL235, COL236, COL237, COL373, COL374, COL375)
		Colon Epithelium	Control, young adult colon

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Bot15	COL238	no	yes (COL238, COL239)		
		Colon Epithelium	PMS2 -/- ##		
Bot16	COL239	no	yes (COL238, COL239)		
		Colon Epithelium	PMS2 -/- ##		
Bot17	SIN230	no	no		
		Small Intestine, Duodenum	Control, child small intestine		
Bot18	COL235	yes (Bot12)	yes (COL235, COL236, COL237, COL373, COL374, COL375)		
		Colon Epithelium, Sigmoid	Control, young adult colon		
Bot19	COL236	yes (Bot13)	yes (COL235, COL236, COL237, COL373, COL374, COL375)		
		Colon Epithelium, Sigmoid	Control, young adult colon		
Bot20	COL373	no	yes (COL235, COL236, COL237, COL373, COL374, COL375)		
		Colon Epithelium	Control, young adult colon		
Bot21	COL374	no	yes (COL235, COL236, COL237, COL373, COL374, COL375)		
		Colon Epithelium	Control, young adult colon		
Bot22	COL375	no	yes (COL235, COL236, COL237, COL373, COL374, COL375)		
		Colon Epithelium	Control, young adult colon		
Bot23	AA_105	yes* (Bot1)	yes (AA_105, AA_124, AA_126)		
		Kidney Cortex	Aristolochic acid-associated UTUC#		
Bot24	AA_124	yes* (Bot2)	yes (AA_105, AA_124, AA_126)		
		Kidney Cortex	Aristolochic acid-associated UTUC#		
Bot25	AA_126	yes* (Bot3)	yes (AA_105, AA_124, AA_126)		
		Kidney Cortex	Aristolochic acid-associated UTUC#		
Bot26	SA_117	yes* (Bot4)	yes (SA_117, SA_118, AA_119)		
		Kidney Cortex	Smoking-assocated UTUC#		
Bot27	SA_118	yes* (Bot5)	yes (SA_117, SA_118, AA_119)		
		Kidney Cortex	Smoking-assocated UTUC#		
Bot28	SA_119	yes* (Bot6)	yes (SA_117, SA_118, AA_119)		
		Kidney Cortex	Smoking-assocated UTUC#		
Bot29	KID034	no	yes (KID034, KID035, KID036, KID037)		
		Kidney Cortex	Control (Nonsmoker), old adult kidney		
Bot30	KID035	no	yes (KID034, KID035, KID036, KID037)		
		Kidney Cortex	Control (Nonsmoker), old adult kidney		
Bot31	KID036	no	yes (KID034, KID035, KID036, KID037)		
		Kidney Cortex	Control		

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(Nonsmoker), old adult kidney
Bot32 KID037 no yes (KID034, KID035, KID036, KID037) Kidney Cortex Control (Nonsmoker), old adult kidney
Bot33 KID038 yes (Bot34, Bot35) no Kidney Cortex, Right Control (Nonsmoker), infant kidney
Bot34 KID038 yes (Bot33, Bot35) no Kidney Cortex, Left Sector 1 Control (Nonsmoker), infant kidney
Bot35 KID038 yes (Bot33, Bot34) no Kidney Cortex, Left Sector 2 Control (Nonsmoker), infant kidney
Bot36 BRA01 no yes (BRA01, BRA02, BRA03) Brain, Frontal Cortex Control, child brain
Bot37 BRA02 no yes (BRA01, BRA02, BRA03) Brain, Frontal Cortex Control, child brain
Bot38 BRA03 no yes (BRA01, BRA02, BRA03) Brain, Frontal Cortex Control, child brain
Bot39 BRA04 no yes (BRA04, BRA05, BRA06) Brain, Frontal Cortex Control, young adult brain
Bot40 BRA05 no yes (BRA04, BRA05, BRA06) Brain, Frontal Cortex Control, young adult brain
Bot41 BRA06 no yes (BRA04, BRA05, BRA06) Brain, Frontal Cortex Control, young adult brain
Bot42 BRA07 no yes (BRA07, BRA08, BRA09) Brain, Frontal Cortex Control, old adult brain
Bot43 BRA08 no yes (BRA07, BRA08, BRA09) Brain, Frontal Cortex Control, old adult brain
Bot44 BRA09 no yes (BRA07, BRA08, BRA09) Brain, Frontal Cortex Control, old adult brain
*100-fold difference in dilution in replicate samples
#Patients previously reported in PMID 23926200
##Patients previously reported in PMID 7661930 (as Family 12), PMID 7632227, and PMID 15077197

Table43.txt

Input DNA quantitated by Qubit (ng)	Fold-dilution of Adapter-ligated Molecules	Number of PCR Cycles	Final Library Peak Size on Agilent TapeStation (bp)*	Ethnicity	Sex	Age (years unless note	BotS Library Prep Date	DNA/Tissue Source
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		522	Taiwanese	F	78	12/9/2013	
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		514	Taiwanese	M	82	12/9/2013	
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		534	Taiwanese	F	78	12/9/2013	
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		536	Taiwanese	M	66	12/9/2013	
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		532	Taiwanese	M	59	12/9/2013	
								Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan
500	10,000,20		484	Taiwanese	M	69	12/9/2013	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		618	African American	M	3	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		616	Caucasian	M	8	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		619	Caucasian	M	98	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		589	Caucasian	F	96	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		619	Caucasian	F	95	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
500	1018		682	Caucasian	M	26	1/24/2014	
								Johns Hopkins School of Medicine, Baltimore, MD
				Caucasian	M	26	1/24/2014	

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500 1018 667
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian M 22 1/24/2014
500 1018 622
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian M 16 12/9/2013
129 20 330
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian F 18 12/9/2013
34 20 316
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian M 6 1/24/2014
500 1018 604
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian M 26 9/22/2014
500 1018 669
Johns Hopkins School of Medicine, Baltimore, MD
Caucasian M 26 9/22/2014
500 1018 657
University of Maryland Brain and Tissue Bank, Baltimore, MD
Caucasian M 36 9/22/2014
824 1018 648
University of Maryland Brain and Tissue Bank, Baltimore, MD
Caucasian M 21 9/22/2014
380 1018 616
University of Maryland Brain and Tissue Bank, Baltimore, MD
Caucasian F 38 9/22/2014
825 1018 565
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese F 78
9/22/2014 nd 1018 611
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese M 82
9/22/2014 500 1018 598
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese F 78
9/22/2014 500 1018 628
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese M 66
9/22/2014 nd 1018 610
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese M 59
9/22/2014 500 1018 587
Drs. C-H Chen and Y-S Pu, National Taiwan University Hospital and College of Medicine, Taipei, Taiwan Taiwanese M 69
9/22/2014 nd 1018 613
Windber Research Institute, Windber, PA
Caucasian F 55 9/22/2014

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1000 1018 659
Windber Research Institute, Windber, PA
Caucasian F 45 9/22/2014
1000 1018 660
Windber Research Institute, Windber, PA
Caucasian F 77 9/22/2014
1000 1018 691
Windber Research Institute, Windber, PA
Caucasian F 80 9/22/2014
1000 1018 619
Windber Research Institute, Windber, PA
Caucasian M 5 months 9/22/2014
1000 1018 646
Windber Research Institute, Windber, PA
Caucasian M 5 months 9/22/2014
1000 1018 650
Windber Research Institute, Windber, PA
Caucasian M 5 months 9/22/2014
1000 1018 695
University of Maryland Brain and Tissue Bank, Baltimore, MD
African American M 54 days 1/23/2015
500 1018 626
University of Maryland Brain and Tissue Bank, Baltimore, MD
African American M 1 year 259 days 1/23/2015
500 1018 650
University of Maryland Brain and Tissue Bank, Baltimore, MD
Caucasian M 8 years 286 days 1/23/2015
500 1018 684
University of Miami Brain Endowment Bank, Miami, FL
African American M 20 1/23/2015
500 1018 636
University of Miami Brain Endowment Bank, Miami, FL
African American M 22 1/23/2015
500 1018 600
University of Miami Brain Endowment Bank, Miami, FL
African American F 25 1/23/2015
500 1018 641
University of Miami Brain Endowment Bank, Miami, FL
Caucasian M 90 1/23/2015
500 1018 631
University of Miami Brain Endowment Bank, Miami, FL
Caucasian F 94 1/23/2015
500 1018 615
University of Miami Brain Endowment Bank, Miami, FL
Caucasian F 95 1/23/2015
500 1018 674

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Illumina Platform	Alignment	% Matching	Number of Sequencing Variants Matched	Run Date	Run Type	Number of Sequencing Cycles	Clusters Pass Filter
HiSeq 2500 Rapid Run	eland_pair	hg19	87% in WGS	2/27/2014	PE	2X100	46,637,831
HiSeq 2500 Rapid Run	eland_pair	hg19	84% in WGS	2/27/2014	PE	2X100	48,702,256
HiSeq 2500 Rapid Run	eland_pair	hg19	86% in WGS	2/27/2014	PE	2X100	57,023,695
HiSeq 2500 Rapid Run	eland_pair	hg19	87% in WGS	2/27/2014	PE	2X100	62,775,107
HiSeq 2500 Rapid Run	eland_pair	hg19	88% in WGS	2/27/2014	PE	2X100	43,516,933
HiSeq 2500 Rapid Run	eland_pair	hg19	83% in WGS	2/27/2014	PE	2X100	44,519,862
HiSeq 2500 Rapid Run	eland_pair	hg19	88% in WGS	5/21/2014	PE	2X100	62,223,353
HiSeq 2500 Rapid Run	eland_pair	hg19	89% in WGS	5/21/2014	PE	2X100	63,368,196
HiSeq 2500 Rapid Run	eland_pair	hg19	89% in WGS	5/21/2014	PE	2X100	65,075,864
HiSeq 2500 Rapid Run	eland_pair	hg19	89% in WGS	5/21/2014	PE	2X100	59,863,503
HiSeq 2500 Rapid Run	eland_pair	hg19	88% in WGS	5/21/2014	PE	2X100	79,111,391
HiSeq 2500 Rapid Run	eland_pair	hg19	86% in WGS	5/21/2014	PE	2X100	64,923,637
HiSeq 2500 Rapid Run	eland_pair	hg19	88% in WGS	5/21/2014	PE	2X100	96,227,518
HiSeq 2500 Rapid Run	eland_pair	hg19	88% in WGS	5/21/2014	PE	2X100	70,564,807
HiSeq 2500 Rapid Run	eland_pair	hg19	45% no WGS	2/27/2014	PE	2X100	187,952,063
HiSeq 2500 Rapid Run	eland_pair	hg19	37% no WGS	2/27/2014	PE	2X100	79,171,450
HiSeq 2500 Rapid Run	eland_pair	hg19	89% in WGS	5/21/2014	PE	2X100	81,123,873
HiSeq 2500 Rapid Run				10/14/2014	PE	2X100	78,976,262

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eland_pair	hg19	86%		5,322,33		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	86,042,845
eland_pair	hg19	88%		4,459,46		
HiSeq 2500 Rapid Run		10/6/2014		PE	2X100	79,589,144
eland_pair	hg19	88%		4,488,37		
HiSeq 2500 Rapid Run		10/6/2014		PE	2X100	63,357,946
eland_pair	hg19	89%		4,455,78		
HiSeq 2500 Rapid Run		10/6/2014		PE	2X100	85,684,748
eland_pair	hg19	90%		4,470,04		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	67,544,525
eland_pair	hg19	89%		4,517,74		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	79,846,290
eland_pair	hg19	84%		4,530,65		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	67,875,326
eland_pair	hg19	84%		4,472,46		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	37,232,047
eland_pair	hg19	87%		4,477,92		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	41,659,940
eland_pair	hg19	86%		4,512,47		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	47,806,459
eland_pair	hg19	86%		4,509,80		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	79,793,770
eland_pair	hg19	89%		4,482,44		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	59,455,178
eland_pair	hg19	89%		4,508,15		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	68,583,262
eland_pair	hg19	89%		4,483,42		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	88,502,675
eland_pair	hg19	89%		4,468,84		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	91,991,340
eland_pair	hg19	89%		4,463,95		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	75,175,483
eland_pair	hg19	89%		4,463,95		
HiSeq 2500 Rapid Run		10/14/2014		PE	2X100	75,375,396
eland_pair	hg19	89%		4,463,95		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	95,664,832
eland_pair	hg19	89%		5,531,90		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	77,202,292
eland_pair	hg19	89%		5,490,83		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	72,675,364
eland_pair	hg19	89%		4,550,46		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	63,145,478
eland_pair	hg19	89%		5,397,98		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	70,791,299
eland_pair	hg19	89%		5,356,99		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	108,709,209
eland_pair	hg19	89%		5,433,34		
HiSeq 2500 Rapid Run		2/11/2015		PE	2X100	98,612,463

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eland_pair	hg19	89%	4,465,50		
HiSeq 2500 Rapid Run	2/11/2015		PE	2X100	63,774,477
eland_pair	hg19	90%	4,487,09		
HiSeq 2500 Rapid Run	2/11/2015		PE	2X100	65,950,850
eland_pair	hg19	90%	4,521,82		
				SUM	3,203,800,239
				AVERAGE	72,813,642
				STDEV	24,013,807
				MEDIAN	69,574,035
				MAX	187,952,063
				MIN	37,232,047

Table44.txt

Table 44. First filtering applied to mtDNA templates as part of BotSeqS pipeline

		Filter						
		Number of Templates Remaining After Applied Filter						
		Frequency						
		mtDNA only						
		-	+	+	+	+	+	
	Median	of templates						
Watson AND Crick duplicate families only (cutoff number of PCR duplicates per family)		-	-	+ (>=1)	+ (>=2)	+ (>=2)	+ (>=2)	
	number	with both						
Exclude templates that include high frequency mutations (i.e. homopolymers, > 1 mutation p		-	-	-	-	+	+	
	of PCR	Watson and Crick						
Exclude templates that map to repeatMasker								
		-	-	-	-	-	+	
		duplicates	duplicates					
BotSeqS Library ID						Sample Name		
Filter A		Filter B	Filter C	Filter D		Filter E	Filter F*	
Filter B	Filter C/Filter B							
Bot01						AA_105		
384019		687	140	134		132	126	
66	20%							
Bot02						AA_124		
626591		1480	371	342		335	317	
37	25%							
Bot03						AA_126		
501708		2639	611	579		569	556	
64	23%							
Bot04						SA_117		
830645		2903	564	535		533	511	
31	19%							
Bot05						SA_118		
425949		475	82	76		76	75	
61	17%							
Bot06						SA_119		
564312		5263	1375	1285		1271	1213	
42	26%							
Bot07						COL229		
5665038		9364	4042	3013		3002	2858	
5	43%							
Bot08						COL231		
5469318		7196	3192	2473		2468	2344	
5	44%							
Bot09						COL232		
3532725		5136	2322	2052		2047	1961	
8	45%							
Bot10						COL233		

Table44.txt

4720633	9629	4328	3581	3575	3411	
6	45%					
Bot11				COL234		
5024306	8581	3825	3267	3263	3111	
7	45%					
Bot12				COL235		
3220085	6788	3067	2718	2712	2573	
8	45%					
Bot13				COL236		
4266043	7670	3551	3225	3215	3055	
11	46%					
Bot14				COL237		
3923375	7760	2825	2608	2598	2484	
11	36%					
Bot15				COL238*		
10913590	145746	15522	2735	2434	2352	
1	11%					
Bot16				COL239*		
461475	1899	237	210	192	181	
6	12%					
Bot17				SIN230		
5561560	9636	4485	3854	3849	3664	
7	47%					
Bot18				COL235		
5072534	10328	5453	4744	4735	4496	
8	53%					
Bot19				COL236		
6838232	11922	6256	5312	5304	5022	
7	52%					
Bot20				COL373		
3927830	7915	3870	3588	3556	3410	
12	49%					
Bot21				COL374		
2447968	9013	4250	4048	4039	3861	
17	47%					
Bot22				COL375		
3083857	9829	4746	4554	4536	4383	
18	48%					
Bot23				AA_105		
6686482	8834	1809	1426	1422	1376	
4	20%					
Bot24				AA_124		
2018059	3853	1173	1090	1081	1042	
17	30%					
Bot25				AA_126		
2619825	9450	2426	2240	2230	2127	
11	26%					
Bot26				SA_117		

Table44.txt

2159999	5649	1091	941	937	897	
7	19%					
Bot27				SA_118		
2235258	1796	341	298	297	285	
8	19%					
Bot28				SA_119		
4191245	18604	4677	4112	4097	3903	
7	25%					
Bot29				KID034		
10115634	70997	36642	20989	20946	19970	
4	52%					
Bot30				KID035		
7731899	52798	23728	13700	13687	13115	
3	45%					
Bot31				KID036		
7007098	34320	17051	11454	11441	10856	
4	50%					
Bot32				KID037		
7384650	36610	19875	17722	17691	16903	
8	54%					
Bot33				KID038		
8023064	14639	7592	6210	6196	5907	
6	52%					
Bot34				KID038		
5172516	8195	3848	3306	3300	3159	
8	47%					
Bot35				KID038		
4382471	8912	3942	3407	3400	3231	
9	44%					
Bot36				BRA01		
4286811	31355	18814	17881	17727	16940	
16	60%					
Bot37				BRA02		
3449630	39215	23820	22407	22372	21352	
12	61%					
Bot38				BRA03		
2055100	31806	19651	18812	18744	17903	
18	62%					
Bot39				BRA04		
3172695	48924	30118	27778	27709	26415	
11	62%					
Bot40				BRA05		
2455396	36028	21272	20396	20242	19345	
17	59%					
Bot41				BRA06		
3780301	56869	34562	33427	33347	31808	
19	61%					
Bot42				BRA07		

Table44.txt

	3208673	20657	11373	10954	10904	10384
21	55%					
	Bot43				BRA08	
	2330483	23005	11750	11092	11063	10531
15	51%					
	Bot44				BRA09	
	2840263	44292	26676	25281	25167	23978
13	60%					
	AVERAGE					
	3972030.57	20196.9773	9030.56818	7496.72727	7464.56818	7122.52273
15	41%					
	STANDARD DEVIATION					
	2529202.17	26000.5306	10171.8717	8685.33072	8661.20791	8262.04426
16	15%					
	MEDIAN					
	3923375	9629	4328	3588	3575	3411
9	45%					
	MAX					
	10913590	145746	36642	33427	33347	31808
66	62%					
	MIN					
	384019	475	82	76	76	75
1	11%					

*Filter F is the final criteria for the BotSeqS pipeline

Table45.txt

Table 45. First filtering applied to nuclear DNA templates as part of BotSeqS pipeline

	Filter					
	Number of Templates Remaining After Applied Filter					
	Frequency					
	Nuclear DNA only					
	-	+	+	+	+	+
Median	of templates					
Watson AND Crick duplicate families only (cutoff number of PCR duplicates per family)	-	-	+ (>=1)	+ (>=2)	+ (>=2)	+ (>=2)
Number	with both					
Exclude templates that include high frequency mutations (i.e. homopolymers, > 1 mutation	-	-	-	-	+	+
of PCR	Watson and Crick					
Exclude templates that map to repetitive DNA or structural variants						
-	-	-	-	-	+	
Duplicates	duplicates					
BotSeqS Library ID					Sample Name	
Filter A	Filter B	Filter C	Filter D	Filter E	Filter F*	Filter B Filter C/Filter B
Bot01				AA_105		
384019	383332	81040	75995	71363	3188	74 21%
Bot02				AA_124		
626591	625111	154275	144908	137703	5944	44 25%
Bot03				AA_126		
501708	499069	107073	100366	93935	3920	68 21%
Bot04				SA_117		
830645	827742	150176	140388	133763	5622	35 18%
Bot05				SA_118		
425949	425474	77785	73172	68781	3004	65 18%
Bot06				SA_119		
564312	559049	130510	121796	115796	5176	42 23%
Bot07				COL229		
5665038	5655674	2425593	1894117	1852142	76474	5 43%
Bot08				COL231		
5469318	5462122	2468654	1987721	1945117	80053	5 45%
Bot09				COL232		
3532725	3527589	1544164	1389818	1353285	55580	9 44%

Table45.txt

Bot10				COL233		
4720633	4711004	2051364	1709635	1671402	69497	6
44%						
Bot11				COL234		
5024306	5015725	2212381	1954408	1906159	79225	8
44%						
Bot12				COL235		
3220085	3213297	1429886	1296856	1261253	51819	9
44%						
Bot13				COL236		
4266043	4258373	1943833	1796629	1744052	71113	12
46%						
Bot14				COL237		
3923375	3915615	1432119	1330812	1288692	52536	12
37%						
Bot15				COL238		
10913590	10767844	875763	136482	134451	6116	1
8%						
Bot16				COL239		
461475	459576	67578	59333	56144	2127	7
15%						
Bot17				SIN230		
5561560	5551924	2538902	2231634	2178131	88550	7
46%						
Bot18				COL235		
5072534	5062206	2710636	2443300	2379414	96067	10
54%						
Bot19				COL236		
6838232	6826310	3622249	3231731	3156140	128559	8
53%						
Bot20				COL373		
3927830	3919915	1854424	1749498	1699084	69474	14
47%						
Bot21				COL374		
2447968	2438955	1116769	1063645	1027825	41441	18
46%						
Bot22				COL375		
3083857	3074028	1424813	1360843	1314834	54777	19
46%						
Bot23				AA_105		
6686482	6677648	1338397	1068698	1045927	45059	4
20%						
Bot24				AA_124		
2018059	2014206	602826	567268	546181	22768	18
30%						
Bot25				AA_126		
2619825	2610375	647673	599001	580580	23773	12
25%						

Table45.txt

Bot26				SA_117		
2159999	2154350	399109	353894	344828	14241	
8	19%					
Bot27				SA_118		
2235258	2233462	427282	385529	375111	15618	
9	19%					
Bot28				SA_119		
4191245	4172641	1079813	961893	937068	38375	
7	26%					
Bot29				KID034		
10115634	10044637	5277007	3219056	3164707	133353	
4	53%					
Bot30				KID035		
7731899	7679101	3518436	2184528	2147222	89421	
4	46%					
Bot31				KID036		
7007098	6972778	3549219	2521538	2475837	102859	
5	51%					
Bot32				KID037		
7384650	7348040	3920526	3576344	3490785	144302	
9	53%					
Bot33				KID038		
8023064	8008425	4231193	3669855	3587946	147220	
7	53%					
Bot34				KID038		
5172516	5164321	2449399	2199573	2144965	86446	
9	47%					
Bot35				KID038		
4382471	4373559	1891298	1713295	1666800	66635	
11	43%					
Bot36				BRA01		
4286811	4255456	2551648	2441604	2364396	95344	
16	60%					
Bot37				BRA02		
3449630	3410415	2042906	1925295	1871365	75495	
12	60%					
Bot38				BRA03		
2055100	2023294	1226314	1171761	1132741	45521	
19	61%					
Bot39				BRA04		
3172695	3123771	1867340	1728254	1682306	68571	
11	60%					
Bot40				BRA05		
2455396	2419368	1380183	1321006	1280222	52339	
16	57%					
Bot41				BRA06		
3780301	3723432	2179063	2083096	2011703	81536	
18	59%					

Table45.txt

Bot42				BRA07		
3208673	3188016	1706550	1631909	1573847	63640	
20	54%					
Bot43				BRA08		
2330483	2307478	1150268	1080825	1048020	43310	
15	50%					
Bot44				BRA09		
2840263	2795971	1640937	1552442	1507205	60641	
13	59%					
AVERAGE						
3972030.568	3951833.591	1715849.409	1460221.614	1422027.909	58334.75	
16	41%					
STANDARD DEVIATION						
2529202.171	2513784.053	1232297.947	982539.0582	961092.0203	39442.11157	
17	15%					
MEDIAN						
3923375	3915615	1706550	1552442	1507205	60641	
11	46%					
MAX						
10913590	10767844	5277007	3669855	3587946	147220	
74	61%					
MIN						
384019	383332	67578	59333	56144	2127	
1	8%					

*Filter F is the final criteria for the BotSeqS pipeline

Table46.txt

Table 46. Second filtering applied to mtDNA changes as part of BotSeqS pipeline

Filter	Number of Changes Remaining After Applied Filter
mtDNA only	-
Single-base substitution only	-
Average quality score >= 30	-
Read 1 >=2 Watson duplicates with >=90% mutation fraction only	-
Read 2 >=2 Crick duplicates with >=90% mutation fraction only	-
Exclude all variants called in WGS	-
Exclude all variants in dbSNP142	-
Exclude calls that map to repeatMasker	-
Exclude visual artifacts and high frequency mutations (i.e. homopolymers, cycle 6 and 7, > 1 change per templ	-

BotSeqS Library ID	Sample Name	Filter A	Filter B	Filter C	Filter D	Filter E	Filter F	Filter G	Filter H	Filter I	Filter J
Bot01	AA_105	7353265	12925	12840	1289	71	104	5	31	48	1
Bot02	AA_124	8904153	20699	20557	2172	177	197	10	26	142	2
Bot03	AA_126	11151270	62891	62529	5216	374	370	15	74	235	6
Bot04	SA_117	10639408	37864	37645	3798	378	339	19	64	158	10
Bot05	SA_118	7507191	8282	8234	868	66					

Table46.txt

| | | |

Table46.txt

506 2 5 1073 17
Bot22 COL375
19063809 64912 64509 11541 678
585 9 10 1158 27
Bot23 AA_105
6008608 9971 9799 4069
1056 1135 48 121 520 19
Bot24 AA_124
6145034 13069 12853 2686 470
427 18 37 418 6
Bot25 AA_126
5351292 23237 22852 5695
1298 1317 35 80 900 23
Bot26 SA_117
22784206 54062 53866 6477 719
563 34 62 286 11
Bot27 SA_118
25358164 19143 19092 2304 272
219 14 35 91 0
Bot28 SA_119
5893301 28764 28152 8412
1977 1942 114 303 1105 47
Bot29 KID034
9394390 85519 84813 27704
3944 3449 68 77 6796 151
Bot30 KID035
6478824 54575 54084 17510
2742 2401 31 31 3799 81
Bot31 KID036
7109836 47160 46724 15801
2530 2237 48 66 4436 113
Bot32 KID037
11623274 67162 66494 15421
1948 1878 43 50 4597 148
Bot33 KID038
38035080 72203 71990 19096 843
687 1 12 1645 2
Bot34 KID038
29937990 49207 49077 11573 534
446 0 10 865 0
Bot35 KID038
29394095 60648 60491 13217 612
510 3 7 921 2
Bot36 BRA01
13461657 126402 124564 34705
4069 3524 8 11 13243 70
Bot37 BRA02
8050528 108409 106382 26794

Table46.txt

| | | |

Table46.txt

+	+	-	+	+	+
-	-	+	+	+	+
-	-	-	-	-	+
Filter K	Filter L	Filter M	Filter N	Filter O	Filter P**
11	1	48	11	1	1
58	2	142	58	2	2
54	3	235	54	3	3
32	6	158	32	6	6
7	1	32	7	1	1
122	15	373	122	15	7
205	1	1851	205	1	0
139	1	864	139	1	1
110	11	717	110	11	11
290	32	1089	289	31	29
288	17	1016	288	17	16
69	9	180	68	8	5
232	6	1067	231	5	5
93	6	616	93	6	2
507	nd	1798	507	nd	5
32	nd	125	32	nd	2
238	2	1302	238	2	2
182	6	380	182	6	5
351	15	1738	350	14	14
336	41	1396	335	40	10
241	7	1073	241	7	7
295	13	1158	294	12	11
68	7	520	68	7	7
166	5	418	166	5	3
262	10	900	262	10	9
53	7	286	52	6	6
23	0	91	23	0	0
364	27	1105	363	26	23
1418	117	6796	1410	109	103
835	53	3799	830	48	44
733	80	4436	729	76	66
803	93	4597	800	90	83
324	2	1645	324	2	1
142	0	865	142	0	0
188	2	921	188	2	2
3165	25	13243	3165	25	3
1011	9	8590	1011	9	9
1347	7	5566	1347	7	6
1251	20	7115	1249	18	18
1581	20	9157	1579	18	14
1908	31	6697	1908	31	28
1137	87	4409	1048	87	21
929	35	3702	928	34	28
1650	76	9326	1648	74	54

Table46.txt

528.40909	21.619048	2535.0455	525.59091	20.785714	15.295455
655.88383	28.79359	3148.8966	653.5907	27.575648	22.450545
251.5	9	1081	251.5	8.5	6.5
3165	117	13243	3165	109	103
7	0	32	7	0	0

Table47.txt

Table 47. Second filtering applied to nuclear DNA changes as part of BotSeqS pipeline

Filter
Number of Changes Remaining After Applied Filter
Nuclear DNA only
Single-base substitution only
Average quality score >= 30
Read 1 >=2 PCR duplicates with >=90% mutation fraction only
Read 2 >=2 PCR duplicates with >=90% mutation fraction only
Exclude all variants called in WGS
Exclude all variants in dbSNP130 and dbSNP142
Exclude calls that map to repetitive DNA or structural variants
Exclude visual artifacts and high frequency mutations (i.e. homopolymers, cycle 6 and 7,

BotSeqS Library ID	Sample Name	Filter A	Filter B	Filter C	Filter D	Filter E	Filter F	Filter G	Filter H	Filter I	Filter J	Filter K
Bot01	AA_105	7353265	7340340	7237286	807611	28814	37342	4246	13586	13649	1460	604
Bot02	AA_124	8904153	8883454	8758675	932863	44178	53411	5314	16848	26220	3124	1219
Bot03	AA_126	11151270	11088379	10956445	983043	36704	42144	4826	13120	17793	2014	766
Bot04	SA_117	10639408	10601544	10453511	1115657	63216	71396	6787	19638	24949	2452	826
Bot05	SA_118											

Table47.txt

7507191	7498909	7391580	819141	32309	41627
3792	14565	13256	1310	493	
Bot06				SA_119	
7205532	7131826	7021957	818195	40851	50672
5010	16831	21878	2363	846	
Bot07				COL229	
6986214	6969914	6594073	1888475	259358	245522
5010	5543	361151	28735	6491	
Bot08				COL231	
6957513	6946254	6584140	1773613	219331	207774
4677	5047	338954	29634	5565	
Bot09				COL232	
6606850	6595494	6289039	1422861	152639	144672
2868	3260	233395	18127	4199	
Bot10				COL233	
5889029	5873480	5545749	1486008	193359	182325
3939	4642	283481	24091	4511	
Bot11				COL234	
7758150	7742676	7337802	1856954	213277	202114
4225	4753	327498	28526	5679	
Bot12				COL235	
6050318	6037392	5734223	1451595	157012	148291
3095	3312	252642	21979	4724	
Bot13				COL236	
10636746	10614897	10173530	2069576	180115	168591
3517	3997	302715	25034	5064	
Bot14				COL237	
13035164	13007143	12573154	2367264	197966	184349
4630	4948	225124	21126	4006	
Bot15				COL238*	
8468813	8227358	7832864	4247553	509117	693137
209420	397326	40828	12077	2852	
Bot16				COL239*	
1498200	1491832	1436720	586033	134753	168676
52469	85524	30287	14151	4882	
Bot17				SIN230	
8814833	8796205	8368317	2018002	230683	218401
5461	6127	378567	32286	6404	
Bot18				COL235	
30510670	30449407	29997173	6888750	207669	185371
6855	7057	451861	39542	8451	
Bot19				COL236	
23099174	23054185	22516671	4717371	242827	218590
8097	7990	520225	43126	8429	
Bot20				COL373	
18215741	18174688	17768605	3475317	162184	153546
3964	6049	284984	23698	4595	
Bot21				COL374	

Table47.txt

15300639	15241256	14933776	2630874	107759	99988	2990	3137	178273	14808	2952	
Bot22											
19063809	18998897	18607230	3495325	133521	127546	4173	5199	224943	16853	3605	
Bot23											
6008608	5998637	5600618	1990132	433440	469601	36848	87570	188151	15840	4713	
Bot24											
6145034	6131965	5874889	1195725	125271	132405	9926	20578	101425	10072	3190	
Bot25											
5351292	5328055	5072090	1131144	170838	178016	12925	26598	105236	9871	3208	
Bot26											
22784206	22730144	22555149	2535277	152657	138074	12023	23875	57181	4761	1238	
Bot27											
25358164	25339021	25142095	2739952	160608	154798	13690	33244	62722	5364	1559	
Bot28											
5893301	5864537	5541114	1530381	265874	296102	20196	58447	169393	15134	4293	
Bot29											
9394390	9308871	8811123	2522376	278086	259252	4567	4984	525015	39254	7951	
Bot30											
6478824	6424249	6050180	1902073	253386	238365	4038	4345	364719	28412	5522	
Bot31											
7109836	7062676	6685763	1845091	221047	205543	3591	3982	415932	32236	6411	
Bot32											
11623274	11556112	10975978	2638608	258210	247549	4485	4870	593406	48244	9790	
Bot33											
38035080	37962877	37365402	9727959	283691	258619	6888	8991	591627	44154	8567	
Bot34											
29937990	29888783	29455484	7064802	210743	191336	5799	6864	354265	27456	5314	
Bot35											
29394095	29333447	28926780	6352408	194788	174626	5487	5837	276375	21934	4320	
Bot36											
13461657	13335255	12828419	2655464	146278	140478	2826	2982	472001	36731	8517	
Bot37											

COL375											
133521	127546	4173	5199	224943	16853	3605					
AA_105											
433440	469601	36848	87570	188151	15840	4713					
AA_124											
125271	132405	9926	20578	101425	10072	3190					
AA_126											
170838	178016	12925	26598	105236	9871	3208					
SA_117											
152657	138074	12023	23875	57181	4761	1238					
SA_118											
160608	154798	13690	33244	62722	5364	1559					
SA_119											
265874	296102	20196	58447	169393	15134	4293					
KID034											
278086	259252	4567	4984	525015	39254	7951					
KID035											
253386	238365	4038	4345	364719	28412	5522					
KID036											
221047	205543	3591	3982	415932	32236	6411					
KID037											
258210	247549	4485	4870	593406	48244	9790					
KID038											
283691	258619	6888	8991	591627	44154	8567					
KID038											
210743	191336	5799	6864	354265	27456	5314					
KID038											
194788	174626	5487	5837	276375	21934	4320					
BRA01											
146278	140478	2826	2982	472001	36731	8517					
BRA02											

Table47.txt

| | | |

Table47.txt

+	+	+	+	+
+	-	-	+	+
+	-	+	+	+
-	+	+	+	+
-	-	-	-	+
Filter L	Filter M	Filter N	Filter O	Filter P**
540	768	26	25	22
1107	1366	42	36	33
682	909	36	34	29
711	1331	41	36	31
405	723	24	20	19
750	1172	33	28	23
4617	19237	124	7	2
4384	17334	57	5	3
2912	12515	77	18	12
3543	14988	64	20	14
4381	17558	88	19	13
3544	13458	70	9	6
3984	15874	70	11	1
3268	11553	47	10	6
2841	727	52	52	45***
4870	410	41	41	34***
4961	19770	85	11	4
6278	24596	137	19	9
6581	27050	112	18	10
3582	15266	64	12	9
2278	9495	46	5	4
2770	11769	46	6	5
3812	10314	193	134	120
2705	5490	112	88	76
2739	5398	135	108	103
953	3077	45	29	25
1185	3244	71	43	39
3350	8924	128	91	78
5906	28464	133	28	21
4272	19134	72	12	9
4933	22346	93	19	16
7410	31302	156	29	20
6400	31312	124	9	5
4004	18508	65	5	1
3251	14400	60	1	1
5970	25200	129	6	2
4617	20482	121	6	1
2237	10533	41	1	1
3795	18540	92	8	4
3076	14024	81	7	1
4427	22474	142	12	3
3580	14795	61	10	10

Table47.txt

2261	9492	40	4	4
8951	13836	89	7	5
3609.61364	13389.9545	81.0227273	24.9772727	19.047619
1934.42848	8888.51043	40.292817	28.9470155	27.2002084
3562	13930	70.5	15	9
8951	31312	193	134	120
405	410	24	1	1

Table48.txt

Table 48. Databases used in BotSeqS pipeline

Number	Table Category	File Name	Genome Assembly	Date Number Downloaded	Number of Rows	Source Description
1	dbSNP	snp130	GRCh37/hg19	3/19/2010	19084576	UCSC Human Genome Browser dbSNP build 130
2	Structural Variant	dgvMerged	GRCh37/hg19	4/28/2014	202430	UCSC Human Genome Browser Database of Genome Variants
3	Structural Variant	genomicSuperDups	GRCh37/hg19	4/28/2014	51599	UCSC Human Genome Browser Segmental Duplications
4	Repetitve DNA	nestedRepeats	GRCh37/hg19	4/28/2014	575600	UCSC Human Genome Browser Fragments of Interrupted Repeats
6	Repetitve DNA	simpleRepeat	GRCh37/hg19	4/28/2014	962714	UCSC Human Genome Browser Simple Tandem Repeats
5	Repetitve DNA	rmsk	GRCh37/hg19	4/28/2014	1048575	UCSC Human Genome Browser Repeat Masker
7	dbSNP	snp142	GRCh37/hg19	3/10/2015	113128211	UCSC Human Genome Browser dbSNP build 142
8	Structural Variant	dgvMerged	GRCh37/hg19	3/10/2015	255676	UCSC Human Genome Browser updated Database of Genome Variants
9	Structural Variant	dgvSupporting	GRCh37/hg19	3/10/2015	3251239	UCSC Human Genome Browser updated Database of Genome Variants
10	Structural Variant	genomicSuperDups	GRCh37/hg19	3/10/2015	51599	UCSC Human Genome Browser updated Segmental Duplications
11	Repetitve DNA	nestedRepeats	GRCh37/hg19	3/10/2015	575600	UCSC Human Genome Browser updated Fragments of Interrupted Repeats
13	Repetitve DNA	simpleRepeat	GRCh37/hg19	3/10/2015	962714	UCSC Human Genome Browser updated Simple Tandem Repeats
12	Repetitve DNA	rmsk	GRCh37/hg19	3/10/2015	5298130	UCSC Human Genome Browser updated Repeat Masker

na, not applicable

*"between" criteria are inclusive; italics indicates field name from corresponding database; human genome coordinate system are 0-start and 1-end and therefore corrected to be compatible with t

Table48.txt

Filter Criteria for Nuclear DNA Changes*
exclude when change maps to single-base substitution variants
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to chrom between chromStart+1 or chromEnd or otherChrom between otherStart+1 and otherEnd
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to genoName between genoStart+1 and genoEnd
exclude when change maps to all variant positions, including at single-base substitution SNPs or between indel SNPs
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to chrom between chromStart+1 and chromEnd or otherChrom between otherStart+1 and otherEnd
exclude when change maps to chrom between chromStart+1 and chromEnd
exclude when change maps to chrom between chromStart-99 and chromEnd+100
exclude when change maps to genoName between genoStart+1 and genoEnd or exclude when change maps to genoName between genoStart-99 an

he BotSeqS pipeline coordinates system (1-start and 1-end)

Filter Criteria for Nuclear DNA Templates*
na
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd or otherChrom between otherStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to genoName between genoStart+1 and genoEnd
na
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd or otherChrom between otherStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart+1 and chromEnd
exclude when left or right end of template maps to chrom between chromStart-99 and chromEnd+100
exclude when left or right end of template maps to genoName between genoStart+1 and

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genoEnd or exclude when left or right end of template maps to genoNa

Filter Criteria for Mitochondrial Changes*
Filter Criteria for Mitochondrial Changes*
Filter Criteria for Mitochondrial Templates*
na
na
na
na
na
na
na
na
na
na
exclude when change maps to all variant positions, including at single-base substitution SNPs or between indel SNPs na
na
na
na
na
na
na
na
na
na
exclude when change maps to genoName between genoStart+1 and genoEnd
exclude when left or right end of template maps to genoName between genoStart+1 and genoEnd

Table49.txt

Table 49. Rare mutations from the mitochondrial genomes evaluated in this study
*Paircoordinates indicate leftmost coordinate of each paired-end read of the template

BotSeqS Library ID	Sample Name	Age	hg19 Chr	Mutation Coordinate	Mutation Strand)	Number of Watson Reads with Mutation (Forward Read 1)	Number of Crick Reads with Mutation (Cycle Duplicates	Number of Watson Reads with Normal Human Match (Forward Read 2)	Number of Crick Reads with Mutation	Fraction of Watson Reads with Mutation	Mutation Tissue	Mutation PairCoordinates*	Mutation Orientation
Bot01	AA_105	78	chrM	13432	C>T	54	83	83	100%	Kidney Cortex	chrMF13379chrMR13578	F
Bot02	AA_124	82	chrM	10848	C>G	20	32	32	100%	Kidney Cortex	chrMF10553chrMR10768	R
Bot02	AA_124	82	chrM	11518	T>C	83	39	39	100%	Kidney Cortex	chrMF11237chrMR11501	R
Bot03	AA_126	78	chrM	1484	A>C	74	54	54	100%	Kidney Cortex	chrMF1411chrMR1613	F
Bot03	AA_126	78	chrM	2779	G>A	59	90	90	100%	Kidney Cortex	chrMF2522chrMR2738	R
Bot03	AA_126	78	chrM	4491	C>T	50	3	3	100%	Kidney Cortex	chrMF4442chrMR4798	F
Bot04	SA_117	66	chrM	3073	T>C	44	42	42	100%	Kidney Cortex	chrMF2752chrMR3017	R
Bot04	SA_117	66	chrM	3847	C>T	13	29	29	100%	Kidney Cortex	chrMF3835chrMR3950	F
Bot04	SA_117	66	chrM	5203	C>T	63	32	32	100%	Kidney Cortex	chrMF5141chrMR5350	F
Bot04	SA_117	66	chrM	8008	G>A	63				Kidney Cortex	chrMF7645chrMR7971	R

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8		8		100%		11		11			
Bot04	SA_117	66			Kidney Cortex						
chrMF12317chrMR12453			chrM		12325		C>T		9		F
10		10		100%		2		2			
Bot04	SA_117	66			Kidney Cortex						
chrMF14307chrMR14492			chrM		14385		G>A		79		F
60		60		100%		35		35			
Bot05	SA_118	59			Kidney Cortex						
chrMF1373chrMR1667			chrM		1421		G>A		49		F
67		67		100%		69		71			
Bot06	SA_119	69			Kidney Cortex						
chrMF4396chrMR4730			chrM		4486		C>T		91		F
10		10		100%		4		4			
Bot06	SA_119	69			Kidney Cortex						
chrMF4255chrMR4584			chrM		4645		T>C		39		R
41		41		100%		44		45			
Bot06	SA_119	69			Kidney Cortex						
chrMF4976chrMR5118			chrM		5018		C>T		43		F
8		8		100%		70		70			
Bot06	SA_119	69			Kidney Cortex						
chrMF5439chrMR5563			chrM		5610		T>C		53		R
25		25		100%		67		67			
Bot06	SA_119	69			Kidney Cortex						
chrMF6759chrMR6902			chrM		6943		C>A		59		R
69		69		100%		63		63			
Bot06	SA_119	69			Kidney Cortex						
chrMF9529chrMR9662			chrM		9617		T>C		89		F
2		2		100%		19		19			
Bot06	SA_119	69			Kidney Cortex						
chrMF14492chrMR14785			chrM		14839		G>A		46		R
22		22		100%		31		31			
Bot08	COL231	8			Colon Epithelium						
chrMF4554chrMR4845			chrM		4561		G>A		8		F
7		7		100%		2		2			
Bot09	COL232	98			Colon Epithelium						
chrMF2789chrMR3047			chrM		3084		G>A		63		R
9		9		100%		12		12			
Bot09	COL232	98			Colon Epithelium						
chrMF2788chrMR3063			chrM		3128		G>A		35		R
13		13		100%		10		10			
Bot09	COL232	98			Colon Epithelium						
chrMF11847chrMR12156			chrM		11881		A>G		35		F
5		5		100%		12		12			
Bot09	COL232	98			Colon Epithelium						
chrMF11705chrMR12220			chrM		12294		G>A		26		R
6		6		100%		8		8			
Bot09	COL232	98			Colon Epithelium						
chrMF12566chrMR12840			chrM		12890		G>A		50		R

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7		7		100%		9		9			
Bot09	COL232	98			Colon Epithelium						
chrMF13824chrMR14402			chrM		14462		T>C	40		R	
7		7		100%		2		2			
Bot09	COL232	98			Colon Epithelium						
chrMF14257chrMR14676			chrM		14740		G>A	36		R	
11		11		100%		3		3			
Bot09	COL232	98			Colon Epithelium						
chrMF15339chrMR15599			chrM		15389		T>C	51		F	
4		4		100%		9		9			
Bot09	COL232	98			Colon Epithelium						
chrMF15845chrMR16279			chrM		15882		T>C	38		F	
3		3		100%		6		6			
Bot09	COL232	98			Colon Epithelium						
chrMF15464chrMR15982			chrM		16040		G>A	42		R	
7		7		100%		5		5			
Bot09	COL232	98			Colon Epithelium						
chrMF15457chrMR15997			chrM		16066		G>A	31		R	
5		5		100%		2		2			
Bot10	COL233	96			Colon Epithelium						
chrMF357chrMR605			chrM		413		C>A	57		F	
4		4		100%		6		6			
Bot10	COL233	96			Colon Epithelium						
chrMF525chrMR929			chrM		943		G>A	86		R	
6		6		100%		6		6			
Bot10	COL233	96			Colon Epithelium						
chrMF930chrMR1485			chrM		1553		G>A	32		R	
3		3		100%		2		2			
Bot10	COL233	96			Colon Epithelium						
chrMF1922chrMR2110			chrM		1954		T>C	33		F	
9		9		100%		11		11			
Bot10	COL233	96			Colon Epithelium						
chrMF1945chrMR2201			chrM		2271		G>A	30		R	
7		7		100%		3		3			
Bot10	COL233	96			Colon Epithelium						
chrMF3411chrMR3781			chrM		3425		G>A	15		F	
6		6		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF3840chrMR4152			chrM		4173		T>C	79		R	
10		10		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF4305chrMR4460			chrM		4533		G>A	27		R	
8		8		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF4172chrMR4676			chrM		4709		T>C	67		R	
4		4		100%		2		2			
Bot10	COL233	96			Colon Epithelium						
chrMF4573chrMR4859			chrM		4942		T>C	17		R	

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2		2		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF5559chrMR6009			chrM		6076		G>C		33		R
3		3		100%		2		2			
Bot10	COL233	96			Colon Epithelium						
chrMF6214chrMR6600			chrM		6228		T>C		15		F
6		6		100%		3		3			
Bot10	COL233	96			Colon Epithelium						
chrMF7581chrMR8005			chrM		7626		T>C		46		F
11		11		100%		3		3			
Bot10	COL233	96			Colon Epithelium						
chrMF8892chrMR9291			chrM		8903		G>A		12		F
2		2		100%		4		4			
Bot10	COL233	96			Colon Epithelium						
chrMF8735chrMR8935			chrM		8996		G>A		39		R
4		4		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF9144chrMR9584			chrM		9656		G>A		28		R
4		4		100%		7		7			
Bot10	COL233	96			Colon Epithelium						
chrMF9197chrMR9769			chrM		9857		T>C		12		R
2		2		100%		4		4			
Bot10	COL233	96			Colon Epithelium						
chrMF10378chrMR10842			chrM		10438		G>A		61		F
7		7		100%		9		9			
Bot10	COL233	96			Colon Epithelium						
chrMF10259chrMR10517			chrM		10600		G>A		17		R
10		10		100%		12		12			
Bot10	COL233	96			Colon Epithelium						
chrMF10976chrMR11162			chrM		11181		G>A		81		R
4		4		100%		8		8			
Bot10	COL233	96			Colon Epithelium						
chrMF12771chrMR13060			chrM		12801		T>C		31		F
3		3		100%		2		2			
Bot10	COL233	96			Colon Epithelium						
chrMF14086chrMR14356			chrM		14440		G>A		16		R
5		5		100%		9		9			
Bot10	COL233	96			Colon Epithelium						
chrMF14705chrMR14854			chrM		14944		T>C		10		R
6		6		100%		10		10			
Bot10	COL233	96			Colon Epithelium						
chrMF15011chrMR15541			chrM		15044		G>A		34		F
3		3		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF15053chrMR15409			chrM		15060		G>A		8		F
3		3		100%		4		4			
Bot10	COL233	96			Colon Epithelium						
chrMF15221chrMR15529			chrM		15247		G>A		27		F

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3		3		100%		5		5			
Bot10	COL233	96			Colon Epithelium						
chrMF15524	chrMR15784		chrM		15844		T>C	40		R	
10		10		100%		7		7			
Bot10	COL233	96			Colon Epithelium						
chrMF15718	chrMR16012		chrM		16035		G>A	77		R	
3		3		100%		16		16			
Bot10	COL233	96			Colon Epithelium						
chrMF16070	chrMR16338		chrM		16142		A>G	73		F	
15		15		100%		7		7			
Bot11	COL234	95			Colon Epithelium						
chrMF1916	chrMR2064		chrM		1975		G>A	60		F	
7		7		100%		10		10			
Bot11	COL234	95			Colon Epithelium						
chrMF1844	chrMR1979		chrM		2017		G>A	62		R	
11		11		100%		8		8			
Bot11	COL234	95			Colon Epithelium						
chrMF3697	chrMR4095		chrM		4106		A>G	89		R	
6		6		100%		6		6			
Bot11	COL234	95			Colon Epithelium						
chrMF5144	chrMR5473		chrM		5233		C>T	90		F	
8		8		100%		4		4			
Bot11	COL234	95			Colon Epithelium						
chrMF6375	chrMR6645		chrM		6682		T>C	63		R	
5		5		100%		7		7			
Bot11	COL234	95			Colon Epithelium						
chrMF7169	chrMR7544		chrM		7204		T>C	36		F	
12		12		100%		5		5			
Bot11	COL234	95			Colon Epithelium						
chrMF10179	chrMR10410		chrM		10204		G>A	26		F	
5		5		100%		11		11			
Bot11	COL234	95			Colon Epithelium						
chrMF10975	chrMR11283		chrM		11373		G>A	10		R	
8		8		100%		8		8			
Bot11	COL234	95			Colon Epithelium						
chrMF12213	chrMR12503		chrM		12573		G>A	30		R	
5		5		100%		10		10			
Bot11	COL234	95			Colon Epithelium						
chrMF12715	chrMR13083		chrM		12747		T>C	33		F	
6		6		100%		3		3			
Bot11	COL234	95			Colon Epithelium						
chrMF13474	chrMR13644		chrM		13677		A>G	67		R	
5		5		100%		14		14			
Bot11	COL234	95			Colon Epithelium						
chrMF14299	chrMR14502		chrM		14352		T>C	54		F	
5		5		100%		8		8			
Bot11	COL234	95			Colon Epithelium						
chrMF14461	chrMR14696		chrM		14531		T>C	71		F	

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11		11		100%		8		8			
Bot11	COL234	95			Colon Epithelium						
chrMF14607chrMR14867			chrM		14901		G>A		66		R
7		7		100%		5		5			
Bot11	COL234	95			Colon Epithelium						
chrMF15000chrMR15483			chrM		15046		G>A		47		F
6		6		100%		5		5			
Bot11	COL234	95			Colon Epithelium						
chrMF15070chrMR15365			chrM		15393		G>A		72		R
3		3		100%		11		11			
Bot12	COL235	26			Colon Epithelium						
chrMF2721chrMR3164			chrM		3182		T>C		82		R
5		5		100%		4		4			
Bot12	COL235	26			Colon Epithelium						
chrMF7370chrMR7633			chrM		7383		G>C		14		F
18		18		100%		15		15			
Bot12	COL235	26			Colon Epithelium						
chrMF7722chrMR8102			chrM		7815		G>A		94		F
5		5		100%		5		5			
Bot12	COL235	26			Colon Epithelium						
chrMF9850chrMR10166			chrM		10231		G>A		35		R
7		7		100%		3		3			
Bot12	COL235	26			Colon Epithelium						
chrMF15844chrMR16469			chrM		16551		C>T		18		R
9		9		100%		3		3			
Bot13	COL236	26			Colon Epithelium						
chrMF1413chrMR1795			chrM		1447		G>A		35		F
16		16		100%		11		11			
Bot13	COL236	26			Colon Epithelium						
chrMF5265chrMR5742			chrM		5792		G>A		50		R
4		4		100%		4		4			
Bot13	COL236	26			Colon Epithelium						
chrMF6514chrMR6859			chrM		6905		G>A		54		R
4		4		100%		3		3			
Bot13	COL236	26			Colon Epithelium						
chrMF6647chrMR6916			chrM		6956		G>A		60		R
7		7		100%		15		15			
Bot13	COL236	26			Colon Epithelium						
chrMF9943chrMR10408			chrM		10458		T>C		50		R
5		5		100%		6		6			
Bot14	COL237	22			Colon Epithelium						
chrMF3448chrMR3807			chrM		3831		T>C		76		R
2		2		100%		13		13			
Bot14	COL237	22			Colon Epithelium						
chrMF15354chrMR15575			chrM		15439		G>A		86		F
22		22		100%		5		5			
Bot15	COL238	16			Colon Epithelium						
chrMF8892chrMR9117			chrM		9196		C>A		21		R

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2		2		100%		2		2			
Bot15	COL238	16			Colon Epithelium						
chrMF9677chrMR10000			chrM		10076		T>C		24		R
2		2		100%		2		2			
Bot15	COL238	16			Colon Epithelium						
chrMF15274chrMR15455			chrM		15333		C>A		60		F
2		2		100%		2		2			
Bot15	COL238	16			Colon Epithelium						
chrMF15397chrMR15546			chrM		15575		C>A		71		R
3		3		100%		3		3			
Bot15	COL238	16			Colon Epithelium						
chrMF15554chrMR15682			chrM		15577		C>T		24		F
3		3		100%		2		2			
Bot16	COL239	18			Colon Epithelium						
chrMF9595chrMR9774			chrM		9672		C>T		78		F
10		10		100%		4		4			
Bot16	COL239	18			Colon Epithelium						
chrMF12593chrMR12706			chrM		12777		T>C		29		R
8		8		100%		12		12			
Bot17	SIN230	6			Small Intestine, Duodenum						
chrMF9339chrMR9833			chrM		9866		T>C		67		R
2		2		100%		2		2			
Bot17	SIN230	6			Small Intestine, Duodenum						
chrMF10136chrMR10473			chrM		10498		C>T		75		R
3		3		100%		9		9			
Bot18	COL235	26			Colon Epithelium						
chrMF3840chrMR4179			chrM		4245		G>A		34		R
9		9		100%		14		14			
Bot18	COL235	26			Colon Epithelium						
chrMF10123chrMR10595			chrM		10675		T>C		20		R
6		6		100%		5		5			
Bot18	COL235	26			Colon Epithelium						
chrMF12280chrMR12460			chrM		12550		C>T		10		R
9		9		100%		14		14			
Bot18	COL235	26			Colon Epithelium						
chrMF13119chrMR13489			chrM		13532		G>A		57		R
4		4		100%		4		4			
Bot18	COL235	26			Colon Epithelium						
chrMF14505chrMR14829			chrM		14541		T>C		37		F
6		6		100%		6		6			
Bot19	COL236	26			Colon Epithelium						
chrMF317chrMR652			chrM		671		T>C		81		R
7		7		100%		5		5			
Bot19	COL236	26			Colon Epithelium						
chrMF721chrMR983			chrM		990		G>A		93		R
3		3		100%		7		7			
Bot19	COL236	26			Colon Epithelium						
chrMF1549chrMR1807			chrM		1879		T>C		28		R

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4		4		100%		3		3			
Bot19	COL236	26			Colon Epithelium						
chrMF1449chrMR1859			chrM		1889		A>G		70		R
4		4		100%		8		8			
Bot19	COL236	26			Colon Epithelium						
chrMF1948chrMR2269			chrM		2024		G>A		77		F
10		10		100%		8		8			
Bot19	COL236	26			Colon Epithelium						
chrMF3955chrMR4331			chrM		4404		G>A		27		R
9		9		100%		12		12			
Bot19	COL236	26			Colon Epithelium						
chrMF4185chrMR4414			chrM		4505		C>T		9		R
4		4		100%		14		14			
Bot19	COL236	26			Colon Epithelium						
chrMF5934chrMR6396			chrM		6019		G>A		86		F
3		3		100%		2		2			
Bot19	COL236	26			Colon Epithelium						
chrMF8331chrMR8686			chrM		8384		T>C		54		F
7		7		100%		6		6			
Bot19	COL236	26			Colon Epithelium						
chrMF8167chrMR8753			chrM		8826		T>C		27		R
4		4		100%		4		4			
Bot19	COL236	26			Colon Epithelium						
chrMF12120chrMR12535			chrM		12566		T>C		69		R
6		6		100%		6		6			
Bot19	COL236	26			Colon Epithelium						
chrMF12887chrMR13201			chrM		12906		T>C		20		F
6		6		100%		5		5			
Bot19	COL236	26			Colon Epithelium						
chrMF12685chrMR13003			chrM		13064		G>A		39		R
2		2		100%		9		9			
Bot19	COL236	26			Colon Epithelium						
chrMF13538chrMR13821			chrM		13569		T>C		32		F
10		10		100%		2		2			
Bot20	COL373	36			Colon Epithelium						
chrMF2557chrMR3012			chrM		3073		T>C		39		R
14		14		100%		8		8			
Bot20	COL373	36			Colon Epithelium						
chrMF3222chrMR3660			chrM		3708		G>A		52		R
7		7		100%		5		5			
Bot20	COL373	36			Colon Epithelium						
chrMF8128chrMR8575			chrM		8214		G>C		87		F
3		3		100%		3		3			
Bot20	COL373	36			Colon Epithelium						
chrMF8754chrMR9019			chrM		8765		G>A		12		F
21		21		100%		13		13			
Bot20	COL373	36			Colon Epithelium						
chrMF9326chrMR9696			chrM		9716		G>A		80		R

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16		16		100%		13		13			
Bot20	COL373	36			Colon Epithelium						
chrMF13252	chrMR13586		chrM		13310		G>A		59		F
12		12		100%		15		15			
Bot20	COL373	36			Colon Epithelium						
chrMF13291	chrMR13645		chrM		13334		G>A		44		F
4		4		100%		4		4			
Bot20	COL373	36			Colon Epithelium						
chrMF14760	chrMR15292		chrM		14767		T>C		8		F
5		5		100%		4		4			
Bot20	COL373	36			Colon Epithelium						
chrMF14814	chrMR15275		chrM		14906		A>G		93		F
6		6		100%		9		9			
Bot20	COL373	36			Colon Epithelium						
chrMF15386	chrMR15812		chrM		15862		T>C		50		R
9		9		100%		7		7			
Bot21	COL374	21			Colon Epithelium						
chrMF821	chrMR1361		chrM		887		T>C		67		F
5		5		100%		6		6			
Bot21	COL374	21			Colon Epithelium						
chrMF1150	chrMR1842		chrM		1229		G>A		80		F
2		2		100%		2		2			
Bot21	COL374	21			Colon Epithelium						
chrMF1015	chrMR1535		chrM		1594		T>C		41		R
8		8		100%		6		6			
Bot21	COL374	21			Colon Epithelium						
chrMF3154	chrMR3494		chrM		3227		G>A		74		F
12		12		100%		14		14			
Bot21	COL374	21			Colon Epithelium						
chrMF12815	chrMR13189		chrM		13269		G>A		20		R
12		12		100%		5		5			
Bot21	COL374	21			Colon Epithelium						
chrMF13539	chrMR13880		chrM		13916		G>A		64		R
11		11		100%		17		17			
Bot21	COL374	21			Colon Epithelium						
chrMF13230	chrMR13834		chrM		13919		T>C		15		R
3		3		100%		3		3			
Bot22	COL375	38			Colon Epithelium						
chrMF1870	chrMR2136		chrM		1886		G>A		17		F
23		23		100%		24		24			
Bot22	COL375	38			Colon Epithelium						
chrMF2729	chrMR3157		chrM		2765		T>C		37		F
9		9		100%		12		12			
Bot22	COL375	38			Colon Epithelium						
chrMF4803	chrMR5005		chrM		5012		A>G		93		R
18		18		100%		25		25			
Bot22	COL375	38			Colon Epithelium						
chrMF6340	chrMR6673		chrM		6686		A>G		87		R

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11		11	100%		14		14				
Bot22	COL375	38			Colon Epithelium						
chrMF6672chrMR7018			chrM		7023		T>C		95		R
12		12	100%		8		8				
Bot22	COL375	38			Colon Epithelium						
chrMF7163chrMR7412			chrM		7192		T>C		30		F
27		27	100%		15		16				
Bot22	COL375	38			Colon Epithelium						
chrMF11386chrMR11819			chrM		11446		T>C		61		F
16		16	100%		7		7				
Bot22	COL375	38			Colon Epithelium						
chrMF12345chrMR12715			chrM		12764		G>A		51		R
14		14	100%		11		11				
Bot22	COL375	38			Colon Epithelium						
chrMF12718chrMR13175			chrM		12770		G>A		53		F
8		8	100%		9		9				
Bot22	COL375	38			Colon Epithelium						
chrMF15611chrMR15867			chrM		15689		C>T		79		F
18		18	100%		15		15				
Bot22	COL375	38			Colon Epithelium						
chrMF15822chrMR16335			chrM		15844		T>C		23		F
14		14	100%		2		2				
Bot23	AA_105	78			Kidney Cortex						
chrMF3302chrMR3522			chrM		3585		A>G		37		R
2		2	100%		3		3				
Bot23	AA_105	78			Kidney Cortex						
chrMF8832chrMR9104			chrM		9111		T>A		93		R
5		5	100%		6		6				
Bot23	AA_105	78			Kidney Cortex						
chrMF9486chrMR9760			chrM		9503		G>C		18		F
6		6	100%		2		2				
Bot23	AA_105	78			Kidney Cortex						
chrMF13027chrMR13191			chrM		13095		T>C		69		F
7		7	100%		6		6				
Bot23	AA_105	78			Kidney Cortex						
chrMF12829chrMR13091			chrM		13100		G>A		91		R
4		4	100%		6		6				
Bot23	AA_105	78			Kidney Cortex						
chrMF13010chrMR13336			chrM		13415		G>A		21		R
2		2	100%		6		6				
Bot23	AA_105	78			Kidney Cortex						
chrMF14096chrMR14396			chrM		14161		G>A		66		F
5		5	100%		4		4				
Bot24	AA_124	82			Kidney Cortex						
chrMF9613chrMR9920			chrM		9988		T>C		32		R
16		16	100%		21		21				
Bot24	AA_124	82			Kidney Cortex						
chrMF15145chrMR15525			chrM		15602		T>C		23		R

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14		14		100%		15		15			
Bot24	AA_124	82			Kidney Cortex						
chrMF16097chrMR16413			chrM		16505		G>A	8		R	
4		4		100%		2		2			
Bot25	AA_126	78			Kidney Cortex						
chrMF701chrMR853			chrM		865		C>G	88		R	
10		10		100%		36		36			
Bot25	AA_126	78			Kidney Cortex						
chrMF1321chrMR1801			chrM		1341		G>A	21		F	
2		2		100%		11		11			
Bot25	AA_126	78			Kidney Cortex						
chrMF3121chrMR3525			chrM		3187		T>C	67		F	
13		13		100%		8		8			
Bot25	AA_126	78			Kidney Cortex						
chrMF11871chrMR12347			chrM		11894		A>G	24		F	
8		8		100%		5		5			
Bot25	AA_126	78			Kidney Cortex						
chrMF12981chrMR13293			chrM		13040		T>C	60		F	
13		13		100%		7		7			
Bot25	AA_126	78			Kidney Cortex						
chrMF13532chrMR13820			chrM		13541		T>C	10		F	
6		6		100%		25		25			
Bot25	AA_126	78			Kidney Cortex						
chrMF14336chrMR14700			chrM		14370		A>C	35		F	
6		6		100%		13		13			
Bot25	AA_126	78			Kidney Cortex						
chrMF16018chrMR16457			chrM		16028		T>C	11		F	
9		9		100%		9		9			
Bot25	AA_126	78			Kidney Cortex						
chrMF16083chrMR16373			chrM		16105		C>T	23		F	
22		22		100%		9		9			
Bot26	SA_117	66			Kidney Cortex						
chrMF3939chrMR4384			chrM		4430		G>A	54		R	
7		7		100%		6		6			
Bot26	SA_117	66			Kidney Cortex						
chrMF6219chrMR6560			chrM		6577		G>A	83		R	
5		5		100%		8		8			
Bot26	SA_117	66			Kidney Cortex						
chrMF12164chrMR12591			chrM		12675		A>G	16		R	
3		3		100%		5		5			
Bot26	SA_117	66			Kidney Cortex						
chrMF13685chrMR13982			chrM		13727		G>A	43		F	
8		8		100%		7		7			
Bot26	SA_117	66			Kidney Cortex						
chrMF16057chrMR16461			chrM		16096		C>T	40		F	
7		7		100%		7		7			
Bot26	SA_117	66			Kidney Cortex						
chrMF15613chrMR16071			chrM		16128		A>G	43		R	

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9		9		100%		7		7		
Bot28	SA_119	69			Kidney Cortex					
chrMF50chrMR379			chrM		60		T>C	11		F
3		3		100%		11		11		
Bot28	SA_119	69			Kidney Cortex					
chrMF792chrMR963			chrM		820		C>T	29		F
10		10		100%		5		5		
Bot28	SA_119	69			Kidney Cortex					
chrMF1015chrMR1387			chrM		1084		A>G	70		F
10		10		100%		3		3		
Bot28	SA_119	69			Kidney Cortex					
chrMF964chrMR1137			chrM		1203		A>G	34		R
8		8		100%		9		9		
Bot28	SA_119	69			Kidney Cortex					
chrMF1275chrMR1655			chrM		1291		G>A	17		F
3		3		100%		11		11		
Bot28	SA_119	69			Kidney Cortex					
chrMF2281chrMR2523			chrM		2356		A>G	76		F
6		6		100%		6		6		
Bot28	SA_119	69			Kidney Cortex					
chrMF3001chrMR3315			chrM		3071		A>G	71		F
10		10		100%		8		8		
Bot28	SA_119	69			Kidney Cortex					
chrMF3340chrMR3565			chrM		3644		G>A	21		R
4		4		100%		4		4		
Bot28	SA_119	69			Kidney Cortex					
chrMF4583chrMR4947			chrM		4994		T>C	53		R
5		5		100%		4		4		
Bot28	SA_119	69			Kidney Cortex					
chrMF6049chrMR6537			chrM		6611		G>A	26		R
3		3		100%		7		7		
Bot28	SA_119	69			Kidney Cortex					
chrMF7979chrMR8372			chrM		8440		A>G	32		R
9		9		100%		6		6		
Bot28	SA_119	69			Kidney Cortex					
chrMF8529chrMR8849			chrM		8539		T>C	11		F
8		8		100%		3		3		
Bot28	SA_119	69			Kidney Cortex					
chrMF10118chrMR10251			chrM		10343		T>C	8		R
7		7		100%		6		6		
Bot28	SA_119	69			Kidney Cortex					
chrMF10731chrMR11009			chrM		10777		T>C	47		F
8		8		100%		10		10		
Bot28	SA_119	69			Kidney Cortex					
chrMF11146chrMR11477			chrM		11158		T>C	13		F
8		8		100%		4		4		
Bot28	SA_119	69			Kidney Cortex					
chrMF12046chrMR12303			chrM		12129		T>C	84		F

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4		4		100%		6		6			
Bot28	SA_119	69			Kidney Cortex						
chrMF12328chrMR12537			chrM		12591		T>C		46		R
10		10		100%		5		5			
Bot28	SA_119	69			Kidney Cortex						
chrMF13245chrMR13467			chrM		13334		G>A		90		F
8		8		100%		8		8			
Bot28	SA_119	69			Kidney Cortex						
chrMF13574chrMR13884			chrM		13617		T>C		44		F
11		11		100%		5		5			
Bot28	SA_119	69			Kidney Cortex						
chrMF13713chrMR14061			chrM		13732		A>T		20		F
8		8		100%		3		3			
Bot28	SA_119	69			Kidney Cortex						
chrMF14997chrMR15510			chrM		15025		G>A		29		F
10		10		100%		2		2			
Bot28	SA_119	69			Kidney Cortex						
chrMF15115chrMR15609			chrM		15615		G>A		94		R
4		4		100%		2		2			
Bot28	SA_119	69			Kidney Cortex						
chrMF15888chrMR16234			chrM		16310		T>G		24		R
7		7		100%		13		13			
Bot29	KID034	55			Kidney Cortex						
chrMF333chrMR657			chrM		408		T>C		76		F
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF417chrMR791			chrM		430		A>C		14		F
3		3		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF503chrMR750			chrM		542		A>G		40		F
2		2		100%		6		6			
Bot29	KID034	55			Kidney Cortex						
chrMF674chrMR878			chrM		685		G>A		12		F
5		5		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF671chrMR957			chrM		1006		G>A		51		R
2		2		100%		5		5			
Bot29	KID034	55			Kidney Cortex						
chrMF600chrMR980			chrM		1033		G>A		47		R
4		4		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF1084chrMR1322			chrM		1105		A>G		22		F
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF1364chrMR1760			chrM		1414		G>A		51		F
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF1375chrMR1691			chrM		1423		G>A		49		F

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3		3		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF1553chrMR2071			chrM		1572		G>A		20		F
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF1008chrMR1518			chrM		1577		T>C		41		R
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF1126chrMR1557			chrM		1598		A>G		59		R
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF1298chrMR1653			chrM		1745		T>C		8		R
5		5		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF1781chrMR2103			chrM		1826		T>C		46		F
6		6		100%		6		6			
Bot29	KID034	55			Kidney Cortex						
chrMF1870chrMR2355			chrM		1922		T>C		53		F
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF1628chrMR1983			chrM		2017		G>A		66		R
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF2071chrMR2358			chrM		2137		A>C		67		F
4		4		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF1871chrMR2184			chrM		2196		T>C		88		R
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF2430chrMR2904			chrM		2910		T>C		94		R
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF2920chrMR3188			chrM		2962		T>C		43		F
4		4		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF3008chrMR3210			chrM		3049		G>A		42		F
5		5		100%		6		6			
Bot29	KID034	55			Kidney Cortex						
chrMF3082chrMR3385			chrM		3098		T>C		17		F
4		4		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF3027chrMR3253			chrM		3115		T>C		89		F
5		5		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF3136chrMR3324			chrM		3154		T>C		19		F
5		5		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF2832chrMR3157			chrM		3168		T>C		89		R

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2		2		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF3521chrMR3790			chrM		3565		A>G		45		F
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF3253chrMR3533			chrM		3606		T>C		27		R
4		4		100%		5		5			
Bot29	KID034	55			Kidney Cortex						
chrMF3558chrMR3943			chrM		3609		G>A		52		F
5		5		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF3648chrMR3911			chrM		3726		T>C		79		F
8		8		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF3829chrMR4199			chrM		3862		A>G		34		F
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF3592chrMR3890			chrM		3974		T>C		16		R
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF3611chrMR4060			chrM		4144		A>G		16		R
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF4259chrMR4422			chrM		4286		T>C		28		F
6		6		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF4025chrMR4323			chrM		4413		G>A		10		R
3		3		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF3993chrMR4399			chrM		4456		A>T		43		R
3		3		100%		6		6			
Bot29	KID034	55			Kidney Cortex						
chrMF4447chrMR4821			chrM		4483		G>A		37		F
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF4334chrMR4698			chrM		4790		G>A		8		R
4		4		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF4789chrMR5008			chrM		4832		G>A		44		F
7		7		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF4944chrMR5396			chrM		5011		T>A		68		F
5		5		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF5551chrMR5997			chrM		5563		T>C		13		F
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF5098chrMR5602			chrM		5628		A>G		74		R

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2	2	100%	3	3						
Bot29	KID034	55		Kidney Cortex						
chrMF5602chrMR5955		chrM	5632	G>A	31	F				
3	3	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF5584chrMR5967		chrM	5670	G>A	87	F				
4	4	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF5707chrMR5978		chrM	5727	T>C	21	F				
2	2	100%	3	3						
Bot29	KID034	55		Kidney Cortex						
chrMF5537chrMR5824		chrM	5858	A>G	66	R				
4	4	100%	6	6						
Bot29	KID034	55		Kidney Cortex						
chrMF5496chrMR5860		chrM	5943	A>G	17	R				
2	2	100%	4	4						
Bot29	KID034	55		Kidney Cortex						
chrMF6651chrMR6976		chrM	6727	T>C	77	F				
6	6	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF7228chrMR7509		chrM	7262	T>C	35	F				
2	2	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF7321chrMR7760		chrM	7383	G>A	63	F				
4	4	100%	4	4						
Bot29	KID034	55		Kidney Cortex						
chrMF7547chrMR7938		chrM	7573	T>C	27	F				
3	3	100%	3	3						
Bot29	KID034	55		Kidney Cortex						
chrMF8694chrMR8914		chrM	8990	G>C	24	R				
4	4	100%	5	5						
Bot29	KID034	55		Kidney Cortex						
chrMF8954chrMR9087		chrM	9140	G>C	47	R				
3	3	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF9306chrMR9758		chrM	9344	G>A	39	F				
4	4	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF9527chrMR9936		chrM	9542	T>C	16	F				
3	3	100%	3	3						
Bot29	KID034	55		Kidney Cortex						
chrMF9559chrMR10084		chrM	9566	G>A	8	F				
2	2	100%	2	2						
Bot29	KID034	55		Kidney Cortex						
chrMF9762chrMR9963		chrM	9841	T>C	80	F				
5	5	100%	5	5						
Bot29	KID034	55		Kidney Cortex						
chrMF9507chrMR9836		chrM	9869	G>A	67	R				

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2	2	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF9908chrMR10131			chrM	9968	T>C	61	F				
3	3	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF9632chrMR9970			chrM	9982	T>C	88	R				
3	3	100%	6	6							
Bot29	KID034	55		Kidney Cortex							
chrMF9528chrMR9920			chrM	9990	T>C	30	R				
2	2	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF9611chrMR9993			chrM	9999	T>C	94	R				
2	2	100%	5	5							
Bot29	KID034	55		Kidney Cortex							
chrMF9976chrMR10333			chrM	10069	G>A	94	F				
3	3	100%	4	4							
Bot29	KID034	55		Kidney Cortex							
chrMF10065chrMR10254			chrM	10130	T>C	66	F				
4	4	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF9784chrMR10163			chrM	10221	A>G	42	R				
5	5	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF10183chrMR10495			chrM	10257	T>C	75	F				
7	7	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF10269chrMR10714			chrM	10327	T>C	59	F				
3	3	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF10356chrMR10771			chrM	10435	T>C	80	F				
4	4	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF10224chrMR10556			chrM	10621	A>G	35	R				
8	8	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF11063chrMR11171			chrM	11154	A>G	92	F				
10	10	100%	11	11							
Bot29	KID034	55		Kidney Cortex							
chrMF11593chrMR11931			chrM	11680	G>A	88	F				
3	3	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF11643chrMR11998			chrM	11691	G>A	49	F				
3	3	100%	2	2							
Bot29	KID034	55		Kidney Cortex							
chrMF11352chrMR11826			chrM	11908	T>C	18	R				
4	4	100%	3	3							
Bot29	KID034	55		Kidney Cortex							
chrMF12029chrMR12412			chrM	12082	T>C	54	F				

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4		4		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF11932	chrMR12201		chrM		12243		A>C		58		R
4		4		100%		5		5			
Bot29	KID034	55			Kidney Cortex						
chrMF12058	chrMR12342		chrM		12350		A>G		92		R
4		4		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF12364	chrMR12654		chrM		12426		A>G		63		F
2		2		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF12429	chrMR12720		chrM		12470		A>G		42		F
3		3		100%		5		5			
Bot29	KID034	55			Kidney Cortex						
chrMF12740	chrMR13026		chrM		12768		G>A		29		F
6		6		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF12721	chrMR13055		chrM		12780		G>A		60		F
4		4		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF12409	chrMR12832		chrM		12912		A>G		20		R
3		3		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF12502	chrMR12898		chrM		12984		T>C		14		R
3		3		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF13399	chrMR13751		chrM		13435		A>G		37		F
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF13786	chrMR14143		chrM		13805		G>A		20		F
5		5		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF13758	chrMR13990		chrM		13817		A>G		60		F
6		6		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF13707	chrMR14035		chrM		14114		T>C		21		R
3		3		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF14357	chrMR14528		chrM		14365		G>A		9		F
3		3		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF14615	chrMR14994		chrM		14648		A>C		34		F
4		4		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF14294	chrMR14712		chrM		14765		A>G		47		R
2		2		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF14846	chrMR15055		chrM		15129		T>C		26		R

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4		4		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15086chrMR15316			chrM		15356		G>A	60		R	
3		3		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15335chrMR15653			chrM		15375		G>A	41		F	
7		7		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF14936chrMR15325			chrM		15400		T>C	25		R	
6		6		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF15019chrMR15382			chrM		15458		C>A	24		R	
5		5		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15416chrMR15596			chrM		15612		G>A	84		R	
5		5		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF15223chrMR15594			chrM		15614		A>G	80		R	
3		3		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF15365chrMR15669			chrM		15730		T>C	39		R	
4		4		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF15374chrMR15852			chrM		15919		T>C	33		R	
2		2		100%		3		3			
Bot29	KID034	55			Kidney Cortex						
chrMF15667chrMR15945			chrM		16035		G>A	10		R	
2		2		100%		2		2			
Bot29	KID034	55			Kidney Cortex						
chrMF15683chrMR15995			chrM		16048		G>A	47		R	
7		7		100%		5		5			
Bot29	KID034	55			Kidney Cortex						
chrMF15738chrMR16006			chrM		16093		T>C	13		R	
6		6		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15719chrMR16042			chrM		16110		A>G	32		R	
2		2		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15922chrMR16243			chrM		16288		C>T	55		R	
2		2		100%		4		4			
Bot29	KID034	55			Kidney Cortex						
chrMF15769chrMR16203			chrM		16291		A>C	12		R	
2		2		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF26chrMR364			chrM		60		T>C	35		F	
3		3		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF506chrMR759			chrM		807		C>T	52		R	

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4	4	100%	2	2							
Bot30	KID035	45		Kidney Cortex							
chrMF456chrMR863		chrM	881	T>C	82	R					
2	2	100%	3	3							
Bot30	KID035	45		Kidney Cortex							
chrMF808chrMR1174		chrM	1207	T>C	67	R					
4	4	100%	4	4							
Bot30	KID035	45		Kidney Cortex							
chrMF2243chrMR2508		chrM	2335	G>A	93	F					
2	2	100%	6	6							
Bot30	KID035	45		Kidney Cortex							
chrMF2098chrMR2366		chrM	2438	G>A	28	R					
4	4	100%	2	2							
Bot30	KID035	45		Kidney Cortex							
chrMF2734chrMR3069		chrM	2756	A>G	23	F					
5	5	100%	5	5							
Bot30	KID035	45		Kidney Cortex							
chrMF2435chrMR2753		chrM	2807	A>G	46	R					
2	2	100%	4	4							
Bot30	KID035	45		Kidney Cortex							
chrMF2212chrMR2756		chrM	2846	G>A	10	R					
5	5	100%	2	2							
Bot30	KID035	45		Kidney Cortex							
chrMF3021chrMR3365		chrM	3413	G>A	52	R					
2	2	100%	2	2							
Bot30	KID035	45		Kidney Cortex							
chrMF3475chrMR3752		chrM	3527	G>A	53	F					
3	3	100%	3	3							
Bot30	KID035	45		Kidney Cortex							
chrMF3720chrMR4077		chrM	3780	G>A	61	F					
2	2	100%	3	3							
Bot30	KID035	45		Kidney Cortex							
chrMF4406chrMR4719		chrM	4452	T>C	47	F					
3	3	100%	4	4							
Bot30	KID035	45		Kidney Cortex							
chrMF4020chrMR4421		chrM	4493	T>G	28	R					
2	2	100%	8	8							
Bot30	KID035	45		Kidney Cortex							
chrMF4460chrMR4725		chrM	4533	G>A	74	F					
4	4	100%	4	4							
Bot30	KID035	45		Kidney Cortex							
chrMF4479chrMR4868		chrM	4892	T>C	76	R					
2	2	100%	2	2							
Bot30	KID035	45		Kidney Cortex							
chrMF5555chrMR5739		chrM	5792	G>A	47	R					
2	2	100%	4	4							
Bot30	KID035	45		Kidney Cortex							
chrMF5798chrMR6297		chrM	6304	G>A	93	R					

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2		2		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF7518chrMR7747			chrM		7606		T>C		89		F
4		4		100%		8		8			
Bot30	KID035	45			Kidney Cortex						
chrMF7204chrMR7731			chrM		7782		A>G		49		R
3		3		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF7684chrMR8066			chrM		8119		G>A		47		R
2		2		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF8728chrMR9040			chrM		8791		G>A		64		F
3		3		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF8442chrMR8831			chrM		8853		G>A		78		R
3		3		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF9181chrMR9572			chrM		9633		A>G		39		R
3		3		100%		5		5			
Bot30	KID035	45			Kidney Cortex						
chrMF10102chrMR10375			chrM		10417		T>C		58		R
3		3		100%		5		5			
Bot30	KID035	45			Kidney Cortex						
chrMF10493chrMR10795			chrM		10562		T>C		70		F
2		2		100%		4		4			
Bot30	KID035	45			Kidney Cortex						
chrMF10624chrMR11099			chrM		11170		G>A		29		R
3		3		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF11986chrMR12304			chrM		12049		T>C		64		F
2		2		100%		4		4			
Bot30	KID035	45			Kidney Cortex						
chrMF12361chrMR12737			chrM		12784		T>C		53		R
4		4		100%		5		5			
Bot30	KID035	45			Kidney Cortex						
chrMF12594chrMR12932			chrM		13002		G>A		30		R
3		3		100%		5		5			
Bot30	KID035	45			Kidney Cortex						
chrMF12811chrMR13295			chrM		13360		G>A		35		R
4		4		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF13257chrMR13614			chrM		13670		G>A		44		R
3		3		100%		5		5			
Bot30	KID035	45			Kidney Cortex						
chrMF13733chrMR14141			chrM		13788		T>C		56		F
2		2		100%		4		4			
Bot30	KID035	45			Kidney Cortex						
chrMF13771chrMR14159			chrM		14232		T>C		27		R

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3		3		100%		8		8			
Bot30	KID035	45			Kidney Cortex						
chrMF13916chrMR14423			chrM		14439		G>A		84		R
2		2		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF14726chrMR15140			chrM		14776		T>C		51		F
2		2		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF14772chrMR15113			chrM		14860		G>A		89		F
5		5		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF14529chrMR14884			chrM		14946		G>A		38		R
2		2		100%		3		3			
Bot30	KID035	45			Kidney Cortex						
chrMF14929chrMR15258			chrM		14997		G>A		69		F
2		2		100%		4		4			
Bot30	KID035	45			Kidney Cortex						
chrMF14805chrMR15033			chrM		15046		G>A		87		R
4		4		100%		4		4			
Bot30	KID035	45			Kidney Cortex						
chrMF15072chrMR15426			chrM		15140		T>C		69		F
5		5		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF15795chrMR16007			chrM		15864		G>A		70		F
2		2		100%		9		9			
Bot30	KID035	45			Kidney Cortex						
chrMF15517chrMR15911			chrM		15928		G>A		83		R
5		5		100%		2		2			
Bot30	KID035	45			Kidney Cortex						
chrMF15925chrMR16364			chrM		16440		G>A		24		R
2		2		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF185chrMR336			chrM		203		G>A		19		F
5		5		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF105chrMR504			chrM		558		A>G		46		R
2		2		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF705chrMR1329			chrM		750		G>A		46		F
2		2		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF1012chrMR1233			chrM		1052		C>A		41		F
8		8		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF1017chrMR1374			chrM		1065		A>G		49		F
3		3		100%		6		6			
Bot31	KID036	77			Kidney Cortex						
chrMF1040chrMR1217			chrM		1074		G>A		35		F

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2		2		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF576chrMR1174			chrM		1237		T>C		37		R
3		3		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF1145chrMR1539			chrM		1576		G>A		63		R
8		8		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF1745chrMR2084			chrM		1778		G>A		34		F
2		2		100%		6		6			
Bot31	KID036	77			Kidney Cortex						
chrMF2213chrMR2669			chrM		2268		T>C		56		F
3		3		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF2206chrMR2631			chrM		2282		C>A		77		F
5		5		100%		8		8			
Bot31	KID036	77			Kidney Cortex						
chrMF2292chrMR2801			chrM		2325		A>C		34		F
2		2		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF1804chrMR2266			chrM		2353		T>C		13		R
2		2		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF2363chrMR2940			chrM		2409		T>C		47		F
3		3		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF2267chrMR2776			chrM		2807		A>T		69		R
2		2		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF2378chrMR2804			chrM		2816		G>A		88		R
5		5		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF2836chrMR3269			chrM		2897		T>C		62		F
4		4		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF3530chrMR3925			chrM		3615		T>C		86		F
2		2		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF3663chrMR4158			chrM		3728		T>C		66		F
3		3		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF4455chrMR4772			chrM		4814		T>C		58		R
5		5		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF4423chrMR4826			chrM		4843		A>G		83		R
4		4		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF4758chrMR5181			chrM		4845		A>G		88		F

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3		3		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF4592chrMR5011			chrM		5098		A>G		13		R
3		3		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF4786chrMR5198			chrM		5260		T>G		38		R
4		4		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF5295chrMR5688			chrM		5315		T>A		21		F
5		5		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF5531chrMR5993			chrM		5601		A>T		71		F
2		2		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF6483chrMR6917			chrM		6538		G>A		56		F
3		3		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF6368chrMR6720			chrM		6736		A>C		84		R
5		5		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF6840chrMR7478			chrM		6865		T>C		26		F
2		2		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF7057chrMR7204			chrM		7070		T>C		14		F
3		3		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF7246chrMR7691			chrM		7331		T>C		86		F
2		2		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF7894chrMR8336			chrM		7930		G>A		37		F
4		4		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF8454chrMR8760			chrM		8781		T>C		79		R
4		4		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF9111chrMR9403			chrM		9451		G>A		52		R
9		9		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF9369chrMR9597			chrM		9655		A>G		42		R
4		4		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF9161chrMR9689			chrM		9766		A>T		23		R
3		3		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF9388chrMR9776			chrM		9867		C>T		9		R
2		2		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF9858chrMR10248			chrM		9877		A>G		20		F

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4		4		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF9989	chrMR10359		chrM		10064		A>G		76		F
2		2		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF9863	chrMR10130		chrM		10204		G>A		26		R
7		7		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF10293	chrMR10745		chrM		10343		T>C		51		F
6		6		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF10472	chrMR10859		chrM		10501		G>A		30		F
5		5		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF10403	chrMR10590		chrM		10659		A>G		31		R
7		7		100%		6		6			
Bot31	KID036	77			Kidney Cortex						
chrMF10675	chrMR11053		chrM		10703		T>C		29		F
2		2		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF10745	chrMR11108		chrM		10771		T>C		27		F
5		5		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF10934	chrMR11224		chrM		10965		A>T		32		F
7		7		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF10941	chrMR11259		chrM		10971		T>C		31		F
3		3		100%		8		8			
Bot31	KID036	77			Kidney Cortex						
chrMF11172	chrMR11478		chrM		11224		T>C		53		F
5		5		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF10786	chrMR11221		chrM		11285		C>A		36		R
4		4		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF11259	chrMR11643		chrM		11648		C>T		95		R
4		4		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF12249	chrMR12528		chrM		12324		T>C		76		F
6		6		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF12328	chrMR12725		chrM		12366		T>C		39		F
3		3		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF12498	chrMR12781		chrM		12582		T>C		85		F
6		6		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF12742	chrMR13078		chrM		12819		G>A		78		F

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6		6		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF12696chrMR13058			chrM		13135		A>G		23		R
2		2		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF13133chrMR13549			chrM		13636		T>C		13		R
2		2		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF13447chrMR13778			chrM		13845		A>G		33		R
3		3		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF14261chrMR14582			chrM		14292		T>C		32		F
10		10		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF14518chrMR15103			chrM		15181		T>C		22		R
5		5		100%		2		2			
Bot31	KID036	77			Kidney Cortex						
chrMF15261chrMR15544			chrM		15330		C>T		70		F
8		8		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF15102chrMR15551			chrM		15640		T>C		11		R
3		3		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF15635chrMR15968			chrM		15984		T>C		84		R
5		5		100%		7		7			
Bot31	KID036	77			Kidney Cortex						
chrMF15950chrMR16231			chrM		16035		G>A		86		F
2		2		100%		5		5			
Bot31	KID036	77			Kidney Cortex						
chrMF15512chrMR15961			chrM		16049		G>A		12		R
3		3		100%		4		4			
Bot31	KID036	77			Kidney Cortex						
chrMF15592chrMR16026			chrM		16055		A>G		71		R
4		4		100%		3		3			
Bot31	KID036	77			Kidney Cortex						
chrMF15977chrMR16317			chrM		16370		T>C		47		R
5		5		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF993chrMR1229			chrM		1262		A>T		67		R
6		6		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF1491chrMR1803			chrM		1576		G>A		86		F
6		6		100%		2		2			
Bot32	KID037	80			Kidney Cortex						
chrMF1596chrMR2148			chrM		1613		G>A		18		F
4		4		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF1740chrMR2073			chrM		2151		G>A		22		R

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2		2		100%		8		8			
Bot32	KID037	80			Kidney Cortex						
chrMF2313chrMR2754			chrM		2347		G>A		35		F
4		4		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF2367chrMR2779			chrM		2451		G>A		85		F
4		4		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF2493chrMR2956			chrM		2512		T>C		20		F
3		3		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF2521chrMR2746			chrM		2780		T>C		66		R
5		5		100%		11		11			
Bot32	KID037	80			Kidney Cortex						
chrMF2420chrMR2772			chrM		2840		A>G		32		R
8		8		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF2948chrMR3186			chrM		2962		T>C		15		F
11		11		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF2931chrMR3218			chrM		3007		A>T		77		F
8		8		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF3016chrMR3351			chrM		3038		G>A		23		F
14		14		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF3049chrMR3280			chrM		3087		A>T		39		F
9		9		100%		7		7			
Bot32	KID037	80			Kidney Cortex						
chrMF2749chrMR3260			chrM		3321		A>G		39		R
5		5		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF2831chrMR3273			chrM		3356		A>G		17		R
6		6		100%		7		7			
Bot32	KID037	80			Kidney Cortex						
chrMF2940chrMR3287			chrM		3372		T>C		15		R
9		9		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF3135chrMR3314			chrM		3381		G>A		33		R
9		9		100%		11		11			
Bot32	KID037	80			Kidney Cortex						
chrMF3089chrMR3354			chrM		3428		G>A		26		R
6		6		100%		9		9			
Bot32	KID037	80			Kidney Cortex						
chrMF3073chrMR3394			chrM		3434		T>C		60		R
8		8		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF3436chrMR3729			chrM		3527		G>A		92		F

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7		7		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF3279chrMR3668			chrM		3708		G>A	60		R	
2		2		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF3534chrMR3863			chrM		3902		G>A	61		R	
3		3		100%		8		8			
Bot32	KID037	80			Kidney Cortex						
chrMF3980chrMR4240			chrM		4038		G>A	59		F	
12		12		100%		15		15			
Bot32	KID037	80			Kidney Cortex						
chrMF4301chrMR4594			chrM		4317		A>G	17		F	
11		11		100%		9		9			
Bot32	KID037	80			Kidney Cortex						
chrMF4498chrMR4786			chrM		4512		T>C	15		F	
5		5		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF4083chrMR4480			chrM		4526		T>C	54		R	
3		3		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF4347chrMR4715			chrM		4753		T>C	62		R	
8		8		100%		10		10			
Bot32	KID037	80			Kidney Cortex						
chrMF4119chrMR4717			chrM		4801		T>C	16		R	
3		3		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF4763chrMR5026			chrM		4819		G>A	57		F	
4		4		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF4345chrMR4766			chrM		4832		G>A	34		R	
5		5		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF4610chrMR5000			chrM		5089		A>G	11		R	
4		4		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF5055chrMR5297			chrM		5333		T>C	64		R	
4		4		100%		2		2			
Bot32	KID037	80			Kidney Cortex						
chrMF6094chrMR6295			chrM		6354		A>G	41		R	
4		4		100%		10		10			
Bot32	KID037	80			Kidney Cortex						
chrMF6101chrMR6462			chrM		6497		C>T	65		R	
6		6		100%		9		9			
Bot32	KID037	80			Kidney Cortex						
chrMF6648chrMR6914			chrM		6679		A>G	32		F	
2		2		100%		13		13			
Bot32	KID037	80			Kidney Cortex						
chrMF6639chrMR7009			chrM		6691		G>A	53		F	

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3		3		100%		2		2			
Bot32	KID037	80			Kidney Cortex						
chrMF6441chrMR6850			chrM		6921		C>A		29		R
7		7		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF6642chrMR6919			chrM		6925		G>A		94		R
7		7		100%		13		14			
Bot32	KID037	80			Kidney Cortex						
chrMF6521chrMR6970			chrM		7024		G>A		46		R
7		7		100%		2		2			
Bot32	KID037	80			Kidney Cortex						
chrMF7234chrMR7663			chrM		7313		T>C		80		F
3		3		100%		2		2			
Bot32	KID037	80			Kidney Cortex						
chrMF7527chrMR7929			chrM		7562		T>C		36		F
6		6		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF7691chrMR7941			chrM		7965		T>C		76		R
5		5		100%		8		8			
Bot32	KID037	80			Kidney Cortex						
chrMF8248chrMR8658			chrM		8676		T>C		82		R
5		5		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF8882chrMR9277			chrM		8955		T>C		74		F
8		8		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF8878chrMR9384			chrM		8970		G>A		93		F
6		6		100%		3		3			
Bot32	KID037	80			Kidney Cortex						
chrMF8751chrMR9132			chrM		9153		T>C		79		R
7		7		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF9092chrMR9392			chrM		9161		T>C		70		F
5		5		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF9166chrMR9626			chrM		9210		G>A		45		F
2		2		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF9269chrMR9564			chrM		9593		T>G		71		R
5		5		100%		5		5			
Bot32	KID037	80			Kidney Cortex						
chrMF9354chrMR9684			chrM		9770		T>C		14		R
6		6		100%		6		6			
Bot32	KID037	80			Kidney Cortex						
chrMF9512chrMR9906			chrM		9985		G>A		21		R
4		4		100%		4		4			
Bot32	KID037	80			Kidney Cortex						
chrMF9598chrMR10032			chrM		10098		A>G		34		R

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6	6	100%	3	3					
Bot32	KID037	80	Kidney Cortex						
chrMF10085	chrMR10357	chrM	10099	G>A	15	F			
2	2	100%	14	14					
Bot32	KID037	80	Kidney Cortex						
chrMF10192	chrMR10552	chrM	10231	G>A	40	F			
7	7	100%	2	2					
Bot32	KID037	80	Kidney Cortex						
chrMF10766	chrMR11189	chrM	10801	T>G	36	F			
5	5	100%	4	4					
Bot32	KID037	80	Kidney Cortex						
chrMF11230	chrMR11598	chrM	11247	G>A	18	F			
7	7	100%	13	13					
Bot32	KID037	80	Kidney Cortex						
chrMF10912	chrMR11288	chrM	11302	T>C	86	R			
6	6	100%	5	5					
Bot32	KID037	80	Kidney Cortex						
chrMF11379	chrMR11795	chrM	11436	G>C	58	F			
2	2	100%	4	4					
Bot32	KID037	80	Kidney Cortex						
chrMF11367	chrMR11822	chrM	11901	G>A	21	R			
3	3	100%	4	4					
Bot32	KID037	80	Kidney Cortex						
chrMF12018	chrMR12401	chrM	12041	A>G	24	F			
2	2	100%	5	5					
Bot32	KID037	80	Kidney Cortex						
chrMF12217	chrMR12423	chrM	12503	T>C	20	R			
14	14	100%	4	4					
Bot32	KID037	80	Kidney Cortex						
chrMF12663	chrMR13022	chrM	12737	G>A	75	F			
6	6	100%	3	3					
Bot32	KID037	80	Kidney Cortex						
chrMF12333	chrMR12742	chrM	12788	T>C	54	R			
8	8	100%	3	3					
Bot32	KID037	80	Kidney Cortex						
chrMF12619	chrMR12962	chrM	13031	T>C	31	R			
7	7	100%	4	4					
Bot32	KID037	80	Kidney Cortex						
chrMF12684	chrMR12966	chrM	13058	A>G	8	R			
2	2	100%	2	2					
Bot32	KID037	80	Kidney Cortex						
chrMF13372	chrMR13709	chrM	13718	A>G	91	R			
4	4	100%	2	2					
Bot32	KID037	80	Kidney Cortex						
chrMF13663	chrMR13818	chrM	13827	G>A	91	R			
3	3	100%	3	3					
Bot32	KID037	80	Kidney Cortex						
chrMF13526	chrMR13858	chrM	13908	A>G	50	R			

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4		4		100%		4		4		
Bot32	KID037	80			Kidney Cortex					
chrMF14033	chrMR14404		chrM		14043		A>G	11		F
6		6		100%		5		5		
Bot32	KID037	80			Kidney Cortex					
chrMF14555	chrMR14895		chrM		14588		A>C	34		F
6		6		100%		12		12		
Bot32	KID037	80			Kidney Cortex					
chrMF15354	chrMR15497		chrM		15438		G>A	85		F
16		16		100%		9		9		
Bot32	KID037	80			Kidney Cortex					
chrMF15182	chrMR15485		chrM		15532		T>C	53		R
4		4		100%		12		12		
Bot32	KID037	80			Kidney Cortex					
chrMF15605	chrMR15911		chrM		15612		G>A	8		F
11		11		100%		16		16		
Bot32	KID037	80			Kidney Cortex					
chrMF15533	chrMR15899		chrM		15618		G>A	86		F
8		8		100%		11		11		
Bot32	KID037	80			Kidney Cortex					
chrMF15401	chrMR15612		chrM		15671		T>C	41		R
4		4		100%		13		13		
Bot32	KID037	80			Kidney Cortex					
chrMF15602	chrMR16012		chrM		16053		C>T	59		R
3		3		100%		6		6		
Bot32	KID037	80			Kidney Cortex					
chrMF15735	chrMR16163		chrM		16190		C>A	73		R
10		10		100%		4		4		
Bot32	KID037	80			Kidney Cortex					
chrMF15881	chrMR16247		chrM		16288		C>T	59		R
6		6		100%		4		4		
Bot32	KID037	80			Kidney Cortex					
chrMF15737	chrMR16232		chrM		16307		A>G	25		R
4		4		100%		6		6		
Bot32	KID037	80			Kidney Cortex					
chrMF16034	chrMR16286		chrM		16307		A>T	79		R
9		9		100%		13		13		
Bot32	KID037	80			Kidney Cortex					
chrMF16232	chrMR16470		chrM		16308		C>T	77		F
8		8		100%		11		11		
Bot32	KID037	80			Kidney Cortex					
chrMF15941	chrMR16254		chrM		16309		A>G	45		R
13		13		100%		9		9		
Bot32	KID037	80			Kidney Cortex					
chrMF16021	chrMR16442		chrM		16467		C>T	75		R
4		4		100%		2		2		
Bot33	KID038	0.416666667			Kidney Cortex, Right					
chrMF4528	chrMR4927		chrM		4933		C>T	94		R

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3		3	100%	7	7					
Bot35	KID038	0.416666667	Kidney Cortex, Left Block 2							
chrMF8256chrMR8598		chrM	8603	T>C	95	R				
5		5	100%	12	12					
Bot35	KID038	0.416666667	Kidney Cortex, Left Block 2							
chrMF11860chrMR12201		chrM	12268	C>G	33	R				
9		9	100%	8	8					
Bot36	BRA01	0.147945205	Brain, Frontal Cortex							
chrMF1215chrMR1510		chrM	1291	G>A	77	F				
5		5	100%	4	4					
Bot36	BRA01	0.147945205	Brain, Frontal Cortex							
chrMF4563chrMR5065		chrM	5106	T>C	59	R				
7		7	100%	13	13					
Bot36	BRA01	0.147945205	Brain, Frontal Cortex							
chrMF14421chrMR14710		chrM	14767	T>C	43	R				
8		8	100%	20	20					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF2400chrMR2759		chrM	2420	A>T	21	F				
8		8	100%	4	4					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF4786chrMR5193		chrM	5225	G>A	68	R				
7		7	100%	5	5					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF6369chrMR6649		chrM	6407	T>C	39	F				
11		11	100%	6	6					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF6130chrMR6497		chrM	6518	G>A	79	R				
3		3	100%	2	2					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF6729chrMR7137		chrM	7156	T>C	81	R				
12		12	100%	2	2					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF8928chrMR9367		chrM	8951	G>A	24	F				
8		8	100%	11	11					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF9134chrMR9449		chrM	9182	A>G	49	F				
6		6	100%	21	21					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF13176chrMR13584		chrM	13670	G>A	14	R				
10		10	100%	8	8					
Bot37	BRA02	1.709589041	Brain, Frontal Cortex							
chrMF15664chrMR16023		chrM	16051	T>C	72	R				
6		6	100%	8	8					
Bot38	BRA03	8.783561644	Brain, Frontal Cortex							
chrMF121chrMR554		chrM	139	T>C	19	F				
2		2	100%	13	13					
Bot38	BRA03	8.783561644	Brain, Frontal Cortex							
chrMF3257chrMR3657		chrM	3665	G>A	92	R				

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6		6	100%		11		11				
Bot38	BRA03	8.783561644		Brain, Frontal Cortex							
chrMF7121chrMR7572		chrM		7638	G>A	34	R				
17		17	100%		13		13				
Bot38	BRA03	8.783561644		Brain, Frontal Cortex							
chrMF8924chrMR9195		chrM		8964	C>T	41	F				
17		17	100%		11		11				
Bot38	BRA03	8.783561644		Brain, Frontal Cortex							
chrMF9240chrMR9661		chrM		9291	C>T	52	F				
14		14	100%		17		17				
Bot38	BRA03	8.783561644		Brain, Frontal Cortex							
chrMF15751chrMR16410		chrM		15823	T>C	73	F				
8		8	100%		9		9				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF105chrMR264		chrM		198	C>T	94	F				
15		15	100%		10		10				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF594chrMR1099		chrM		685	G>A	92	F				
6		6	100%		11		11				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF1145chrMR1326		chrM		1394	A>G	32	R				
12		12	100%		10		10				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF2762chrMR2985		chrM		3020	A>G	65	R				
12		12	100%		13		13				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF4253chrMR4657		chrM		4272	G>A	20	F				
5		5	100%		6		6				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF6460chrMR6740		chrM		6752	T>C	88	R				
5		5	100%		9		9				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF7097chrMR7635		chrM		7106	C>T	10	F				
3		3	100%		9		9				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF8443chrMR8887		chrM		8960	G>A	27	R				
10		10	100%		10		10				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF9356chrMR9531		chrM		9414	C>T	59	F				
13		13	100%		12		12				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF11516chrMR12048		chrM		12084	T>C	64	R				
3		3	100%		4		4				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF12138chrMR12657		chrM		12173	A>G	36	F				
4		4	100%		5		5				
Bot39	BRA04	20		Brain, Frontal Cortex							
chrMF12166chrMR12487		chrM		12186	G>A	21	F				

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15		15		100%		9		9			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF13613chrMR13907			chrM		13664		A>G		52		F
10		10		100%		6		6			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF13652chrMR13813			chrM		13889		T>C		24		R
22		22		100%		8		8			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF14667chrMR15088			chrM		14735		T>C		69		F
8		8		100%		9		9			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF14954chrMR15399			chrM		15044		G>A		91		F
4		4		100%		10		10			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF15005chrMR15223			chrM		15302		A>G		21		R
11		11		100%		13		13			
Bot39	BRA04	20			Brain, Frontal Cortex						
chrMF15724chrMR16195			chrM		16203		C>T		92		R
3		3		100%		10		10			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF201chrMR470			chrM		237		A>T		37		F
11		11		100%		13		13			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF3619chrMR3950			chrM		3658		C>T		40		F
16		16		100%		9		9			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF3887chrMR4271			chrM		3936		G>A		50		F
18		18		100%		6		6			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF4857chrMR5396			chrM		4951		T>C		95		F
4		4		100%		12		12			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF4658chrMR5060			chrM		5113		G>A		47		R
14		14		100%		13		13			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF5363chrMR5647			chrM		5720		G>A		27		R
19		19		100%		13		13			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF5670chrMR6004			chrM		6086		A>G		18		R
19		19		100%		9		9			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF6802chrMR7168			chrM		6853		G>A		52		F
7		7		100%		6		6			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF9391chrMR9783			chrM		9839		G>C		44		R
9		9		100%		12		12			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF10152chrMR10460			chrM		10160		C>T		9		F

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11		11		100%		18		18			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF14026chrMR14338			chrM		14430		C>A		8		R
17		17		100%		23		23			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF15270chrMR15572			chrM		15592		G>A		80		R
9		9		100%		11		11			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF15394chrMR15720			chrM		15746		C>A		74		R
15		15		100%		19		19			
Bot40	BRA05	22			Brain, Frontal Cortex						
chrMF15673chrMR16028			chrM		15766		G>A		94		F
13		13		100%		20		20			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF1163chrMR1612			chrM		1212		T>C		50		F
8		8		100%		9		9			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF1363chrMR1729			chrM		1424		G>A		62		F
15		15		100%		11		11			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF1383chrMR1780			chrM		1794		G>A		86		R
15		15		100%		15		15			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF2255chrMR2588			chrM		2291		G>A		37		F
20		20		100%		11		12			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF2999chrMR3270			chrM		3021		G>A		23		F
20		20		100%		23		23			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF3324chrMR3779			chrM		3346		T>C		23		F
10		10		100%		8		8			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF3501chrMR3965			chrM		4046		T>C		19		R
5		5		100%		7		7			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF4694chrMR4978			chrM		5028		C>T		50		R
9		9		100%		17		17			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF7018chrMR7333			chrM		7088		A>G		71		F
21		21		100%		10		10			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF7740chrMR8173			chrM		7794		G>A		55		F
13		13		100%		12		12			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF7568chrMR7901			chrM		7950		A>G		51		R
10		10		100%		14		14			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF7540chrMR8014			chrM		8077		C>G		37		R

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13		13		100%		13		13			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF8698	chrMR9093		chrM		8787		T>C		90		F
11		11		100%		22		22			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF8975	chrMR9422		chrM		8990		G>A		16		F
12		12		100%		11		11			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF8814	chrMR9178		chrM		9183		G>A		95		R
17		17		100%		6		6			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF9638	chrMR9921		chrM		9988		T>C		33		R
2		2		100%		20		20			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF10118	chrMR10777		chrM		10852		G>A		25		R
10		10		100%		7		7			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF10953	chrMR11264		chrM		11011		T>C		59		F
15		15		100%		14		14			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF11709	chrMR12364		chrM		11783		C>T		75		F
6		6		100%		4		4			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF11835	chrMR12245		chrM		12299		T>A		46		R
11		11		100%		14		14			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF11926	chrMR12413		chrM		12475		C>A		38		R
14		14		100%		10		10			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF12535	chrMR13059		chrM		12544		C>G		10		F
3		3		100%		7		7			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF13673	chrMR14017		chrM		14064		T>C		53		R
14		14		100%		13		13			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF14181	chrMR14686		chrM		14737		C>T		49		R
7		7		100%		4		4			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF14827	chrMR15244		chrM		15284		T>C		60		R
11		11		100%		9		9			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF15657	chrMR16012		chrM		16031		C>T		81		R
14		14		100%		14		14			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF15622	chrMR16028		chrM		16096		C>T		32		R
14		14		100%		10		10			
Bot41	BRA06	25			Brain, Frontal Cortex						
chrMF15638	chrMR16065		chrM		16115		C>T		50		R

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15		15		100%		15		15	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF1822chrMR2243			chrM		1833		G>A	12	F
18		18		100%		17		17	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF2881chrMR3062			chrM		3093		G>A	69	R
14		14		100%		37		37	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF3316chrMR3747			chrM		3381		G>A	66	F
11		11		100%		3		3	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF3212chrMR3530			chrM		3543		T>C	87	R
15		15		100%		13		13	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF4220chrMR4578			chrM		4267		A>G	48	F
16		16		100%		8		8	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF4426chrMR4678			chrM		4510		T>C	85	F
14		14		100%		13		13	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF4220chrMR4514			chrM		4554		T>C	60	R
21		21		100%		16		16	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF4571chrMR4889			chrM		4624		T>C	54	F
2		2		100%		2		2	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF4253chrMR4649			chrM		4706		T>C	43	R
13		13		100%		21		21	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF5548chrMR6014			chrM		5583		A>G	36	F
16		16		100%		9		9	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF5908chrMR6206			chrM		5974		G>A	67	F
3		3		100%		2		2	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF7722chrMR8059			chrM		7776		G>A	55	F
15		15		100%		11		11	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF8451chrMR8859			chrM		8489		C>T	39	F
18		18		100%		6		6	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF11328chrMR11530			chrM		11560		G>A	70	R
30		30		100%		30		30	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF11676chrMR12408			chrM		11751		A>G	76	F
5		5		100%		8		8	
Bot42	BRA07	90			Brain, Frontal Cortex				
chrMF12024chrMR12145			chrM		12114		G>A	91	F

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21		21		100%		8		8			
Bot42	BRA07	90			Brain, Frontal Cortex						
chrMF12347chrMR12665			chrM		12750		T>C		15		R
25		25		100%		17		17			
Bot42	BRA07	90			Brain, Frontal Cortex						
chrMF12792chrMR12932			chrM		12969		C>T		63		R
12		12		100%		22		22			
Bot42	BRA07	90			Brain, Frontal Cortex						
chrMF12646chrMR13022			chrM		13064		G>A		58		R
11		11		100%		4		4			
Bot42	BRA07	90			Brain, Frontal Cortex						
chrMF13183chrMR13632			chrM		13269		G>A		87		F
11		11		100%		11		11			
Bot42	BRA07	90			Brain, Frontal Cortex						
chrMF13559chrMR14049			chrM		14056		C>T		93		R
9		9		100%		8		8			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF592chrMR852			chrM		682		T>C		91		F
10		10		100%		17		17			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF1634chrMR2181			chrM		1649		T>C		16		F
7		7		100%		7		7			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF1639chrMR1975			chrM		1670		T>G		32		F
16		16		100%		13		13			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF1389chrMR1658			chrM		1749		G>A		9		R
16		16		100%		20		20			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF3071chrMR3308			chrM		3094		T>C		24		F
16		16		100%		16		16			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF3289chrMR3550			chrM		3580		A>G		70		R
20		20		100%		15		15			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF4609chrMR4952			chrM		4960		G>A		92		R
12		12		100%		12		12			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF4458chrMR4930			chrM		4976		G>A		54		R
4		4		100%		3		3			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF5661chrMR5937			chrM		5668		G>A		8		F
12		12		100%		12		12			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF5480chrMR5914			chrM		5922		A>T		92		R
4		4		100%		11		11			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF5493chrMR5937			chrM		5966		T>C		71		R

Table49.txt

6		6		100%		6		6			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF5531chrMR5953			chrM		6022		G>A		31		R
6		6		100%		13		13			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF6101chrMR6438			chrM		6165		C>T		65		F
7		7		100%		10		10			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF6238chrMR6681			chrM		6769		G>A		12		R
7		7		100%		6		6			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF6928chrMR7195			chrM		6958		G>A		31		F
16		16		100%		17		17			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF6929chrMR7126			chrM		7208		G>A		18		R
20		20		100%		3		3			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF8329chrMR8796			chrM		8878		T>C		18		R
7		7		100%		8		8			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF8533chrMR8871			chrM		8939		A>G		32		R
12		12		100%		11		11			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF8771chrMR9265			chrM		9311		T>C		54		R
5		5		100%		10		10			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF9756chrMR10303			chrM		9775		G>A		20		F
2		2		100%		2		2			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF9782chrMR10074			chrM		9838		G>A		57		F
10		10		100%		17		17			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF9935chrMR10475			chrM		10523		G>A		52		R
7		7		100%		7		7			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF11780chrMR12221			chrM		11848		G>A		69		F
13		13		100%		7		7			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF11786chrMR12070			chrM		11874		A>T		89		F
12		12		100%		9		9			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF13561chrMR13812			chrM		13839		C>T		73		R
22		22		100%		15		15			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF14310chrMR14550			chrM		14596		A>T		54		R
20		20		100%		13		13			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF15379chrMR15733			chrM		15400		T>C		22		F

Table49.txt

21		21		100%		19		19			
Bot43	BRA08	94			Brain, Frontal Cortex						
chrMF16143chrMR16346			chrM		16368		C>T	78		R	
5		5		100%		4		4			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF396chrMR865			chrM		471		C>A	76		F	
8		8		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF555chrMR973			chrM		563		A>G	9		F	
6		6		100%		10		10			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF483chrMR970			chrM		566		G>A	84		F	
8		8		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF325chrMR667			chrM		703		G>A	64		R	
9		9		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF838chrMR1216			chrM		895		G>A	58		F	
11		11		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF965chrMR1298			chrM		1340		A>G	58		R	
14		14		100%		16		16			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF1181chrMR1562			chrM		1576		G>A	86		R	
5		5		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF1883chrMR2083			chrM		1952		T>C	70		F	
14		14		100%		28		28			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF1757chrMR2085			chrM		2175		G>A	10		R	
7		7		100%		19		19			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF2197chrMR2637			chrM		2287		T>C	91		F	
6		6		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF3022chrMR3527			chrM		3065		G>A	44		F	
6		6		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF2745chrMR3064			chrM		3094		T>C	70		R	
14		14		100%		4		4			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF2656chrMR3076			chrM		3106		T>C	70		R	
4		4		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF3305chrMR3955			chrM		3358		G>A	54		F	
3		3		100%		2		2			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF3127chrMR3412			chrM		3495		C>T	17		R	

Table49.txt

21		21		100%		12		12			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF3366chrMR3682			chrM		3738		T>C		44		R
9		9		100%		16		16			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF4352chrMR4985			chrM		4422		G>A		71		F
9		9		100%		2		2			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF3847chrMR4386			chrM		4461		T>C		25		R
9		9		100%		15		15			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF4753chrMR5286			chrM		4777		G>A		25		F
11		11		100%		6		6			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF4898chrMR5249			chrM		4949		T>A		52		F
15		15		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF5453chrMR5973			chrM		5494		T>C		42		F
4		4		100%		10		10			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF5894chrMR6199			chrM		5971		G>A		78		F
11		11		100%		12		12			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF6237chrMR6639			chrM		6318		C>T		82		F
10		10		100%		4		4			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF6390chrMR6669			chrM		6463		T>C		74		F
10		10		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF6195chrMR6698			chrM		6710		G>A		88		R
6		6		100%		11		11			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF6787chrMR7013			chrM		6845		T>C		59		F
27		27		100%		17		17			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF6797chrMR7175			chrM		7237		G>A		38		R
10		10		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF7123chrMR7237			chrM		7325		A>G		12		R
14		14		100%		13		13			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF7287chrMR7616			chrM		7358		T>C		72		F
7		7		100%		6		6			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF7319chrMR7704			chrM		7394		G>A		76		F
11		11		100%		15		15			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF8727chrMR9304			chrM		9372		C>T		32		R

Table49.txt

4		4		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF9519	chrMR9850		chrM		9554		G>A		36		F
15		15		100%		11		11			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF9663	chrMR10191		chrM		10255		G>A		36		R
13		13		100%		5		5			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF10234	chrMR10710		chrM		10323		T>C		90		F
2		2		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF10004	chrMR10381		chrM		10408		G>A		73		R
20		20		100%		12		12			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF11234	chrMR11639		chrM		11712		G>A		27		R
10		10		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF12699	chrMR13064		chrM		12774		G>A		76		F
10		10		100%		9		9			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF12244	chrMR12795		chrM		12852		T>C		43		R
7		7		100%		6		6			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF12560	chrMR12982		chrM		13007		T>C		75		R
9		9		100%		5		5			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13442	chrMR13884		chrM		13911		T>C		73		R
10		10		100%		7		7			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13529	chrMR14017		chrM		14034		T>C		83		R
8		8		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13983	chrMR14290		chrM		14051		T>G		69		F
12		12		100%		11		11			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13412	chrMR14009		chrM		14082		G>A		27		R
4		4		100%		3		3			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF14104	chrMR14418		chrM		14136		T>C		33		F
17		17		100%		7		7			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13926	chrMR14247		chrM		14275		A>G		72		R
6		6		100%		7		7			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF13915	chrMR14404		chrM		14450		A>G		54		R
6		6		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF14535	chrMR14826		chrM		14588		A>G		54		F

Table49.txt

16		16		100%		16		17			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF14244	chrMR14599		chrM		14613		G>A	86		R	
9		9		100%		11		11			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF14992	chrMR15262		chrM		15013		T>C	22		F	
8		8		100%		17		17			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF14621	chrMR14975		chrM		15049		G>A	26		R	
7		7		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF15519	chrMR16064		chrM		15559		A>G	41		F	
13		13		100%		8		8			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF15518	chrMR15810		chrM		15897		A>G	13		R	
9		9		100%		18		18			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF15717	chrMR16116		chrM		16191		C>T	25		R	
7		7		100%		6		6			
Bot44	BRA09	95			Brain, Frontal Cortex						
chrMF15725	chrMR16206		chrM		16249		A>G	57		R	
9		9		100%		7		7			

Mutation Fraction of Crick Duplicates	Total Number of Reads with Mutation	Total Number of Reads
100%	210	210
100%	93	93
100%	77	77
100%	120	120
99%	196	197
100%	66	66
100%	86	86
98%	91	92
100%	34	34
100%	19	19
100%	12	12
100%	95	95
97%	136	138
100%	14	14
98%	85	86
100%	78	78
100%	92	92
100%	132	132

Table49.txt

100%	21	21
100%	53	53
100%	9	9
100%	21	21
100%	23	23
100%	17	17
100%	14	14
100%	16	16
100%	9	9
100%	14	14
100%	13	13
100%	9	9
100%	12	12
100%	7	7
100%	10	10
100%	12	12
100%	5	5
100%	20	20
100%	10	10
100%	11	11
100%	15	15
100%	13	13
100%	6	6
100%	7	7
100%	5	5
100%	9	9
100%	14	14
100%	6	6
100%	9	9
100%	11	11
100%	6	6
100%	16	16
100%	22	22
100%	12	12
100%	5	5
100%	14	14
100%	16	16
100%	8	8
100%	7	7
100%	8	8
100%	17	17
100%	19	19
100%	22	22
100%	17	17
100%	19	19
100%	12	12
100%	12	12
100%	12	12

Table49.txt

100%	17	17
100%	16	16
100%	16	16
100%	15	15
100%	9	9
100%	19	19
100%	13	13
100%	19	19
100%	12	12
100%	11	11
100%	14	14
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100%	33	33
100%	10	10
100%	10	10
100%	12	12
100%	27	27
100%	8	8
100%	7	7
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100%	14	14
100%	20	20
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100%	12	12
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100%	7	7
100%	12	12
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100%	13	13
100%	8	8
100%	12	12

Table49.txt

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100%	12	12
100%	22	22
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100%	6	6
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100%	27	27
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100%	25	25
100%	20	20
94%	42	43
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100%	25	25
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100%	8	8
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100%	37	37
100%	29	29
100%	6	6
100%	46	46
100%	13	13
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100%	31	31
100%	19	19

Table49.txt

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100%	31	31
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100%	7	7

Table49.txt

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100%	11	11
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100%	9	9
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100%	6	6
100%	4	4
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100%	5	5
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100%	9	9

Table49.txt

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100%	11	11
100%	21	21
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100%	5	5
100%	7	7
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100%	8	8
100%	6	6
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100%	9	9
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100%	7	7
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100%	6	6
100%	6	6
100%	6	6
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100%	7	7
100%	11	11
100%	9	9
100%	9	9
100%	7	7
100%	6	6
100%	7	7
100%	5	5
100%	4	4
100%	12	12
100%	10	10
100%	6	6
100%	6	6
100%	5	5
100%	5	5
100%	6	6
100%	5	5
100%	8	8
100%	8	8
100%	6	6
100%	10	10
100%	6	6
100%	7	7
100%	4	4

Table49.txt

100%	6	6
100%	5	5
100%	7	7
100%	10	10
100%	8	8
100%	4	4
100%	6	6
100%	4	4
100%	12	12
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100%	6	6
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100%	9	9
100%	8	8
100%	6	6
100%	8	8
100%	6	6
100%	11	11
100%	4	4
100%	5	5
100%	7	7
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100%	6	6
100%	8	8
100%	7	7
100%	11	11
100%	7	7
100%	5	5
100%	10	10
100%	4	4
100%	6	6
100%	13	13
100%	9	9
100%	9	9
100%	5	5
100%	11	11
100%	8	8
100%	6	6
100%	13	13
100%	7	7
100%	5	5
100%	6	6

Table49.txt

100%	6	6
100%	10	10
100%	8	8
100%	4	4
100%	5	5
100%	12	12
100%	6	6
100%	6	6
100%	7	7
100%	7	7
100%	7	7
100%	7	7
100%	10	10
100%	8	8
100%	5	5
100%	8	8
100%	6	6
100%	11	11
100%	9	9
100%	12	12
100%	7	7
100%	5	5
100%	5	5
100%	6	6
100%	4	4
100%	9	9
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100%	10	10
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Table49.txt

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Table49.txt

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Table49.txt

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Table49.txt

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Table49.txt

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Table49.txt

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100%	13	13
100%	14	14
94%	32	33
100%	20	20
100%	25	25
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100%	21	21
100%	27	27
100%	13	13
100%	16	16

Table50.txt

Table 50. Rare mutations from the nuclear genomes evaluated in this study
*Paircoordinates indicate leftmost coordinate of each paired-end read of the template

BotSeqS Library ID	Sample Name	Age	Tissue	Chr	hg19 Coordinate	Mutation (Forward Strand)	Mutation	Exon Number	Intron Number	Intergenic Number	Intragenic Number	UCSC Human Genome Browser Gene Name(s), PairCoordinates*
Bot01	AA_105	78	Kidney Cortex	chr1	82209726	G>T	intron		8		intragenic	LPHN2 chr1F82209719chr1R82210099
Bot01	AA_105	78	Kidney Cortex	chr1	181458238	T>A	intron		41		intragenic	CACNA1E chr1F181457825chr1R181458179
Bot01	AA_105	78	Kidney Cortex	chr2	7883728	A>G	na		64		intergenic	na chr2F7883665chr2R7883945
Bot01	AA_105	78	Kidney Cortex	chr2	68803983	C>G	intron		41		intragenic	APLF chr2F68803806chr2R68803924
Bot01	AA_105	78	Kidney Cortex	chr4	100733096	G>T	na		34		intergenic	na chr4F100733063chr4R100733254
Bot01	AA_105	78	Kidney Cortex	chr5	4160164	T>A	na		9		intergenic	na chr5F4159942chr5R4160073
Bot01	AA_105	78	Kidney Cortex	chr5	158510315	G>A	intron		93		intragenic	EBF1 chr5F158509971chr5R158510308
Bot01	AA_105	78	Kidney Cortex	chr5	178455845	C>T	na		72		intergenic	na chr5F178455774chr5R178456026
Bot01	AA_105	78	Kidney Cortex	chr6	142831557	G>T	na		63		intergenic	na chr6F142831495chr6R142831773
Bot01	AA_105	78	Kidney Cortex	chr6	166320840	C>A	intron		74		intragenic	AK090688 chr6F166320620chr6R166320814

Table50.txt

Bot01	AA_105	78	chr7F43520857chr7R43521345	intragenic	HECW1	Kidney Cortex	chr7	43520934	G>T	intron	78
Bot01	AA_105	78	chr10F75351850chr10R75351993	intergenic	na	Kidney Cortex	chr10	75351861	C>T	na	12
Bot01	AA_105	78	chr10F91064240chr10R91064506	intragenic	LIPA	Kidney Cortex	chr10	91064260	C>T	intron	21
Bot01	AA_105	78	chr11F40467077chr11R40467322	intragenic	LRRC4C	Kidney Cortex	chr11	40467409	G>A	intron	13
Bot01	AA_105	78	chr12F103890661chr12R103890908	intergenic	na	Kidney Cortex	chr12	103890986	G>A	na	22
Bot01	AA_105	78	chr12F110212740chr12R110213233	intergenic	na	Kidney Cortex	chr12	110213310	C>G	na	23
Bot01	AA_105	78	chr13F44268445chr13R44268648	intragenic	ENOX1	Kidney Cortex	chr13	44268731	G>A	intron	17
Bot01	AA_105	78	chr13F106861216chr13R106861584	intergenic	na	Kidney Cortex	chr13	106861614	A>G	na	70
Bot01	AA_105	78	chr18F73674632chr18R73674920	intergenic	na	Kidney Cortex	chr18	73674679	C>T	na	48
Bot01	AA_105	78	chrXF43901677chrXR43901925	intergenic	na	Kidney Cortex	chrX	43901950	T>A	na	75
Bot01	AA_105	78	chrXF118370831chrXR118371006	intragenic	PGRMC1	Kidney Cortex	chrX	118371089	G>A	intron	17
Bot01	AA_105	78	chrXF132360285chrXR132360506	intergenic	na	Kidney Cortex	chrX	132360304	G>T	na	20
Bot02	AA_124	82	chr1F177357374chr1R177357712	intergenic	na	Kidney Cortex	chr1	177357730	A>T	na	82
Bot02	AA_124	82	chr2F60020146chr2R60020397	intergenic	na	Kidney Cortex	chr2	60020455	A>T	na	42
Bot02	AA_124	82	chr2F71525235chr2R71525518	intragenic	ZNF638	Kidney Cortex	chr2	71525540	G>A	intron	78
Bot02	AA_124	82	chr2F165037077chr2R165037394	intergenic	na	Kidney Cortex	chr2	165037132	T>A	na	56

Table50.txt

Bot02	AA_124	82	Kidney Cortex								
chr2F174657874	chr2R174658320		chr2	174657925	A>T						
intergenic	na				na	52					
Bot02	AA_124	82	Kidney Cortex								
chr2F176225850	chr2R176226030		chr2	176225907	A>T						
intergenic	na				na	58					
Bot02	AA_124	82	Kidney Cortex								
chr2F198308613	chr2R198308807		chr2	198308643	C>T						
intergenic	na				na	31					
Bot02	AA_124	82	Kidney Cortex								
chr2F223886312	chr2R223886654		chr2	223886405	G>T						
intergenic	na				na	94					
Bot02	AA_124	82	Kidney Cortex								
chr3F47954249	chr3R47954459		chr3	47954290	C>T						
intragenic	MAP4				intron	42					
Bot02	AA_124	82	Kidney Cortex								
chr4F74206684	chr4R74207114		chr4	74207178	C>A						
intergenic	na				na	36					
Bot02	AA_124	82	Kidney Cortex								
chr4F176688405	chr4R176688826		chr4	176688913	G>A						
intragenic	GPM6A				intron	13					
Bot02	AA_124	82	Kidney Cortex								
chr5F150465226	chr5R150465695		chr5	150465235	C>T						
intragenic	TNIP1				intron	10					
Bot02	AA_124	82	Kidney Cortex								
chr6F21061954	chr6R21062185		chr6	21062272	C>A						
intragenic	CDKAL1				intron	13					
Bot02	AA_124	82	Kidney Cortex								
chr6F23231538	chr6R23231735		chr6	23231819	G>A						
intergenic	na				na	16					
Bot02	AA_124	82	Kidney Cortex								
chr6F70148431	chr6R70148646		chr6	70148440	T>A						
intergenic	na				na	10					
Bot02	AA_124	82	Kidney Cortex								
chr8F10953056	chr8R10953326		chr8	10953383	G>A						
intragenic	XKR6				intron	43					
Bot02	AA_124	82	Kidney Cortex								
chr8F113748349	chr8R113748500		chr8	113748546	C>A						
intragenic	CSMD3				intron	54					
Bot02	AA_124	82	Kidney Cortex								
chr8F123881272	chr8R123881566		chr8	123881329	C>G						
intragenic	ZHX2				intron	58					
Bot02	AA_124	82	Kidney Cortex								
chr9F91636852	chr9R91636952		chr9	91637040	G>C						
intragenic	SHC3				intron	12					
Bot02	AA_124	82	Kidney Cortex								
chr10F86414217	chr10R86414512		chr10	86414581	G>A						
intergenic	na				na	31					

Table50.txt

Bot02	AA_124	82	chr10F97789908	chr10R97790114	Kidney Cortex	chr10	97790191	C>G		
intragenic	ENTPD1-AS1, CC2D2B							intron	23	
Bot02	AA_124	82	chr10F98278694	chr10R98279154	Kidney Cortex	chr10	98279212	C>A		
intragenic	TM9SF3							exon	42	
Bot02	AA_124	82	chr10F121771696	chr10R121772029	Kidney Cortex	chr10	121771736	C>T		
intergenic	na							na	41	
Bot02	AA_124	82	chr11F45104920	chr11R45105046	Kidney Cortex	chr11	45105105	G>A		
intergenic	na							na	41	
Bot02	AA_124	82	chr11F105850049	chr11R105850333	Kidney Cortex	chr11	105850124	C>T		
intragenic	GRIA4							intron	76	
Bot02	AA_124	82	chr12F43965680	chr12R43966063	Kidney Cortex	chr12	43966103	T>A		
intergenic	na							na	60	
Bot02	AA_124	82	chr14F79462547	chr14R79462812	Kidney Cortex	chr14	79462868	A>T		
intragenic	NRXN3							intron	44	
Bot02	AA_124	82	chr15F83629649	chr15R83629879	Kidney Cortex	chr15	83629943	C>G		
intragenic	BC044934							intron	36	
Bot02	AA_124	82	chr16F55404082	chr16R55404338	Kidney Cortex	chr16	55404423	A>G		
intergenic	na							na	15	
Bot02	AA_124	82	chr18F50792325	chr18R50792535	Kidney Cortex	chr18	50792351	C>T		
intragenic	DCC							intron	27	
Bot02	AA_124	82	chr20F38244796	chr20R38245117	Kidney Cortex	chr20	38245168	G>A		
intergenic	na							na	49	
Bot02	AA_124	82	chr21F34489382	chr21R34489687	Kidney Cortex	chr21	34489452	C>T		
intergenic	na							na	71	
Bot02	AA_124	82	chr22F33418316	chr22R33418537	Kidney Cortex	chr22	33418575	A>T		
intragenic	SYN3							intron	62	
Bot03	AA_126	78	chr1F18494300	chr1R18494570	Kidney Cortex	chr1	18494307	G>C		
intragenic	IGSF21							intron	8	
Bot03	AA_126	78	chr1F66357026	chr1R66357280	Kidney Cortex	chr1	66357110	T>A		
intragenic	PDE4B							intron	85	
Bot03	AA_126	78	chr1F205246985	chr1R205247297	Kidney Cortex	chr1	205247370	T>G		
intergenic	na							na	27	

Table50.txt

Bot03	AA_126	78	chr2F164877957	chr2R164878130	Kidney Cortex	chr2	164877984	G>C	intergenic	na	28
Bot03	AA_126	78	chr2F180502249	chr2R180502496	Kidney Cortex	chr2	180502258	C>T	intragenic	ZNF385B	10
Bot03	AA_126	78	chr3F24263575	chr3R24264102	Kidney Cortex	chr3	24263587	C>T	intragenic	THRB	13
Bot03	AA_126	78	chr3F28008166	chr3R28008521	Kidney Cortex	chr3	28008611	G>A	intergenic	na	10
Bot03	AA_126	78	chr4F182191102	chr4R182191386	Kidney Cortex	chr4	182191475	G>A	intergenic	na	11
Bot03	AA_126	78	chr6F24218837	chr6R24219079	Kidney Cortex	chr6	24219163	G>A	intragenic	DCDC2	16
Bot03	AA_126	78	chr6F45710431	chr6R45710771	Kidney Cortex	chr6	45710779	A>T	intergenic	na	92
Bot03	AA_126	78	chr6F105918850	chr6R105919206	Kidney Cortex	chr6	105919277	A>T	intergenic	na	29
Bot03	AA_126	78	chr6F154015927	chr6R154016165	Kidney Cortex	chr6	154015940	G>C	intergenic	na	14
Bot03	AA_126	78	chr8F28889307	chr8R28889600	Kidney Cortex	chr8	28889317	C>T	intragenic	HMBOX1	11
Bot03	AA_126	78	chr8F53081401	chr8R53081604	Kidney Cortex	chr8	53081444	C>T	intragenic	ST18	44
Bot03	AA_126	78	chr8F96392043	chr8R96392322	Kidney Cortex	chr8	96392052	G>T	intragenic	LOC100616530	10
Bot03	AA_126	78	chr8F116738095	chr8R116738604	Kidney Cortex	chr8	116738672	A>G	intergenic	na	32
Bot03	AA_126	78	chr8F134483933	chr8R134484137	Kidney Cortex	chr8	134483990	G>T	intragenic	ST3GAL1	58
Bot03	AA_126	78	chr9F109081649	chr9R109081875	Kidney Cortex	chr9	109081927	A>T	intragenic	BC039487	48
Bot03	AA_126	78	chr10F22767494	chr10R22767818	Kidney Cortex	chr10	22767543	G>T	intergenic	na	50

Table50.txt

Bot03	AA_126	78	chr10F44114817	chr10R44115081	Kidney Cortex	chr10	44114862	C>T		
intergenic	na							na		46
Bot03	AA_126	78	chr10F105672291	chr10R105672485	Kidney Cortex	chr10	105672574	C>A		
intragenic	OBFC1							intron		11
Bot03	AA_126	78	chr12F104524069	chr12R104524645	Kidney Cortex	chr12	104524705	G>A		
intragenic	NFYB							intron		40
Bot03	AA_126	78	chr13F38369199	chr13R38369512	Kidney Cortex	chr13	38369214	T>A		
intragenic	TRPC4							intron		16
Bot03	AA_126	78	chr13F72961196	chr13R72961479	Kidney Cortex	chr13	72961206	C>T		
intergenic	na							na		11
Bot03	AA_126	78	chr15F89319811	chr15R89320008	Kidney Cortex	chr15	89320030	C>A		
intergenic	na							na		78
Bot03	AA_126	78	chr16F49215002	chr16R49215259	Kidney Cortex	chr16	49215304	C>A		
intergenic	na							na		55
Bot03	AA_126	78	chr19F31225870	chr19R31226243	Kidney Cortex	chr19	31225897	C>T		
intergenic	na							na		28
Bot03	AA_126	78	chrXF17284302	chrXR17284523	Kidney Cortex	chrX	17284314	C>T		
intergenic	na							na		13
Bot03	AA_126	78	chrXF121641773	chrXR121641879	Kidney Cortex	chrX	121641957	G>A		
intergenic	na							na		22
Bot04	SA_117	66	chr1F47108651	chr1R47108942	Kidney Cortex	chr1	47108958	C>A		
intragenic	ATPAF1							exon		84
Bot04	SA_117	66	chr1F52224815	chr1R52225184	Kidney Cortex	chr1	52224825	C>T		
intragenic	OSBPL9							intron		11
Bot04	SA_117	66	chr1F52865830	chr1R52866291	Kidney Cortex	chr1	52866382	G>A		
intragenic	ORC1							intron		9
Bot04	SA_117	66	chr1F110529393	chr1R110529505	Kidney Cortex	chr1	110529591	G>A		
intragenic	AHCYL1							intron		14
Bot04	SA_117	66	chr1F156458756	chr1R156459344	Kidney Cortex	chr1	156458781	A>T		
intragenic	MEF2D							intron		26
Bot04	SA_117	66	chr3F57284705	chr3R57284939	Kidney Cortex	chr3	57284717	C>T		
intragenic	APPL1							intron		13

Table50.txt

Bot04	SA_117	66	Kidney Cortex						
chr3F62375390	chr3R62375491		chr3	62375397	G>T				
intergenic	na				na	8			
Bot04	SA_117	66	Kidney Cortex						
chr3F99614569	chr3R99614706		chr3	99614770	G>A				
intragenic	MIR548G,CMSS1, FILIP1L				intron	36			
Bot04	SA_117	66	Kidney Cortex						
chr4F55357795	chr4R55358088		chr4	55357805	C>T				
intergenic	na				na	11			
Bot04	SA_117	66	Kidney Cortex						
chr4F183160846	chr4R183161105		chr4	183160914	G>T				
intragenic	TENM3				intron	69			
Bot04	SA_117	66	Kidney Cortex						
chr5F136366027	chr5R136366245		chr5	136366042	C>T				
intragenic	SPOCK1				intron	16			
Bot04	SA_117	66	Kidney Cortex						
chr5F156674145	chr5R156674467		chr5	156674472	G>A				
intragenic	ITK				intron	95			
Bot04	SA_117	66	Kidney Cortex						
chr6F139470543	chr6R139470904		chr6	139470979	G>A				
intragenic	HECA				intron	25			
Bot04	SA_117	66	Kidney Cortex						
chr7F103758443	chr7R103758755		chr7	103758450	C>T				
intergenic	na				na	8			
Bot04	SA_117	66	Kidney Cortex						
chr7F121395892	chr7R121396238		chr7	121395908	C>T				
intergenic	na				na	17			
Bot04	SA_117	66	Kidney Cortex						
chr8F29199220	chr8R29199496		chr8	29199565	C>G				
intragenic	DUSP4				intron	31			
Bot04	SA_117	66	Kidney Cortex						
chr8F29640264	chr8R29640486		chr8	29640309	C>T				
intragenic	BC082237, BC015784				intron	46			
Bot04	SA_117	66	Kidney Cortex						
chr8F40685257	chr8R40685637		chr8	40685676	G>A				
intragenic	ZMAT4				intron	61			
Bot04	SA_117	66	Kidney Cortex						
chr10F44671077	chr10R44671294		chr10	44671385	A>G				
intergenic	na				na	9			
Bot04	SA_117	66	Kidney Cortex						
chr10F101416745	chr10R101417049		chr10	101417080	G>A				
intragenic	SLC25A28				intron	69			
Bot04	SA_117	66	Kidney Cortex						
chr11F109651412	chr11R109651939		chr11	109651433	C>T				
intergenic	na				na	22			
Bot04	SA_117	66	Kidney Cortex						
chr12F10204142	chr12R10204422		chr12	10204513	G>A				
intragenic	CLEC9A				intron	9			

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Bot04	SA_117	66	chr12F70218438chr12R70218713	intergenic	na	Kidney Cortex	chr12	70218449	G>C	na	12
Bot04	SA_117	66	chr13F103294897chr13R103295170	intragenic	TPP2	Kidney Cortex	chr13	103294966	C>T	intron	70
Bot04	SA_117	66	chr16F64679081chr16R64679512	intergenic	na	Kidney Cortex	chr16	64679522	G>A	na	90
Bot04	SA_117	66	chr17F11783651chr17R11783778	intragenic	DNAH9	Kidney Cortex	chr17	11783851	G>A	intron	27
Bot04	SA_117	66	chr17F70630084chr17R70630500	intragenic	LINC00511	Kidney Cortex	chr17	70630554	G>A	intron	46
Bot04	SA_117	66	chrXF25967688chrXR25967893	intergenic	na	Kidney Cortex	chrX	25967701	C>T	na	14
Bot04	SA_117	66	chrXF71695428chrXR71695654	intragenic	HDAC8	Kidney Cortex	chrX	71695436	C>T	intron	9
Bot04	SA_117	66	chrXF131880572chrXR131880836	intragenic	HS6ST2	Kidney Cortex	chrX	131880891	G>A	intron	45
Bot04	SA_117	66	chrXF133315887chrXR133316073	intergenic	na	Kidney Cortex	chrX	133316162	G>A	na	11
Bot05	SA_118	59	chr1F111505708chr1R111505813	intragenic	LRIF1	Kidney Cortex	chr1	111505870	C>T	intron	43
Bot05	SA_118	59	chr1F174674603chr1R174674858	intragenic	RABGAP1L	Kidney Cortex	chr1	174674621	C>T	intron	19
Bot05	SA_118	59	chr1F204462205chr1R204462367	intragenic	PIK3C2B	Kidney Cortex	chr1	204462223	G>T	intron	19
Bot05	SA_118	59	chr1F217116689chr1R217116824	intragenic	ESRRG	Kidney Cortex	chr1	217116710	G>T	intron	22
Bot05	SA_118	59	chr2F113780294chr2R113780498	intragenic	IL36B	Kidney Cortex	chr2	113780547	A>G	intron	51
Bot05	SA_118	59	chr3F40114532chr3R40115111	intragenic	MYRIP	Kidney Cortex	chr3	40114550	C>T	intron	19
Bot05	SA_118	59	chr3F65379638chr3R65379866	intragenic	MAGI1	Kidney Cortex	chr3	65379685	C>T	intron	48

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Bot05	SA_118	59	Kidney Cortex						
chr4F23315018	chr4R23315256		chr4	23315025	C>T				
intergenic	na				na	8			
Bot05	SA_118	59	Kidney Cortex						
chr5F40437843	chr5R40438177		chr5	40437870	C>T				
intergenic	na				na	28			
Bot05	SA_118	59	Kidney Cortex						
chr5F57363780	chr5R57364001		chr5	57364058	C>A				
intergenic	na				na	43			
Bot05	SA_118	59	Kidney Cortex						
chr10F91188185	chr10R91188453		chr10	91188215	C>T				
intergenic	na				na	31			
Bot05	SA_118	59	Kidney Cortex						
chr11F27512920	chr11R27513035		chr11	27512954	C>T				
intergenic	na				na	35			
Bot05	SA_118	59	Kidney Cortex						
chr12F5514326	chr12R5514487		chr12	5514365	C>T				
intergenic	na				na	40			
Bot05	SA_118	59	Kidney Cortex						
chr13F41959777	chr13R41959914		chr13	41959790	G>T				
intergenic	na				na	14			
Bot05	SA_118	59	Kidney Cortex						
chr17F33230103	chr17R33230363		chr17	33230442	C>A				
intergenic	na				na	21			
Bot05	SA_118	59	Kidney Cortex						
chr17F35874436	chr17R35874883		chr17	35874961	G>A				
intragenic	SYNRG				exon	22			
Bot05	SA_118	59	Kidney Cortex						
chr18F3520057	chr18R3520206		chr18	3520295	C>G				
intragenic	DLGAP1				intron	11			
Bot05	SA_118	59	Kidney Cortex						
chrXF100999555	chrXR100999658		chrX	100999743	G>A				
intergenic	na				na	15			
Bot05	SA_118	59	Kidney Cortex						
chrYF17280514	chrYR17280690		chrY	17280737	C>A				
intergenic	na				na	53			
Bot06	SA_119	69	Kidney Cortex						
chr1F95262445	chr1R95262651		chr1	95262664	C>A				
intragenic	BC030750				intron	87			
Bot06	SA_119	69	Kidney Cortex						
chr1F222083493	chr1R222083733		chr1	222083546	C>T				
intergenic	na				na	54			
Bot06	SA_119	69	Kidney Cortex						
chr2F29041543	chr2R29041729		chr2	29041582	G>C				
intragenic	SPDYA				intron	40			
Bot06	SA_119	69	Kidney Cortex						
chr2F66693507	chr2R66693642		chr2	66693553	G>T				
intragenic	MEIS1				intron	47			

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Bot06	SA_119	69	chr2F104492535chr2R104492708	intergenic	na	Kidney Cortex	chr2	104492581	G>T	na	47
Bot06	SA_119	69	chr3F188659955chr3R188660276	intergenic	na	Kidney Cortex	chr3	188659987	C>T	na	33
Bot06	SA_119	69	chr5F67383727chr5R67383969	intergenic	na	Kidney Cortex	chr5	67383788	C>T	na	62
Bot06	SA_119	69	chr5F88064899chr5R88065064	intragenic	MEF2C	Kidney Cortex	chr5	88065129	G>A	intron	35
Bot06	SA_119	69	chr6F10191840chr6R10192032	intragenic	MRDS1	Kidney Cortex	chr6	10191851	T>G	intron	12
Bot06	SA_119	69	chr6F43686591chr6R43686694	intergenic	na	Kidney Cortex	chr6	43686606	G>T	na	16
Bot06	SA_119	69	chr6F151135393chr6R151135848	intragenic	PLEKHG1	Kidney Cortex	chr6	151135478	C>T	intron	86
Bot06	SA_119	69	chr6F164162753chr6R164163024	intragenic	AK093114	Kidney Cortex	chr6	164162794	C>T	intron	42
Bot06	SA_119	69	chr9F79750371chr9R79750772	intergenic	na	Kidney Cortex	chr9	79750845	C>G	na	27
Bot06	SA_119	69	chr11F120400264chr11R120400581	intragenic	GRIK4	Kidney Cortex	chr11	120400272	G>C	intron	9
Bot06	SA_119	69	chr12F42860309chr12R42860557	intragenic	PRICKLE1	Kidney Cortex	chr12	42860583	G>A	intron	74
Bot06	SA_119	69	chr14F53866824chr14R53867172	intergenic	na	Kidney Cortex	chr14	53866850	G>T	na	27
Bot06	SA_119	69	chr14F73148138chr14R73148450	intragenic	DPF3	Kidney Cortex	chr14	73148208	C>T	intron	71
Bot06	SA_119	69	chr14F78567797chr14R78568031	intergenic	na	Kidney Cortex	chr14	78567844	C>T	na	48
Bot06	SA_119	69	chr15F99482300chr15R99482610	intragenic	IGF1R	Kidney Cortex	chr15	99482701	C>G	intron	9
Bot06	SA_119	69	chr20F58707698chr20R58707845	intergenic	na	Kidney Cortex	chr20	58707753	C>T	na	56

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Bot06	SA_119	69	chr21F30013192chr21R30013424	intergenic	na	Kidney Cortex	chr21	30013226	C>T	na	35
Bot06	SA_119	69	chrXF109824763chrXR109824898	intergenic	na	Kidney Cortex	chrX	109824802	C>T	na	40
Bot06	SA_119	69	chrXF131517681chrXR131517934	intragenic	MBNL3	Kidney Cortex	chrX	131518012	C>A	intron	22
Bot07	COL229	3	chr1F245020827chr1R245021068	intragenic	HNRNPU	Colon Epithelium	chr1	245021115	C>G	intron	53
Bot07	COL229	3	chr21F34052344chr21R34052624	intragenic	SYNJ1	Colon Epithelium	chr21	34052632	T>G	intron	92
Bot08	COL231	8	chr2F6477068chr2R6477470	intergenic	na	Colon Epithelium	chr2	6477082	G>C	na	15
Bot08	COL231	8	chr4F42336476chr4R42336819	intergenic	na	Colon Epithelium	chr4	42336868	C>A	na	51
Bot08	COL231	8	chr12F16757057chr12R16757295	intragenic	LMO3	Colon Epithelium	chr12	16757376	C>T	intron	19
Bot09	COL232	98	chr1F161160627chr1R161160983	intragenic	ADAMTS4	Colon Epithelium	chr1	161160699	G>T	exon	73
Bot09	COL232	98	chr1F164920334chr1R164920610	intergenic	na	Colon Epithelium	chr1	164920389	G>A	na	56
Bot09	COL232	98	chr5F2692356chr5R2692620	intergenic	na	Colon Epithelium	chr5	2692407	C>T	na	52
Bot09	COL232	98	chr5F94220778chr5R94221319	intragenic	MCTP1	Colon Epithelium	chr5	94221336	G>A	intron	83
Bot09	COL232	98	chr7F35301600chr7R35301913	intergenic	na	Colon Epithelium	chr7	35301660	C>T	na	61
Bot09	COL232	98	chr7F123427302chr7R123427795	intergenic	na	Colon Epithelium	chr7	123427345	A>G	na	44
Bot09	COL232	98	chr7F155916186chr7R155916606	intergenic	na	Colon Epithelium	chr7	155916626	G>A	na	80
Bot09	COL232	98	chr8F35687633chr8R35688089	intergenic	na	Colon Epithelium	chr8	35687640	A>G	na	8

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Bot09	COL232	98	chr11F26707819chr11R26708447	intragenic	SLC5A12	Colon Epithelium	chr11	26708509	C>A	intron	38
Bot09	COL232	98	chr13F90976504chr13R90976763	intergenic	na	Colon Epithelium	chr13	90976821	T>A	na	42
Bot09	COL232	98	chr15F69320353chr15R69320942	intragenic	NOX5	Colon Epithelium	chr15	69320373	G>A	intron	21
Bot09	COL232	98	chr17F60004986chr17R60005294	intergenic	na	Colon Epithelium	chr17	60005381	T>A	na	13
Bot10	COL233	96	chr1F42314201chr1R42314624	intragenic	HIVEP3	Colon Epithelium	chr1	42314663	C>G	intron	61
Bot10	COL233	96	chr1F82225383chr1R82225693	intragenic	LPHN2	Colon Epithelium	chr1	82225416	G>A	intron	34
Bot10	COL233	96	chr2F60021226chr2R60021522	intergenic	na	Colon Epithelium	chr2	60021250	G>C	na	25
Bot10	COL233	96	chr2F215849817chr2R215850021	intragenic	ABCA12	Colon Epithelium	chr2	215849900	G>A	intron	84
Bot10	COL233	96	chr3F187385605chr3R187386103	intergenic	na	Colon Epithelium	chr3	187385634	C>G	na	30
Bot10	COL233	96	chr3F188747957chr3R188748413	intragenic	TPRG1	Colon Epithelium	chr3	188748426	C>T	intron	87
Bot10	COL233	96	chr4F141247439chr4R141247836	intragenic	SCOC, LOC100129858	Colon Epithelium	chr4	141247881	T>G	intron	55
Bot10	COL233	96	chr7F95850418chr7R95850927	intragenic	SLC25A13	Colon Epithelium	chr7	95850447	C>T	intron	30
Bot10	COL233	96	chr8F136822775chr8R136823061	intergenic	na	Colon Epithelium	chr8	136823113	G>A	na	48
Bot10	COL233	96	chr10F62603485chr10R62603802	intergenic	na	Colon Epithelium	chr10	62603492	G>C	na	8
Bot10	COL233	96	chr10F102613680chr10R102614027	intergenic	na	Colon Epithelium	chr10	102614096	C>A	na	31
Bot10	COL233	96	chr14F49681121chr14R49681280	intergenic	na	Colon Epithelium	chr14	49681369	C>A	na	11

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Bot10	COL233	96	chrXF9693132chrXR9693562	intragenic	GPR143	Colon Epithelium	chrX	9693598	G>C
exon	64								
Bot10	COL233	96	chrXF13589537chrXR13589727	intragenic	EGFL6	Colon Epithelium	chrX	13589614	C>T
intron	78								
Bot11	COL234	95	chr1F60797526chr1R60797734	intergenic	na	Colon Epithelium	chr1	60797791	C>G
na	43								
Bot11	COL234	95	chr2F126182558chr2R126182909	intergenic	na	Colon Epithelium	chr2	126182988	T>C
na	21								
Bot11	COL234	95	chr2F181518904chr2R181519237	intergenic	na	Colon Epithelium	chr2	181519304	C>T
na	33								
Bot11	COL234	95	chr4F165231553chr4R165231744	intragenic	MARCH1	Colon Epithelium	chr4	165231640	T>C
intron	88								
Bot11	COL234	95	chr4F173691779chr4R173692064	intragenic	GALNTL6	Colon Epithelium	chr4	173691855	C>T
intron	77								
Bot11	COL234	95	chr5F147122721chr5R147123239	intragenic	JAKMIP2	Colon Epithelium	chr5	147123271	G>A
intron	68								
Bot11	COL234	95	chr8F87398051chr8R87398237	intragenic	WWP1	Colon Epithelium	chr8	87398324	C>A
intron	13								
Bot11	COL234	95	chr8F97157436chr8R97157754	intragenic	GDF6	Colon Epithelium	chr8	97157842	G>C
intron	12								
Bot11	COL234	95	chr11F59100124chr11R59100407	intergenic	na	Colon Epithelium	chr11	59100415	G>C
na	92								
Bot11	COL234	95	chr11F112362078chr11R112362473	intergenic	na	Colon Epithelium	chr11	112362103	G>C
na	26								
Bot11	COL234	95	chr11F115905760chr11R115906011	intergenic	na	Colon Epithelium	chr11	115906067	C>T
na	44								
Bot11	COL234	95	chr21F41690585chr21R41690752	intragenic	DSCAM	Colon Epithelium	chr21	41690653	G>A
intron	69								
Bot11	COL234	95	chrXF135318863chrXR135319319	intragenic	MAP7D3	Colon Epithelium	chrX	135319332	G>A
intron	87								
Bot12	COL235	26	chr4F144140126chr4R144140427	intragenic	USP38	Colon Epithelium	chr4	144140488	C>T
intron	39								

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Bot12	COL235	26	Colon Epithelium						
chr5F131280728	chr5R131281089		chr5	131281140	G>T				
intragenic	LOC728637, ACSL6					exon	49		
Bot12	COL235	26	Colon Epithelium						
chr11F14839530	chr11R14839977		chr11	14839552	A>G				
intragenic	PDE3B					intron	23		
Bot12	COL235	26	Colon Epithelium						
chr11F47150165	chr11R47150642		chr11	47150660	G>T				
intragenic	C11ORF49					intron	82		
Bot12	COL235	26	Colon Epithelium						
chr11F105919470	chr11R105919965		chr11	105919970	T>C				
intergenic	na					na	95		
Bot12	COL235	26	Colon Epithelium						
chr12F116732057	chr12R116732740		chr12	116732099	G>C				
intergenic	na					na	43		
Bot13	COL236	26	Colon Epithelium						
chr7F148161716	chr7R148161977		chr7	148162007	C>G				
intergenic	na					na	70		
Bot14	COL237	22	Colon Epithelium						
chr2F6055380	chr2R6055715		chr2	6055795	C>T				
intergenic	na					na	20		
Bot14	COL237	22	Colon Epithelium						
chr4F155705224	chr4R155705492		chr4	155705294	G>A				
intragenic	RBM46					intron	71		
Bot14	COL237	22	Colon Epithelium						
chr5F115164372	chr5R115164783		chr5	115164453	A>G				
intragenic	ATG12					exon	82		
Bot14	COL237	22	Colon Epithelium						
chr10F24359600	chr10R24360024		chr10	24360115	T>G				
intragenic	KIAA1217					intron	9		
Bot14	COL237	22	Colon Epithelium						
chr13F54010341	chr13R54010662		chr13	54010352	G>C				
intergenic	na					na	12		
Bot14	COL237	22	Colon Epithelium						
chrXF83464617	chrXR83464943		chrX	83464960	G>C				
intergenic	na					na	83		
Bot15	COL238	16	Colon Epithelium						
chr1F34058034	chr1R34058135		chr1	34058068	G>T				
intragenic	CSMD2					intron	35		
Bot15	COL238	16	Colon Epithelium						
chr1F85142993	chr1R85143134		chr1	85143056	G>T				
intragenic	SSX2IP					intron	64		
Bot15	COL238	16	Colon Epithelium						
chr1F94101025	chr1R94101234		chr1	94101054	G>C				
intragenic	BCAR3					intron	30		
Bot15	COL238	16	Colon Epithelium						
chr1F101552362	chr1R101552468		chr1	101552409	T>A				
intragenic	BX538249, BC045807, AK021551					exon	48		

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Bot15	COL238	16	chr1F109243994	chr1R109244215	intragenic	PRPF38B	Colon Epithelium	chr1	109244069	C>T
exon	76									
Bot15	COL238	16	chr1F208021158	chr1R208021331	intergenic	na	Colon Epithelium	chr1	208021342	G>A
na	89									
Bot15	COL238	16	chr1F233497786	chr1R233497930	intragenic	KIAA1804	Colon Epithelium	chr1	233497998	G>A
exon	32									
Bot15	COL238	16	chr2F27860980	chr2R27861208	intragenic	GPN1	Colon Epithelium	chr2	27861006	C>T
intron	27									
Bot15	COL238	16	chr2F100193141	chr2R100193262	intragenic	AFF3	Colon Epithelium	chr2	100193168	G>T
intron	28									
Bot15	COL238	16	chr2F103157681	chr2R103157824	intergenic	na	Colon Epithelium	chr2	103157877	G>A
na	47									
Bot15	COL238	16	chr3F160167966	chr3R160168163	intergenic	na	Colon Epithelium	chr3	160167987	C>T
na	22									
Bot15	COL238	16	chr5F71259052	chr5R71259191	intergenic	na	Colon Epithelium	chr5	71259085	C>T
na	34									
Bot15	COL238	16	chr5F126313289	chr5R126313483	intragenic	MARCH3	Colon Epithelium	chr5	126313496	G>A
intron	87									
Bot15	COL238	16	chr6F3421935	chr6R3422044	intragenic	SLC22A23	Colon Epithelium	chr6	3422125	G>A
intron	19									
Bot15	COL238	16	chr6F11435981	chr6R11436113	intragenic	BC030116	Colon Epithelium	chr6	11436151	G>A
intron	62									
Bot15	COL238	16	chr6F26536620	chr6R26536721	intergenic	na	Colon Epithelium	chr6	26536636	G>T
na	17									
Bot15	COL238	16	chr6F37069820	chr6R37069961	intergenic	na	Colon Epithelium	chr6	37069909	G>C
na	90									
Bot15	COL238	16	chr6F37275947	chr6R37276068	intragenic	TBC1D22B	Colon Epithelium	chr6	37276083	G>C
intron	85									
Bot15	COL238	16	chr6F45759022	chr6R45759147	intergenic	na	Colon Epithelium	chr6	45759074	G>T
na	53									
Bot15	COL238	16	chr6F56532947	chr6R56533119	intragenic	DST	Colon Epithelium	chr6	56533004	G>T
intron	58									

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Bot15	COL238	16	chr6F166785554	chr6R166785688	intragenic	MPC1	Colon Epithelium	chr6	166785752	G>A	intron	36
Bot15	COL238	16	chr8F116682223	chr8R116682360	intergenic	na	Colon Epithelium	chr8	116682263	G>C	na	41
Bot15	COL238	16	chr9F20550970	chr9R20551142	intragenic	MLLT3	Colon Epithelium	chr9	20551202	C>G	intron	40
Bot15	COL238	16	chr9F111875632	chr9R111875799	intragenic	TMEM245	Colon Epithelium	chr9	111875826	C>G	intron	73
Bot15	COL238	16	chr9F129999893	chr9R130000110	intergenic	na	Colon Epithelium	chr9	130000186	G>A	na	24
Bot15	COL238	16	chr10F11358275	chr10R11358414	intragenic	CELF2	Colon Epithelium	chr10	11358453	T>G	intron	61
Bot15	COL238	16	chr11F73590277	chr11R73590421	intragenic	PAAF1	Colon Epithelium	chr11	73590504	G>A	intron	17
Bot15	COL238	16	chr11F78210939	chr11R78211188	intragenic	NARS2	Colon Epithelium	chr11	78210969	C>T	intron	31
Bot15	COL238	16	chr11F114956437	chr11R114956616	intergenic	na	Colon Epithelium	chr11	114956455	G>C	na	19
Bot15	COL238	16	chr11F120755877	chr11R120756034	intragenic	GRIK4	Colon Epithelium	chr11	120755944	C>T	intron	68
Bot15	COL238	16	chr11F121779566	chr11R121779753	intergenic	na	Colon Epithelium	chr11	121779580	C>T	na	15
Bot15	COL238	16	chr11F121897873	chr11R121898107	intergenic	na	Colon Epithelium	chr11	121898197	G>A	na	10
Bot15	COL238	16	chr11F128220831	chr11R128221009	intergenic	na	Colon Epithelium	chr11	128221097	C>A	na	12
Bot15	COL238	16	chr12F3212364	chr12R3212509	intragenic	TSPAN9	Colon Epithelium	chr12	3212542	G>A	intron	67
Bot15	COL238	16	chr15F99328338	chr15R99328493	intragenic	IGF1R	Colon Epithelium	chr15	99328501	T>C	intron	92
Bot15	COL238	16	chr16F7711949	chr16R7712092	intragenic	RBFOX1	Colon Epithelium	chr16	7711960	G>T	intron	12

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Bot15	COL238	16	chr16F27888831	chr16R27888935	Colon Epithelium	chr16	27889013	C>A		
intragenic	GSG1L							intron	22	
Bot15	COL238	16	chr16F60641914	chr16R60642062	Colon Epithelium	chr16	60642072	A>G		
intergenic	na							na	90	
Bot15	COL238	16	chr17F29820275	chr17R29820429	Colon Epithelium	chr17	29820487	C>A		
intragenic	RAB11FIP4							intron	42	
Bot15	COL238	16	chr17F46874422	chr17R46874717	Colon Epithelium	chr17	46874456	C>T		
intragenic	TTLL6							exon	35	
Bot15	COL238	16	chrXF44703946	chrXR44704122	Colon Epithelium	chrX	44703960	G>T		
intragenic	DUSP21							exon	15	
Bot15	COL238	16	chrXF150798996	chrXR150799103	Colon Epithelium	chrX	150799138	G>A		
intragenic	PASD1							intron	65	
Bot15	COL238	16	chrYF18044563	chrYR18044686	Colon Epithelium	chrY	18044738	G>A		
intergenic	na							na	48	
Bot16	COL239	18	chr1F57263810	chr1R57263913	Colon Epithelium	chr1	57263878	G>T		
intragenic	C1ORF168							intron	69	
Bot16	COL239	18	chr1F73491990	chr1R73492203	Colon Epithelium	chr1	73492264	G>A		
intergenic	na							na	39	
Bot16	COL239	18	chr2F104537356	chr2R104537553	Colon Epithelium	chr2	104537584	G>T		
intergenic	na							na	69	
Bot16	COL239	18	chr3F69844446	chr3R69844558	Colon Epithelium	chr3	69844472	G>T		
intragenic	MITF							intron	27	
Bot16	COL239	18	chr3F143581252	chr3R143581528	Colon Epithelium	chr3	143581319	G>T		
intergenic	na							na	68	
Bot16	COL239	18	chr3F149238029	chr3R149238130	Colon Epithelium	chr3	149238202	C>G		
intragenic	WWTR1							exon	28	
Bot16	COL239	18	chr3F188624541	chr3R188624694	Colon Epithelium	chr3	188624589	C>T		
intergenic	na							na	49	
Bot16	COL239	18	chr4F36394092	chr4R36394201	Colon Epithelium	chr4	36394228	C>T		
intergenic	na							na	73	
Bot16	COL239	18	chr4F182103242	chr4R182103463	Colon Epithelium	chr4	182103514	C>G		
intergenic	na							na	49	

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Bot16	COL239	18	chr5F57382522chr5R57382675	intergenic	na	Colon Epithelium	chr5	57382567	G>T	na	46
Bot16	COL239	18	chr5F59230699chr5R59230818	intragenic	PDE4D	Colon Epithelium	chr5	59230870	G>A	intron	48
Bot16	COL239	18	chr6F12692031chr6R12692172	intergenic	na	Colon Epithelium	chr6	12692058	T>A	na	28
Bot16	COL239	18	chr6F119631249chr6R119631396	intragenic	MAN1A1	Colon Epithelium	chr6	119631409	G>A	intron	87
Bot16	COL239	18	chr6F127770959chr6R127771084	intragenic	KIAA0408, SOGA3	Colon Epithelium	chr6	127771029	C>T	exon	71
Bot16	COL239	18	chr6F143246409chr6R143246627	intragenic	HIVEP2	Colon Epithelium	chr6	143246660	G>A	intron	67
Bot16	COL239	18	chr6F153325145chr6R153325257	intergenic	na	Colon Epithelium	chr6	153325202	C>T	na	58
Bot16	COL239	18	chr8F93516357chr8R93516475	intergenic	na	Colon Epithelium	chr8	93516539	G>A	na	36
Bot16	COL239	18	chr10F22911939chr10R22912073	intragenic	PIP4K2A	Colon Epithelium	chr10	22912131	G>A	intron	42
Bot16	COL239	18	chr10F61979623chr10R61979866	intragenic	ANK3	Colon Epithelium	chr10	61979679	G>T	intron	57
Bot16	COL239	18	chr10F95905715chr10R95905917	intragenic	PLCE1	Colon Epithelium	chr10	95905975	G>A	intron	42
Bot16	COL239	18	chr10F99546719chr10R99546835	intergenic	na	Colon Epithelium	chr10	99546727	G>T	na	9
Bot16	COL239	18	chr11F124355587chr11R124355822	intergenic	na	Colon Epithelium	chr11	124355904	C>G	na	18
Bot16	COL239	18	chr12F10208980chr12R10209212	intragenic	CLEC9A	Colon Epithelium	chr12	10209266	G>A	intron	46
Bot16	COL239	18	chr12F15394330chr12R15394466	intergenic	na	Colon Epithelium	chr12	15394386	C>T	na	57
Bot16	COL239	18	chr12F54221778chr12R54221896	intergenic	na	Colon Epithelium	chr12	54221786	C>T	na	9

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Bot16	COL239	18	chr12F54725464	chr12R54725603	Colon Epithelium	chr12	54725677	C>A	
intragenic	COPZ1							intron	26
Bot16	COL239	18	chr12F76119101	chr12R76119223	Colon Epithelium	chr12	76119293	G>A	
intergenic	na							na	30
Bot16	COL239	18	chr15F90549865	chr15R90550040	Colon Epithelium	chr15	90550109	A>T	
intragenic	ZNF710							intron	31
Bot16	COL239	18	chr15F101209090	chr15R101209240	Colon Epithelium	chr15	101209304	G>A	
intergenic	na							na	36
Bot16	COL239	18	chr17F28569116	chr17R28569285	Colon Epithelium	chr17	28569200	C>T	
intergenic	na							na	85
Bot16	COL239	18	chr19F31091228	chr19R31091371	Colon Epithelium	chr19	31091457	G>A	
intergenic	na							na	14
Bot16	COL239	18	chr21F27487980	chr21R27488163	Colon Epithelium	chr21	27487998	G>T	
intragenic	APP							intron	19
Bot16	COL239	18	chrXF93150303	chrXR93150409	Colon Epithelium	chrX	93150482	T>G	
intergenic	na							na	27
Bot17	SIN230	6	chr1F95266592	chr1R95266885	Small Intestine	chr1	95266604	G>T	
intragenic	BC030750							intron	13
Bot17	SIN230	6	chr3F140835107	chr3R140835368	Small Intestine	chr3	140835186	C>T	
intragenic	SPSB4							intron	80
Bot17	SIN230	6	chr10F95652518	chr10R95652874	Small Intestine	chr10	95652929	C>G	
intergenic	na							na	45
Bot17	SIN230	6	chr11F120747641	chr11R120747931	Small Intestine	chr11	120747668	G>A	
intragenic	GRIK4							intron	28
Bot18	COL235	26	chr1F52730812	chr1R52731143	Colon Epithelium	chr1	52731157	A>G	
intragenic	ZFYVE9							intron	86
Bot18	COL235	26	chr1F177255203	chr1R177255637	Colon Epithelium	chr1	177255676	G>A	
intergenic	na							na	61
Bot18	COL235	26	chr3F77053182	chr3R77053513	Colon Epithelium	chr3	77053526	C>A	
intragenic	ROBO2							intron	87
Bot18	COL235	26	chr4F141229559	chr4R141230018	Colon Epithelium	chr4	141229580	G>T	
intragenic	SCOC, LOC100129858							intron	22

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Bot18	COL235	26	chr10F119152507	chr10R119152681	Colon Epithelium	chr10	119152533	C>T	intergenic	na	27
Bot18	COL235	26	chr17F43413443	chr17R43413913	Colon Epithelium	chr17	43413931	T>G	intergenic	na	82
Bot18	COL235	26	chr18F22139754	chr18R22140151	Colon Epithelium	chr18	22140237	C>T	intergenic	na	14
Bot18	COL235	26	chr18F52459699	chr18R52460210	Colon Epithelium	chr18	52459793	G>C	intergenic	na	95
Bot18	COL235	26	chrXF47415346	chrXR47415802	Colon Epithelium	chrX	47415838	G>A	intergenic	na	64
Bot19	COL236	26	chr3F85414091	chr3R85414389	Colon Epithelium	chr3	85414469	A>G	intragenic	CADM2	20
Bot19	COL236	26	chr4F137235856	chr4R137236363	Colon Epithelium	chr4	137235949	G>C	intergenic	na	94
Bot19	COL236	26	chr4F176267763	chr4R176267979	Colon Epithelium	chr4	176267849	C>T	intergenic	na	87
Bot19	COL236	26	chr6F123387485	chr6R123387790	Colon Epithelium	chr6	123387804	C>T	intergenic	na	86
Bot19	COL236	26	chr8F32284149	chr8R32284509	Colon Epithelium	chr8	32284584	T>G	intragenic	NRG1	25
Bot19	COL236	26	chr8F34359154	chr8R34359474	Colon Epithelium	chr8	34359246	C>A	intergenic	na	93
Bot19	COL236	26	chr10F64463952	chr10R64464419	Colon Epithelium	chr10	64464510	C>T	intergenic	na	9
Bot19	COL236	26	chr11F30434143	chr11R30434554	Colon Epithelium	chr11	30434206	G>A	intragenic	MPPED2	64
Bot19	COL236	26	chr12F66070900	chr12R66071221	Colon Epithelium	chr12	66071277	G>A	intergenic	na	44
Bot19	COL236	26	chrXF81551761	chrXR81551965	Colon Epithelium	chrX	81551786	G>A	intergenic	na	26
Bot20	COL373	36	chr4F101398075	chr4R101398372	Colon Epithelium	chr4	101398104	C>T	intragenic	EMCN	30

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Bot20	COL373	36	Colon Epithelium						
chr5F60977874	chr5R60978189		chr5	60977964	T>C				
intragenic	C5ORF64, BC043229,BC043516, BC043261				intron	91			
Bot20	COL373	36	Colon Epithelium						
chr5F88476510	chr5R88477189		chr5	88477194	C>T				
intergenic	na				na	95			
Bot20	COL373	36	Colon Epithelium						
chr6F40799997	chr6R40800272		chr6	40800293	G>A				
intergenic	na				na	79			
Bot20	COL373	36	Colon Epithelium						
chr8F77880765	chr8R77880996		chr8	77881026	C>T				
intergenic	na				na	70			
Bot20	COL373	36	Colon Epithelium						
chr12F14833442	chr12R14833787		chr12	14833851	C>T				
intragenic	GUCY2C				intron	36			
Bot20	COL373	36	Colon Epithelium						
chr17F50186558	chr17R50186908		chr17	50186570	A>T				
intragenic	CA10				intron	13			
Bot20	COL373	36	Colon Epithelium						
chrXF118214483	chrXR118214737		chrX	118214514	T>A				
intragenic	KIAA1210				exon	32			
Bot20	COL373	36	Colon Epithelium						
chrYF18926220	chrYR18926329		chrY	18926388	C>T				
intergenic	na				na	41			
Bot21	COL374	21	Colon Epithelium						
chr2F50327073	chr2R50327337		chr2	50327395	G>A				
intragenic	NRXN1				intron	42			
Bot21	COL374	21	Colon Epithelium						
chr3F153393631	chr3R153394132		chr3	153394164	T>C				
intergenic	na				na	68			
Bot21	COL374	21	Colon Epithelium						
chr14F92220042	chr14R92220346		chr14	92220055	A>G				
intergenic	na				na	14			
Bot21	COL374	21	Colon Epithelium						
chr17F50216316	chr17R50216688		chr17	50216719	A>T				
intragenic	CA10				intron	69			
Bot22	COL375	38	Colon Epithelium						
chr2F14872521	chr2R14872811		chr2	14872884	T>A				
intergenic	na				na	27			
Bot22	COL375	38	Colon Epithelium						
chr4F183080933	chr4R183081290		chr4	183080958	C>T				
intragenic	TENM3				intron	26			
Bot22	COL375	38	Colon Epithelium						
chr7F130523776	chr7R130524258		chr7	130523818	G>A				
intergenic	na				na	43			
Bot22	COL375	38	Colon Epithelium						
chr8F51618855	chr8R51619223		chr8	51619241	T>C				
intragenic	SNTG1				intron	82			

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Bot22	COL375	38	chrXF30674123chrXR30674346	Colon Epithelium	chrX	30674417	T>C		
intragenic	GK						intron	29	
Bot23	AA_105	78	chr1F61556220chr1R61556525	Kidney Cortex	chr1	61556256	G>T		
intragenic	NFIA						intron	37	
Bot23	AA_105	78	chr1F68503318chr1R68503625	Kidney Cortex	chr1	68503708	G>A		
intragenic	GNG12-AS1						intron	17	
Bot23	AA_105	78	chr1F82529215chr1R82529802	Kidney Cortex	chr1	82529282	C>T		
intergenic	na						na	68	
Bot23	AA_105	78	chr1F159628151chr1R159628446	Kidney Cortex	chr1	159628479	T>A		
intergenic	na						na	67	
Bot23	AA_105	78	chr1F173165272chr1R173165416	Kidney Cortex	chr1	173165350	G>T		
intragenic	TNFSF4						intron	79	
Bot23	AA_105	78	chr1F181579264chr1R181579505	Kidney Cortex	chr1	181579573	T>A		
intragenic	CACNA1E						intron	32	
Bot23	AA_105	78	chr1F213794502chr1R213794759	Kidney Cortex	chr1	213794808	G>A		
intergenic	na						na	51	
Bot23	AA_105	78	chr1F214535875chr1R214535980	Kidney Cortex	chr1	214535929	G>T		
intragenic	PTPN14						intron	55	
Bot23	AA_105	78	chr1F217026773chr1R217027138	Kidney Cortex	chr1	217027158	A>T		
intragenic	ESRRG						intron	80	
Bot23	AA_105	78	chr1F230523389chr1R230523700	Kidney Cortex	chr1	230523786	C>A		
intragenic	PGBD5						intron	14	
Bot23	AA_105	78	chr2F17729014chr2R17729179	Kidney Cortex	chr2	17729106	T>C		
intragenic	VSNL1						intron	93	
Bot23	AA_105	78	chr2F60097476chr2R60097638	Kidney Cortex	chr2	60097675	C>G		
intergenic	na						na	63	
Bot23	AA_105	78	chr2F104051407chr2R104051721	Kidney Cortex	chr2	104051434	C>A		
intergenic	na						na	28	
Bot23	AA_105	78	chr2F145626208chr2R145626570	Kidney Cortex	chr2	145626261	C>T		
intragenic	TEX41						intron	54	
Bot23	AA_105	78	chr2F147768690chr2R147768924	Kidney Cortex	chr2	147768739	C>T		
intergenic	na						na	50	

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Bot23	AA_105	78		Kidney Cortex						
chr2F171850584	chr2R171850945			chr2	171850968		G>A			
intragenic	TLK1						intron	77		
Bot23	AA_105	78		Kidney Cortex						
chr2F201399188	chr2R201399532			chr2	201399561		G>A			
intragenic	SGOL2						intron	71		
Bot23	AA_105	78		Kidney Cortex						
chr2F201680657	chr2R201680894			chr2	201680727		G>T			
intragenic	BZW1						intron	71		
Bot23	AA_105	78		Kidney Cortex						
chr2F211454791	chr2R211455132			chr2	211454845		C>T			
intragenic	CPS1						exon	55		
Bot23	AA_105	78		Kidney Cortex						
chr3F25145245	chr3R25145421			chr3	25145265		C>T			
intergenic	na						na	21		
Bot23	AA_105	78		Kidney Cortex						
chr3F53954122	chr3R53954470			chr3	53954137		A>T			
intergenic	na						na	16		
Bot23	AA_105	78		Kidney Cortex						
chr3F104860222	chr3R104860652			chr3	104860728		G>A			
intergenic	na						na	24		
Bot23	AA_105	78		Kidney Cortex						
chr3F159514646	chr3R159514978			chr3	159514670		C>T			
intragenic	IQCJ-SCHIP1, SCHIP1						intron	25		
Bot23	AA_105	78		Kidney Cortex						
chr3F182401086	chr3R182401404			chr3	182401494		C>A			
intergenic	na						na	10		
Bot23	AA_105	78		Kidney Cortex						
chr3F183793815	chr3R183794010			chr3	183793875		C>T			
intergenic	na						na	61		
Bot23	AA_105	78		Kidney Cortex						
chr4F24521614	chr4R24521876			chr4	24521641		C>T			
intergenic	na						na	28		
Bot23	AA_105	78		Kidney Cortex						
chr4F47367974	chr4R47368316			chr4	47368334		G>A			
intragenic	GABRB1						intron	82		
Bot23	AA_105	78		Kidney Cortex						
chr4F67658092	chr4R67658478			chr4	67658487		A>T			
intergenic	na						na	91		
Bot23	AA_105	78		Kidney Cortex						
chr4F74465883	chr4R74466058			chr4	74466095		G>A			
intragenic	RASSF6						intron	63		
Bot23	AA_105	78		Kidney Cortex						
chr4F82123910	chr4R82124173			chr4	82124240		T>A			
intragenic	PRKG2						intron	33		
Bot23	AA_105	78		Kidney Cortex						
chr4F82184128	chr4R82184460			chr4	82184552		C>A			
intergenic	na						na	8		

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Bot23	AA_105	78	chr4F88745552chr4R88745911	intragenic	MEPE	Kidney Cortex	chr4	88745577	C>T	intron	26
Bot23	AA_105	78	chr4F96204635chr4R96205023	intragenic	UNC5C	Kidney Cortex	chr4	96204718	T>A	intron	84
Bot23	AA_105	78	chr4F97358800chr4R97359097	intergenic	na	Kidney Cortex	chr4	97358865	C>T	na	66
Bot23	AA_105	78	chr4F123354491chr4R123354776	intergenic	na	Kidney Cortex	chr4	123354813	T>A	na	63
Bot23	AA_105	78	chr4F154936341chr4R154936718	intergenic	na	Kidney Cortex	chr4	154936385	C>T	na	45
Bot23	AA_105	78	chr5F3790623chr5R3790932	intergenic	na	Kidney Cortex	chr5	3790631	C>T	na	9
Bot23	AA_105	78	chr5F68116842chr5R68117282	intergenic	na	Kidney Cortex	chr5	68116934	C>T	na	93
Bot23	AA_105	78	chr5F151849320chr5R151849750	intergenic	na	Kidney Cortex	chr5	151849817	C>A	na	33
Bot23	AA_105	78	chr5F154450117chr5R154450482	intergenic	na	Kidney Cortex	chr5	154450540	G>A	na	42
Bot23	AA_105	78	chr5F160018571chr5R160018774	intragenic	ATP10B	Kidney Cortex	chr5	160018650	A>T	intron	80
Bot23	AA_105	78	chr6F14875907chr6R14876317	intergenic	na	Kidney Cortex	chr6	14875924	G>T	na	18
Bot23	AA_105	78	chr6F35022404chr6R35022670	intragenic	ANKS1A	Kidney Cortex	chr6	35022748	C>G	intron	22
Bot23	AA_105	78	chr6F43528437chr6R43528658	intragenic	XPO5	Kidney Cortex	chr6	43528744	C>G	exon	14
Bot23	AA_105	78	chr6F50036253chr6R50036646	intergenic	na	Kidney Cortex	chr6	50036720	T>A	na	26
Bot23	AA_105	78	chr6F56821932chr6R56822228	intragenic	BEND6	Kidney Cortex	chr6	56822235	A>T	intron	93
Bot23	AA_105	78	chr6F83405192chr6R83405644	intergenic	na	Kidney Cortex	chr6	83405730	C>G	na	14

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Bot23	AA_105	78	Kidney Cortex								
chr6F88292230chr6R88292588			chr6	88292675	G>A						
intragenic	RARS2						intron	13			
Bot23	AA_105	78	Kidney Cortex								
chr6F88621346chr6R88621783			chr6	88621357	C>T						
intragenic	AY927641						intron	12			
Bot23	AA_105	78	Kidney Cortex								
chr6F89494291chr6R89494626			chr6	89494310	G>C						
intragenic	RNGTT						intron	20			
Bot23	AA_105	78	Kidney Cortex								
chr6F96768115chr6R96768484			chr6	96768122	C>T						
intergenic	na						na	8			
Bot23	AA_105	78	Kidney Cortex								
chr6F102267978chr6R102268234			chr6	102268008	C>T						
intragenic	GRIK2						intron	31			
Bot23	AA_105	78	Kidney Cortex								
chr6F108480276chr6R108480668			chr6	108480678	T>C						
intergenic	na						na	90			
Bot23	AA_105	78	Kidney Cortex								
chr6F126132881chr6R126133059			chr6	126132912	G>T						
intragenic	NCOA7						intron	32			
Bot23	AA_105	78	Kidney Cortex								
chr6F127225046chr6R127225363			chr6	127225080	C>T						
intragenic	AK127472						intron	35			
Bot23	AA_105	78	Kidney Cortex								
chr7F21334173chr7R21334487			chr7	21334569	G>A						
intergenic	na						na	18			
Bot23	AA_105	78	Kidney Cortex								
chr7F37030634chr7R37030926			chr7	37030713	T>A						
intragenic	ELMO1						intron	80			
Bot23	AA_105	78	Kidney Cortex								
chr8F66975538chr8R66975834			chr8	66975605	A>T						
intragenic	DNAJC5B						intron	68			
Bot23	AA_105	78	Kidney Cortex								
chr8F72137969chr8R72138306			chr8	72138396	G>A						
intragenic	EYA1						intron	10			
Bot23	AA_105	78	Kidney Cortex								
chr8F87411960chr8R87412253			chr8	87412048	G>C						
intragenic	WWP1						intron	89			
Bot23	AA_105	78	Kidney Cortex								
chr8F104496555chr8R104496837			chr8	104496617	G>C						
intergenic	na						na	63			
Bot23	AA_105	78	Kidney Cortex								
chr8F108064036chr8R108064396			chr8	108064101	G>T						
intergenic	na						na	66			
Bot23	AA_105	78	Kidney Cortex								
chr9F2642132chr9R2642255			chr9	2642161	G>T						
intragenic	VLDLR						intron	30			

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Bot23	AA_105	78	chr9F97754467chr9R97754708	intragenic	C9ORF3	Kidney Cortex	chr9	97754479	G>T	intron	13
Bot23	AA_105	78	chr9F128472537chr9R128472941	intergenic	na	Kidney Cortex	chr9	128472588	G>T	na	52
Bot23	AA_105	78	chr10F22436216chr10R22436417	intergenic	na	Kidney Cortex	chr10	22436267	A>G	na	52
Bot23	AA_105	78	chr10F25755394chr10R25755670	intragenic	GPR158	Kidney Cortex	chr10	25755462	T>A	intron	69
Bot23	AA_105	78	chr10F30364142chr10R30364453	intragenic	KIAA1462	Kidney Cortex	chr10	30364222	C>T	intron	81
Bot23	AA_105	78	chr10F78028487chr10R78028815	intragenic	C10ORF11	Kidney Cortex	chr10	78028893	G>A	intron	22
Bot23	AA_105	78	chr10F93721313chr10R93721471	intragenic	BTAF1	Kidney Cortex	chr10	93721547	C>A	intron	24
Bot23	AA_105	78	chr10F98290408chr10R98290633	intragenic	TM9SF3	Kidney Cortex	chr10	98290724	A>G	intron	9
Bot23	AA_105	78	chr10F101090437chr10R101090834	intragenic	CNNM1	Kidney Cortex	chr10	101090446	C>T	intron	10
Bot23	AA_105	78	chr10F104621708chr10R104622031	intragenic	C10ORF32	Kidney Cortex	chr10	104621741	G>C	intron	34
Bot23	AA_105	78	chr10F105587596chr10R105587940	intragenic	SH3PXD2A	Kidney Cortex	chr10	105588001	A>G	intron	39
Bot23	AA_105	78	chr10F106143213chr10R106143323	intragenic	CCDC147	Kidney Cortex	chr10	106143410	A>T	intron	13
Bot23	AA_105	78	chr11F19628490chr11R19628744	intragenic	NAV2	Kidney Cortex	chr11	19628765	G>A	intron	79
Bot23	AA_105	78	chr11F27527464chr11R27527761	intragenic	LIN7C	Kidney Cortex	chr11	27527504	G>T	intron	41
Bot23	AA_105	78	chr11F44781519chr11R44781784	intergenic	na	Kidney Cortex	chr11	44781544	C>T	na	26
Bot23	AA_105	78	chr11F117787607chr11R117787834	intragenic	TMPRSS13	Kidney Cortex	chr11	117787916	G>A	exon	18

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Bot23	AA_105	78	chr12F89344907	chr12R89345227	Kidney Cortex	chr12	89344947	G>C			
intergenic	na								na		41
Bot23	AA_105	78	chr12F101932094	chr12R101932464	Kidney Cortex	chr12	101932513	A>G			
intergenic	na								na		51
Bot23	AA_105	78	chr12F108839938	chr12R108840238	Kidney Cortex	chr12	108840284	A>T			
intergenic	na								na		54
Bot23	AA_105	78	chr12F110564475	chr12R110564724	Kidney Cortex	chr12	110564549	G>C			
intragenic	IFT81								intron		75
Bot23	AA_105	78	chr12F123751360	chr12R123751727	Kidney Cortex	chr12	123751376	T>C			
intragenic	CDK2AP1								intron		17
Bot23	AA_105	78	chr13F27430839	chr13R27430981	Kidney Cortex	chr13	27430868	G>T			
intergenic	na								na		30
Bot23	AA_105	78	chr13F34319409	chr13R34319776	Kidney Cortex	chr13	34319463	C>T			
intergenic	na								na		55
Bot23	AA_105	78	chr13F36368909	chr13R36369079	Kidney Cortex	chr13	36369000	G>T			
intragenic	DCLK1								intron		92
Bot23	AA_105	78	chr13F78221414	chr13R78221711	Kidney Cortex	chr13	78221782	T>A			
intergenic	na								na		29
Bot23	AA_105	78	chr13F92348580	chr13R92348874	Kidney Cortex	chr13	92348887	T>A			
intragenic	GPC5								intron		87
Bot23	AA_105	78	chr14F37056904	chr14R37057157	Kidney Cortex	chr14	37057197	G>A			
intergenic	na								na		60
Bot23	AA_105	78	chr14F51640416	chr14R51640729	Kidney Cortex	chr14	51640429	G>T			
intergenic	na								na		14
Bot23	AA_105	78	chr14F54389596	chr14R54390006	Kidney Cortex	chr14	54390017	G>A			
intergenic	na								na		89
Bot23	AA_105	78	chr14F75551201	chr14R75551477	Kidney Cortex	chr14	75551218	T>G			
intragenic	NEK9								intron		18
Bot23	AA_105	78	chr14F85815889	chr14R85816184	Kidney Cortex	chr14	85815905	T>A			
intergenic	na								na		17
Bot23	AA_105	78	chr14F86102085	chr14R86102514	Kidney Cortex	chr14	86102164	G>T			
intergenic	na								na		80

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Bot23	AA_105	78	chr14F86107044	chr14R86107360	Kidney Cortex	chr14	86107081	C>T	intergenic	na	38
Bot23	AA_105	78	chr14F94425377	chr14R94425933	Kidney Cortex	chr14	94426022	G>A	intragenic	ASB2	11
Bot23	AA_105	78	chr15F43545630	chr15R43545788	Kidney Cortex	chr15	43545649	G>T	intragenic	TGM5	20
Bot23	AA_105	78	chr15F50289003	chr15R50289346	Kidney Cortex	chr15	50289406	G>A	intragenic	ATP8B4	40
Bot23	AA_105	78	chr15F91360332	chr15R91360551	Kidney Cortex	chr15	91360340	C>T	intergenic	na	9
Bot23	AA_105	78	chr15F93534695	chr15R93535015	Kidney Cortex	chr15	93534738	C>T	intragenic	CHD2	44
Bot23	AA_105	78	chr16F27127019	chr16R27127258	Kidney Cortex	chr16	27127326	A>G	intergenic	na	32
Bot23	AA_105	78	chr16F50608240	chr16R50608512	Kidney Cortex	chr16	50608599	C>A	intragenic	NKD1	13
Bot23	AA_105	78	chr16F53527665	chr16R53527898	Kidney Cortex	chr16	53527943	G>A	intragenic	AKTIP	55
Bot23	AA_105	78	chr16F68432641	chr16R68432863	Kidney Cortex	chr16	68432723	G>C	intragenic	SMPD3	83
Bot23	AA_105	78	chr17F38654245	chr17R38654524	Kidney Cortex	chr17	38654263	G>C	intragenic	TNS4	19
Bot23	AA_105	78	chr18F36492805	chr18R36493115	Kidney Cortex	chr18	36493136	T>C	intergenic	na	79
Bot23	AA_105	78	chr19F17252154	chr19R17252415	Kidney Cortex	chr19	17252173	G>C	intragenic	MYO9B	20
Bot23	AA_105	78	chr19F32865549	chr19R32865877	Kidney Cortex	chr19	32865949	C>G	intragenic	ZNF507	28
Bot23	AA_105	78	chr20F20289639	chr20R20290087	Kidney Cortex	chr20	20289711	G>C	intragenic	C20orf26	73
Bot23	AA_105	78	chr20F38526648	chr20R38527062	Kidney Cortex	chr20	38526656	C>T	intergenic	na	9

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Bot23	AA_105	78	chr21F35166427chr21R35166688	intragenic	DONSON, ITSN1	Kidney Cortex	chr21	35166467	G>C	intron	41
Bot23	AA_105	78	chr21F43377193chr21R43377415	intergenic	na	Kidney Cortex	chr21	43377442	C>G	na	73
Bot23	AA_105	78	chr22F33382250chr22R33382494	intragenic	SYN3	Kidney Cortex	chr22	33382280	G>T	intron	31
Bot23	AA_105	78	chrXF9817270chrXR9817658	intragenic	SHROOM2	Kidney Cortex	chrX	9817677	A>G	intron	81
Bot23	AA_105	78	chrXF23164349chrXR23164525	intragenic	LOC100873065	Kidney Cortex	chrX	23164596	C>A	intron	29
Bot23	AA_105	78	chrXF23833711chrXR23834076	intergenic	na	Kidney Cortex	chrX	23833722	C>T	na	12
Bot23	AA_105	78	chrXF45053949chrXR45054203	intragenic	CXorf36	Kidney Cortex	chrX	45054240	C>A	intron	63
Bot23	AA_105	78	chrXF98244107chrXR98244423	intergenic	na	Kidney Cortex	chrX	98244137	G>T	na	31
Bot23	AA_105	78	chrXF102411664chrXR102411974	intergenic	na	Kidney Cortex	chrX	102411696	C>T	na	33
Bot24	AA_124	82	chr1F69110260chr1R69110570	intergenic	na	Kidney Cortex	chr1	69110326	T>C	na	67
Bot24	AA_124	82	chr1F84221723chr1R84221963	intragenic	BC036594	Kidney Cortex	chr1	84221808	G>C	intron	86
Bot24	AA_124	82	chr1F109913539chr1R109913798	intragenic	SORT1	Kidney Cortex	chr1	109913860	G>A	intron	38
Bot24	AA_124	82	chr1F212008016chr1R212008434	intergenic	na	Kidney Cortex	chr1	212008034	T>A	na	19
Bot24	AA_124	82	chr1F231473234chr1R231473488	intragenic	EXOC8	Kidney Cortex	chr1	231473309	G>T	exon	76
Bot24	AA_124	82	chr2F13053449chr2R13053658	intergenic	na	Kidney Cortex	chr2	13053474	A>T	na	26
Bot24	AA_124	82	chr2F41427201chr2R41427396	intergenic	na	Kidney Cortex	chr2	41427258	A>T	na	58

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Bot24	AA_124	82	chr2F71557544	chr2R71557828	Kidney Cortex	chr2	71557888	G>A	intragenic	ZNF638	intron	40
Bot24	AA_124	82	chr2F72411962	chr2R72412183	Kidney Cortex	chr2	72412255	A>C	intragenic	EXOC6B	intron	28
Bot24	AA_124	82	chr2F79876724	chr2R79876987	Kidney Cortex	chr2	79877005	A>T	intragenic	CTNNA2	intron	82
Bot24	AA_124	82	chr2F115926749	chr2R115927106	Kidney Cortex	chr2	115927169	T>A	intragenic	DPP10	intron	37
Bot24	AA_124	82	chr2F161109300	chr2R161109646	Kidney Cortex	chr2	161109366	T>C	intragenic	ITGB6	intron	67
Bot24	AA_124	82	chr2F161764730	chr2R161765009	Kidney Cortex	chr2	161765065	T>A	intergenic	na	na	44
Bot24	AA_124	82	chr2F204923438	chr2R204923657	Kidney Cortex	chr2	204923488	A>T	intergenic	na	na	51
Bot24	AA_124	82	chr2F215303169	chr2R215303501	Kidney Cortex	chr2	215303236	A>C	intragenic	VWC2L	intron	68
Bot24	AA_124	82	chr2F226255383	chr2R226255768	Kidney Cortex	chr2	226255463	A>T	intergenic	na	na	81
Bot24	AA_124	82	chr3F22407351	chr3R22407685	Kidney Cortex	chr3	22407772	G>A	intragenic	ZNF385D	intron	13
Bot24	AA_124	82	chr3F88268140	chr3R88268711	Kidney Cortex	chr3	88268172	A>T	intergenic	na	na	33
Bot24	AA_124	82	chr3F88663151	chr3R88663430	Kidney Cortex	chr3	88663227	A>T	intergenic	na	na	77
Bot24	AA_124	82	chr3F111628346	chr3R111628629	Kidney Cortex	chr3	111628658	A>T	intragenic	PHLDB2	intron	71
Bot24	AA_124	82	chr3F113656780	chr3R113656951	Kidney Cortex	chr3	113657019	G>A	intragenic	GRAMD1C	intron	32
Bot24	AA_124	82	chr3F194964613	chr3R194964916	Kidney Cortex	chr3	194964661	T>A	intragenic	XXYLT1	intron	49
Bot24	AA_124	82	chr4F128001137	chr4R128001432	Kidney Cortex	chr4	128001222	T>A	intergenic	na	na	86

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Bot24	AA_124	82	chr4F159332116chr4R159332490	intergenic	na	Kidney Cortex	chr4	159332125	G>T	na	10
Bot24	AA_124	82	chr4F171307571chr4R171307965	intergenic	na	Kidney Cortex	chr4	171308038	G>A	na	27
Bot24	AA_124	82	chr5F67483587chr5R67483746	intergenic	na	Kidney Cortex	chr5	67483837	G>A	na	9
Bot24	AA_124	82	chr5F77135373chr5R77135613	intergenic	na	Kidney Cortex	chr5	77135680	A>T	na	33
Bot24	AA_124	82	chr5F165010614chr5R165010798	intergenic	na	Kidney Cortex	chr5	165010890	G>A	na	8
Bot24	AA_124	82	chr6F23205655chr6R23205888	intergenic	na	Kidney Cortex	chr6	23205927	C>A	na	61
Bot24	AA_124	82	chr6F23784075chr6R23784523	intergenic	na	Kidney Cortex	chr6	23784142	T>A	na	68
Bot24	AA_124	82	chr6F45758746chr6R45759231	intergenic	na	Kidney Cortex	chr6	45759320	C>G	na	11
Bot24	AA_124	82	chr6F64860169chr6R64860465	intergenic	na	Kidney Cortex	chr6	64860247	T>G	na	79
Bot24	AA_124	82	chr6F89488476chr6R89488639	intragenic	RNGTT	Kidney Cortex	chr6	89488670	T>A	intron	69
Bot24	AA_124	82	chr6F98645094chr6R98645415	intergenic	na	Kidney Cortex	chr6	98645461	A>T	na	54
Bot24	AA_124	82	chr6F122062511chr6R122062718	intergenic	na	Kidney Cortex	chr6	122062790	A>T	na	28
Bot24	AA_124	82	chr7F21784360chr7R21784592	intragenic	DNAH11	Kidney Cortex	chr7	21784652	A>T	exon	40
Bot24	AA_124	82	chr7F50810670chr7R50810923	intragenic	GRB10	Kidney Cortex	chr7	50810969	T>G	intron	54
Bot24	AA_124	82	chr7F108164714chr7R108165161	intragenic	PNPLA8	Kidney Cortex	chr7	108164721	G>C	intron	8
Bot24	AA_124	82	chr8F120423620chr8R120423898	intergenic	na	Kidney Cortex	chr8	120423633	G>T	na	14

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Bot24	AA_124	82	Kidney Cortex						
chr8F131603602	chr8R131603830		chr8	131603881	G>A				
intergenic	na				na	49			
Bot24	AA_124	82	Kidney Cortex						
chr9F91962213	chr9R91962646		chr9	91962233	C>T				
intragenic	SECISBP2				intron	21			
Bot24	AA_124	82	Kidney Cortex						
chr9F98495168	chr9R98495552		chr9	98495180	C>A				
intergenic	na				na	13			
Bot24	AA_124	82	Kidney Cortex						
chr9F128299779	chr9R128300110		chr9	128300179	G>A				
intragenic	MAPKAP1				intron	31			
Bot24	AA_124	82	Kidney Cortex						
chr10F11472140	chr10R11472441		chr10	11472513	T>A				
intergenic	na				na	28			
Bot24	AA_124	82	Kidney Cortex						
chr10F25079133	chr10R25079536		chr10	25079186	C>T				
intergenic	na				na	54			
Bot24	AA_124	82	Kidney Cortex						
chr10F124491675	chr10R124491996		chr10	124491725	A>T				
intergenic	na				na	51			
Bot24	AA_124	82	Kidney Cortex						
chr11F19380942	chr11R19381298		chr11	19381375	G>A				
intragenic	NAV2				intron	23			
Bot24	AA_124	82	Kidney Cortex						
chr11F31906677	chr11R31906969		chr11	31907020	A>T				
intragenic	DKFZp686K1684, RCN1				intron	49			
Bot24	AA_124	82	Kidney Cortex						
chr11F57582688	chr11R57583135		chr11	57583166	A>T				
intragenic	CTNND1				intron	69			
Bot24	AA_124	82	Kidney Cortex						
chr11F59254956	chr11R59255412		chr11	59255477	A>T				
intergenic	na				na	35			
Bot24	AA_124	82	Kidney Cortex						
chr11F109763875	chr11R109764173		chr11	109764230	A>C				
intergenic	na				na	43			
Bot24	AA_124	82	Kidney Cortex						
chr11F118214952	chr11R118215267		chr11	118215272	G>A				
intragenic	CD3G				intron	95			
Bot24	AA_124	82	Kidney Cortex						
chr12F26301285	chr12R26301750		chr12	26301831	C>A				
intragenic	BC041929				intron	19			
Bot24	AA_124	82	Kidney Cortex						
chr12F89515240	chr12R89515383		chr12	89515472	G>A				
intergenic	na				na	11			
Bot24	AA_124	82	Kidney Cortex						
chr13F84492301	chr13R84492610		chr13	84492699	G>A				
intergenic	na				na	11			

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Bot24	AA_124	82	chr14F55649812	chr14R55650185	Kidney Cortex	chr14	55650214	T>A	intragenic	DLGAP5	intron	71
Bot24	AA_124	82	chr14F72943703	chr14R72944146	Kidney Cortex	chr14	72943727	G>C	intragenic	RGS6	intron	25
Bot24	AA_124	82	chr14F75820206	chr14R75820715	Kidney Cortex	chr14	75820263	T>A	intergenic	na	na	58
Bot24	AA_124	82	chr14F98728763	chr14R98729165	Kidney Cortex	chr14	98729224	G>A	intergenic	na	na	41
Bot24	AA_124	82	chr15F67557388	chr15R67557705	Kidney Cortex	chr15	67557735	A>T	intragenic	IQCH	intron	70
Bot24	AA_124	82	chr15F99225097	chr15R99225230	Kidney Cortex	chr15	99225110	A>T	intragenic	IGF1R	intron	14
Bot24	AA_124	82	chr16F24787954	chr16R24788185	Kidney Cortex	chr16	24788194	A>T	intragenic	TNRC6A	intron	91
Bot24	AA_124	82	chr16F47104200	chr16R47104466	Kidney Cortex	chr16	47104207	C>T	intergenic	na	na	8
Bot24	AA_124	82	chr16F55116869	chr16R55117206	Kidney Cortex	chr16	55116953	A>T	intergenic	na	na	85
Bot24	AA_124	82	chr17F11733833	chr17R11734188	Kidney Cortex	chr17	11733851	T>A	intragenic	DNAH9	intron	19
Bot24	AA_124	82	chr17F70627618	chr17R70627736	Kidney Cortex	chr17	70627814	G>A	intragenic	LINC00511	intron	22
Bot24	AA_124	82	chr18F56304596	chr18R56304850	Kidney Cortex	chr18	56304603	C>T	intergenic	na	na	8
Bot24	AA_124	82	chr20F20926964	chr20R20927233	Kidney Cortex	chr20	20927038	A>T	intergenic	na	na	75
Bot24	AA_124	82	chr20F58830973	chr20R58831451	Kidney Cortex	chr20	58831516	C>T	intragenic	LOC284757	intron	35
Bot24	AA_124	82	chr21F25820247	chr21R25820698	Kidney Cortex	chr21	25820735	T>A	intragenic	AK124194	intron	63
Bot24	AA_124	82	chr22F41257073	chr22R41257309	Kidney Cortex	chr22	41257124	C>T	intragenic	XPNPEP3, DNAJB7	intron	52

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Bot24	AA_124	82	chrXF10710381chrXR10710536	intragenic	MID1	Kidney Cortex	chrX	10710624	G>A	intron	12
Bot24	AA_124	82	chrXF18021516chrXR18021788	intergenic	na	Kidney Cortex	chrX	18021591	A>T	na	76
Bot24	AA_124	82	chrXF36708540chrXR36708884	intergenic	na	Kidney Cortex	chrX	36708625	C>T	na	86
Bot24	AA_124	82	chrXF72669087chrXR72669363	intragenic	CDX4	Kidney Cortex	chrX	72669454	T>A	intron	9
Bot24	AA_124	82	chrXF145921650chrXR145921931	intergenic	na	Kidney Cortex	chrX	145921732	A>T	na	83
Bot25	AA_126	78	chr1F64302735chr1R64303058	intragenic	ROR1	Kidney Cortex	chr1	64302813	A>T	intron	79
Bot25	AA_126	78	chr1F68990481chr1R68990732	intragenic	BC020917	Kidney Cortex	chr1	68990792	T>A	intron	40
Bot25	AA_126	78	chr1F77697019chr1R77697288	intergenic	na	Kidney Cortex	chr1	77697302	G>A	na	86
Bot25	AA_126	78	chr1F161333746chr1R161334057	intragenic	SDHC	Kidney Cortex	chr1	161333759	A>T	exon	14
Bot25	AA_126	78	chr1F164638751chr1R164639254	intragenic	PBX1, AX748175	Kidney Cortex	chr1	164638758	C>T	intron	8
Bot25	AA_126	78	chr1F173638928chr1R173639234	intragenic	ANKRD45	Kidney Cortex	chr1	173638945	C>T	intron	18
Bot25	AA_126	78	chr1F184224153chr1R184224291	intergenic	na	Kidney Cortex	chr1	184224339	A>T	na	52
Bot25	AA_126	78	chr1F212240805chr1R212241157	intragenic	DTL	Kidney Cortex	chr1	212240876	A>T	intron	72
Bot25	AA_126	78	chr1F220794354chr1R220794836	intragenic	MARK1	Kidney Cortex	chr1	220794433	T>A	intron	80
Bot25	AA_126	78	chr2F22195774chr2R22196118	intergenic	na	Kidney Cortex	chr2	22195805	T>A	na	32
Bot25	AA_126	78	chr2F50666124chr2R50666349	intragenic	NRXN1	Kidney Cortex	chr2	50666184	A>T	intron	61

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Bot25	AA_126	78	chr2F65556606chr2R65556904	Kidney Cortex	chr2	65556978	T>C	intragenic	SPRED2	intron 26
Bot25	AA_126	78	chr2F72101134chr2R72101411	Kidney Cortex	chr2	72101226	T>A	intergenic	na	na 93
Bot25	AA_126	78	chr2F73674572chr2R73675021	Kidney Cortex	chr2	73675099	C>G	intragenic	ALMS1	exon 22
Bot25	AA_126	78	chr2F95700384chr2R95700832	Kidney Cortex	chr2	95700400	A>T	intragenic	MAL	intron 17
Bot25	AA_126	78	chr2F100569229chr2R100569757	Kidney Cortex	chr2	100569807	T>A	intragenic	AFF3	intron 50
Bot25	AA_126	78	chr2F115849271chr2R115849631	Kidney Cortex	chr2	115849329	T>A	intragenic	DPP10	intron 59
Bot25	AA_126	78	chr2F180623473chr2R180623843	Kidney Cortex	chr2	180623906	T>A	intragenic	ZNF385B	intron 37
Bot25	AA_126	78	chr2F197980483chr2R197980773	Kidney Cortex	chr2	197980492	T>A	intragenic	ANKRD44	intron 10
Bot25	AA_126	78	chr2F208083880chr2R208084119	Kidney Cortex	chr2	208083963	C>T	intergenic	na	na 84
Bot25	AA_126	78	chr3F16146812chr3R16147156	Kidney Cortex	chr3	16146856	C>T	intragenic	GALNT15	intron 45
Bot25	AA_126	78	chr3F39559124chr3R39559772	Kidney Cortex	chr3	39559199	C>T	intragenic	MOBP	intron 76
Bot25	AA_126	78	chr3F42448751chr3R42448932	Kidney Cortex	chr3	42448993	T>A	intragenic	LYZL4	intron 39
Bot25	AA_126	78	chr3F72640063chr3R72640674	Kidney Cortex	chr3	72640130	T>A	intergenic	na	na 68
Bot25	AA_126	78	chr3F78888938chr3R78889308	Kidney Cortex	chr3	78888949	C>T	intragenic	ROBO1	intron 12
Bot25	AA_126	78	chr3F88655009chr3R88655517	Kidney Cortex	chr3	88655546	T>A	intergenic	na	na 71
Bot25	AA_126	78	chr3F117654547chr3R117654781	Kidney Cortex	chr3	117654867	T>A	intergenic	na	na 14

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Bot25	AA_126	78	chr3F118190657	chr3R118191218	Kidney Cortex	chr3	118191275	T>A		
intergenic	na							na		43
Bot25	AA_126	78	chr3F148417433	chr3R148417727	Kidney Cortex	chr3	148417740	T>A		
intragenic	AGTR1							intron		87
Bot25	AA_126	78	chr4F23345013	chr4R23345571	Kidney Cortex	chr4	23345044	T>A		
intergenic	na							na		32
Bot25	AA_126	78	chr4F37060720	chr4R37061133	Kidney Cortex	chr4	37060751	A>T		
intergenic	na							na		32
Bot25	AA_126	78	chr4F182077072	chr4R182077472	Kidney Cortex	chr4	182077506	T>A		
intragenic	LINC00290							intron		66
Bot25	AA_126	78	chr4F183005543	chr4R183005776	Kidney Cortex	chr4	183005557	C>T		
intragenic	AK056196							intron		15
Bot25	AA_126	78	chr4F184118850	chr4R184119346	Kidney Cortex	chr4	184118902	A>T		
intragenic	WWC2							intron		53
Bot25	AA_126	78	chr5F31922099	chr5R31922517	Kidney Cortex	chr5	31922598	G>A		
intragenic	PDZD2							intron		19
Bot25	AA_126	78	chr5F60498242	chr5R60498583	Kidney Cortex	chr5	60498650	T>C		
intergenic	na							na		33
Bot25	AA_126	78	chr5F67411292	chr5R67411793	Kidney Cortex	chr5	67411845	T>A		
intergenic	na							na		48
Bot25	AA_126	78	chr5F87256103	chr5R87256379	Kidney Cortex	chr5	87256154	T>C		
intergenic	na							na		52
Bot25	AA_126	78	chr5F90585797	chr5R90586258	Kidney Cortex	chr5	90585811	A>T		
intergenic	na							na		15
Bot25	AA_126	78	chr5F116471823	chr5R116472196	Kidney Cortex	chr5	116472252	T>A		
intergenic	na							na		44
Bot25	AA_126	78	chr5F135609265	chr5R135609577	Kidney Cortex	chr5	135609657	A>T		
intragenic	TRPC7							intron		20
Bot25	AA_126	78	chr5F138543363	chr5R138543673	Kidney Cortex	chr5	138543434	C>T		
intergenic	na							na		72
Bot25	AA_126	78	chr5F148004303	chr5R148004724	Kidney Cortex	chr5	148004370	T>A		
intragenic	HTR4, SH3TC2							intron		68

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Bot25	AA_126	78	chr6F6778867chr6R6779392	intergenic	na	Kidney Cortex	chr6	6778892	A>G	26
Bot25	AA_126	78	chr6F50432064chr6R50432391	intergenic	na	Kidney Cortex	chr6	50432110	A>T	47
Bot25	AA_126	78	chr6F71741591chr6R71741905	intergenic	na	Kidney Cortex	chr6	71741618	C>T	28
Bot25	AA_126	78	chr6F97384952chr6R97385269	intragenic	KLHL32	Kidney Cortex	chr6	97385326	G>A	43
Bot25	AA_126	78	chr6F123431022chr6R123431226	intergenic	na	Kidney Cortex	chr6	123431255	A>T	71
Bot25	AA_126	78	chr6F133768379chr6R133768788	intragenic	EYA4, AK093513	Kidney Cortex	chr6	133768398	A>T	20
Bot25	AA_126	78	chr6F149005217chr6R149005577	intergenic	na	Kidney Cortex	chr6	149005607	A>T	70
Bot25	AA_126	78	chr6F154059479chr6R154059994	intergenic	na	Kidney Cortex	chr6	154060033	A>T	61
Bot25	AA_126	78	chr7F147613786chr7R147614067	intragenic	CNTNAP2	Kidney Cortex	chr7	147613795	A>T	10
Bot25	AA_126	78	chr8F49491548chr8R49491769	intergenic	na	Kidney Cortex	chr8	49491572	C>T	25
Bot25	AA_126	78	chr8F53057749chr8R53057971	intragenic	ST18	Kidney Cortex	chr8	53057769	T>C	21
Bot25	AA_126	78	chr8F53166604chr8R53167031	intragenic	ST18	Kidney Cortex	chr8	53167100	T>C	31
Bot25	AA_126	78	chr8F59190509chr8R59190850	intergenic	na	Kidney Cortex	chr8	59190935	G>A	15
Bot25	AA_126	78	chr8F75542452chr8R75542893	intragenic	FLJ39080	Kidney Cortex	chr8	75542909	G>A	84
Bot25	AA_126	78	chr8F78567088chr8R78567460	intergenic	na	Kidney Cortex	chr8	78567096	C>T	9
Bot25	AA_126	78	chr9F89624990chr9R89625504	intragenic	LOC440173	Kidney Cortex	chr9	89625517	C>A	87

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Bot25	AA_126	78	Kidney Cortex							
chr9F89805598	chr9R89805975		chr9	89805626	C>T					
intergenic	na				na	29				
Bot25	AA_126	78	Kidney Cortex							
chr10F21186231	chr10R21186569		chr10	21186624	G>A					
intragenic	NEBL				intron	45				
Bot25	AA_126	78	Kidney Cortex							
chr10F21248667	chr10R21249051		chr10	21248692	T>A					
intragenic	NEBL				intron	26				
Bot25	AA_126	78	Kidney Cortex							
chr10F22435527	chr10R22435895		chr10	22435973	C>A					
intergenic	na				na	22				
Bot25	AA_126	78	Kidney Cortex							
chr10F96333571	chr10R96333958		chr10	96333646	A>T					
intragenic	HELLS				intron	76				
Bot25	AA_126	78	Kidney Cortex							
chr10F97115573	chr10R97115869		chr10	97115641	A>G					
intragenic	SORBS1, KIAA0894				intron	69				
Bot25	AA_126	78	Kidney Cortex							
chr10F120551734	chr10R120552255		chr10	120551752	G>T					
intergenic	na				na	19				
Bot25	AA_126	78	Kidney Cortex							
chr11F15469099	chr11R15469433		chr11	15469445	A>T					
intergenic	na				na	88				
Bot25	AA_126	78	Kidney Cortex							
chr11F45234700	chr11R45235027		chr11	45234712	G>T					
intragenic	PRDM11, AK097878				exon	13				
Bot25	AA_126	78	Kidney Cortex							
chr11F79668948	chr11R79669340		chr11	79669001	A>T					
intergenic	na				na	54				
Bot25	AA_126	78	Kidney Cortex							
chr11F113868011	chr11R113868437		chr11	113868513	G>A					
intergenic	na				na	24				
Bot25	AA_126	78	Kidney Cortex							
chr11F126896922	chr11R126897218		chr11	126897289	G>A					
intergenic	na				na	29				
Bot25	AA_126	78	Kidney Cortex							
chr12F110366165	chr12R110366474		chr12	110366176	G>C					
intragenic	TCHP				intron	12				
Bot25	AA_126	78	Kidney Cortex							
chr12F118268494	chr12R118268793		chr12	118268536	C>T					
intragenic	KSR2				intron	43				
Bot25	AA_126	78	Kidney Cortex							
chr12F128775509	chr12R128775807		chr12	128775522	T>A					
intragenic	TMEM132C				intron	14				
Bot25	AA_126	78	Kidney Cortex							
chr13F31436833	chr13R31437307		chr13	31436847	T>A					
intergenic	na				na	15				

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Bot25	AA_126	78	chr13F59676299	chr13R59676434	intergenic	na	Kidney Cortex	chr13	59676520	G>A
na	14									
Bot25	AA_126	78	chr13F102537220	chr13R102537656	intragenic	FGF14	Kidney Cortex	chr13	102537713	G>A
intron	43									
Bot25	AA_126	78	chr13F106597509	chr13R106597734	intergenic	na	Kidney Cortex	chr13	106597529	T>A
na	21									
Bot25	AA_126	78	chr14F58118138	chr14R58118635	intragenic	SLC35F4	Kidney Cortex	chr14	58118215	A>T
intron	78									
Bot25	AA_126	78	chr14F59484690	chr14R59485126	intergenic	na	Kidney Cortex	chr14	59484756	A>T
na	67									
Bot25	AA_126	78	chr15F98420731	chr15R98421106	intergenic	na	Kidney Cortex	chr15	98420824	C>T
na	94									
Bot25	AA_126	78	chr16F13197264	chr16R13197636	intragenic	SHISA9	Kidney Cortex	chr16	13197294	A>T
intron	31									
Bot25	AA_126	78	chr16F50137356	chr16R50137602	intragenic	HEATR3	Kidney Cortex	chr16	50137369	C>T
intron	14									
Bot25	AA_126	78	chr18F6558305	chr18R6558651	intragenic	LOC100130480	Kidney Cortex	chr18	6558349	C>T
intron	45									
Bot25	AA_126	78	chr18F13412962	chr18R13413343	intragenic	LDLRAD4	Kidney Cortex	chr18	13413367	T>A
intron	76									
Bot25	AA_126	78	chr18F19340119	chr18R19340417	intragenic	MIB1	Kidney Cortex	chr18	19340460	C>A
intron	57									
Bot25	AA_126	78	chr18F28438993	chr18R28439377	intergenic	na	Kidney Cortex	chr18	28439017	C>T
na	25									
Bot25	AA_126	78	chr18F37686108	chr18R37686479	intergenic	na	Kidney Cortex	chr18	37686570	A>T
na	9									
Bot25	AA_126	78	chr18F50788590	chr18R50788853	intragenic	DCC	Kidney Cortex	chr18	50788643	C>T
intron	54									
Bot25	AA_126	78	chr18F51654500	chr18R51654850	intergenic	na	Kidney Cortex	chr18	51654887	G>A
na	63									
Bot25	AA_126	78	chr18F53536650	chr18R53536982	intergenic	na	Kidney Cortex	chr18	53536994	A>T
na	88									

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Bot25	AA_126	78	chr18F71708660chr18R71708951	intergenic	na	Kidney Cortex	chr18	71708959	G>A	92
Bot25	AA_126	78	chr20F32590272chr20R32590543	intragenic	RALY	Kidney Cortex	chr20	32590622	T>A	21
Bot25	AA_126	78	chr20F42186383chr20R42186672	intragenic	SGK2	Kidney Cortex	chr20	42186391	G>T	9
Bot25	AA_126	78	chr20F58733487chr20R58733862	intragenic	LOC284757	Kidney Cortex	chr20	58733922	A>T	40
Bot25	AA_126	78	chr21F46557118chr21R46557434	intragenic	ADARB1	Kidney Cortex	chr21	46557178	G>T	61
Bot25	AA_126	78	chrXF21782070chrXR21782310	intergenic	na	Kidney Cortex	chrX	21782400	C>G	10
Bot25	AA_126	78	chrXF31337041chrXR31337224	intragenic	DMD	Kidney Cortex	chrX	31337306	A>T	18
Bot25	AA_126	78	chrXF79285053chrXR79285514	intragenic	TBX22	Kidney Cortex	chrX	79285082	T>A	30
Bot25	AA_126	78	chrXF119838638chrXR119839045	intergenic	na	Kidney Cortex	chrX	119838712	G>T	75
Bot25	AA_126	78	chrXF137566689chrXR137566984	intergenic	na	Kidney Cortex	chrX	137567066	A>T	18
Bot25	AA_126	78	chrXF150561100chrXR150561541	intergenic	na	Kidney Cortex	chrX	150561161	G>C	62
Bot25	AA_126	78	chrYF14295786chrYR14296019	intergenic	na	Kidney Cortex	chrY	14295794	C>T	9
Bot26	SA_117	66	chr1F59123126chr1R59123562	intragenic	MYSM1	Kidney Cortex	chr1	59123142	C>T	17
Bot26	SA_117	66	chr1F209712429chr1R209712746	intergenic	na	Kidney Cortex	chr1	209712476	G>C	48
Bot26	SA_117	66	chr1F216850859chr1R216851131	intragenic	ESRRG	Kidney Cortex	chr1	216851142	C>G	89
Bot26	SA_117	66	chr2F50609854chr2R50610152	intragenic	NRXN1	Kidney Cortex	chr2	50609872	C>T	19

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Bot26	SA_117	66	chr2F135540445	chr2R135540774	Kidney Cortex	chr2	135540813	G>A	intergenic	na	61
Bot26	SA_117	66	chr2F173207504	chr2R173207920	Kidney Cortex	chr2	173207518	C>T	intergenic	na	15
Bot26	SA_117	66	chr4F151106917	chr4R151107264	Kidney Cortex	chr4	151106991	C>T	intragenic	DCLK2	75
Bot26	SA_117	66	chr5F65691255	chr5R65691611	Kidney Cortex	chr5	65691702	G>A	intergenic	na	9
Bot26	SA_117	66	chr6F14903993	chr6R14904293	Kidney Cortex	chr6	14904382	C>A	intergenic	na	11
Bot26	SA_117	66	chr6F125910401	chr6R125910779	Kidney Cortex	chr6	125910462	G>C	intergenic	na	62
Bot26	SA_117	66	chr8F34497916	chr8R34498270	Kidney Cortex	chr8	34498304	C>A	intergenic	na	66
Bot26	SA_117	66	chr10F32390258	chr10R32390565	Kidney Cortex	chr10	32390644	G>A	intergenic	na	21
Bot26	SA_117	66	chr10F120137542	chr10R120137816	Kidney Cortex	chr10	120137837	A>T	intergenic	na	79
Bot26	SA_117	66	chr11F69077828	chr11R69078035	Kidney Cortex	chr11	69077877	G>T	intragenic	MYEOV	50
Bot26	SA_117	66	chr12F63412103	chr12R63412585	Kidney Cortex	chr12	63412677	G>A	intergenic	na	8
Bot26	SA_117	66	chr13F28365025	chr13R28365373	Kidney Cortex	chr13	28365043	C>T	intergenic	na	19
Bot26	SA_117	66	chr14F56948896	chr14R56949190	Kidney Cortex	chr14	56948949	C>T	intergenic	na	54
Bot26	SA_117	66	chr15F99343350	chr15R99343645	Kidney Cortex	chr15	99343680	T>G	intragenic	IGF1R	65
Bot26	SA_117	66	chr16F65678940	chr16R65679312	Kidney Cortex	chr16	65679375	G>A	intergenic	na	37
Bot26	SA_117	66	chr17F61819388	chr17R61819704	Kidney Cortex	chr17	61819398	C>T	intergenic	na	11

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Bot26	SA_117	66	chr18F22767273	chr18R22767653	Kidney Cortex	chr18	22767343	C>T	intragenic	ZNF521	71
Bot26	SA_117	66	chr18F73526498	chr18R73526864	Kidney Cortex	chr18	73526538	G>C	intergenic	na	41
Bot26	SA_117	66	chr20F58088935	chr20R58089109	Kidney Cortex	chr20	58088969	C>T	intergenic	na	35
Bot26	SA_117	66	chr21F16134156	chr21R16134532	Kidney Cortex	chr21	16134239	C>T	intergenic	na	84
Bot26	SA_117	66	chrXF84187869	chrXR84188173	Kidney Cortex	chrX	84187957	C>T	intergenic	na	89
Bot27	SA_118	59	chr1F218742514	chr1R218742910	Kidney Cortex	chr1	218742534	C>T	intergenic	na	21
Bot27	SA_118	59	chr1F237221388	chr1R237221602	Kidney Cortex	chr1	237221693	G>A	intragenic	RYR2	9
Bot27	SA_118	59	chr2F164845553	chr2R164845893	Kidney Cortex	chr2	164845979	C>A	intergenic	na	14
Bot27	SA_118	59	chr2F182155651	chr2R182155860	Kidney Cortex	chr2	182155925	G>A	intragenic	AK125001	35
Bot27	SA_118	59	chr3F31510048	chr3R31510627	Kidney Cortex	chr3	31510073	G>T	intergenic	na	26
Bot27	SA_118	59	chr3F71569559	chr3R71569815	Kidney Cortex	chr3	71569580	G>T	intragenic	FOXP1	22
Bot27	SA_118	59	chr3F134615063	chr3R134615336	Kidney Cortex	chr3	134615073	C>T	intragenic	EPHB1	11
Bot27	SA_118	59	chr3F187367433	chr3R187367794	Kidney Cortex	chr3	187367450	G>T	intergenic	na	18
Bot27	SA_118	59	chr3F195026351	chr3R195026558	Kidney Cortex	chr3	195026648	G>A	intragenic	ACAP2	10
Bot27	SA_118	59	chr4F81215453	chr4R81215635	Kidney Cortex	chr4	81215465	C>T	intergenic	na	13
Bot27	SA_118	59	chr4F183867725	chr4R183868077	Kidney Cortex	chr4	183867787	C>T	intergenic	na	63

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Bot27	SA_118	59	chr5F138489616	chr5R138489921	Kidney Cortex	chr5	138489983	G>A	intragenic	SIL1	intron 38
Bot27	SA_118	59	chr6F21930370	chr6R21930611	Kidney Cortex	chr6	21930385	G>C	intragenic	LINC00340	intron 16
Bot27	SA_118	59	chr6F97527758	chr6R97528039	Kidney Cortex	chr6	97528050	G>A	intragenic	KLHL32	intron 89
Bot27	SA_118	59	chr6F112436921	chr6R112437228	Kidney Cortex	chr6	112437303	G>A	intragenic	LAMA4	intron 25
Bot27	SA_118	59	chr7F36228092	chr7R36228308	Kidney Cortex	chr7	36228397	G>A	intragenic	EEPD1	intron 11
Bot27	SA_118	59	chr7F44605914	chr7R44606112	Kidney Cortex	chr7	44606198	C>G	intragenic	DDX56	intron 14
Bot27	SA_118	59	chr8F54294852	chr8R54295139	Kidney Cortex	chr8	54295144	G>A	intergenic	na	na 95
Bot27	SA_118	59	chr8F81436803	chr8R81437154	Kidney Cortex	chr8	81436879	G>C	intragenic	ZBTB10	exon 77
Bot27	SA_118	59	chr10F31999406	chr10R31999669	Kidney Cortex	chr10	31999413	C>T	intergenic	na	na 8
Bot27	SA_118	59	chr10F103769371	chr10R103769612	Kidney Cortex	chr10	103769384	G>T	intragenic	C10orf76	intron 14
Bot27	SA_118	59	chr10F130741514	chr10R130741768	Kidney Cortex	chr10	130741844	G>A	intergenic	na	na 24
Bot27	SA_118	59	chr11F20936771	chr11R20936991	Kidney Cortex	chr11	20937064	G>A	intragenic	NELL1	intron 27
Bot27	SA_118	59	chr11F109745874	chr11R109746070	Kidney Cortex	chr11	109745884	C>G	intergenic	na	na 11
Bot27	SA_118	59	chr11F132542367	chr11R132542675	Kidney Cortex	chr11	132542432	G>A	intragenic	OPCML	intron 66
Bot27	SA_118	59	chr12F13747715	chr12R13747925	Kidney Cortex	chr12	13748014	C>G	intragenic	GRIN2B	intron 11
Bot27	SA_118	59	chr12F14002120	chr12R14002386	Kidney Cortex	chr12	14002476	C>G	intragenic	GRIN2B	intron 10

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Bot27	SA_118	59	Kidney Cortex								
chr12F30641775	chr12R30641899		chr12	30641991	G>A						
intergenic	na				na	8					
Bot27	SA_118	59	Kidney Cortex								
chr12F112159649	chr12R112159951		chr12	112159668	C>T						
intragenic	ACAD10				exon	20					
Bot27	SA_118	59	Kidney Cortex								
chr12F126647904	chr12R126648200		chr12	126647915	C>T						
intergenic	na				na	12					
Bot27	SA_118	59	Kidney Cortex								
chr13F48527536	chr13R48527829		chr13	48527904	C>A						
intragenic	SUCLA2				intron	25					
Bot27	SA_118	59	Kidney Cortex								
chr14F78712121	chr14R78712467		chr14	78712138	C>T						
intragenic	NRXN3				intron	18					
Bot27	SA_118	59	Kidney Cortex								
chr16F25916946	chr16R25917054		chr16	25917124	G>A						
intragenic	HS3ST4				intron	30					
Bot27	SA_118	59	Kidney Cortex								
chr17F69899602	chr17R69899929		chr17	69899995	C>A						
intergenic	na				na	34					
Bot27	SA_118	59	Kidney Cortex								
chr18F36288045	chr18R36288323		chr18	36288359	T>C						
intergenic	na				na	64					
Bot27	SA_118	59	Kidney Cortex								
chr18F53188607	chr18R53188922		chr18	53188668	C>T						
intragenic	TCF4				intron	62					
Bot27	SA_118	59	Kidney Cortex								
chr19F32547928	chr19R32548364		chr19	32548021	C>T						
intergenic	na				na	94					
Bot27	SA_118	59	Kidney Cortex								
chr21F41628015	chr21R41628343		chr21	41628022	G>T						
intragenic	DSCAM				intron	8					
Bot27	SA_118	59	Kidney Cortex								
chrXF9276569	chrXR9276954		chrX	9276588	C>T						
intergenic	na				na	20					
Bot28	SA_119	69	Kidney Cortex								
chr1F15167012	chr1R15167229		chr1	15167257	G>A						
intragenic	KAZN				intron	72					
Bot28	SA_119	69	Kidney Cortex								
chr1F66289809	chr1R66290105		chr1	66290173	A>T						
intragenic	PDE4B				intron	32					
Bot28	SA_119	69	Kidney Cortex								
chr1F84303118	chr1R84303425		chr1	84303129	C>T						
intragenic	BC036594, MIR548AP, AK097722				intron	12					
Bot28	SA_119	69	Kidney Cortex								
chr1F109847346	chr1R109847761		chr1	109847353	T>A						
intragenic	MYBPHL				intron	8					

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Bot28	SA_119	69	chr1F110919846	chr1R110920195	Kidney Cortex	chr1	110920275	G>A	intragenic	SLC16A4	intron	20
Bot28	SA_119	69	chr1F118176297	chr1R118176679	Kidney Cortex	chr1	118176767	G>A	intergenic	na	na	12
Bot28	SA_119	69	chr1F174969208	chr1R174969604	Kidney Cortex	chr1	174969221	G>A	intragenic	CACYBP	exon	14
Bot28	SA_119	69	chr1F203645502	chr1R203645792	Kidney Cortex	chr1	203645824	C>G	intragenic	ATP2B4	intron	68
Bot28	SA_119	69	chr1F229688787	chr1R229689319	Kidney Cortex	chr1	229689355	C>G	intragenic	ABCB10	intron	64
Bot28	SA_119	69	chr2F31991231	chr2R31991539	Kidney Cortex	chr2	31991613	G>A	intergenic	na	na	26
Bot28	SA_119	69	chr2F42929385	chr2R42929589	Kidney Cortex	chr2	42929676	G>A	intragenic	MTA3	intron	13
Bot28	SA_119	69	chr2F157940553	chr2R157941002	Kidney Cortex	chr2	157940621	G>C	intergenic	na	na	69
Bot28	SA_119	69	chr2F172547385	chr2R172547768	Kidney Cortex	chr2	172547831	C>G	intragenic	DYNC1I2	intron	37
Bot28	SA_119	69	chr2F176139886	chr2R176140096	Kidney Cortex	chr2	176139957	T>A	intergenic	na	na	72
Bot28	SA_119	69	chr2F211527387	chr2R211527697	Kidney Cortex	chr2	211527402	G>C	intragenic	CPS1	intron	16
Bot28	SA_119	69	chr2F224065640	chr2R224065746	Kidney Cortex	chr2	224065796	C>G	intergenic	na	na	50
Bot28	SA_119	69	chr3F38177656	chr3R38177989	Kidney Cortex	chr3	38178081	A>G	intragenic	ACAA1	intron	8
Bot28	SA_119	69	chr3F39174973	chr3R39175219	Kidney Cortex	chr3	39175027	C>T	intragenic	TTC21A	intron	55
Bot28	SA_119	69	chr3F69915174	chr3R69915571	Kidney Cortex	chr3	69915229	C>T	intragenic	MITF	intron	56
Bot28	SA_119	69	chr3F70574118	chr3R70574319	Kidney Cortex	chr3	70574206	G>C	intergenic	na	na	89

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Bot28	SA_119	69	Kidney Cortex								
chr3F82024227	chr3R82024455		chr3	82024489	C>T						
intergenic	na				na	66					
Bot28	SA_119	69	Kidney Cortex								
chr3F101571541	chr3R101571871		chr3	101571549	T>C						
intragenic	NFKBIZ				intron	9					
Bot28	SA_119	69	Kidney Cortex								
chr3F156361165	chr3R156361537		chr3	156361182	A>T						
intergenic	na				na	18					
Bot28	SA_119	69	Kidney Cortex								
chr4F54355194	chr4R54355564		chr4	54355638	G>A						
intragenic	PDGFRA, LNX1				intron	26					
Bot28	SA_119	69	Kidney Cortex								
chr4F87954882	chr4R87955232		chr4	87955248	G>A						
intragenic	AFF1				intron	84					
Bot28	SA_119	69	Kidney Cortex								
chr4F106842769	chr4R106843008		chr4	106842842	G>C						
intragenic	NPNT				intron	74					
Bot28	SA_119	69	Kidney Cortex								
chr4F121025230	chr4R121025493		chr4	121025243	C>T						
intergenic	na				na	14					
Bot28	SA_119	69	Kidney Cortex								
chr4F140798908	chr4R140799031		chr4	140799112	C>A						
intragenic	MAML3				intron	19					
Bot28	SA_119	69	Kidney Cortex								
chr5F68028077	chr5R68028444		chr5	68028115	C>T						
intergenic	na				na	39					
Bot28	SA_119	69	Kidney Cortex								
chr5F141531621	chr5R141531863		chr5	141531923	G>A						
intragenic	NDFIP1				exon	40					
Bot28	SA_119	69	Kidney Cortex								
chr5F168988770	chr5R168989170		chr5	168988791	C>T						
intergenic	na				na	22					
Bot28	SA_119	69	Kidney Cortex								
chr6F9454390	chr6R9454618		chr6	9454685	G>A						
intergenic	na				na	33					
Bot28	SA_119	69	Kidney Cortex								
chr6F14174041	chr6R14174184		chr6	14174062	C>T						
intergenic	na				na	22					
Bot28	SA_119	69	Kidney Cortex								
chr7F39401551	chr7R39401892		chr7	39401611	G>T						
intragenic	POU6F2				intron	61					
Bot28	SA_119	69	Kidney Cortex								
chr7F47453226	chr7R47453426		chr7	47453288	C>T						
intragenic	TNS3				intron	63					
Bot28	SA_119	69	Kidney Cortex								
chr7F95306127	chr7R95306447		chr7	95306204	C>A						
intergenic	na				na	78					

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Bot28	SA_119	69	Kidney Cortex								
chr7F106222558chr7R106222810			chr7	106222587	C>T						
intragenic	AF086203				intron	30					
Bot28	SA_119	69	Kidney Cortex								
chr7F155005649chr7R155006006			chr7	155005678	C>A						
intergenic	na				na	30					
Bot28	SA_119	69	Kidney Cortex								
chr8F38187145chr8R38187451			chr8	38187216	G>C						
intragenic	WHSC1L1				exon	72					
Bot28	SA_119	69	Kidney Cortex								
chr8F123826833chr8R123827346			chr8	123826863	C>T						
intragenic	ZHX2				intron	31					
Bot28	SA_119	69	Kidney Cortex								
chr9F91953485chr9R91953809			chr9	91953899	G>A						
intragenic	SECISBP2				intron	10					
Bot28	SA_119	69	Kidney Cortex								
chr9F109060010chr9R109060595			chr9	109060019	G>T						
intragenic	BC039487				intron	10					
Bot28	SA_119	69	Kidney Cortex								
chr9F111661550chr9R111661936			chr9	111661999	G>C						
intragenic	IKBKAP				intron	37					
Bot28	SA_119	69	Kidney Cortex								
chr9F129845726chr9R129845932			chr9	129845814	C>T						
intragenic	RALGPS1				intron	89					
Bot28	SA_119	69	Kidney Cortex								
chr10F104928420chr10R104928824			chr10	104928440	A>C						
intragenic	NT5C2				intron	21					
Bot28	SA_119	69	Kidney Cortex								
chr11F15430462chr11R15430790			chr11	15430851	G>A						
intergenic	na				na	39					
Bot28	SA_119	69	Kidney Cortex								
chr11F15581337chr11R15581627			chr11	15581639	G>T						
intergenic	na				na	88					
Bot28	SA_119	69	Kidney Cortex								
chr11F59578120chr11R59578254			chr11	59578144	C>T						
intragenic	MRPL16				intron	25					
Bot28	SA_119	69	Kidney Cortex								
chr11F118754111chr11R118754505			chr11	118754595	G>A						
intragenic	CXCR5				intron	10					
Bot28	SA_119	69	Kidney Cortex								
chr11F125330142chr11R125330406			chr11	125330456	G>A						
intragenic	FEZ1				intron	50					
Bot28	SA_119	69	Kidney Cortex								
chr12F39897837chr12R39898096			chr12	39898154	G>A						
intergenic	na				na	42					
Bot28	SA_119	69	Kidney Cortex								
chr13F44827245chr13R44827401			chr13	44827463	G>A						
intergenic	na				na	38					

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Bot28	SA_119	69	chr13F59999102	chr13R59999320	intergenic	na	Kidney Cortex	chr13	59999382	G>A	na	38
Bot28	SA_119	69	chr13F79796124	chr13R79796309	intergenic	na	Kidney Cortex	chr13	79796323	A>T	na	86
Bot28	SA_119	69	chr13F90919072	chr13R90919321	intergenic	na	Kidney Cortex	chr13	90919412	C>G	na	9
Bot28	SA_119	69	chr13F95630666	chr13R95630924	intergenic	na	Kidney Cortex	chr13	95630676	C>G	na	11
Bot28	SA_119	69	chr13F110918302	chr13R110918649	intragenic	COL4A1	Kidney Cortex	chr13	110918330	G>T	intron	29
Bot28	SA_119	69	chr14F56653978	chr14R56654285	intragenic	PELI2	Kidney Cortex	chr14	56654299	G>A	intron	86
Bot28	SA_119	69	chr14F69871145	chr14R69871485	intragenic	SLC39A9	Kidney Cortex	chr14	69871543	G>A	intron	42
Bot28	SA_119	69	chr14F74230250	chr14R74230386	intragenic	ELMSAN1	Kidney Cortex	chr14	74230279	C>T	intron	30
Bot28	SA_119	69	chr15F65520978	chr15R65521329	intergenic	na	Kidney Cortex	chr15	65520996	C>T	na	19
Bot28	SA_119	69	chr15F69315139	chr15R69315529	intragenic	MIR548H4, NOX5	Kidney Cortex	chr15	69315191	C>T	intron	53
Bot28	SA_119	69	chr15F79592985	chr15R79593285	intergenic	na	Kidney Cortex	chr15	79593346	C>A	na	39
Bot28	SA_119	69	chr15F88646859	chr15R88647158	intragenic	NTRK3	Kidney Cortex	chr15	88646873	C>T	intron	15
Bot28	SA_119	69	chr16F23142926	chr16R23143256	intragenic	USP31	Kidney Cortex	chr16	23142953	G>T	intron	28
Bot28	SA_119	69	chr16F49166127	chr16R49166579	intergenic	na	Kidney Cortex	chr16	49166637	G>A	na	42
Bot28	SA_119	69	chr17F45302298	chr17R45302456	intergenic	na	Kidney Cortex	chr17	45302545	G>A	na	11
Bot28	SA_119	69	chr17F69028311	chr17R69028596	intergenic	na	Kidney Cortex	chr17	69028349	C>T	na	39

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Bot28	SA_119	69	chr17F69803660chr17R69803926	intergenic	na	Kidney Cortex	chr17	69803977	G>A	na	49
Bot28	SA_119	69	chr18F33464687chr18R33464997	intergenic	na	Kidney Cortex	chr18	33464699	C>T	na	13
Bot28	SA_119	69	chr18F36557904chr18R36558155	intergenic	na	Kidney Cortex	chr18	36558198	T>A	na	57
Bot28	SA_119	69	chr18F59537367chr18R59537690	intragenic	RNF152	Kidney Cortex	chr18	59537774	G>A	intron	16
Bot28	SA_119	69	chr19F13321887chr19R13322181	intragenic	CACNA1A	Kidney Cortex	chr19	13321959	C>T	intron	73
Bot28	SA_119	69	chr21F26742637chr21R26743037	intergenic	na	Kidney Cortex	chr21	26742721	G>C	na	85
Bot28	SA_119	69	chr22F31283203chr22R31283571	intragenic	OSBP2	Kidney Cortex	chr22	31283659	G>A	intron	12
Bot28	SA_119	69	chrXF135155861chrXR135156108	intergenic	na	Kidney Cortex	chrX	135156116	C>A	na	92
Bot28	SA_119	69	chrXF145141978chrXR145142213	intergenic	na	Kidney Cortex	chrX	145142044	C>T	na	67
Bot28	SA_119	69	chrYF17468598chrYR17468801	intergenic	na	Kidney Cortex	chrY	17468891	C>A	na	10
Bot29	KID034	55	chr1F177173373chr1R177173666	intragenic	FAM5B	Kidney Cortex	chr1	177173730	C>G	intron	36
Bot29	KID034	55	chr2F41926355chr2R41926567	intergenic	na	Kidney Cortex	chr2	41926608	A>G	na	59
Bot29	KID034	55	chr2F86703213chr2R86703625	intragenic	KDM3A	Kidney Cortex	chr2	86703708	C>A	intron	17
Bot29	KID034	55	chr2F162871127chr2R162871409	intragenic	DPP4	Kidney Cortex	chr2	162871210	T>C	intron	84
Bot29	KID034	55	chr2F177924202chr2R177924586	intergenic	na	Kidney Cortex	chr2	177924656	T>G	na	30
Bot29	KID034	55	chr4F125586839chr4R125587046	intragenic	ANKRD50	Kidney Cortex	chr4	125586886	A>T	intron	48

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Bot29	KID034	55	chr5F126499742chr5R126500032	intergenic	na	Kidney Cortex	chr5	126499785	A>G	na	44
Bot29	KID034	55	chr6F112669479chr6R112669865	intragenic	RFPL4B	Kidney Cortex	chr6	112669503	T>A	intron	25
Bot29	KID034	55	chr6F146060428chr6R146060705	intragenic	LOC100507557	Kidney Cortex	chr6	146060498	G>A	intron	71
Bot29	KID034	55	chr7F37295693chr7R37295966	intragenic	ELMO1	Kidney Cortex	chr7	37296004	A>T	intron	62
Bot29	KID034	55	chr7F69633662chr7R69634049	intragenic	AUTS2	Kidney Cortex	chr7	69634078	T>A	intron	71
Bot29	KID034	55	chr10F120015378chr10R120015765	intergenic	na	Kidney Cortex	chr10	120015419	G>A	na	42
Bot29	KID034	55	chr11F33892178chr11R33892519	intragenic	LMO2	Kidney Cortex	chr11	33892205	G>A	intron	28
Bot29	KID034	55	chr11F105501580chr11R105501938	intragenic	GRIA4	Kidney Cortex	chr11	105502000	T>C	intron	38
Bot29	KID034	55	chr13F28329529chr13R28329980	intergenic	na	Kidney Cortex	chr13	28329615	G>C	na	87
Bot29	KID034	55	chr13F53339695chr13R53339902	intergenic	na	Kidney Cortex	chr13	53339785	C>A	na	91
Bot29	KID034	55	chr14F37544718chr14R37545124	intragenic	SLC25A21	Kidney Cortex	chr14	37544791	T>C	intron	74
Bot29	KID034	55	chr18F10556769chr18R10557106	intergenic	na	Kidney Cortex	chr18	10557175	A>G	na	31
Bot29	KID034	55	chr18F22945152chr18R22945511	intergenic	na	Kidney Cortex	chr18	22945184	C>G	na	33
Bot29	KID034	55	chrXF28825253chrXR28825757	intragenic	IL1RAPL1	Kidney Cortex	chrX	28825817	G>A	intron	40
Bot29	KID034	55	chrXF43649340chrXR43649546	intragenic	MAOB	Kidney Cortex	chrX	43649564	A>G	intron	82
Bot30	KID035	45	chr6F83752182chr6R83752485	intragenic	UBE3D	Kidney Cortex	chr6	83752557	C>A	intron	28

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Bot30	KID035	45	chr6F148748862chr6R148749261	intragenic	SASH1	Kidney Cortex	chr6	148748916	C>T	intron	55
Bot30	KID035	45	chr7F148218453chr7R148218867	intergenic	na	Kidney Cortex	chr7	148218528	T>C	na	76
Bot30	KID035	45	chr8F62186579chr8R62187073	intergenic	na	Kidney Cortex	chr8	62186609	A>G	na	31
Bot30	KID035	45	chr10F126967206chr10R126967443	intergenic	na	Kidney Cortex	chr10	126967460	G>T	na	83
Bot30	KID035	45	chr15F70415533chr15R70415842	intergenic	na	Kidney Cortex	chr15	70415579	T>G	na	47
Bot30	KID035	45	chr15F99398951chr15R99399515	intragenic	IGF1R	Kidney Cortex	chr15	99398966	A>G	intron	16
Bot30	KID035	45	chrXF19321490chrXR19321909	intergenic	na	Kidney Cortex	chrX	19321571	G>A	na	82
Bot30	KID035	45	chrXF104226656chrXR104226839	intragenic	IL1RAPL2	Kidney Cortex	chrX	104226872	C>G	intron	67
Bot31	KID036	77	chr1F63018025chr1R63018312	intragenic	DOCK7	Kidney Cortex	chr1	63018101	A>C	intron	77
Bot31	KID036	77	chr1F94031238chr1R94031599	intragenic	BCAR3	Kidney Cortex	chr1	94031682	G>A	intron	17
Bot31	KID036	77	chr2F100060611chr2R100061062	intragenic	REV1	Kidney Cortex	chr2	100061072	C>T	intron	90
Bot31	KID036	77	chr2F104545202chr2R104545596	intergenic	na	Kidney Cortex	chr2	104545234	T>G	na	33
Bot31	KID036	77	chr2F221773651chr2R221774169	intergenic	na	Kidney Cortex	chr2	221774203	A>G	na	66
Bot31	KID036	77	chr2F235496993chr2R235497435	intergenic	na	Kidney Cortex	chr2	235497017	C>T	na	25
Bot31	KID036	77	chr3F32928963chr3R32929441	intragenic	TRIM71	Kidney Cortex	chr3	32929484	C>T	intron	57
Bot31	KID036	77	chr4F30799196chr4R30799465	intragenic	PCDH7	Kidney Cortex	chr4	30799487	C>T	intron	78

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Bot31	KID036	77	chr4F42280683	chr4R42280911	Kidney Cortex	chr4	42280748	T>A	intergenic	na	66
Bot31	KID036	77	chr6F131801704	chr6R131802141	Kidney Cortex	chr6	131802225	T>G	intergenic	na	16
Bot31	KID036	77	chr6F143442936	chr6R143443181	Kidney Cortex	chr6	143442965	A>T	intragenic	AIG1	30
Bot31	KID036	77	chr11F128208905	chr11R128209245	Kidney Cortex	chr11	128208968	T>A	intergenic	na	64
Bot31	KID036	77	chr13F93904526	chr13R93904868	Kidney Cortex	chr13	93904561	T>G	intragenic	GPC6	36
Bot31	KID036	77	chr19F44839306	chr19R44839567	Kidney Cortex	chr19	44839620	T>A	intragenic	ZFP112	47
Bot31	KID036	77	chrXF17968018	chrXR17968381	Kidney Cortex	chrX	17968051	G>T	intergenic	na	34
Bot31	KID036	77	chrXF122360363	chrXR122360930	Kidney Cortex	chrX	122360435	C>A	intragenic	GRIA3	73
Bot32	KID037	80	chr1F117610572	chr1R117610892	Kidney Cortex	chr1	117610612	T>C	intragenic	TTF2	41
Bot32	KID037	80	chr1F150117142	chr1R150117543	Kidney Cortex	chr1	150117598	A>G	intergenic	na	45
Bot32	KID037	80	chr2F116311139	chr2R116311397	Kidney Cortex	chr2	116311211	G>A	intragenic	DPP10	73
Bot32	KID037	80	chr2F197174816	chr2R197175007	Kidney Cortex	chr2	197175040	T>A	intragenic	HECW2	67
Bot32	KID037	80	chr2F199321577	chr2R199321990	Kidney Cortex	chr2	199321626	A>C	intergenic	na	50
Bot32	KID037	80	chr4F74642612	chr4R74642954	Kidney Cortex	chr4	74643013	A>G	intergenic	na	41
Bot32	KID037	80	chr4F113929867	chr4R113930216	Kidney Cortex	chr4	113930308	T>A	intragenic	ANK2	8
Bot32	KID037	80	chr5F94364359	chr5R94364714	Kidney Cortex	chr5	94364382	T>C	intragenic	MCTP1	24

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Bot32	KID037	80	Kidney Cortex								
chr8F57131170	chr8R57131617		chr8	57131182	T>A						
intergenic	na				na	13					
Bot32	KID037	80	Kidney Cortex								
chr8F140569378	chr8R140569737		chr8	140569409	A>G						
intergenic	na				na	32					
Bot32	KID037	80	Kidney Cortex								
chr10F128141420	chr10R128141992		chr10	128141506	G>T						
intragenic	C10orf90				intron	87					
Bot32	KID037	80	Kidney Cortex								
chr11F128457922	chr11R128458251		chr11	128457929	A>C						
intergenic	na				na	8					
Bot32	KID037	80	Kidney Cortex								
chr12F111706266	chr12R111706595		chr12	111706621	C>T						
intragenic	CUX2				intron	74					
Bot32	KID037	80	Kidney Cortex								
chr15F88601170	chr15R88601437		chr15	88601217	G>A						
intragenic	NTRK3				intron	48					
Bot32	KID037	80	Kidney Cortex								
chr16F50243894	chr16R50244138		chr16	50243939	T>C						
intragenic	PAPD5				intron	46					
Bot32	KID037	80	Kidney Cortex								
chr17F42961061	chr17R42961307		chr17	42961098	A>T						
intragenic	EFTUD2				intron	38					
Bot32	KID037	80	Kidney Cortex								
chrXF33003609	chrXR33003868		chrX	33003616	A>C						
intragenic	DMD				intron	8					
Bot32	KID037	80	Kidney Cortex								
chrXF36801602	chrXR36802027		chrX	36801684	A>G						
intergenic	na				na	83					
Bot32	KID037	80	Kidney Cortex								
chrXF86217414	chrXR86217790		chrX	86217797	C>T						
intergenic	na				na	93					
Bot32	KID037	80	Kidney Cortex								
chrXF104143467	chrXR104143911		chrX	104143969	G>A						
intragenic	IL1RAPL2				intron	42					
Bot33	KID038	0.416666667	Kidney Cortex, Right								
chr2F20976479	chr2R20976749		chr2	20976488	G>C						
intragenic	C2orf43				intron	10					
Bot33	KID038	0.416666667	Kidney Cortex, Right								
chr3F39884532	chr3R39884830		chr3	39884539	G>C						
intragenic	MYRIP				intron	8					
Bot33	KID038	0.416666667	Kidney Cortex, Right								
chr7F106148235	chr7R106148648		chr7	106148672	C>A						
intragenic	AF086203				intron	76					
Bot33	KID038	0.416666667	Kidney Cortex, Right								
chr10F125768425	chr10R125768917		chr10	125768997	C>A						
intragenic	CHST15				exon	20					

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Bot33	KID038	0.416666667	Kidney Cortex, Right						
chr15F71126851	chr15R71127244		chr15	71127315	C>G				
intragenic	LARP6				intron	29			
Bot34	KID038	0.416666667	Kidney Cortex, Left Block 1						
chr5F81835904	chr5R81836284		chr5	81835973	G>C				
intergenic	na				na	70			
Bot35	KID038	0.416666667	Kidney Cortex, Left Block 2						
chr5F57807946	chr5R57808210		chr5	57807976	G>C				
intergenic	na				na	31			
Bot36	BRA01	0.147945205	Brain, Frontal Cortex						
chr4F123249019	chr4R123249323		chr4	123249382	C>A				
intragenic	KIAA1109				exon	41			
Bot36	BRA01	0.147945205	Brain, Frontal Cortex						
chr8F61419192	chr8R61419498		chr8	61419565	C>G				
intergenic	na				na	33			
Bot37	BRA02	1.709589041	Brain, Frontal Cortex						
chr6F9794654	chr6R9794979		chr6	9794732	T>A				
intragenic	MRDS1, OFCC1				intron	79			
Bot38	BRA03	8.783561644	Brain, Frontal Cortex						
chr1F203371978	chr1R203372345		chr1	203372027	C>G				
intergenic	na				na	50			
Bot39	BRA04	20	Brain, Frontal Cortex						
chr2F190487795	chr2R190488265		chr2	190488356	C>T				
intergenic	na				na	9			
Bot39	BRA04	20	Brain, Frontal Cortex						
chr6F37354275	chr6R37354525		chr6	37354581	C>G				
intragenic	RNF8				intron	44			
Bot39	BRA04	20	Brain, Frontal Cortex						
chr16F13246886	chr16R13247448		chr16	13247490	C>G				
intragenic	SHISA9				intron	58			
Bot39	BRA04	20	Brain, Frontal Cortex						
chr17F67499567	chr17R67500009		chr17	67499589	A>G				
intragenic	MAP2K6				intron	23			
Bot40	BRA05	22	Brain, Frontal Cortex						
chr4F44159768	chr4R44160135		chr4	44160206	C>A				
intergenic	na				na	29			
Bot41	BRA06	25	Brain, Frontal Cortex						
chr1F234140461	chr1R234140892		chr1	234140503	G>A				
intragenic	SLC35F3				intron	43			
Bot41	BRA06	25	Brain, Frontal Cortex						
chr4F164105679	chr4R164106165		chr4	164105705	C>T				
intergenic	na				na	27			
Bot41	BRA06	25	Brain, Frontal Cortex						
chr14F42346020	chr14R42346308		chr14	42346102	C>T				
intragenic	LRFN5				intron	83			
Bot42	BRA07	90	Brain, Frontal Cortex						
chr1F68258955	chr1R68259519		chr1	68259527	T>G				
intragenic	GNG12				intron	92			

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Bot42	BRA07	90	chr4F30729249chr4R30729569	intragenic	PCDH7	Brain, Frontal Cortex	chr4	30729269	A>G	intron 21
Bot42	BRA07	90	chr5F169966310chr5R169966781	intragenic	KCNIP1	Brain, Frontal Cortex	chr5	169966807	G>A	intron 74
Bot42	BRA07	90	chr6F117777847chr6R117778344	intragenic	GOPC	Brain, Frontal Cortex	chr6	117778408	A>G	intron 36
Bot42	BRA07	90	chr6F159002175chr6R159002429	intragenic	TMEM181	Brain, Frontal Cortex	chr6	159002187	G>C	intron 13
Bot42	BRA07	90	chr7F106160472chr7R106160801	intragenic	AF086203	Brain, Frontal Cortex	chr7	106160869	A>G	intron 32
Bot42	BRA07	90	chr8F11546742chr8R11547059	intragenic	GATA4	Brain, Frontal Cortex	chr8	11547104	T>G	intron 55
Bot42	BRA07	90	chr14F62409166chr14R62409443	intergenic	na	Brain, Frontal Cortex	chr14	62409455	T>G	na 88
Bot42	BRA07	90	chr20F22217330chr20R22217647	intergenic	na	Brain, Frontal Cortex	chr20	22217369	T>G	na 40
Bot42	BRA07	90	chr21F38466766chr21R38467143	intragenic	TTC3	Brain, Frontal Cortex	chr21	38466788	G>T	intron 23
Bot43	BRA08	94	chr2F208687224chr2R208687474	intragenic	PLEKHM3	Brain, Frontal Cortex	chr2	208687282	T>C	exon 59
Bot43	BRA08	94	chr3F63978391chr3R63978676	intragenic	ATXN7	Brain, Frontal Cortex	chr3	63978420	G>C	intron 30
Bot43	BRA08	94	chr6F14144710chr6R14145210	intergenic	na	Brain, Frontal Cortex	chr6	14144802	C>T	na 93
Bot43	BRA08	94	chr8F120546936chr8R120547388	intergenic	na	Brain, Frontal Cortex	chr8	120546997	G>A	na 62
Bot44	BRA09	95	chr1F110851674chr1R110852053	intragenic	LOC440600	Brain, Frontal Cortex	chr1	110852137	T>A	intron 16
Bot44	BRA09	95	chr1F159162962chr1R159163179	intragenic	CADM3	Brain, Frontal Cortex	chr1	159163218	C>T	exon 61
Bot44	BRA09	95	chr1F231509433chr1R231509783	intragenic	EGLN1	Brain, Frontal Cortex	chr1	231509825	C>T	exon 58

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Bot44	BRA09	95	Brain, Frontal Cortex								
chr2F190516070	chr2R190516474		chr2	190516488	A>C						
intergenic	na				na	86					
Bot44	BRA09	95	Brain, Frontal Cortex								
chr6F125909247	chr6R125909573		chr6	125909608	T>C						
intergenic	na				na	65					

Mutation	Number of Watson Reads with Mutation (Read 1)	Number of Reads	Number of Watson Reads	Mutation Number of Sanger Sequencing Result	Fraction of Watson Duplicates	Number of Crick Reads with Mutation (Read 2)	Number of Crick Reads
Fraction of Match Crick Orientation		Total					
F	75	75	75		100%	88	88
100%	163	163	absent in Sanger				
R	49	49	49		100%	67	67
100%	116	116	absent in Sanger				
F	6	6	6		100%	77	77
100%	83	83	not performed				
R	142	142	142		100%	6	6
100%	148	148	absent in Sanger				
F	8	8	8		100%	108	110
98%	116	118	absent in Sanger				
R	123	123	123		100%	135	137
99%	258	260	absent in Sanger				
R	7	7	7		100%	93	94
99%	100	101	absent in Sanger				
F	14	14	14		100%	10	10
100%	24	24	not performed				
F	10	10	10		100%	60	60
100%	70	70	absent in Sanger				
R	91	91	91		100%	112	112
100%	203	203	absent in Sanger				
F	37	37	37		100%	52	52
100%	89	89	absent in Sanger				
F	78	78	78		100%	102	102
100%	180	180	absent in Sanger				
F	80	80	80		100%	46	47
98%	126	127	absent in Sanger				
R	109	109	109		100%	90	90
100%	199	199	not performed				
R	46	46	46		100%	114	114
100%	160	160	absent in Sanger				

Table50.txt

R	9	9	100%	30	30	100%
39	39	absent in Sanger				
R	26	26	100%	90	91	99%
116	117	absent in Sanger				
R	18	18	100%	67	67	100%
85	85	absent in Sanger				
F	6	6	100%	28	28	100%
34	34	absent in Sanger				
R	111	111	100%	69	69	100%
180	180	absent in Sanger				
R	38	38	100%	33	33	100%
71	71	not performed				
F	106	107	99%	129	131	98%
235	238	absent in Sanger				
R	24	24	100%	11	11	100%
35	35	not performed				
R	23	23	100%	47	47	100%
70	70	not performed				
R	2	2	100%	50	50	100%
52	52	absent in Sanger				
F	34	34	100%	37	37	100%
71	71	absent in Sanger				
F	32	32	100%	30	30	100%
62	62	absent in Sanger				
F	82	82	100%	56	56	100%
138	138	absent in Sanger				
F	42	42	100%	40	40	100%
82	82	not performed				
F	9	9	100%	9	9	100%
18	18	not performed				
F	25	25	100%	52	52	100%
77	77	absent in Sanger				
R	30	30	100%	34	34	100%
64	64	absent in Sanger				
R	19	19	100%	27	27	100%
46	46	absent in Sanger				
F	17	17	100%	22	22	100%
39	39	not performed				
R	57	57	100%	34	34	100%
91	91	absent in Sanger				
R	56	56	100%	70	73	96%
126	129	absent in Sanger				
F	53	53	100%	81	81	100%
134	134	absent in Sanger				
R	10	10	100%	46	47	98%
56	57	not performed				
R	54	54	100%	63	63	100%
117	117	not performed				

Table50.txt

F	7	7	100%	28	28	
100%	35	35	absent in Sanger			
R	50	50	100%	11	11	
100%	61	61	absent in Sanger			
R	17	17	100%	43	43	
100%	60	60	not performed			
R	47	47	100%	52	52	
100%	99	99	not performed			
R	25	25	100%	4	4	
100%	29	29	absent in Sanger			
F	8	8	100%	28	28	
100%	36	36	not performed			
R	34	34	100%	47	47	
100%	81	81	absent in Sanger			
F	34	34	100%	2	2	
100%	36	36	absent in Sanger			
R	38	38	100%	17	17	
100%	55	55	not performed			
R	56	56	100%	55	55	
100%	111	111	absent in Sanger			
R	58	58	100%	61	61	
100%	119	119	absent in Sanger			
R	48	48	100%	41	41	
100%	89	89	absent in Sanger			
F	42	42	100%	53	53	
100%	95	95	absent in Sanger			
R	19	19	100%	42	42	
100%	61	61	absent in Sanger			
F	55	55	100%	57	57	
100%	112	112	absent in Sanger			
R	49	49	100%	25	25	
100%	74	74	absent in Sanger			
F	71	71	100%	52	52	
100%	123	123	not performed			
F	120	121	99%	127	127	
100%	247	248	absent in Sanger			
R	66	66	100%	59	59	
100%	125	125	absent in Sanger			
F	76	76	100%	118	118	
100%	194	194	absent in Sanger			
F	34	34	100%	33	33	
100%	67	67	absent in Sanger			
F	4	4	100%	34	36	
94%	38	40	absent in Sanger			
R	6	6	100%	25	25	
100%	31	31	absent in Sanger			
R	27	27	100%	52	52	
100%	79	79	not performed			

Table50.txt

R	104		104		100%	100	104
96%	204	208		absent in Sanger			
R	62		62		100%	70	71
99%	132	133		not performed			
R	66		67		99%	13	13
100%	79	80		absent in Sanger			
F	57		57		100%	113	113
100%	170	170		absent in Sanger			
F	22		22		100%	70	70
100%	92	92		not performed			
F	51		51		100%	89	90
99%	140	141		absent in Sanger			
F	107		107		100%	56	56
100%	163	163		not performed			
R	44		44		100%	57	57
100%	101	101		absent in Sanger			
F	37		37		100%	81	81
100%	118	118		not performed			
R	98		98		100%	110	110
100%	208	208		not performed			
F	61		61		100%	66	67
99%	127	128		absent in Sanger			
F	97		101		96%	105	107
98%	202	208		absent in Sanger			
R	67		67		100%	14	14
100%	81	81		absent in Sanger			
R	18		18		100%	17	17
100%	35	35		absent in Sanger			
F	62		62		100%	93	96
97%	155	158		not performed			
F	6		6		100%	90	90
100%	96	96		absent in Sanger			
R	93		93		100%	102	102
100%	195	195		not performed			
R	14		14		100%	69	70
99%	83	84		absent in Sanger			
F	23		23		100%	8	8
100%	31	31		absent in Sanger			
F	59		59		100%	117	118
99%	176	177		absent in Sanger			
R	5		5		100%	101	101
100%	106	106		absent in Sanger			
R	40		40		100%	45	46
98%	85	86		not performed			
F	11		11		100%	41	41
100%	52	52		absent in Sanger			
R	2		2		100%	21	21
100%	23	23		not performed			

Table50.txt

R	48	48	100%	67	67	
100%	115	115	not performed			
F	5	5	100%	5	5	
100%	10	10	not performed			
F	2	2	100%	15	15	
100%	17	17	not performed			
F	47	52	90%	47	47	
100%	94	99	absent in Sanger			
R	52	52	100%	62	62	
100%	114	114	absent in Sanger			
F	8	8	100%	27	27	
100%	35	35	absent in Sanger			
F	40	40	100%	57	57	
100%	97	97	absent in Sanger			
F	21	21	100%	45	45	
100%	66	66	not performed			
R	15	15	100%	28	28	
100%	43	43	absent in Sanger			
R	2	2	100%	28	28	
100%	30	30	absent in Sanger			
F	29	29	100%	38	40	
95%	67	69	not performed			
F	3	3	100%	7	7	
100%	10	10	not performed			
R	48	48	100%	52	52	
100%	100	100	absent in Sanger			
F	18	18	100%	7	7	
100%	25	25	absent in Sanger			
R	23	23	100%	29	29	
100%	52	52	absent in Sanger			
R	3	3	100%	41	42	
98%	44	45	absent in Sanger			
R	40	40	100%	48	48	
100%	88	88	absent in Sanger			
F	22	22	100%	21	21	
100%	43	43	absent in Sanger			
R	51	51	100%	41	41	
100%	92	92	not performed			
F	46	46	100%	5	5	
100%	51	51	absent in Sanger			
F	4	4	100%	40	40	
100%	44	44	absent in Sanger			
R	2	2	100%	16	16	
100%	18	18	not performed			
R	24	24	100%	71	71	
100%	95	95	absent in Sanger			
R	14	14	100%	20	20	
100%	34	34	absent in Sanger			

Table50.txt

F	4	4	100%	55	56	98%	59	60	absent in Sanger
F	4	4	100%	38	39	97%	42	43	absent in Sanger
R	2	2	100%	45	45	100%	47	47	not performed
R	26	26	100%	71	71	100%	97	97	absent in Sanger
R	78	78	100%	13	13	100%	91	91	absent in Sanger
F	6	6	100%	101	101	100%	107	107	absent in Sanger
F	56	56	100%	90	91	99%	146	147	absent in Sanger
F	53	53	100%	17	18	94%	70	71	not performed
R	45	45	100%	94	94	100%	139	139	absent in Sanger
F	27	27	100%	26	26	100%	53	53	not performed
F	2	2	100%	104	105	99%	106	107	absent in Sanger
F	81	81	100%	2	2	100%	83	83	absent in Sanger
F	8	8	100%	57	57	100%	65	65	absent in Sanger
R	95	95	100%	90	90	100%	185	185	not performed
F	19	19	100%	79	79	100%	98	98	absent in Sanger
F	5	5	100%	128	128	100%	133	133	not performed
F	37	37	100%	94	94	100%	131	131	absent in Sanger
F	54	54	100%	95	96	99%	149	150	absent in Sanger
R	79	81	98%	61	62	98%	140	143	not performed
R	32	32	100%	37	37	100%	69	69	not performed
R	39	39	100%	100	100	100%	139	139	not performed
R	81	81	100%	112	112	100%	193	193	absent in Sanger
R	95	95	100%	114	114	100%	209	209	absent in Sanger
R	58	60	97%	5	5	100%	63	65	not performed

Table50.txt

F	19	19	100%	52	52	
100%	71	71	not performed			
F	12	12	100%	73	73	
100%	85	85	absent in Sanger			
F	58	58	100%	66	67	
99%	124	125	absent in Sanger			
F	15	15	100%	76	76	
100%	91	91	absent in Sanger			
F	6	6	100%	40	40	
100%	46	46	not performed			
F	46	47	98%	8	8	
100%	54	55	absent in Sanger			
R	29	29	100%	3	3	
100%	32	32	not performed			
F	56	56	100%	65	65	
100%	121	121	absent in Sanger			
F	71	71	100%	35	35	
100%	106	106	absent in Sanger			
F	2	2	100%	9	9	
100%	11	11	absent in Sanger			
F	27	27	100%	34	34	
100%	61	61	absent in Sanger			
R	21	21	100%	13	13	
100%	34	34	absent in Sanger			
F	3	3	100%	12	12	
100%	15	15	absent in Sanger			
R	6	6	100%	55	55	
100%	61	61	absent in Sanger			
F	54	54	100%	41	41	
100%	95	95	not performed			
F	28	28	100%	31	31	
100%	59	59	absent in Sanger			
F	28	28	100%	16	16	
100%	44	44	absent in Sanger			
R	21	21	100%	20	20	
100%	41	41	absent in Sanger			
F	7	7	100%	44	44	
100%	51	51	absent in Sanger			
F	57	57	100%	42	43	
98%	99	100	absent in Sanger			
F	2	2	100%	60	60	
100%	62	62	absent in Sanger			
R	11	11	100%	40	40	
100%	51	51	absent in Sanger			
R	5	5	100%	8	8	
100%	13	13	not performed			
R	6	6	100%	7	7	
100%	13	13	absent in Sanger			

Table50.txt

F	2		2	100%	9	9	
100%	11	11	absent in Sanger				
R	4		4	100%	3	3	
100%	7	7	absent in Sanger				
R	4		4	100%	3	3	
100%	7	7	absent in Sanger				
F	5		5	100%	5	5	
100%	10	10	not performed				
F	8		8	100%	9	9	
100%	17	17	not performed				
F	6		6	100%	8	8	
100%	14	14	not performed				
R	3		3	100%	2	2	
100%	5	5	absent in Sanger				
F	7		7	100%	7	7	
100%	14	14	absent in Sanger				
F	6		6	100%	6	6	
100%	12	12	absent in Sanger				
R	5		5	100%	10	10	
100%	15	15	absent in Sanger				
F	3		3	100%	8	8	
100%	11	11	absent in Sanger				
R	5		5	100%	4	4	
100%	9	9	not performed				
R	7		7	100%	5	5	
100%	12	12	absent in Sanger				
F	6		6	100%	2	2	
100%	8	8	not performed				
R	2		2	100%	10	10	
100%	12	12	absent in Sanger				
R	2		2	100%	3	3	
100%	5	5	absent in Sanger				
F	6		6	100%	3	3	
100%	9	9	absent in Sanger				
F	4		4	100%	10	10	
100%	14	14	not performed				
F	7		7	100%	12	12	
100%	19	19	not performed				
F	4		4	100%	5	5	
100%	9	9	absent in Sanger				
R	6		6	100%	9	9	
100%	15	15	absent in Sanger				
R	5		5	100%	8	8	
100%	13	13	not performed				
F	5		5	100%	2	2	
100%	7	7	absent in Sanger				
R	11		11	100%	7	7	
100%	18	18	absent in Sanger				

Table50.txt

F	2	2	100%	5	5	100%	7
7	absent in Sanger						
R	4	4	100%	3	3	100%	7
7	absent in Sanger						
R	5	5	100%	10	10	100%	15
15	absent in Sanger						
R	5	5	100%	4	4	100%	9
9	not performed						
F	4	4	100%	4	4	100%	8
8	absent in Sanger						
R	9	9	100%	7	7	100%	16
16	not performed						
R	11	11	100%	8	8	100%	19
19	not performed						
R	6	6	100%	7	7	100%	13
13	absent in Sanger						
F	8	8	100%	6	6	100%	14
14	not performed						
F	3	3	100%	6	6	100%	9
9	not performed						
R	3	3	100%	3	3	100%	6
6	absent in Sanger						
R	8	8	100%	6	6	100%	14
14	absent in Sanger						
R	6	6	100%	6	6	100%	12
12	absent in Sanger						
R	8	8	100%	7	7	100%	15
15	absent in Sanger						
F	4	4	100%	3	3	100%	7
7	absent in Sanger						
R	8	8	100%	8	8	100%	16
16	not performed						
F	8	8	100%	9	9	100%	17
17	absent in Sanger						
R	2	2	100%	5	5	100%	7
7	absent in Sanger						
R	14	14	100%	16	16	100%	30
30	absent in Sanger						
R	7	7	100%	7	7	100%	14
14	absent in Sanger						
F	6	6	100%	14	14	100%	20
20	absent in Sanger						
R	5	5	100%	4	4	100%	9
9	absent in Sanger						
R	7	7	100%	12	12	100%	19
19	absent in Sanger						
F	3	3	100%	3	3	100%	6
6	absent in Sanger						

Table50.txt

R	14	14	100%	16	16	100%	30
30	absent in Sanger						
R	9	9	100%	8	8	100%	17
17	absent in Sanger						
F	22	22	100%	17	17	100%	39
39	absent in Sanger						
F	17	17	100%	8	8	100%	25
25	absent in Sanger						
R	13	13	100%	10	10	100%	23
23	absent in Sanger						
F	9	9	100%	16	16	100%	25
25	absent in Sanger						
R	7	7	100%	9	9	100%	16
16	not performed						
F	3	3	100%	2	2	100%	5
5	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	3	3	100%	5
5	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	2	2	100%	3	3	100%	5
5	absent in Sanger						
F	2	2	100%	4	4	100%	6
6	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	3	3	100%	5
5	absent in Sanger						
R	2	2	100%	4	4	100%	6
6	absent in Sanger						
R	2	2	100%	3	3	100%	5
5	absent in Sanger						
R	3	3	100%	3	3	100%	6
6	absent in Sanger						
F	3	3	100%	2	2	100%	5
5	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						

Table50.txt

R	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	3	3	100%	3	3	100%	6	6
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	4	4	100%	2	2	100%	6	6
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	3	3	100%	2	2	100%	5	5
absent in Sanger								
F	3	3	100%	2	2	100%	5	5
not performed								
F	2	2	100%	3	3	100%	5	5
not performed								
F	3	3	100%	2	2	100%	5	5
absent in Sanger								
F	3	3	100%	2	2	100%	5	5
absent in Sanger								
R	2	2	100%	4	4	100%	6	6
absent in Sanger								
R	3	3	100%	2	2	100%	5	5
absent in Sanger								
R	3	3	100%	2	2	100%	5	5
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	3	3	100%	2	2	100%	5	5
absent in Sanger								
R	2	2	100%	3	3	100%	5	5
absent in Sanger								
F	3	3	100%	2	2	100%	5	5
absent in Sanger								
F	2	2	100%	2	2	100%	4	4
absent in Sanger								

Table50.txt

R	2	2	100%	2	2	100%	4	4
absent in Sanger								
R	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	7	7	100%	4	4	100%	11	11
absent in Sanger								
R	7	7	100%	7	7	100%	14	14
absent in Sanger								
R	7	7	100%	3	3	100%	10	10
absent in Sanger								
F	11	11	100%	4	4	100%	15	15
absent in Sanger								
F	11	12	92%	4	4	100%	15	16
absent in Sanger								
R	3	3	100%	11	11	100%	14	14
absent in Sanger								
F	5	5	100%	6	6	100%	11	11
absent in Sanger								
R	6	6	100%	10	10	100%	16	16
absent in Sanger								
R	7	7	100%	7	7	100%	14	14
absent in Sanger								
F	3	3	100%	12	12	100%	15	15
absent in Sanger								
R	3	3	100%	8	8	100%	11	11
absent in Sanger								
F	6	6	100%	6	6	100%	12	12
absent in Sanger								
R	2	2	100%	3	3	100%	5	5
absent in Sanger								
F	7	7	100%	6	6	100%	13	13
absent in Sanger								
R	9	9	100%	3	3	100%	12	12
absent in Sanger								
F	9	9	100%	7	7	100%	16	16
absent in Sanger								
R	16	16	100%	12	12	100%	28	28
absent in Sanger								
R	9	9	100%	8	8	100%	17	17
absent in Sanger								
F	5	5	100%	6	6	100%	11	11
absent in Sanger								
R	7	7	100%	4	4	100%	11	11
absent in Sanger								
F	5	5	100%	8	8	100%	13	13
absent in Sanger								
R	2	2	100%	4	4	100%	6	6
absent in Sanger								

Table50.txt

R	10	10	100%	3	3	100%	13	13
absent in Sanger								
F	13	13	100%	8	8	100%	21	21
absent in Sanger								
F	5	5	100%	4	4	100%	9	9
absent in Sanger								
R	2	2	100%	8	8	100%	10	10
absent in Sanger								
R	3	3	100%	8	8	100%	11	11
absent in Sanger								
R	5	5	100%	15	15	100%	20	20
not performed								
R	8	8	100%	6	6	100%	14	14
absent in Sanger								
F	3	3	100%	6	6	100%	9	9
absent in Sanger								
R	4	4	100%	8	8	100%	12	12
absent in Sanger								
F	7	7	100%	7	7	100%	14	14
absent in Sanger								
R	2	2	100%	5	5	100%	7	7
absent in Sanger								
F	10	11	91%	4	4	100%	14	15
not performed								
F	5	5	100%	10	10	100%	15	15
absent in Sanger								
R	4	4	100%	5	5	100%	9	9
absent in Sanger								
F	6	6	100%	6	6	100%	12	12
not performed								
R	4	4	100%	8	8	100%	12	12
absent in Sanger								
R	4	4	100%	3	3	100%	7	7
not performed								
R	13	13	100%	7	7	100%	20	20
absent in Sanger								
F	4	4	100%	2	2	100%	6	6
absent in Sanger								
F	11	11	100%	19	19	100%	30	30
absent in Sanger								
R	5	5	100%	6	6	100%	11	11
absent in Sanger								
R	2	2	100%	8	8	100%	10	10
absent in Sanger								
F	8	8	100%	8	8	100%	16	16
absent in Sanger								
R	2	2	100%	6	6	100%	8	8
absent in Sanger								

Table50.txt

R	9		9	100%	6	6
100%	15	15	absent in Sanger			
F	2		2	100%	5	5
100%	7	7	absent in Sanger			
F	13		13	100%	11	11
100%	24	24	absent in Sanger			
R	5		5	100%	7	7
100%	12	12	absent in Sanger			
R	6		6	100%	2	2
100%	8	8	absent in Sanger			
F	12		12	100%	9	9
100%	21	21	not performed			
R	5		5	100%	7	7
100%	12	12	not performed			
F	8		8	100%	6	6
100%	14	14	not performed			
R	12		12	100%	11	11
100%	23	23	absent in Sanger			
F	8		8	100%	7	7
100%	15	15	not performed			
F	7		7	100%	18	18
100%	25	25	not performed			
F	21		21	100%	14	14
100%	35	35	not performed			
R	3		3	100%	6	6
100%	9	9	absent in Sanger			
R	14		14	100%	13	13
100%	27	27	not performed			
R	13		13	100%	14	14
100%	27	27	absent in Sanger			
R	3		3	100%	11	11
100%	14	14	absent in Sanger			
F	16		16	100%	5	5
100%	21	21	absent in Sanger			
F	9		9	100%	19	19
100%	28	28	not performed			
R	15		15	100%	15	15
100%	30	30	not performed			
R	18		18	100%	14	14
100%	32	32	absent in Sanger			
R	7		7	100%	15	15
100%	22	22	not performed			
F	16		16	100%	12	12
100%	28	28	not performed			
R	6		6	100%	13	13
100%	19	19	absent in Sanger			
R	18		18	100%	4	4
100%	22	22	absent in Sanger			

Table50.txt

F	15	15	100%	17	17	100%	32	32	absent in Sanger
F	12	12	100%	11	11	100%	23	23	not performed
R	10	10	100%	20	20	100%	30	30	absent in Sanger
R	15	15	100%	23	23	100%	38	38	absent in Sanger
F	2	2	100%	3	3	100%	5	5	absent in Sanger
R	10	10	100%	4	4	100%	14	14	absent in Sanger
F	6	6	100%	2	2	100%	8	8	not performed
R	7	7	100%	5	5	100%	12	12	absent in Sanger
F	14	14	100%	11	11	100%	25	25	absent in Sanger
R	7	7	100%	12	12	100%	19	19	absent in Sanger
R	3	3	100%	3	3	100%	6	6	absent in Sanger
F	2	2	100%	10	10	100%	12	12	not performed
R	7	7	100%	6	6	100%	13	13	absent in Sanger
R	4	4	100%	4	4	100%	8	8	not performed
F	9	9	100%	9	9	100%	18	18	absent in Sanger
R	6	6	100%	6	6	100%	12	12	not performed
F	8	8	100%	10	10	100%	18	18	not performed
F	2	2	100%	8	8	100%	10	10	absent in Sanger
F	5	5	100%	6	6	100%	11	11	absent in Sanger
R	4	4	100%	5	5	100%	9	9	not performed
R	5	5	100%	3	3	100%	8	8	absent in Sanger
F	4	4	100%	3	3	100%	7	7	absent in Sanger
F	4	4	100%	4	4	100%	8	8	absent in Sanger
F	4	4	100%	6	6	100%	10	10	not performed

Table50.txt

F	6	6	100%	5	5	100%	11	11	not performed
R	6	6	100%	4	4	100%	10	10	absent in Sanger
F	12	12	100%	3	3	100%	15	15	absent in Sanger
R	9	9	100%	7	7	100%	16	16	absent in Sanger
F	11	11	100%	4	4	100%	15	15	absent in Sanger
F	8	8	100%	2	2	100%	10	10	absent in Sanger
R	2	2	100%	5	5	100%	7	7	not performed
R	2	2	100%	3	3	100%	5	5	not performed
R	2	2	100%	4	4	100%	6	6	not performed
R	9	9	100%	3	3	100%	12	12	absent in Sanger
R	3	3	100%	5	5	100%	8	8	not performed
F	2	2	100%	4	4	100%	6	6	not performed
F	2	2	100%	2	2	100%	4	4	absent in Sanger
F	9	9	100%	6	6	100%	15	15	not performed
R	4	4	100%	3	3	100%	7	7	not performed
F	2	2	100%	5	5	100%	7	7	absent in Sanger
F	5	5	100%	4	4	100%	9	9	not performed
F	3	3	100%	2	2	100%	5	5	absent in Sanger
R	2	2	100%	4	4	100%	6	6	absent in Sanger
R	3	3	100%	6	6	100%	9	9	not performed
F	5	5	100%	7	7	100%	12	12	absent in Sanger
F	3	3	100%	5	5	100%	8	8	absent in Sanger
R	3	3	100%	8	8	100%	11	11	absent in Sanger
R	5	5	100%	5	5	100%	10	10	absent in Sanger

Table50.txt

R	7	7	100%	4	4	100%	11	11	not performed
R	6	6	100%	6	6	100%	12	12	absent in Sanger
R	2	2	100%	3	3	100%	5	5	absent in Sanger
R	4	4	100%	6	6	100%	10	10	not performed
F	4	4	100%	3	3	100%	7	7	absent in Sanger
F	7	7	100%	4	4	100%	11	11	not performed
F	2	2	100%	6	6	100%	8	8	absent in Sanger
F	2	2	100%	3	3	100%	5	5	absent in Sanger
R	6	6	100%	5	5	100%	11	11	not performed
F	5	5	100%	4	4	100%	9	9	absent in Sanger
F	4	4	100%	3	3	100%	7	7	not performed
R	4	4	100%	6	6	100%	10	10	absent in Sanger
F	2	2	100%	3	3	100%	5	5	absent in Sanger
F	4	4	100%	7	7	100%	11	11	absent in Sanger
R	6	6	100%	12	12	100%	18	18	absent in Sanger
F	2	2	100%	7	7	100%	9	9	not performed
F	3	3	100%	7	7	100%	10	10	not performed
F	6	6	100%	3	3	100%	9	9	not performed
F	3	3	100%	9	9	100%	12	12	not performed
F	3	3	100%	7	7	100%	10	10	absent in Sanger
F	2	2	100%	5	5	100%	7	7	absent in Sanger
F	8	8	100%	11	11	100%	19	19	not performed
F	4	4	100%	3	3	100%	7	7	absent in Sanger
F	7	7	100%	3	3	100%	10	10	not performed

Table50.txt

R	7	7	100%	5	5	
100%	12	12	not performed			
R	11	11	100%	8	8	
100%	19	19	absent in Sanger			
R	6	6	100%	7	7	
100%	13	13	absent in Sanger			
F	2	2	100%	2	2	
100%	4	4	absent in Sanger			
F	2	2	100%	6	6	
100%	8	8	absent in Sanger			
R	3	3	100%	5	5	
100%	8	8	absent in Sanger			
R	11	11	100%	3	3	
100%	14	14	absent in Sanger			
R	2	2	100%	4	4	
100%	6	6	absent in Sanger			
F	6	6	100%	6	6	
100%	12	12	absent in Sanger			
F	2	2	100%	2	2	
100%	4	4	not performed			
R	8	8	100%	3	3	
100%	11	11	absent in Sanger			
F	4	4	100%	7	7	
100%	11	11	absent in Sanger			
R	4	4	100%	2	2	
100%	6	6	not performed			
R	7	7	100%	3	3	
100%	10	10	absent in Sanger			
F	7	7	100%	3	3	
100%	10	10	not performed			
F	2	2	100%	4	4	
100%	6	6	absent in Sanger			
F	3	3	100%	4	4	
100%	7	7	absent in Sanger			
F	2	2	100%	6	6	
100%	8	8	absent in Sanger			
F	5	5	100%	9	10	
90%	14	15	not performed			
R	3	3	100%	8	8	
100%	11	11	not performed			
R	3	3	100%	6	6	
100%	9	9	absent in Sanger			
R	5	5	100%	6	6	
100%	11	11	absent in Sanger			
F	7	7	100%	3	3	
100%	10	10	absent in Sanger			
R	6	6	100%	4	4	
100%	10	10	absent in Sanger			

Table50.txt

F	3	3	100%	3	3	100%	6	6
not performed								
F	5	5	100%	3	3	100%	8	8
absent in Sanger								
F	3	3	100%	8	8	100%	11	11
absent in Sanger								
F	2	2	100%	6	6	100%	8	8
absent in Sanger								
R	3	3	100%	6	6	100%	9	9
absent in Sanger								
F	3	3	100%	7	7	100%	10	10
absent in Sanger								
R	5	5	100%	4	4	100%	9	9
absent in Sanger								
F	2	2	100%	2	2	100%	4	4
absent in Sanger								
F	10	10	100%	5	5	100%	15	15
not performed								
R	7	7	100%	4	4	100%	11	11
absent in Sanger								
R	10	10	100%	5	5	100%	15	15
absent in Sanger								
R	6	6	100%	8	8	100%	14	14
absent in Sanger								
F	5	5	100%	2	2	100%	7	7
absent in Sanger								
F	3	3	100%	5	5	100%	8	8
absent in Sanger								
R	6	6	100%	5	5	100%	11	11
absent in Sanger								
F	4	4	100%	4	4	100%	8	8
absent in Sanger								
R	2	2	100%	4	4	100%	6	6
not performed								
F	3	3	100%	2	2	100%	5	5
absent in Sanger								
F	2	2	100%	7	7	100%	9	9
absent in Sanger								
F	2	2	100%	3	3	100%	5	5
absent in Sanger								
R	5	5	100%	4	4	100%	9	9
absent in Sanger								
F	10	10	100%	5	5	100%	15	15
not performed								
R	3	3	100%	2	2	100%	5	5
not performed								
R	2	2	100%	6	6	100%	8	8
absent in Sanger								

Table50.txt

F	5	5	100%	2	2	100%	7	7	not performed
R	3	3	100%	8	8	100%	11	11	not performed
F	3	3	100%	5	5	100%	8	8	absent in Sanger
F	3	3	100%	6	6	100%	9	9	not performed
F	9	10	90%	16	16	100%	25	26	absent in Sanger
F	13	13	100%	21	21	100%	34	34	absent in Sanger
R	28	28	100%	16	16	100%	44	44	absent in Sanger
F	6	6	100%	12	12	100%	18	18	not performed
F	18	19	95%	29	29	100%	47	48	not performed
F	21	21	100%	30	30	100%	51	51	not performed
F	30	30	100%	20	20	100%	50	50	not performed
R	2	2	100%	15	15	100%	17	17	not performed
R	33	33	100%	20	20	100%	53	53	absent in Sanger
R	21	21	100%	2	2	100%	23	23	absent in Sanger
R	17	17	100%	5	5	100%	22	22	not performed
F	2	2	100%	2	2	100%	4	4	absent in Sanger
R	17	17	100%	26	26	100%	43	43	absent in Sanger
F	27	27	100%	23	23	100%	50	50	not performed
F	31	31	100%	20	20	100%	51	51	absent in Sanger
F	12	12	100%	11	11	100%	23	23	absent in Sanger
R	12	12	100%	10	10	100%	22	22	not performed
F	8	8	100%	6	6	100%	14	14	not performed
F	24	25	96%	22	22	100%	46	47	absent in Sanger
R	17	17	100%	22	22	100%	39	39	not performed

R	5		5	100%	9	9	
100%	14	14		not performed			
F	3		3	100%	13	13	
100%	16	16		absent in Sanger			
F	16		16	100%	16	16	
100%	32	32		not performed			
F	9		9	100%	15	15	
100%	24	24		absent in Sanger			
R	2		2	100%	18	18	
100%	20	20		not performed			
R	21		21	100%	27	27	
100%	48	48		absent in Sanger			
R	26		26	100%	22	22	
100%	48	48		absent in Sanger			
R	6		6	100%	10	10	
100%	16	16		not performed			
R	8		8	100%	18	18	
100%	26	26		absent in Sanger			
F	14		14	100%	16	16	
100%	30	30		not performed			
R	3		3	100%	19	19	
100%	22	22		absent in Sanger			
F	9		9	100%	22	22	
100%	31	31		absent in Sanger			
R	24		24	100%	33	33	
100%	57	57		absent in Sanger			
R	25		25	100%	21	21	
100%	46	46		absent in Sanger			
R	35		35	100%	20	20	
100%	55	55		absent in Sanger			
R	21		21	100%	7	7	
100%	28	28		not performed			
R	7		7	100%	22	22	
100%	29	29		absent in Sanger			
F	17		17	100%	19	19	
100%	36	36		absent in Sanger			
F	4		4	100%	23	23	
100%	27	27		not performed			
R	8		8	100%	15	15	
100%	23	23		not performed			
F	7		7	100%	6	6	
100%	13	13		absent in Sanger			
F	4		4	100%	10	10	
100%	14	14		absent in Sanger			
R	6		6	100%	18	18	
100%	24	24		absent in Sanger			
R	3		3	100%	18	18	
100%	21	21		absent in Sanger			

F	11		11	100%	17	17	
100%	28	28	absent in Sanger				
F	2		2	100%	20	20	
100%	22	22	absent in Sanger				
R	6		6	100%	22	22	
100%	28	28	absent in Sanger				
R	17		17	100%	9	9	
100%	26	26	not performed				
R	18		18	100%	17	17	
100%	35	35	absent in Sanger				
R	10		10	100%	7	7	
100%	17	17	absent in Sanger				
R	16		16	100%	33	33	
100%	49	49	absent in Sanger				
R	10		10	100%	22	22	
100%	32	32	absent in Sanger				
R	6		6	100%	13	13	
100%	19	19	absent in Sanger				
R	6		6	100%	28	28	
100%	34	34	not performed				
R	20		20	100%	23	23	
100%	43	43	not performed				
R	17		17	100%	20	20	
100%	37	37	absent in Sanger				
F	6		6	100%	8	8	
100%	14	14	absent in Sanger				
F	11		11	100%	20	21	
95%	31	32	not performed				
R	13		13	100%	16	16	
100%	29	29	not performed				
R	14		14	100%	25	25	
100%	39	39	absent in Sanger				
F	13		13	100%	28	28	
100%	41	41	absent in Sanger				
R	4		4	100%	21	21	
100%	25	25	absent in Sanger				
F	29		29	100%	25	25	
100%	54	54	not performed				
F	26		26	100%	10	10	
100%	36	36	absent in Sanger				
F	20		20	100%	10	10	
100%	30	30	not performed				
R	11		11	100%	23	23	
100%	34	34	absent in Sanger				
F	13		13	100%	21	21	
100%	34	34	absent in Sanger				
F	25		26	96%	18	18	
100%	43	44	absent in Sanger				

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R	13		13		100%	11	11	
100%	24	24		absent in Sanger				
R	13		13		100%	14	14	
100%	27	27		absent in Sanger				
F	13		13		100%	23	23	
100%	36	36		absent in Sanger				
R	13		13		100%	27	27	
100%	40	40		absent in Sanger				
F	14		14		100%	17	17	
100%	31	31		absent in Sanger				
F	16		16		100%	12	12	
100%	28	28		not performed				
R	28		28		100%	22	22	
100%	50	50		absent in Sanger				
F	27		27		100%	14	14	
100%	41	41		absent in Sanger				
F	14		14		100%	18	18	
100%	32	32		absent in Sanger				
R	16		16		100%	19	19	
100%	35	35		absent in Sanger				
R	14		14		100%	14	14	
100%	28	28		not performed				
F	17		17		100%	14	14	
100%	31	31		absent in Sanger				
F	2		2		100%	13	13	
100%	15	15		absent in Sanger				
F	6		6		100%	14	14	
100%	20	20		absent in Sanger				
R	20		20		100%	4	4	
100%	24	24		absent in Sanger				
F	20		20		100%	13	13	
100%	33	33		absent in Sanger				
F	9		9		100%	9	9	
100%	18	18		not performed				
F	16		16		100%	10	10	
100%	26	26		absent in Sanger				
F	10		10		100%	9	9	
100%	19	19		absent in Sanger				
R	12		12		100%	14	14	
100%	26	26		absent in Sanger				
F	18		18		100%	19	19	
100%	37	37		not performed				
R	10		10		100%	7	7	
100%	17	17		not performed				
F	7		7		100%	9	9	
100%	16	16		absent in Sanger				
R	6		6		100%	5	5	
100%	11	11		absent in Sanger				

F	15		15	100%	21	21	
100%	36	36	not performed				
R	19		19	100%	16	16	
100%	35	35	not performed				
F	12		12	100%	23	23	
100%	35	35	absent in Sanger				
F	22		22	100%	13	13	
100%	35	35	absent in Sanger				
F	4		4	100%	9	9	
100%	13	13	not performed				
F	5		5	100%	5	5	
100%	10	10	not performed				
R	18		18	100%	12	12	
100%	30	30	absent in Sanger				
F	6		6	100%	3	3	
100%	9	9	absent in Sanger				
F	19		19	100%	17	17	
100%	36	36	absent in Sanger				
R	11		11	100%	17	17	
100%	28	28	not performed				
R	23		23	100%	19	19	
100%	42	42	absent in Sanger				
R	3		3	100%	14	14	
100%	17	17	not performed				
R	22		22	100%	9	9	
100%	31	31	absent in Sanger				
F	8		8	100%	4	4	
100%	12	12	absent in Sanger				
F	10		10	100%	13	13	
100%	23	23	not performed				
R	11		11	100%	15	15	
100%	26	26	absent in Sanger				
F	6		6	100%	22	22	
100%	28	28	not performed				
F	6		6	100%	6	6	
100%	12	12	not performed				
R	3		3	100%	13	13	
100%	16	16	absent in Sanger				
R	13		13	100%	9	9	
100%	22	22	not performed				
R	5		5	100%	8	8	
100%	13	13	absent in Sanger				
F	17		17	100%	20	20	
100%	37	37	absent in Sanger				
F	13		13	100%	9	9	
100%	22	22	absent in Sanger				
R	11		11	100%	14	14	
100%	25	25	absent in Sanger				

R	7		7		100%	7	7	
100%	14	14		absent in Sanger				
F	12		12		100%	13	13	
100%	25	25		absent in Sanger				
F	6		6		100%	8	8	
100%	14	14		absent in Sanger				
F	8		8		100%	3	3	
100%	11	11		not performed				
F	15		15		100%	12	12	
100%	27	27		absent in Sanger				
F	7		7		100%	17	17	
100%	24	24		absent in Sanger				
R	21		21		100%	16	16	
100%	37	37		absent in Sanger				
R	19		19		100%	15	15	
100%	34	34		not performed				
F	8		8		100%	12	12	
100%	20	20		absent in Sanger				
R	6		6		100%	13	13	
100%	19	19		absent in Sanger				
R	3		3		100%	13	13	
100%	16	16		not performed				
F	16		16		100%	18	18	
100%	34	34		absent in Sanger				
F	15		15		100%	23	23	
100%	38	38		absent in Sanger				
F	14		14		100%	18	18	
100%	32	32		not performed				
R	10		10		100%	4	4	
100%	14	14		absent in Sanger				
R	11		11		100%	12	12	
100%	23	23		absent in Sanger				
R	4		4		100%	18	18	
100%	22	22		not performed				
F	7		7		100%	8	8	
100%	15	15		absent in Sanger				
R	12		12		100%	7	7	
100%	19	19		absent in Sanger				
F	7		7		100%	12	12	
100%	19	19		not performed				
R	8		8		100%	15	15	
100%	23	23		absent in Sanger				
F	12		12		100%	9	9	
100%	21	21		absent in Sanger				
R	6		6		100%	14	14	
100%	20	20		not performed				
F	14		14		100%	11	11	
100%	25	25		absent in Sanger				

F	6		6	100%	8	8	
100%	14	14	absent in Sanger				
F	5		5	100%	4	4	
100%	9	9	absent in Sanger				
R	23		23	100%	9	9	
100%	32	32	absent in Sanger				
F	7		7	100%	11	11	
100%	18	18	absent in Sanger				
F	2		2	100%	6	6	
100%	8	8	absent in Sanger				
R	4		4	100%	2	2	
100%	6	6	absent in Sanger				
R	2		2	100%	16	16	
100%	18	18	not performed				
F	7		7	100%	8	8	
100%	15	15	not performed				
F	11		11	100%	18	18	
100%	29	29	absent in Sanger				
F	2		2	100%	12	12	
100%	14	14	absent in Sanger				
F	11		11	100%	16	16	
100%	27	27	absent in Sanger				
R	12		12	100%	20	20	
100%	32	32	absent in Sanger				
R	5		5	100%	8	8	
100%	13	13	not performed				
F	12		12	100%	18	18	
100%	30	30	not performed				
F	12		12	100%	10	10	
100%	22	22	absent in Sanger				
F	8		8	100%	15	15	
100%	23	23	absent in Sanger				
F	3		3	100%	7	7	
100%	10	10	absent in Sanger				
F	15		15	100%	16	16	
100%	31	31	not performed				
F	18		18	100%	15	15	
100%	33	33	not performed				
F	6		6	100%	11	11	
100%	17	17	absent in Sanger				
R	8		8	100%	21	21	
100%	29	29	not performed				
R	21		21	100%	18	18	
100%	39	39	absent in Sanger				
F	10		10	100%	13	13	
100%	23	23	absent in Sanger				
R	14		14	100%	6	6	
100%	20	20	absent in Sanger				

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F	13	13	100%	21	21	100%	34
34	not performed						
R	9	9	100%	17	17	100%	26
26	absent in Sanger						
R	14	14	100%	14	14	100%	28
28	absent in Sanger						
R	6	6	100%	9	9	100%	15
15	not performed						
R	3	3	100%	11	11	100%	14
14	absent in Sanger						
F	9	9	100%	17	17	100%	26
26	absent in Sanger						
R	6	6	100%	9	9	100%	15
15	not performed						
F	6	6	100%	16	16	100%	22
22	not performed						
R	17	17	100%	19	19	100%	36
36	absent in Sanger						
R	17	17	100%	16	16	100%	33
33	absent in Sanger						
F	7	7	100%	6	6	100%	13
13	absent in Sanger						
F	6	6	100%	13	13	100%	19
19	absent in Sanger						
R	7	7	100%	18	18	100%	25
25	absent in Sanger						
F	12	12	100%	11	11	100%	23
23	absent in Sanger						
F	2	2	100%	14	14	100%	16
16	absent in Sanger						
F	3	3	100%	6	6	100%	9
9	absent in Sanger						
F	2	2	100%	9	9	100%	11
11	absent in Sanger						
R	11	11	100%	14	14	100%	25
25	not performed						
F	14	14	100%	10	10	100%	24
24	absent in Sanger						
R	7	7	100%	13	13	100%	20
20	absent in Sanger						
F	5	5	100%	8	8	100%	13
13	absent in Sanger						
F	8	8	100%	2	2	100%	10
10	absent in Sanger						
R	3	3	100%	3	3	100%	6
6	absent in Sanger						
R	5	5	100%	8	8	100%	13
13	not performed						

F	6	6	100%	8	8	
100%	14	14	absent in Sanger			
R	7	7	100%	6	6	
100%	13	13	not performed			
R	2	2	100%	10	10	
100%	12	12	not performed			
R	10	10	100%	14	14	
100%	24	24	absent in Sanger			
F	15	15	100%	10	11	
91%	25	26	absent in Sanger			
R	3	3	100%	7	7	
100%	10	10	absent in Sanger			
F	6	6	100%	14	14	
100%	20	20	absent in Sanger			
F	3	3	100%	12	12	
100%	15	15	not performed			
R	12	12	100%	9	9	
100%	21	21	absent in Sanger			
R	4	4	100%	8	8	
100%	12	12	absent in Sanger			
F	4	4	100%	5	5	
100%	9	9	absent in Sanger			
F	4	4	100%	9	9	
100%	13	13	absent in Sanger			
F	12	12	100%	5	5	
100%	17	17	absent in Sanger			
F	9	9	100%	3	3	
100%	12	12	not performed			
F	2	2	100%	14	14	
100%	16	16	not performed			
F	9	9	100%	10	10	
100%	19	19	absent in Sanger			
F	8	8	100%	13	13	
100%	21	21	absent in Sanger			
R	2	2	100%	11	11	
100%	13	13	not performed			
R	5	5	100%	6	6	
100%	11	11	absent in Sanger			
R	2	2	100%	21	21	
100%	23	23	not performed			
F	5	5	100%	2	2	
100%	7	7	absent in Sanger			
F	5	5	100%	9	9	
100%	14	14	absent in Sanger			
F	5	5	100%	9	9	
100%	14	14	absent in Sanger			
F	2	2	100%	2	2	
100%	4	4	absent in Sanger			

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R	11		11	100%	8	8	
100%	19	19	not performed				
F	8		8	100%	17	17	
100%	25	25	absent in Sanger				
F	13		13	100%	8	8	
100%	21	21	absent in Sanger				
R	13		13	100%	16	16	
100%	29	29	absent in Sanger				
F	5		5	100%	14	14	
100%	19	19	not performed				
R	12		12	100%	22	22	
100%	34	34	absent in Sanger				
R	2		2	100%	14	14	
100%	16	16	absent in Sanger				
R	5		5	100%	13	13	
100%	18	18	absent in Sanger				
R	2		2	100%	15	15	
100%	17	17	not performed				
R	20		20	100%	12	13	
92%	32	33	not performed				
F	11		11	100%	3	3	
100%	14	14	not performed				
F	13		13	100%	11	11	
100%	24	24	not performed				
F	14		14	100%	11	11	
100%	25	25	absent in Sanger				
R	7		7	100%	11	12	
92%	18	19	not performed				
R	13		13	100%	15	15	
100%	28	28	not performed				
F	3		3	100%	2	2	
100%	5	5	not performed				
F	6		6	100%	8	8	
100%	14	14	absent in Sanger				
R	2		2	100%	12	12	
100%	14	14	absent in Sanger				
R	9		9	100%	10	11	
91%	19	20	absent in Sanger				
R	32		32	100%	14	14	
100%	46	46	absent in Sanger				
F	15		15	100%	16	16	
100%	31	31	not performed				
F	3		3	100%	8	8	
100%	11	11	not performed				
R	16		16	100%	17	17	
100%	33	33	absent in Sanger				
F	6		6	100%	11	11	
100%	17	17	absent in Sanger				

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R	12	12	100%	24	24	100%	36
36	absent in Sanger						
R	6	6	100%	13	13	100%	19
19	absent in Sanger						
R	8	8	100%	7	7	100%	15
15	absent in Sanger						
F	8	8	100%	19	19	100%	27
27	absent in Sanger						
F	5	5	100%	2	2	100%	7
7	not performed						
F	8	8	100%	5	5	100%	13
13	not performed						
F	7	7	100%	3	3	100%	10
10	absent in Sanger						
R	9	9	100%	8	8	100%	17
17	not performed						
R	6	6	100%	11	11	100%	17
17	not performed						
F	4	4	100%	5	5	100%	9
9	absent in Sanger						
F	3	3	100%	4	4	100%	7
7	not performed						
R	8	8	100%	10	10	100%	18
18	absent in Sanger						
R	2	2	100%	10	10	100%	12
12	absent in Sanger						
F	6	6	100%	3	3	100%	9
9	not performed						
R	4	4	100%	2	2	100%	6
6	not performed						
R	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	2	2	100%	10	10	100%	12
12	absent in Sanger						
R	4	4	100%	3	3	100%	7
7	not performed						
F	3	3	100%	4	4	100%	7
7	not performed						
R	4	4	100%	6	6	100%	10
10	not performed						
F	6	6	100%	4	4	100%	10
10	absent in Sanger						
F	7	7	100%	5	5	100%	12
12	absent in Sanger						
R	17	17	100%	14	14	100%	31
31	absent in Sanger						
R	5	5	100%	14	14	100%	19
19	not performed						

Table50.txt

F	2	2	100%	12	12	100%	14	14	not performed
F	2	2	100%	7	7	100%	9	9	absent in Sanger
F	4	4	100%	9	10	90%	13	14	absent in Sanger
R	9	9	100%	7	7	100%	16	16	absent in Sanger
F	13	13	100%	8	8	100%	21	21	absent in Sanger
F	6	6	100%	9	9	100%	15	15	absent in Sanger
R	5	5	100%	10	10	100%	15	15	absent in Sanger
R	2	2	100%	9	9	100%	11	11	absent in Sanger
F	8	8	100%	12	12	100%	20	20	absent in Sanger
F	2	2	100%	6	6	100%	8	8	absent in Sanger
R	12	12	100%	9	9	100%	21	21	absent in Sanger
F	3	3	100%	10	10	100%	13	13	absent in Sanger
R	5	5	100%	16	16	100%	21	21	not performed
F	2	2	100%	11	11	100%	13	13	absent in Sanger
R	6	6	100%	11	11	100%	17	17	absent in Sanger
F	7	7	100%	10	10	100%	17	17	not performed
F	2	2	100%	6	6	100%	8	8	absent in Sanger
F	9	9	100%	8	8	100%	17	17	not performed
F	6	6	100%	11	11	100%	17	17	not performed
F	8	8	100%	8	8	100%	16	16	not performed
F	2	2	100%	10	10	100%	12	12	absent in Sanger
F	5	5	100%	7	7	100%	12	12	absent in Sanger
F	6	6	100%	8	8	100%	14	14	not performed
R	6	6	100%	6	6	100%	12	12	absent in Sanger

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F	2	2	100%	3	3	100%	5	5
absent in Sanger								
R	6	6	100%	3	3	100%	9	9
absent in Sanger								
F	7	7	100%	13	13	100%	20	20
not performed								
F	8	8	100%	7	7	100%	15	15
absent in Sanger								
R	7	7	100%	11	11	100%	18	18
absent in Sanger								
R	6	6	100%	6	6	100%	12	12
absent in Sanger								
F	3	3	100%	5	5	100%	8	8
not performed								
R	2	2	100%	10	10	100%	12	12
absent in Sanger								
R	2	2	100%	13	13	100%	15	15
absent in Sanger								
R	4	4	100%	14	14	100%	18	18
absent in Sanger								
R	14	14	100%	8	8	100%	22	22
absent in Sanger								
R	8	8	100%	10	10	100%	18	18
absent in Sanger								
R	3	3	100%	5	5	100%	8	8
not performed								
R	4	4	100%	15	15	100%	19	19
not performed								
F	5	5	100%	3	3	100%	8	8
not performed								
F	7	7	100%	4	4	100%	11	11
absent in Sanger								
R	12	12	100%	6	6	100%	18	18
absent in Sanger								
R	2	2	100%	8	8	100%	10	10
not performed								
F	13	13	100%	11	11	100%	24	24
absent in Sanger								
F	5	5	100%	7	7	100%	12	12
not performed								
F	8	8	100%	6	6	100%	14	14
absent in Sanger								
R	11	11	100%	7	7	100%	18	18
not performed								
F	3	3	100%	4	4	100%	7	7
absent in Sanger								
F	10	11	91%	9	9	100%	19	20
not performed								

Table50.txt

R	4	4	100%	4	4	100%	8
8	absent in Sanger						
R	4	4	100%	5	5	100%	9
9	absent in Sanger						
F	6	6	100%	11	11	100%	17
17	absent in Sanger						
R	2	2	100%	7	7	100%	9
9	not performed						
F	5	5	100%	7	7	100%	12
12	not performed						
R	11	11	100%	15	15	100%	26
26	absent in Sanger						
R	9	9	100%	11	11	100%	20
20	absent in Sanger						
F	9	9	100%	8	8	100%	17
17	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	4	4	100%	2	2	100%	6
6	absent in Sanger						
R	9	9	100%	3	3	100%	12
12	absent in Sanger						
F	5	5	100%	16	16	100%	21
21	not performed						
R	15	15	100%	6	6	100%	21
21	absent in Sanger						
R	3	3	100%	6	6	100%	9
9	not performed						
R	8	8	100%	4	4	100%	12
12	absent in Sanger						
R	5	5	100%	4	4	100%	9
9	absent in Sanger						
F	2	2	100%	5	5	100%	7
7	absent in Sanger						
R	3	3	100%	6	6	100%	9
9	absent in Sanger						
F	5	5	100%	7	7	100%	12
12	absent in Sanger						
F	3	3	100%	3	3	100%	6
6	not performed						
F	3	3	100%	3	3	100%	6
6	not performed						
F	7	7	100%	2	2	100%	9
9	absent in Sanger						
R	4	4	100%	6	6	100%	10
10	absent in Sanger						
R	4	4	100%	3	3	100%	7
7	not performed						

Table50.txt

F	7	7	100%	5	5	100%	12
12	not performed						
F	2	2	100%	3	3	100%	5
5	absent in Sanger						
R	4	4	100%	3	3	100%	7
7	not performed						
F	2	2	100%	2	2	100%	4
4	not performed						
F	3	3	100%	2	2	100%	5
5	absent in Sanger						
F	4	4	100%	8	8	100%	12
12	absent in Sanger						
R	5	5	100%	2	2	100%	7
7	absent in Sanger						
F	4	4	100%	3	3	100%	7
7	not performed						
R	2	2	100%	4	4	100%	6
6	absent in Sanger						
R	3	3	100%	4	4	100%	7
7	not performed						
R	2	2	100%	4	4	100%	6
6	absent in Sanger						
F	4	4	100%	3	3	100%	7
7	not performed						
F	8	8	100%	2	2	100%	10
10	not performed						
F	2	2	100%	2	2	100%	4
4	not performed						
R	8	8	100%	6	6	100%	14
14	not performed						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
F	2	2	100%	2	2	100%	4
4	absent in Sanger						
R	5	5	100%	3	3	100%	8
8	not performed						
F	3	3	100%	6	6	100%	9
9	absent in Sanger						
R	2	2	100%	6	6	100%	8
8	not performed						
R	3	3	100%	2	2	100%	5
5	absent in Sanger						
F	2	2	100%	4	4	100%	6
6	absent in Sanger						
R	5	5	100%	2	2	100%	7
7	not performed						

F	3	3	100%	4	4	100%	7	7	not performed
R	2	2	100%	2	2	100%	4	4	absent in Sanger
R	5	5	100%	10	10	100%	15	15	not performed
F	2	2	100%	4	4	100%	6	6	absent in Sanger
R	2	2	100%	6	6	100%	8	8	not performed
F	3	3	100%	9	9	100%	12	12	absent in Sanger
F	6	6	100%	2	2	100%	8	8	absent in Sanger
F	7	7	100%	6	6	100%	13	13	not performed
R	4	4	100%	3	3	100%	7	7	not performed
F	3	3	100%	4	4	100%	7	7	absent in Sanger
F	6	6	100%	4	4	100%	10	10	absent in Sanger
F	6	6	100%	8	8	100%	14	14	not performed
R	6	6	100%	11	11	100%	17	17	absent in Sanger
F	6	6	100%	4	4	100%	10	10	absent in Sanger
R	4	4	100%	8	8	100%	12	12	not performed
F	2	2	100%	4	4	100%	6	6	not performed
R	9	9	100%	9	9	100%	18	18	absent in Sanger
R	9	9	100%	6	6	100%	15	15	absent in Sanger
F	4	4	100%	4	4	100%	8	8	not performed
F	3	3	100%	8	8	100%	11	11	absent in Sanger
F	4	4	100%	8	8	100%	12	12	absent in Sanger
F	5	5	100%	6	6	100%	11	11	absent in Sanger
F	7	7	100%	6	6	100%	13	13	absent in Sanger
R	6	6	100%	7	7	100%	13	13	absent in Sanger

Table50.txt

F	9	9	100%	5	5	100%	14	14	absent in Sanger
F	5	5	100%	3	3	100%	8	8	absent in Sanger
F	6	6	100%	6	6	100%	12	12	absent in Sanger
F	7	7	100%	7	7	100%	14	14	absent in Sanger
F	5	5	100%	4	4	100%	9	9	absent in Sanger
R	5	5	100%	8	8	100%	13	13	absent in Sanger
R	4	4	100%	9	9	100%	13	13	absent in Sanger
F	5	5	100%	10	10	100%	15	15	absent in Sanger
F	5	5	100%	5	5	100%	10	10	absent in Sanger
R	11	11	100%	2	2	100%	13	13	absent in Sanger
R	2	2	100%	3	3	100%	5	5	absent in Sanger
R	4	4	100%	10	10	100%	14	14	absent in Sanger
F	9	9	100%	7	7	100%	16	16	not performed
F	13	13	100%	11	11	100%	24	24	not performed
R	19	19	100%	22	22	100%	41	41	not performed
R	18	18	100%	12	12	100%	30	30	not performed
F	8	8	100%	3	3	100%	11	11	not performed
F	13	13	100%	15	15	100%	28	28	not performed
R	5	5	100%	5	5	100%	10	10	not performed
R	3	3	100%	20	20	100%	23	23	not performed
R	4	4	100%	3	3	100%	7	7	not performed
F	6	6	100%	10	10	100%	16	16	not performed
R	6	6	100%	14	14	100%	20	20	not performed
F	9	9	100%	10	10	100%	19	19	not performed

Table50.txt

F	11	11	100%	14	15
93%	25	26	not performed		
F	3	3	100%	22	22
100%	25	25	not performed		
R	9	9	100%	5	5
100%	14	14	not performed		
F	13	13	100%	14	14
100%	27	27	not performed		
R	9	9	100%	14	14
100%	23	23	not performed		
R	9	9	100%	14	14
100%	23	23	not performed		
F	10	10	100%	21	21
100%	31	31	not performed		
R	18	18	100%	14	14
100%	32	32	not performed		
R	10	10	100%	15	15
100%	25	25	not performed		
R	16	16	100%	16	16
100%	32	32	not performed		
F	19	19	100%	7	7
100%	26	26	not performed		
F	17	17	100%	10	10
100%	27	27	not performed		
F	15	15	100%	16	17
94%	31	32	not performed		
F	7	7	100%	2	2
100%	9	9	not performed		
F	5	5	100%	10	10
100%	15	15	not performed		
F	11	11	100%	8	8
100%	19	19	not performed		
R	8	8	100%	6	6
100%	14	14	not performed		
R	14	14	100%	14	14
100%	28	28	not performed		
R	13	13	100%	4	4
100%	17	17	not performed		
R	13	13	100%	3	3
100%	16	16	not performed		
R	17	17	100%	10	10
100%	27	27	not performed		

Table51.txt

Table 51. Summary of mutation frequencies and spectra in this study

mtDNA

BotS Library ID	Sample Name	Number of Normal Tissue	Total Number of Molecules Sequenced	Unique Molecules Sequenced	Number of bp Sequenced	Mutation Frequency (mutation/bp)	Cohort	Human Age (years)	C:G>T:A	A:T>G:C	C:G>G:C	A:T>C:G	C:G>A:T	A:T>T:A	Mutations
Bot01	AA_105	Kidney Cortex*	78	100%	0%	0%	0%	Aristolochic acid-associated UTUC	78	0%	0%	0%	0%	0%	1
Bot02	AA_124	Kidney Cortex*	82	0%	50%	50%	0%	Aristolochic acid-associated UTUC	82	0%	0%	0%	0%	0%	2
Bot03	AA_126	Kidney Cortex*	78	67%	0%	0%	33%	Aristolochic acid-associated UTUC	78	0%	0%	0%	0%	0%	3
Bot04	SA_117	Kidney Cortex*	66	83%	17%	0%	0%	Smoking-assocated UTUC	66	0%	0%	0%	0%	0%	6
Bot05	SA_118	Kidney Cortex*	59	100%	0%	0%	0%	Smoking-assocated UTUC	59	0%	0%	0%	0%	0%	1
Bot06	SA_119	Kidney Cortex*	69	43%	43%	0%	14%	Smoking-assocated UTUC	69	0%	0%	0%	0%	0%	7
Bot07	COL229	Colon Epithelium, Splenic Flexure	3	0%	0%	0%	0%	Control	3	0%	0%	0%	0%	0%	0
Bot08	COL231	Colon Epithelium, Cecum	8	100%	0%	0%	0%	Control	8	0%	0%	0%	0%	0%	1
Bot09	COL232	Colon Epithelium, Cecum	98	64%	36%	0%	0%	Control	98	0%	0%	0%	0%	0%	11
Bot10	COL233	Colon Epithelium,Cecum	96	55%	38%	3%	0%	Control	96	0%	0%	0%	3%	0%	29
Bot11	COL234	Colon Epithelium, Cecum	95	56%	44%	0%	0%	Control	95	0%	0%	0%	0%	0%	

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0%	16	3111	547536	2.92218E-05									
Bot12	COL235	Colon Epithelium, Sigmoid**	Control										
26	60%	20%	20%	0%	0%								
0%	5	2573	452848	1.10412E-05									
Bot13	COL236	Colon Epithelium, Sigmoid**	Control										
26	80%	20%	0%	0%	0%								
0%	5	3055	537680	9.29921E-06									
Bot14	COL237	Colon Epithelium	Control										
22	50%	50%	0%	0%	0%								
0%	2	2484	437184	4.57473E-06									
Bot15	COL238	Colon Epithelium	PMS2 -/-										
16	20%	0%	0%	0%	60%								
0%	5	2352	413952	1.20787E-05									
Bot16	COL239	Colon Epithelium	PMS2 -/-										
18	50%	50%	0%	0%	0%								
0%	2	181	31856	6.27825E-05									
Bot17	SIN230	Small Intestine, Duodenum	Control										
6	50%	50%	0%	0%	0%								
0%	2	3664	644864	3.10143E-06									
Bot18	COL235	Colon Epithelium, Sigmoid**	Control										
26	60%	40%	0%	0%	0%								
0%	5	4496	791296	6.31875E-06									
Bot19	COL236	Colon Epithelium, Sigmoid**	Control										
26	43%	57%	0%	0%	0%								
0%	14	5022	883872	1.58394E-05									
Bot20	COL373	Colon Epithelium	Control										
36	50%	40%	10%	0%	0%								
0%	10	3410	600160	1.66622E-05									
Bot21	COL374	Colon Epithelium	Control										
21	57%	43%	0%	0%	0%								
0%	7	3861	679536	1.03011E-05									
Bot22	COL375	Colon Epithelium	Control										
38	36%	64%	0%	0%	0%								
0%	11	4383	771408	1.42596E-05									
Bot23	AA_105	Kidney Cortex*	Aristolochic acid-associated UTUC										
78	43%	29%	14%	0%	0%	14%							
7	1376	242176	2.89046E-05										
Bot24	AA_124	Kidney Cortex*	Aristolochic acid-associated UTUC										
82	33%	67%	0%	0%	0%	0%							
3	1042	183392	1.63584E-05										
Bot25	AA_126	Kidney Cortex*	Aristolochic acid-associated UTUC										
78	22%	56%	11%	11%	0%	0%							
9	2127	374352	2.40415E-05										
Bot26	SA_117	Kidney Cortex*	Smoking-assocated UTUC										
66	67%	33%	0%	0%	0%								
0%	6	897	157872	3.80055E-05									
Bot27	SA_118	Kidney Cortex*	Smoking-assocated UTUC										
59	0%	0%	0%	0%	0%								

Table51.txt

0%	0	285	50160	0					
Bot28	SA_119	Kidney Cortex*						Smoking-assocated UTUC	
	69	30%	61%	0%	4%	0%			
4%	23	3903	686928	3.34824E-05					
Bot29	KID034	Kidney Cortex						Control (Nonsmoker)	
	55	31%	59%	2%	5%	1%			
2%	103	19970	3514720	2.93053E-05					
Bot30	KID035	Kidney Cortex						Control (Nonsmoker)	
	45	57%	41%	0%	2%	0%			
0%	44	13115	2308240	1.90621E-05					
Bot31	KID036	Kidney Cortex						Control (Nonsmoker)	
	77	26%	58%	0%	5%	5%			
8%	66	10856	1910656	3.45431E-05					
Bot32	KID037	Kidney Cortex						Control (Nonsmoker)	
	80	41%	47%	1%	4%	2%			
5%	83	16903	2974928	2.78998E-05					
Bot33	KID038	Kidney Cortex, Right***						Control (Nonsmoker)	
	0.417	100%	0%	0%	0%	0%			
0%	1	5907	1039632	9.61879E-07					
Bot34	KID038	Kidney Cortex, Left, Sector 1***						Control (Nonsmoker)	
	0.417	0%	0%	0%	0%	0%			
0%	0	3159	555984	0					
Bot35	KID038	Kidney Cortex, Left, Sector 2***						Control (Nonsmoker)	
	0.417	0%	50%	50%	0%	0%			
0%	2	3231	568656	3.51706E-06					
Bot36	BRA01	Brain, Frontal Cortex						Control	
	0.148	33%	67%	0%	0%	0%			
0%	3	16940	2981440	1.00623E-06					
Bot37	BRA02	Brain, Frontal Cortex						Control	
	1.71	44%	44%	0%	0%	0%			
11%	9	21352	3757952	2.39492E-06					
Bot38	BRA03	Brain, Frontal Cortex						Control	
	8.784	67%	33%	0%	0%	0%			
0%	6	17903	3150928	1.9042E-06					
Bot39	BRA04	Brain, Frontal Cortex						Control	
	20	50%	50%	0%	0%	0%			
0%	18	26415	4649040	3.87177E-06					
Bot40	BRA05	Brain, Frontal Cortex						Control	
	22	57%	14%	7%	0%	14%			
7%	14	19345	3404720	4.11194E-06					
Bot41	BRA06	Brain, Frontal Cortex						Control	
	25	50%	36%	7%	0%	4%			
4%	28	31808	5598208	5.0016E-06					
Bot42	BRA07	Brain, Frontal Cortex						Control	
	90	57%	43%	0%	0%	0%			
0%	21	10384	1827584	1.14906E-05					
Bot43	BRA08	Brain, Frontal Cortex						Control	
	94	54%	32%	0%	4%	0%			

Table51.txt

| | | |

Table51.txt

58%	5%	5%	0%	32%	0%	19	3004
528704	3.59369E-05	2.1					
52%	0%	17%	4%	26%	0%	23	5176
910976	2.52476E-05	1.3					
0%	0%	50%	50%	0%	0%	2	76474
13459424	1.48595E-07	0.0					
33%	0%	33%	0%	33%	0%	3	80053
14089328	2.12927E-07	11.4					
50%	17%	0%	0%	17%	17%	12	55580
9782080	1.22673E-06	26.0					
43%	0%	36%	7%	14%	0%	14	69497
12231472	1.14459E-06	42.2					
46%	15%	31%	0%	8%	0%	13	79225
13943600	9.32327E-07	31.3					
17%	33%	17%	0%	33%	0%	6	51819
9120144	6.57884E-07	16.8					
0%	0%	100%	0%	0%	0%	1	71113
12515888	7.98984E-08	116.4					
33%	17%	33%	17%	0%	0%	6	52536
9246336	6.48906E-07	7.0					
49%	5%	16%	2%	26%	2%	43	6116
1076416	3.99474E-05	0.3					
55%	0%	9%	3%	27%	6%	33	2127
374352	8.81523E-05	0.7					
50%	0%	25%	0%	25%	0%	4	88550
15584800	2.5666E-07	12.1					
44%	11%	11%	11%	22%	0%	9	96067
16907792	5.32299E-07	11.9					
60%	10%	10%	10%	10%	0%	10	
128559	22626384	4.41962E-07	35.8				
67%	11%	0%	0%	0%	22%	9	69474
12227424	7.3605E-07	22.6					
25%	50%	0%	0%	0%	25%	4	41441
7293616	5.48425E-07	18.8					
40%	40%	0%	0%	0%	20%	5	54777
9640752	5.18632E-07	27.5					
38%	8%	14%	1%	23%	16%	120	45059
7930384	1.51317E-05	1.9					
30%	3%	5%	7%	8%	47%	76	22768
4007168	1.8966E-05	0.9					
30%	7%	4%	0%	8%	51%	103	23773
4184048	2.46173E-05	1.0					
64%	0%	16%	4%	12%	4%	25	14241
2506416	9.9744E-06	3.8					
62%	3%	15%	0%	21%	0%	39	15618
2748768	1.41882E-05	0.0					
58%	3%	17%	1%	14%	8%	78	38375
6754000	1.15487E-05	2.9					

Table51.txt

19%	33%	14%	5%	10%	19%	21	
133353	23470128	8.94754E-07	32.8				
22%	33%	11%	11%	22%	0%	9	89421
15738096	5.71861E-07	33.3					
31%	6%	0%	25%	13%	25%	16	
102859	18103184	8.83822E-07	39.1				
25%	35%	0%	15%	5%	20%	20	
144302	25397152	7.8749E-07	35.4				
0%	0%	60%	0%	40%	0%	5	
147220	25910720	1.9297E-07	5.0				
0%	0%	100%	0%	0%	0%	1	86446
15214496	6.57268E-08	0.0					
0%	0%	100%	0%	0%	0%	1	66635
11727760	8.52678E-08	41.2					
0%	0%	50%	0%	50%	0%	2	95344
16780544	1.19186E-07	8.4					
0%	0%	0%	0%	0%	100%	1	75495
13287120	7.52609E-08	31.8					
0%	0%	100%	0%	0%	0%	1	45521
8011696	1.24818E-07	15.3					
25%	25%	50%	0%	0%	0%	4	68571
12068496	3.31441E-07	11.7					
0%	0%	0%	0%	100%	0%	1	52339
9211664	1.08558E-07	37.9					
100%	0%	0%	0%	0%	0%	3	81536
14350336	2.09054E-07	23.9					
10%	30%	10%	40%	10%	0%	10	63640
11200640	8.92806E-07	12.9					
50%	25%	25%	0%	0%	0%	4	43310
7622560	5.24758E-07	28.8					
40%	20%	0%	20%	0%	20%	5	60641
10672816	4.6848E-07	27.3					
na	na	na	na	na	na	876	
2566729	451744304	na	na				
35%	11%	23%	5%	15%	11%	20	
58334.75	10266916	1.00511E-05	17.8				
24%	13%	29%	11%	18%	19%	27	
39442.11157	6941811.636	1.78953E-05	20.8				
39%	4%	13%	0%	11%	0%	10	
58110.5	10227448	6.96967E-07	12.0				
100%	50%	100%	50%	100%	100%	120	
147220	25910720	8.81523E-05	116.4				
0%	0%	0%	0%	0%	0%	1	2127
374352	6.57268E-08	0.0					

Table52.txt

Table 52. Safe-SeqS with Endogenous UIDs

Conventional Analysis	Capture	Inverse PCR
High quality bp	106,958,863	1,041,346,645
Mean high quality bp read depth	38,620W	2,085,600W
Mutations identified	25,563	234,352
Mutations/bp	2.40E-04	2.30E-04
Safe-SeqS Analysis		
High quality bp	106,958,863	1,041,346,645
Mean high quality bp read depth	38,620W	2,085,600W
UID-families	69,505	1,057
Average # of members/UID-family	40	21,688
Median # of members/UID-family	19	4
Super-mutants identified	8	0
Super-mutants/bp	3.50E-06	0

Table53.txt

Table 53. Safe-SeqS with Exogenous UIDs

A. Polymerase Fidelity	Mean	Standard Deviation
Conventional analysis of 7 replicates		
High quality bp	996,855,791	64,030,757
Total mutations identified	198,638	22,515
Mutations/bp	2.00E-04	1.70E-05
Calculated Phusion Error Rate (errors/bp/cycle)	9.10E-06	7.70E-07
Safe-SeqS analysis of 7 replicates		
High quality bp	996,855,791	64,030,757
UID-families	624,678	421,274
Members/UID-family	107	122
Total super-mutants identified	197	143
Super-mutants/bp	9.90E-06	2.30E-06
Calculated Phusion Error Rate (errors/bp/cycle)	4.50E-07	1.00E-07
B. CTNNB1 mutations in DNA from normal human cells		
Conventional analysis of 3 individuals		
High quality bp	559,334,774	66,600,749
Total mutations identified	118,488	11,357
Mutations/bp	2.10E-04	1.60E-05
Safe-SeqS analysis of 3 individuals		
High quality bp	559,334,774	66,600,749
UID-families	374,553	263,105
Members/UID-family	68	38
Total super-mutants identified	99	78
Super-mutants/bp	9.00E-06	3.10E-06
C. Mitochondrial mutations in DNA from normal human cells		
Conventional analysis of 7 individuals		
High quality bp	147,673,456	

Table53.txt

54,308,546			
Total mutations identified		30,599	
12,970			
Mutations/bp		2.10E-04	
9.40E-05			
Safe-SeqS analysis of 7 individuals			
High quality bp		147,673,456	
54,308,546			
UID-families		515,600	
89,985			
Members/UID-family		15	6
Total super-mutants identified		135	61
Super-mutants/bp		1.40E-05	
6.80E-06			

Table54.txt

Table 54. Fraction of Single Base Substitutions, Insertions, and Deletions with Exogenous UIDs

A. Polymerase Fidelity	Mean	Standard Deviation
Conventional analysis of 7 replicates		
Total mutations identified	198,638	22,515
Fraction of mutations represented by single base substitutions	99%	0%
Fraction of mutations represented by deletions	1%	0%
Fraction of mutations represented by insertions	0%	0%
Safe-SeqS analysis of 7 replicates		
Total super-mutants identified	197	143
Fraction of super-mutants represented by single base substituti	99%	2%
Fraction of super-mutants represented by deletions	1%	2%
Fraction of super-mutants represented by insertions	0%	0%
B. CTNNB1 mutations in DNA from normal human cells		
Conventional analysis of 3 individuals		
Total mutations identified	118,488	11,357
Fraction of mutations represented by single base substitutions	97%	0%
Fraction of mutations represented by deletions	3%	0%
Fraction of mutations represented by insertions	0%	0%
Safe-SeqS analysis of 3 individuals		
Total super-mutants identified	99	78
Fraction of super-mutants represented by single base substituti	100%	1%
Fraction of super-mutants represented by deletions	0%	1%
Fraction of super-mutants represented by insertions	0%	0%
C. Mitochondrial mutations in DNA from normal human cells		
Conventional analysis of 7 individuals		

Table54.txt

Total mutations identified	30,599	12,970
Fraction of mutations represented by single base substitutions	98%	1%
Fraction of mutations represented by deletions	2%	1%
Fraction of mutations represented by insertions	0%	0%
Safe-SeqS analysis of 7 individuals		
Total super-mutants identified	135	61
Fraction of super-mutants represented by single base substituti	99%	1%
Fraction of super-mutants represented by deletions	1%	1%
Fraction of super-mutants represented by insertions	0%	0%

Table55.txt

Table 55. Observed and Expected Number of Errors Generated by Phusion Polymerase

A. Experiment 1	Observed	Expected (mean 1 SD) *
Mutations represented by 1 super-mutant	10	19 1 3.7
Mutations represented by 2 super-mutants	8	5.8 1 2.3
Mutations represented by 3 super-mutants	4	1.3 1 1.1
Mutations represented by 4 super-mutants	4	1.8 1 1.3
Mutations represented by 5 super-mutants	2	0.61 1 0.75
Mutations represented by 6 super-mutants	2	0.22 1 0.44
Mutations represented by 7 super-mutants	0	0.01 1 0.10
Mutations represented by 8 super-mutants	0	0.87 1 0.86
Mutations represented by 9 super-mutants	2	0.28 1 0.51
Mutations represented by 10 super-mutants	0	0.14 1 0.38
Mutations represented by >10 super-mutants	3	1.5 1 2.7
Distinct mutations	35	32 1 4.2
B. Experiment 2		
Mutations represented by 1 super-mutant	19	23 1 4.1
Mutations represented by 2 super-mutants	5	9.5 1 2.8
Mutations represented by 3 super-mutants	4	2.7 1 1.6
Mutations represented by 4 super-mutants	7	2.7 1 1.7
Mutations represented by 5 super-mutants	2	0.88 1 0.94
Mutations represented by 6 super-mutants	1	0.40 1 0.60
Mutations represented by 7 super-mutants	3	0.16 1 0.42
Mutations represented by 8 super-mutants	1	0.99 1 1.0
Mutations represented by 9 super-mutants	1	0.39 1 0.68
Mutations represented by 10 super-mutants	0	0.17 1 0.43
Mutations represented by >10 super-mutants	9	1.8 1 3.4
Distinct mutations	52	43 1 5.1
C. Experiment 3		
Mutations represented by 1 super-mutant	7	17 1 3.4
Mutations represented by 2 super-mutants	9	5.4 1 2.0
Mutations represented by 3 super-mutants	4	1.2 1 1.1
Mutations represented by 4 super-mutants	4	1.7 1 1.4
Mutations represented by 5 super-mutants	2	0.50 1 0.70
Mutations represented by 6 super-mutants	0	0.17 1 0.45
Mutations represented by 7 super-mutants	1	0.03 1 0.17
Mutations represented by 8 super-mutants	0	0.59 1 0.74
Mutations represented by 9 super-mutants	0	0.24 1 0.50
Mutations represented by 10 super-mutants	1	0.07 1 0.29
Mutations represented by >10 super-mutants	5	1.5 1 2.6
Distinct mutations	33	28 1 3.7

Table55.txt

D. Experiment 4		
Mutations represented by 1 super-mutant	7	15 1 3.7
Mutations represented by 2 super-mutants	8	4.1 1 1.7
Mutations represented by 3 super-mutants	2	0.70 1 0.74
Mutations represented by 4 super-mutants	1	1.5 1 1.3
Mutations represented by 5 super-mutants	3	0.21 1 0.52
Mutations represented by 6 super-mutants	2	0.08 1 0.27
Mutations represented by 7 super-mutants	1	0.0 1 0.0
Mutations represented by 8 super-mutants	2	0.65 1 0.77
Mutations represented by 9 super-mutants	2	0.17 1 0.43
Mutations represented by 10 super-mutants	0	0.05 1 0.22
Mutations represented by >10 super-mutants	1	0.92 1 2.1
Distinct mutations	29	23 1 3.2
E. Experiment 5		
Mutations represented by 1 super-mutant	9	23 1 4.1
Mutations represented by 2 super-mutants	6	9.5 1 2.8
Mutations represented by 3 super-mutants	5	2.7 1 1.6
Mutations represented by 4 super-mutants	3	2.7 1 1.7
Mutations represented by 5 super-mutants	6	0.88 1 0.94
Mutations represented by 6 super-mutants	2	0.40 1 0.60
Mutations represented by 7 super-mutants	1	0.16 1 0.42
Mutations represented by 8 super-mutants	2	0.99 1 1.0
Mutations represented by 9 super-mutants	2	0.39 1 0.68
Mutations represented by 10 super-mutants	3	0.17 1 0.43
Mutations represented by >10 super-mutants	7	1.8 1 3.4
Distinct mutations	46	43 1 5.1
F. Experiment 6		
Mutations represented by 1 super-mutant	4	6.7 1 2.8
Mutations represented by 2 super-mutants	7	1.5 1 1.2
Mutations represented by 3 super-mutants	1	0.10 1 0.33
Mutations represented by 4 super-mutants	2	0.60 1 0.82
Mutations represented by 5 super-mutants	0	0.07 1 0.26
Mutations represented by 6 super-mutants	0	0.01 1 0.10
Mutations represented by 7 super-mutants	1	0.0 1 0.0
Mutations represented by 8 super-mutants	1	0.39 1 0.60
Mutations represented by 9 super-mutants	0	0.01 1 0.10
Mutations represented by 10 super-mutants	0	0.0 1 0.0
Mutations represented by >10 super-mutants	2	0.50 1 1.1
Distinct mutations	18	9.9 1 1.4
G. Experiment 7		
Mutations represented by 1 super-mutant	8	2.9 1 1.6
Mutations represented by 2 super-mutants	2	0.61 1 0.79

Table55.txt

Mutations represented by 3 super-mutants	0	0.04	1	0.24
Mutations represented by 4 super-mutants	0	0.41	1	0.59
Mutations represented by 5 super-mutants	1	0.01	1	0.10
Mutations represented by 6 super-mutants	0	0.0	1	0.0
Mutations represented by 7 super-mutants	0	0.0	1	0.0
Mutations represented by 8 super-mutants	0	0.14	1	0.35
Mutations represented by 9 super-mutants	0	0.01	1	0.10
Mutations represented by 10 super-mutants	0	0.0	1	0.0
Mutations represented by >10 super-mutants	0	0.32	1	0.93
Distinct mutations	11	4.5	1	0.62

*See Application Text for details of the simulations

Table56.txt

Table 56. Phosphoramidite- vs Phusion-Synthesized DNA: Transitions vs Transversions Comparison

Phosphoramidites	Exp. 1	Exp. 2	Exp. 3	Exp. 4	Exp. 5	Exp. 6	Exp. 7	Average	Standard Deviation
Transition super-mutants:	496	509	471	396	323	273	470	420	92
Transversion super-mutants:	1494	1499	1521	1154	944	907	1626	1306	298
p-value*	3.40E-05								
Phusion									
Transition super-mutants:	63	275	127	5	87	182	103	120	87
Transversion super-mutants:	14	124	77	12	57	191	63	77	63
p-value*	0.08								

*p-values were calculated using a two-tailed paired t-test

Table57.txt

Table 57. Oligonucleotides Used

Font Legend:
REGION COMPLEMENTARY TO TEMPLATES
TEMPLATE-SPECIFIC UID SEQUENCE
UNIVERSAL SEQUENCE
EXPERIMENT-SPECIFIC INDEX SEQUENCE
ILLUMINA GRAFTING PRIMERS (FOR HYBRIDIZATION TO FLOW CELL)

Symbol Legend:
/5Phos/ = 5' Phosphate
* = Phosphorothioate linkage

Endogenous UIDs

Capture	Sequence	SEQ ID NO
Adapter - strand 1	/5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG	810
Adapter - strand 2	ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	811
Whole Genome Amplification - for	AATGATACGGCGACCACCGAGATCTACACACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	812
Whole Genome Amplification - rev	CAAGCAGAAGACGGCATACGAGATCTCGGCATTCCTGCTGAACCGCTCTTCCGAT*C*T	813
Post-Capture Amplification - for	AATGATACGGCGACCACCGAGATCTACACACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	814
Post-Capture Amplification - rev	CAAGCAGAAGACGGCATACGAGATCTCGGCATTCCTGCTGAACCGCTCTTCCGAT*C*T	815
Sequencing Primer, Read 1 (Illumina; San Diego, CA)	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	816
Sequencing Primer, Read 2 (Illumina; San Diego, CA)	CTCGGCATTCCTGCTGAACCGCTCTTCCGATCT	817

Inverse PCR

Adapter - strand 1	/5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG	818
Adapter - strand 2	ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	819
Whole Genome Amplification - for-1	/5Phos/CGTGATACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	820
Whole Genome Amplification - for-2	/5Phos/ACATCGACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T	

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821
Whole Genome Amplification - for-3
/5Phos/GCCTAAACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
822
Whole Genome Amplification - for-4
/5Phos/TGGTCAACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
823
Whole Genome Amplification - for-5
/5Phos/CACTGTACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
824
Whole Genome Amplification - for-6
/5Phos/ATTGGCACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
825
Whole Genome Amplification - for-7
/5Phos/GATCTGACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
826
Whole Genome Amplification - for-8
/5Phos/TCAAGTACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
827
Whole Genome Amplification - for-9
/5Phos/CTGATCACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
828
Whole Genome Amplification - for-10
/5Phos/AAGCTAACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
829
Whole Genome Amplification - for-11
/5Phos/GTAGCCACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
830
Whole Genome Amplification - for-12
/5Phos/TACAAGACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
831
Whole Genome Amplification - rev
/5Phos/CTCGGCATTCCTGCTGAACCGCTCTTCCGAT*C*T
832
Inverse PCR - antisense
AATGATACGGCGACCACCGAGATCTACACCAGCAGGCCTTATAATAAAAATAATGA
833
Inverse PCR - for
CAAGCAGAAGACGGCATACGAGATTGACTGAATATAAACTTGTGGTAGTTG
834
Sequencing Primer 1 (to read internal sequences)
ACACTCTTTCCCTACACGACGCTCTTCCGATCT
835
Sequencing Primer 2 (to read internal sequences)
CTCGGCATTCCTGCTGAACCGCTCTTCCGATCT
836
Index Primer 1 (to read experiment indexes) CGGAAGAGCGTCGTGTAGGGAAAGAGTGT
837

Table57.txt

Index Primer 2 (to read experiment indexes)	CGGAAGAGCGGTTCAGCAGGAATGCCGAG 838
Exogenous UIDs	
Polymerase Fidelity	
Digital PCR Amplification - for	GGTTACAGGCTCATGATGTAACC 839
Digital PCR Amplification - rev	GATACCAGCTTGGTAATGGCA 840

UID Assignment Amplification - for
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNGGTTACAGGCTCATGATGTAACC
841

UID Assignment Amplification - rev
CACACAGGAAACAGCTATGACCATGGATACCAGCTTGGTAATGGCA
842

Library Amplification - for-1
AATGATACGGCGACCACCGAGATCTACACCGTGATCGACGTAAAACGACGGCCA*G*T
843

Library Amplification - for-2
AATGATACGGCGACCACCGAGATCTACACACATCGCGACGTAAAACGACGGCCA*G*T
844

Library Amplification - for-3
AATGATACGGCGACCACCGAGATCTACACGCCTAACGACGTAAAACGACGGCCA*G*T
845

Library Amplification - for-4
AATGATACGGCGACCACCGAGATCTACACTGGTCACGACGTAAAACGACGGCCA*G*T
846

Library Amplification - for-5
AATGATACGGCGACCACCGAGATCTACACCACTGTCGACGTAAAACGACGGCCA*G*T
847

Library Amplification - for-6
AATGATACGGCGACCACCGAGATCTACACATTGGCCGACGTAAAACGACGGCCA*G*T
848

Library Amplification - for-7
AATGATACGGCGACCACCGAGATCTACACGATCTGCGACGTAAAACGACGGCCA*G*T
849

Library Amplification - for-8
AATGATACGGCGACCACCGAGATCTACACTCAAGTCGACGTAAAACGACGGCCA*G*T
850

Library Amplification - for-9
AATGATACGGCGACCACCGAGATCTACACCTGATCCGACGTAAAACGACGGCCA*G*T
851

Library Amplification - for-10
AATGATACGGCGACCACCGAGATCTACACAAGCTACGACGTAAAACGACGGCCA*G*T
852

Library Amplification - rev
CAAGCAGAAGACGGCATACGAGATCACACAGGAAACAGCTATGACCA*T*G
853

Table57.txt

Sequencing Primer (to read UID and internal sequences)CGACGTAAAACGACGGCCAGT
854
Index Primer (to read experiment indexes) ACTGGCCGTCGTTTTACGTCG
855

CTNNB1 mutations in DNA from normal human cells
UID Assignment Amplification - for
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGCAGCAACAGTCTTACCTGGACT
856
UID Assignment Amplification - rev
CACACAGGAAACAGCTATGACCATGTCCACATCCTCTTCCTCAGGATT
857
Library Amplification - for
AATGATACGGCGACCACCGAGATCTACACCGACGTAAAACGACGGCCA*G*T
858
Library Amplification - rev-1
CAAGCAGAAGACGGCATACGAGATATCACGCACACAGGAAACAGCTATGACCA*T*G
859
Library Amplification - rev-2
CAAGCAGAAGACGGCATACGAGATCGATGTCACACAGGAAACAGCTATGACCA*T*G
860
Library Amplification - rev-3
CAAGCAGAAGACGGCATACGAGATTGACCACACACAGGAAACAGCTATGACCA*T*G
861
Library Amplification - rev-4
CAAGCAGAAGACGGCATACGAGATGCCAATCACACAGGAAACAGCTATGACCA*T*G
862
Library Amplification - rev-5
CAAGCAGAAGACGGCATACGAGATCAGATCCACACAGGAAACAGCTATGACCA*T*G
863
Library Amplification - rev-6
CAAGCAGAAGACGGCATACGAGATACTTGACACACAGGAAACAGCTATGACCA*T*G
864
Library Amplification - rev-7
CAAGCAGAAGACGGCATACGAGATGATCAGCACACAGGAAACAGCTATGACCA*T*G
865
Library Amplification - rev-8
CAAGCAGAAGACGGCATACGAGATTAGCTTCACACAGGAAACAGCTATGACCA*T*G
866
Library Amplification - rev-9
CAAGCAGAAGACGGCATACGAGATGGCTACCACACAGGAAACAGCTATGACCA*T*G
867
Library Amplification - rev-10
CAAGCAGAAGACGGCATACGAGATCTTGTACACACAGGAAACAGCTATGACCA*T*G
868
Sequencing Primer (to read UID and internal sequences)CGACGTAAAACGACGGCCAGT
869
Index Primer (to read experiment indexes) CATGGTCATAGCTGTTTCCTGTGTG

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870

Mitochondrial mutations in DNA from normal human cells
UID Assignment Amplification - for
CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNTTACCGAGAAAGCTCACAAGAA
871
UID Assignment Amplification - rev
CACACAGGAAACAGCTATGACCATGATGCTAAGGCGAGGATGAAA
872
Library Amplification - for-1
AATGATACGGCGACCACCGAGATCTACACACATCGCGACGTAAAACGACGGCCA*G*T
873
Library Amplification - for-2
AATGATACGGCGACCACCGAGATCTACACGCCTAACGACGTAAAACGACGGCCA*G*T
874
Library Amplification - for-3
AATGATACGGCGACCACCGAGATCTACACTGGTCACGACGTAAAACGACGGCCA*G*T
875
Library Amplification - for-4
AATGATACGGCGACCACCGAGATCTACACATTGGCCGACGTAAAACGACGGCCA*G*T
876
Library Amplification - for-5
AATGATACGGCGACCACCGAGATCTACACGATCTGCGACGTAAAACGACGGCCA*G*T
877
Library Amplification - for-6
AATGATACGGCGACCACCGAGATCTACACTCAAGTCGACGTAAAACGACGGCCA*G*T
878
Library Amplification - for-7
AATGATACGGCGACCACCGAGATCTACACCTGATCCGACGTAAAACGACGGCCA*G*T
879
Library Amplification - rev
CAAGCAGAAGACGGCATACGAGATCACACAGGAAACAGCTATGACCA*T*G
880
Sequencing Primer 1 (to read UIDs) CGACGTAAAACGACGGCCAGT
881
Sequencing Primer 2 (to read internal sequences) CCTAATTCCCCCCATCCTTAC
882
Index Primer (to read experiment indexes) ACTGGCCGTCGTTTTACGTCG
883

Analysis of Phosphoramidite Oligonucleotide Composition
Synthesized template, wt
GGTTACAGGCTCATGATGTAACCTCTGTGTCTTGGTGTAACTTTAAAACATATTTTTGCCATTACCAAGCTGGTATC
884
Synthesized template, mut (S = 50/50 mix of C and G)
GGTTACAGGCTCATGATGTAACCTCTGTGTCTTGGTGSAACTTTAAAACATATTTTTGCCATTACCAAGCTGGTATC
885
UID Assignment Amplification - for

Table57.txt

ACACTCTTTCCCTACACGACGCTCNNNNNNNNNNNNGGTGAGTCTGTGCAGGCAT
886
UID Assignment Amplification - rev
CTCGAGCACTGTCCTGACTGAGACGATACCAGCTTGGTAATGGCA
887
Library Amplification - for
AATGATACGGCGACCACCGAGATCTACACCGTGATACACTCTTTCCCTACACGACGC*T*C
888
Library Amplification - rev
CAAGCAGAAGACGGCATACGAGATCTCGAGCACTGTCCTGACTGAG*A*C
889
Sequencing Primer (to read UID and internal sequences)ACACTCTTTCCCTACACGACGCTC
890

Table58.txt

Table 58. Rules for tissue recognition extracted from the random forest model

condition	pred
CA125>102.76 & sFas<=830.345 & gender %in% c('F')	Ovarian
CA199>37.65 & CYFRA211<=14640.67 & CD44>15.67 & Midkine>289.485 & PAR>4580.45 & sHER2>6935.375	Pancreas
AFP>17774.49 & TIMP2<=61777.34 & Galectin3<=16.72 & Mesothelin<=27.71	Liver
CA199<=71.53 & Leptin>12927.9 & sFas>411.525 & TIMP1<=59700.835 & TIMP2<=37667.97 & gender %in% c('F')	Breast
CA125<=104.41 & CA153<=16.22 & CA199<=117.275 & HGF<=465.81 & Leptin<=7244.265 & SHBG>29.53	CRC
Prolactin>37214.25 & sFas>1046.435 & TIMP1<=93517.645 & DKK1<=1.095 & sHER2<=6054.825 & gender %in% c('M')	Lung
CA153<=15.285 & IL8>39.235 & IL8<=163.64 & sFas<=1098.015 & Myeloperoxidase>19.325 & sHER2<=5172.43	st_eso
AFP<=2867.07 & CA153>9.505 & Prolactin>37962.925 & sFas>688.47 & Myeloperoxidase<=11.935 & Thrombospondin2<=3273.685	Lung
AFP<=36492.58 & CA125<=10.475 & Prolactin<=275955.405 & sFas<=1351.39 & AXL>1999.77 & sHER2<=10172.47	CRC
CEA<=1892.955 & sFas<=1076.05 & TIMP2>40306.87 & CD44<=26.915 & sHER2<=9959.43 & gender %in% c('F')	Ovarian
Leptin<=5186.325 & OPN>94670.57 & TIMP1>75617.725 & SHBG<=141.115 & sHER2<=8369.265 & Thrombospondin2<=17040.89	st_eso
AFP<=40375.115 & CA153<=20.835 & CEA>3057.27 & Leptin<=237948.935 & OPN<=250628.405 & TIMP2<=68136.905	CRC
AFP<=299906.424 & sFas>1100.55 & TIMP1<=85064.65 & TIMP2<=53195.905 & DKK1<=1.285 & gender %in% c('F')	Breast
Leptin>8839.01 & sFas<=1745.34 & TIMP1>63205.505 & CD44<=19.735 & Mesothelin<=39.705 & gender %in% c('F')	CRC
AFP<=5369.16 & CA153<=16.21 & CEA>1374.755 & Myeloperoxidase<=368.56 & Midkine<=4401.495 & sHER2<=10713.16	CRC
TIMP2<=61631.2 & Myeloperoxidase>23.725 & SHBG<=96.985 & DKK1<=1.335 & Midkine<=348.515 & sHER2<=5523.84	st_eso
CA125<=56.21 & HGF<=928.54 & Prolactin>65977.55 & sFas<=2849.195 & Mesothelin>13.68 & AXL<=2093.75	Lung
CA199<=36.795 & CEA<=115717.2 & HE4<=15657.71 & Leptin>15287.95 & sFas>716.205 & gender %in% c('F')	Breast
Else	CRC

Table59.txt

Table 59. CancerSEEK tests complement each other

Official	Official Name	CancerSeek Neoadjuvant (Postive/Negative)	Aneuploidy Result (Postive/Negative Adjuvant at 99% Specificity)	Genome Wide Aneuploidy Score	Cancer	Histopathology	Stage	Grade	Treatment	Treatment
PANC 303	PANC 303 PLS	#N/A	Negative	0.57626	Pancreas	Adenocarcinoma	IV	NA	No	No
PANC 304	PANC 304 PLS	#N/A	Negative	0.08806	Pancreas	Adenocarcinoma	IB	3	No	No
PANC 305	PANC 305 PLS	#N/A	Positive	0.78591	Pancreas	Adenocarcinoma	IIB	2	No	No
PANC 306	PANC 306 PLS	#N/A	Negative	0.32406	Pancreas	Adenocarcinoma	IV	2	Yes	No
PANC 307	PANC 307 PLS	#N/A	Negative	0.01861	Pancreas	Adenocarcinoma	IV	2	Yes	No
PANC 308	PANC 308 PLS	#N/A	Negative	0.01696	Pancreas	Adenocarcinoma	III	3	No	No
PANC 323	PANC 323 PLS1	#N/A	Positive	0.61882	Pancreas	Adenocarcinoma	IIB	3	No	No
PANC 333	PANC 333 PLS1	#N/A	Negative	0.07737	Pancreas	Adenocarcinoma	IIB	3	No	No
PANC 335	PANC 335 PLS1	#N/A	Negative	0.04829	Pancreas	Adenocarcinoma	IIB	3	No	No
PANC 336	PANC 336 PLS1	#N/A	Negative	0.29898	Pancreas	Adenocarcinoma	IIB	2	No	No
PANC 336	PANC 336 PLS 2	#N/A	Positive	0.80988	Pancreas	Adenocarcinoma	IIB	2	No	No
PANC 339	PANC 339 PLS1	#N/A	Negative	0.28375	Pancreas	Adenocarcinoma	IIB	3	No	No
PANC 339	PANC 339 PLS 2	#N/A	Positive	0.81002	Pancreas	Adenocarcinoma				

Table59.txt

IIB 3 No No
PANC 343 PANC 343 PLS 1 #N/A Negative
0.05096 Pancreas Adenocarcinoma
IV NA No No
PANC 344 PANC 344 PLS1 #N/A Negative
0.32738 Pancreas Adenocarcinoma
IV NA Yes No
PANC 345 PANC 345 PLS1 #N/A Negative
0.12341 Pancreas Adenocarcinoma
IIA 2 No No
PANC 346 PANC 346 PLS1 #N/A Negative
0.05190 Pancreas Adenocarcinoma
IIB 2 No No
PANC 347 PANC 347 PLS1 #N/A Negative
0.11426 Pancreas adenocarcinoma
IIB 2 No No
PANC 348 PANC 348 PLS1 #N/A Negative
0.05639 Pancreas Adenocarcinoma
IIB 3 No No
PANC 349 PANC 349 PLS1 #N/A Negative
0.28613 Pancreas Adenocarcinoma
IIB 2 No No
PANC 350 PANC 350 PLS1 #N/A Negative
0.06007 Pancreas cholangiocarcinoma
IIB 2 No No
PANC 352 PANC 352 PLS1 #N/A Negative
0.32801 Pancreas Adenocarcinoma
IIA 2 No No
PANC 353 PANC 353 PLS1 #N/A Negative
0.54425 Pancreas Adenocarcinoma
IIA 3 No No
PANC 354 PANC 354 PLS1 #N/A Negative
0.15818 Pancreas NA
NA NA No No
PANC 355 PANC 355 PLS1 #N/A Negative
0.06384 Pancreas Adenocarcinoma
IIB 2 No No
PANC 356 PANC 356 PLS1 #N/A Negative
0.13274 Pancreas NA
NA NA No No
PANC 357 PANC 357 PLS1 #N/A Negative
0.15339 Pancreas Adenocarcinoma
IV 2 No No
PANC 358 PANC 358 PLS1 #N/A Negative
0.10841 Pancreas Adenocarcinoma
IIB 2 No No
PANC 359 PANC 359 PLS1 #N/A Negative
0.41113 Pancreas adenocarcinoma

Table59.txt

IIB 3 No No
PANC 361 PANC 361 PLS1 #N/A Positive
1.00000 Pancreas NA
NA NA No No
PANC 362 PANC 362 PLS1 #N/A Negative
0.10634 Pancreas NA
NA NA No No
PANC 363 PANC 363 PLS1 #N/A Negative
0.18515 Pancreas NA
NA NA No No
PANC 364 PANC 364 PLS1 #N/A Negative
0.18855 Pancreas Adenocarcinoma
IV NA No No
PANC 372 PANC 372 PLS #N/A Negative
0.01852 Pancreas Adenocarcinoma
III NA No No
PANC 373 PANC 373 PLS #N/A Positive
0.74800 Pancreas Adenocarcinoma
IB NA No No
PANC 375 PANC 375 PLS #N/A Negative
0.48355 Pancreas NA
NA NA No No
PANC 376 PANC 376 PLS #N/A Positive
0.74926 Pancreas NA
NA NA No No
PANC 377 PANC 377 PLS #N/A Negative
0.39875 Pancreas NA
NA NA No No
PANC 378 PANC 378 PLS #N/A Negative
0.42663 Pancreas Adenocarcinoma
IV NA No No
PANC 381 PANC 381 PLS #N/A Positive
0.77486 Pancreas NA
NA NA No No
PANC 382 PANC 382 PLS #N/A Negative
0.46863 Pancreas NA
NA NA No No
PANC 383 PANC 383 PLS #N/A Negative
0.05065 Pancreas NA
NA NA No No
PANC 384 PANC 384 PLS #N/A Negative
0.24653 Pancreas NA
NA NA No No
PANC 385 PANC 385 PLS #N/A Negative
0.44139 Pancreas NA
NA NA No No
PANC 386 PANC 386 PLS #N/A Negative
0.19829 Pancreas Adenocarcinoma

Table59.txt

IB	NA				Yes	No			
PANC 387		PANC 387 PLS		#N/A		Negative			
0.20822		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 388		PANC 388 PLS		#N/A		Positive			
0.63691		Pancreas		NA					
NA	NA				No	No			
PANC 389		PANC 389 PLS		#N/A		Negative			
0.20227		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 390		PANC 390 PLS		#N/A		Negative			
0.05308		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 391		PANC 391 PLS		#N/A		Negative			
0.57315		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 392		PANC 392 PLS		#N/A		Negative			
0.01162		Pancreas		NA					
NA	NA				No	No			
PANC 393		PANC 393 PLS 1		#N/A		Negative			
0.29474		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 394		PANC 394 PLS 1		#N/A		Negative			
0.04107		Pancreas		Adenocarcinoma					
IIA	3				No	No			
PANC 395		PANC 395 PLS 1		#N/A		Negative			
0.08918		Pancreas		Adenocarcinoma					
IA	3				No	No			
PANC 396		PANC 396 PLS 1		#N/A		Positive			
0.73578		Pancreas		Adenocarcinoma					
IA	2				No	No			
PANC 397		PANC 397 PLS 1		#N/A		Negative			
0.19877		Pancreas		Adenocarcinoma					
IV	NA				No	No			
PANC 398		PANC 398 PLS 1		#N/A		Negative			
0.13617		Pancreas		Adenocarcinoma					
IV	3				No	No			
PANC 399		PANC 399 PLS 1		#N/A		Negative			
0.31227		Pancreas		Adenocarcinoma					
IV	3				No	No			
PANC 400		PANC 400 PLS 1		#N/A		Negative			
0.15411		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 401		PANC 401 PLS 1		#N/A		Negative			
0.12399		Pancreas		NA					
NA	NA				No	No			
PANC 402		PANC 402 PLS 1		#N/A		Negative			
0.10068		Pancreas		Adenocarcinoma					

Table59.txt

```
   IIB      3                          No              No
PANC 403          PANC 403 PLS 1     #N/A               Negative
0.05177         Pancreas      Adenocarcinoma
   IB       2                          No              No
PANC 404          PANC 404 PLS 1     #N/A               Negative
0.03241         Pancreas      Adenocarcinoma
   IIA      2                          No              No
PANC 405          PANC 405 PLS 1     #N/A               Negative
0.59228         Pancreas      Adenocarcinoma
   IV       NA                         No              No
PANC 406          PANC 406 PLS 1     #N/A               Negative
0.06764         Pancreas      Adenocarcinoma
   IB       2                          No              No
PANC 407          PANC 407 PLS 1     #N/A               Negative
0.08242         Pancreas      Adenocarcinoma
   IB       1                          No              No
PANC 408          PANC 408 PLS 1     #N/A               Negative
0.29797         Pancreas      NA
   NA       NA                         No              No
PANC 409          PANC 409 PLS 1     #N/A               Negative
0.04739         Pancreas      Adenocarcinoma
   IB       2                          No              No
PANC 417          PANC 417 PLS       #N/A               Negative
0.25583         Pancreas      Adenocarcinoma
   IV       NA                         No              No
PANC 418          PANC 418 PLS       #N/A               Negative
0.02742         Pancreas      Adenocarcinoma
   IIA      Well differentiated        No              No
PANC 419          PANC 419 PLS       #N/A               Positive
0.62104         Pancreas      Adenocarcinoma
   IV       NA                         No              No
PANC 420          PANC 420 PLS       #N/A               Negative
0.09079         Pancreas      Adenocarcinoma
   IIB      moderate to poorly differentNo             No
PANC 421          PANC 421 PLS       #N/A               Negative
0.52414         Pancreas      Adenocarcinoma
   IV       NA                         No              No
PANC 422          PANC 422 PLS       #N/A               Positive
0.62310         Pancreas      Adenocarcinoma
   IIB      poorly differentiated      No              No
PANC 423          PANC 423 PLS       #N/A               Positive
0.84895         Pancreas      Adenocarcinoma
   IIA      Moderately differentiated  No              No
PANC 424          PANC 424 PLS       #N/A               Negative
0.09550         Pancreas      Adenocarcinoma
   IIA      poorly differentiated      Yes             No
PANC 425          PANC 425 PLS       #N/A               Negative
0.10377         Pancreas      Adenocarcinoma
```

Table59.txt

IIB Moderately differentiated No No
PANC 426 PANC 426 PLS #N/A Negative
0.28264 Pancreas Adenocarcinoma
locally unresectable pancreatic adenoNo No
PANC 427 PANC 427 PLS #N/A Negative
0.04751 Pancreas Adenocarcinoma
IIA Moderately differentiated No No
PANC 428 PANC 428 PLS #N/A Positive
0.80073 Pancreas Adenocarcinoma
IIB or IVModerately differentiated No No
PANC 429 PANC 429 PLS #N/A Positive
0.78076 Pancreas Adenocarcinoma
locally unresectable pancreatic adenoNo No
PANC 430 PANC 430 PLS #N/A Negative
0.13889 Pancreas Adenocarcinoma
IV poorly differentiated No No
PANC 431 PANC 431 PLS #N/A Negative
0.10279 Pancreas Adenocarcinoma
IV Moderately differentiated Yes No
PANC 432 PANC 432 PLS #N/A Negative
0.31366 Pancreas Adenocarcinoma
IIA Moderately differentiated Yes No
PANC 433 PANC 433 PLS #N/A Negative
0.05198 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANC 434 PANC 434 PLS #N/A Negative
0.10902 Pancreas Adenocarcinoma
NA NA No No
PANC 435 PANC 435 PLS #N/A Negative
0.39447 Pancreas Adenocarcinoma
IIB poorly differentiated No No
PANC 436 PANC 436 PLS #N/A Negative
0.18780 Pancreas Adenocarcinoma
IV Poorly differentiated No No
PANC 437 PANC 437 PLS #N/A Positive
0.70164 Pancreas Adenocarcinoma
IB Well differentiated No No
PANC 438 PANC 438 PLS #N/A Negative
0.25838 Pancreas Adenocarcinoma
IIA Moderately differentiated No No
PANC 439 PANC 439 PLS #N/A Negative
0.22659 Pancreas Adenocarcinoma
IA Well differentiated No No
PANC 440 PANC 440 PLS #N/A Negative
0.32853 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANC 441 PANC 441 PLS #N/A Negative
0.36779 Pancreas Adenocarcinoma

Table59.txt

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   IIB      poorly differentiated       No              No
PANC 442          PANC 442 PLS       #N/A               Negative
0.27618         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANC 443          PANC 443 PLS       #N/A               Negative
0.21184         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANC 444          PANC 444 PLS       #N/A               Negative
0.53160         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 445          PANC 445 PLS       #N/A               Negative
0.37994         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 446          PANC 446 PLS       #N/A               Negative
0.11076         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 447          PANC 447 PLS       #N/A               Negative
0.48583         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 448          PANC 448 PLS       #N/A               Positive
0.70740         Pancreas      Adenocarcinoma
   IIA      poorly differentiated       No              No
PANC 449          PANC 449 PLS       #N/A               Positive
0.67483         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 450          PANC 450 PLS       #N/A               Positive
0.83966         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANC 451          PANC 451 PLS       #N/A               Negative
0.21690         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 452          PANC 452 PLS       #N/A               Negative
0.09063         Pancreas      Adenocarcinoma
   IIA      poorly differentiated       No              No
PANC 453          PANC 453 PLS       #N/A               Negative
0.43391         Pancreas      Adenocarcinoma
   IIA      Moderately differentiated   Yes             No
PANC 454          PANC 454 PLS       #N/A               Positive
0.60171         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 455          PANC 455 PLS       #N/A               Negative
0.15961         Pancreas      adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 456          PANC 456 PLS       #N/A               Negative
0.12512         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANC 457          PANC 457 PLS       #N/A               Negative
0.08761         Pancreas      Adenocarcinoma
```

Table59.txt

IIB Moderately differentiated No No
PANC 458 PANC 458 PLS #N/A Negative
0.19066 Pancreas Adenocarcinoma
IIA Moderately differentiated No No
PANC 459 PANC 459 PLS1 #N/A Negative
0.18441 Pancreas NA
NA NA No No
PANC 462 PANC 462 PLS1 #N/A Positive
0.64829 Pancreas Adenocarcinoma
IV NA No No
PANC 463 PANC 463 PLS1 #N/A Negative
0.09908 Pancreas Adenocarcinoma
IIB 3 No No
PANC 464 PANC 464 PLS1 #N/A Positive
0.73067 Pancreas Adenocarcinoma
IB 3 No No
PANC 465 PANC 465 PLS1 #N/A Negative
0.40222 Pancreas Adenocarcinoma
IIB 3 No No
PANC 466 PANC 466 PLS1 #N/A Negative
0.18171 Pancreas Adenocarcinoma
IIB 2 No No
PANC 467 PANC 467 PLS1 #N/A Negative
0.18895 Pancreas Adenocarcinoma
IIB 2 No No
PANC 468 PANC 468 PLS1 #N/A Negative
0.40014 Pancreas Adenocarcinoma
IIB 3 No No
PANC 469 PANC 469 PLS1 #N/A Negative
0.27993 Pancreas Adenocarcinoma
IIB 3 No No
PANC 470 PANC 470 PLS1 #N/A Negative
0.07469 Pancreas Adenocarcinoma
IA 2 No No
PANC 471 PANC 471 PLS1 #N/A Negative
0.21777 Pancreas Adenocarcinoma
IIB 2 No No
PANC 472 PANC 472 PLS1 #N/A Negative
0.15648 Pancreas Adenocarcinoma
IV NA No No
PANC 473 PANC 473 PLS 1 #N/A Negative
0.06966 Pancreas NA
NA NA No No
PANC 489 PANC 489 PLS 1 #N/A Negative
0.11086 Pancreas adenocarcinoma
IIB 3 No No
PANC 489 PANC 489 PLS 2 #N/A Negative
0.31693 Pancreas adenocarcinoma

Table59.txt

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   IIB      3                          No              No
PANC 496          PANC 496 PLS 1     #N/A               Negative
0.33122         Pancreas      Adenocarcinoma
   IIB      1                          No              No
PANC 496          PANC 496 PLS 2     #N/A               Negative
0.37125         Pancreas      Adenocarcinoma
   IIB      1                          No              No
PANC 496          PANC 496 PLS 3     #N/A               Negative
0.36133         Pancreas      Adenocarcinoma
   IIB      1                          No              No
PANC 498          PANC 498 PLS 1     #N/A               Negative
0.54162         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 498          PANC 498 PLS 2     #N/A               Negative
0.14922         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 500          PANC 500 PLS 1     #N/A               Positive
0.76841         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 500          PANC 500 PLS 2     #N/A               Positive
0.84293         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 500          PANC 500 PLS 3     #N/A               Positive
0.82012         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 502          PANC 502 PLS 1     #N/A               Negative
0.20065         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 502          PANC 502 PLS 2     #N/A               Negative
0.42074         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 502          PANC 502 PLS 3     #N/A               Negative
0.23142         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 505          PANC 505 PLS 1     #N/A               Negative
0.05133         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 505          PANC 505 PLS 2     #N/A               Positive
0.76069         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 505          PANC 505 PLS 3     #N/A               Positive
0.81154         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 508          PANC 508 PLS 1     #N/A               Negative
0.08250         Pancreas      Adenocarcinoma
   IIA      1                          No              No
PANC 508          PANC 508 PLS 2     #N/A               Negative
0.01460         Pancreas      Adenocarcinoma
```

Table59.txt

IIA 1 No No
PANC 508 PANC 508 PLS 3 #N/A Negative
0.17912 Pancreas Adenocarcinoma
IIA 1 No No
PANC 511 PANC 511 PLS 1 #N/A Negative
0.52947 Pancreas Adenocarcinoma
IIB 2 No No
PANC 511 PANC 511 PLS 2 #N/A Positive
0.80723 Pancreas Adenocarcinoma
IIB 2 No No
PANC 511 PANC 511 PLS 3 #N/A Positive
0.81229 Pancreas Adenocarcinoma
IIB 2 No No
PANC 514 PANC 514 PLS 1 #N/A Negative
0.18782 Pancreas Adenocarcinoma
IA 2 No No
PANC 515 PANC 515 PLS 1 #N/A Negative
0.58286 Pancreas Adenocarcinoma
IIB 3 No No
PANC 515 PANC 515 PLS 2 #N/A Positive
0.73949 Pancreas Adenocarcinoma
IIB 3 No No
PANC 515 PANC 515 PLS 3 #N/A Positive
0.60757 Pancreas Adenocarcinoma
IIB 3 No No
PANC 522 PANC 522 PLS 2 #N/A Negative
0.17036 Pancreas NA
NA NA No No
PANC 526 PANC 526 PLS 2 #N/A Negative
0.45232 Pancreas NA
NA NA No No
PANC 527 PANC 527 PLS 2 #N/A Positive
0.61334 Pancreas NA
NA NA No No
PANC 529 PANC 529 PLS 2 #N/A Negative
0.01128 Pancreas Adenocarcinoma
IIA Poor No No
PANC 530 PANC 530 PLS 2 #N/A Negative
0.50723 Pancreas NA
NA NA No No
PANC 531 PANC 531 PLS 2 #N/A Negative
0.41367 Pancreas Adenocarcinoma
III Poor-Moderate No No
PANC 681 PANC 681 PLS 1 #N/A Negative
0.03804 Pancreas Adenocarcinoma
IIB G2 No No
PANC 682 PANC 682 PLS 1 #N/A Negative
0.45444 Pancreas Adenocarcinoma

Table59.txt

IIB G2 No No
PANC 683 PANC 683 PLS 1 #N/A Positive
0.77469 Pancreas Adenocarcinoma
IIB G3 No No
PANC 684 PANC 684 PLS 1 #N/A Negative
0.05925 Pancreas Adenocarcinoma
IV G2/G3 No No
PANC 685 PANC 685 PLS 1 #N/A Negative
0.02204 Pancreas Adenocarcinoma
IIB G2 No No
PANC 687 PANC 687 PLS 1 #N/A Negative
0.39625 Pancreas Adenocarcinoma
IIB G2 No No
PANC 688 PANC 688 PLS 1 #N/A Positive
0.78036 Pancreas Adenocarcinoma
IV NA No No
PANC 689 PANC 689 PLS 1 #N/A Negative
0.11034 Pancreas Adenocarcinoma
IIB G3 No No
PANC 689 PANC 689 PLS 2 #N/A Negative
0.07670 Pancreas Adenocarcinoma
IIB G3 No No
PANC 689 PANC 689 PLS 3 #N/A Negative
0.03973 Pancreas Adenocarcinoma
IIB G3 No No
PANC 690 PANC 690 PLS 1 #N/A Negative
0.32652 Pancreas Adenocarcinoma
IIB G3 No No
PANC 691 PANC 691 PLS 1 #N/A Negative
0.05077 Pancreas Adenocarcinoma
IB G2 No No
PANC 691 PANC 691 PLS 2 #N/A Positive
0.63564 Pancreas Adenocarcinoma
IB G2 No No
PANC 691 PANC 691 PLS 3 #N/A Positive
0.77194 Pancreas Adenocarcinoma
IB G2 No No
PANC 692 PANC 692 PLS 1 #N/A Negative
0.08002 Pancreas Adenocarcinoma
IIB G4 No No
PANC 693 PANC 693 PLS 1 #N/A Positive
0.74982 Pancreas NA
NA NA No No
PANC 693 PANC 693 PLS 3 #N/A Positive
0.82039 Pancreas NA
NA NA No No
PANC 693 PANC 693 PLS 2 #N/A Positive
0.83445 Pancreas NA

Table59.txt

NA	NA			No	No		
PANC 731	PANC 731 PLS 1	#N/A	Negative	0.27100	Pancreas	adenocarcinoma	
IIB	2			No	No		
PANC 732	PANC 732 PLS 1	#N/A	Negative	0.13914	Pancreas	Adenocarcinoma	
IIB	3			No	No		
PANC 733	PANC 733 PLS 1	#N/A	Negative	0.09448	Pancreas	Adenocarcinoma	
IV	NA			No	No		
PANC 734	PANC 734 PLS 1	#N/A	Negative	0.04807	Pancreas	adenocarcinoma	
IIB	3			No	No		
PANC 735	PANC 735 PLS 1	#N/A	Negative	0.47461	Pancreas	Adenocarcinoma	
IIB	1			No	No		
PANC 736	PANC 736 PLS 1	#N/A	Negative	0.19535	Pancreas	Adenocarcinoma	
IA	2			No	No		
PANC 736	PANC 736 PLS 2	#N/A	Negative	0.30271	Pancreas	Adenocarcinoma	
IA	2			No	No		
PANC 736	PANC 736 PLS 3	#N/A	Negative	0.23567	Pancreas	Adenocarcinoma	
IA	2			No	No		
PANC 737	PANC 737 PLS 1	#N/A	Negative	0.23956	Pancreas	adenocarcinoma	
III	2			No	No		
PANC 738	PANC 738 PLS 1	#N/A	Positive	0.81096	Pancreas	Adenocarcinoma	
IIB	2			No	No		
PANC 739	PANC 739 PLS 1	#N/A	Negative	0.09983	Pancreas	Adenocarcinoma	
IIB	2			No	No		
PANC 740	PANC 740 PLS 1	#N/A	Negative	0.03300	Pancreas	Adenocarcinoma	
IIA	NA			No	No		
PANC 741	PANC 741 PLS 1	#N/A	Negative	0.31160	Pancreas	Adenocarcinoma	
IIB	NA			No	No		
PANC 742	PANC 742 PLS 1	#N/A	Negative	0.02688	Pancreas	adenocarcinoma	
IA	2			No	No		
PANC 743	PANC 743 PLS 1	#N/A	Negative	0.04730	Pancreas	Adenocarcinoma	
IIB	3			No	No		
PANC 744	PANC 744 PLS 1	#N/A	Negative	0.15098	Pancreas	Adenocarcinoma	

Table59.txt

IIB 3 No No
PANC 745 PANC 745 PLS 1 #N/A Negative
0.36001 Pancreas Adenocarcinoma
IV 2 No No
PANC 746 PANC 746 PLS 1 #N/A Positive
0.81132 Pancreas Adenocarcinoma
IV NA No No
PANC 747 PANC 747 PLS 1 #N/A Negative
0.09044 Pancreas Adenocarcinoma
IIA 3 No No
PANC 748 PANC 748 PLS 1 #N/A Negative
0.53168 Pancreas Adenocarcinoma
IA 2 No No
PANC 749 PANC 749 PLS 1 #N/A Positive
0.62804 Pancreas Adenocarcinoma
IB 2 No No
PANC 750 PANC 750 PLS 1 #N/A Negative
0.47393 Pancreas Adenocarcinoma
IIB 2 No No
PANC 751 PANC 751 PLS 1 #N/A Negative
0.23797 Pancreas Adenocarcinoma
IV NA No No
PANC 752 PANC 752 PLS 1 #N/A Negative
0.20976 Pancreas Adenocarcinoma
IA 1 No No
PANC 753 PANC 753 PLS 1 #N/A Negative
0.24916 Pancreas Adenocarcinoma
IIB 2 No No
PANC 754 PANC 754 PLS 1 #N/A Positive
0.80677 Pancreas Adenocarcinoma
III 3 No No
PANC 755 PANC 755 PLS 1 #N/A Positive
0.68767 Pancreas Adenocarcinoma
IIB 3 No No
PANC 755 PANC 755 PLS 2 #N/A Positive
0.83928 Pancreas Adenocarcinoma
IIB 3 No No
PANC 755 PANC 755 PLS 3 #N/A Positive
0.81499 Pancreas Adenocarcinoma
IIB 3 No No
PANC 756 PANC 756 PLS 1 #N/A Negative
0.09204 Pancreas Adenocarcinoma
IIB 4 No No
PANC 756 PANC 756 PLS 2 #N/A Positive
0.74631 Pancreas Adenocarcinoma
IIB 4 No No
PANC 756 PANC 756 PLS 3 #N/A Positive
0.75846 Pancreas Adenocarcinoma

Table59.txt

IIB 4 No No
PANC 757 PANC 757 PLS 1 Negative Negative
0.09720 Pancreas Adenocarcinoma
IIB G3 No No
PANC 757 PANC 757 PLS 2 Negative Negative
0.05554 Pancreas Adenocarcinoma
IIB G3 No No
PANC 758 PANC 758 PLS 1 Positive Negative
0.04004 Pancreas Adenocarcinoma
IIB G3 No No
PANC 758 PANC 758 PLS 2 Positive Negative
0.38492 Pancreas Adenocarcinoma
IIB G3 No No
PANC 759 PANC 759 PLS 1 Positive Negative
0.09979 Pancreas Adenocarcinoma
IIB G2-G3 No No
PANC 759 PANC 759 PLS 2 Positive Positive
0.60586 Pancreas Adenocarcinoma
IIB G2-G3 No No
PANC 760 PANC 760 PLS 1 Positive Negative
0.31042 Pancreas Adenocarcinoma
IIB G1 No No
PANC 760 PANC 760 PLS 2 Positive Positive
0.73086 Pancreas Adenocarcinoma
IIB G1 No No
PANC 761 PANC 761 PLS 1 Positive Negative
0.18819 Pancreas Adenocarcinoma
IIA G3 No No
PANC 761 PANC 761 PLS 2 Positive Negative
0.16307 Pancreas Adenocarcinoma
IIA G3 No No
PANC 762 PANC 762 PLS 1 Positive Negative
0.13566 Pancreas Adenocarcinoma
IIB G2 No No
PANC 762 PANC 762 PLS 2 Positive Negative
0.04323 Pancreas Adenocarcinoma
IIB G2 No No
PANC 763 PANC 763 PLS 1 #N/A Negative
0.49897 Pancreas NA
NA NA No No
PANC 763 PANC 763 PLS 2 #N/A Negative
0.25550 Pancreas NA
NA NA No No
PANC 764 PANC 764 PLS 1 Positive Negative
0.33807 Pancreas Adenocarcinoma
IIB G2 No No
PANC 764 PANC 764 PLS 2 Positive Negative
0.16504 Pancreas Adenocarcinoma

Table59.txt

IIB	G2			No	No			
PANC 765	PANC 765 PLS 1	Positive	Negative	0.56842	Pancreas	Adenocarcinoma		
IIB	G2			No	No			
PANC 766	PANC 766 PLS 1	Positive	Negative	0.13417	Pancreas	Adenocarcinoma		
IB	NA			No	No			
PANC 766	PANC 766 PLS 2	Positive	Negative	0.32539	Pancreas	Adenocarcinoma		
IB	NA			No	No			
PANC 767	PANC 767 PLS 1	Negative	Negative	0.03786	Pancreas	Adenocarcinoma		
IIB	G2			No	No			
PANC 767	PANC 767 PLS 2	Negative	Negative	0.06603	Pancreas	Adenocarcinoma		
IIB	G2			No	No			
PANC 768	PANC 768 PLS 1	Negative	Negative	0.42216	Pancreas	Adenocarcinoma		
IIA	G2			No	No			
PANC 768	PANC 768 PLS 2	Negative	Negative	0.17950	Pancreas	Adenocarcinoma		
IIA	G2			No	No			
PANC 769	PANC 769 PLS 1	Negative	Negative	0.25880	Pancreas	Adenocarcinoma		
IIB	G3			No	No			
PANC 769	PANC 769 PLS 2	Negative	Negative	0.35345	Pancreas	Adenocarcinoma		
IIB	G3			No	No			
PANC 973	PANC 973 PLS 1	#N/A	Negative	0.47405	Pancreas	NA		
NA	NA			No	No			
PANC 974	PANC 974 PLS 1	#N/A	Negative	0.24853	Pancreas	NA		
NA	NA			No	No			
PANC 975	PANC 975 PLS 1	#N/A	Negative	0.22287	Pancreas	NA		
NA	NA			No	No			
PANC 976	PANC 976 PLS 1	#N/A	Negative	0.04678	Pancreas	NA		
NA	NA			No	No			
PANC 977	PANC 977 PLS 1	#N/A	Negative	0.10081	Pancreas	NA		
NA	NA			No	No			
PANC 978	PANC 978 PLS 1	#N/A	Negative	0.46927	Pancreas	NA		
NA	NA			No	No			
PANC 979	PANC 979 PLS 1	#N/A	Negative	0.39143	Pancreas	NA		

Table59.txt

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Table59.txt

NA	NA			No	No			
PANC 998	PANC 998 PLS 1	#N/A	Negative	0.43999	Pancreas	NA		
NA	NA			No	No			
PANC 999	PANC 999 PLS 1	#N/A	Negative	0.09602	Pancreas	NA		
NA	NA			No	No			
PANCA 1001	PANCA 1001 PLS 1	Positive	Negative	0.36234	Pancreas	Adenocarcinoma		
IIA	Moderately differentiated		No	No				
PANCA 1002	PANCA 1002 PLS 1	#N/A	Negative	0.25208	Pancreas	NA		
NA	NA			No	No			
PANCA 1003	PANCA 1003 PLS 1	#N/A	Negative	0.27589	Pancreas	NA		
NA	NA			No	No			
PANCA 1004	PANCA 1004 PLS 1	Positive	Negative	0.29575	Pancreas	Adenocarcinoma		
IIB	Moderately differentiated		No	No				
PANCA 1005	PANCA 1005 PLS 1	Positive	Negative	0.28979	Pancreas	Adenocarcinoma		
IIB	poorly differentiated		No	No				
PANCA 1006	PANCA 1006 PLS 1	Positive	Positive	0.66786	Pancreas	Adenocarcinoma		
IIB	Moderately differentiated		No	No				
PANCA 1008	PANCA 1008 PLS 1	Positive	Negative	0.31829	Pancreas	Adenocarcinoma		
IIA	Moderately differentiated		No	No				
PANCA 1009	PANCA 1009 PLS 1	Positive	Negative	0.51278	Pancreas	Adenocarcinoma		
IIB	poorly differentiated		No	No				
PANC 682	PANC 682 PLS 2	#N/A	Positive	0.70129	Pancreas	Adenocarcinoma		
IIB	G2		No	No				
PANC 682	PANC 682 PLS 3	#N/A	Negative	0.46312	Pancreas	Adenocarcinoma		
IIB	G2		No	No				
PANC 707	PANC 707 PLS 2	#N/A	Negative	0.15495	Pancreas	Adenocarcinoma		
IIA	2		No	No				
PANC 749	PANC 749 PLS 2	#N/A	Negative	0.17302	Pancreas	Adenocarcinoma		
IB	2		No	No				
PANC 750	PANC 750 PLS 2	#N/A	Negative	0.10586	Pancreas	Adenocarcinoma		
IIB	2		No	No				
PANC 945	PANC 945 PLS 1	#N/A	Negative	0.03058	Pancreas	NA		

Table59.txt

NA NA No No
PANC 946 PANC 946 PLS 1 #N/A Positive
1.00000 Pancreas NA
NA NA No No
PANC 947 PANC 947 PLS 1 #N/A Negative
0.20031 Pancreas NA
NA NA No No
PANC 948 PANC 948 PLS 1 #N/A Negative
0.10967 Pancreas NA
NA NA No No
PANC 949 PANC 949 PLS 1 #N/A Negative
0.41794 Pancreas NA
NA NA No No
PANC 950 PANC 950 PLS 1 #N/A Negative
0.14007 Pancreas NA
NA NA No No
PANC 951 PANC 951 PLS 1 #N/A Negative
0.35998 Pancreas NA
NA NA No No
PANC 952 PANC 952 PLS 1 #N/A Positive
0.74746 Pancreas NA
NA NA No No
PANC 953 PANC 953 PLS 1 #N/A Negative
0.49959 Pancreas NA
NA NA No No
PANC 954 PANC 954 PLS 1 #N/A Negative
0.29186 Pancreas NA
NA NA No No
PANC 955 PANC 955 PLS 1 #N/A Negative
0.09269 Pancreas NA
NA NA No No
PANC 956 PANC 956 PLS 1 #N/A Negative
0.16057 Pancreas NA
NA NA No No
PANC 957 PANC 957 PLS 1 #N/A Negative
0.09387 Pancreas NA
NA NA No No
PANC 961 PANC 961 PLS 1 #N/A Negative
0.08168 Pancreas NA
NA NA No No
PANC 962 PANC 962 PLS 1 #N/A Negative
0.10938 Pancreas NA
NA NA No No
PANC 963 PANC 963 PLS 1 #N/A Negative
0.06629 Pancreas NA
NA NA No No
PANC 964 PANC 964 PLS 1 #N/A Negative
0.48197 Pancreas NA

Table59.txt

NA	NA			No	No				
PANC 965	PANC 965 PLS 1	#N/A	Negative	0.12718	Pancreas	NA			
NA	NA			No	No				
PANC 966	PANC 966 PLS 1	#N/A	Positive	0.61785	Pancreas	NA			
NA	NA			No	No				
PANC 967	PANC 967 PLS 1	#N/A	Negative	0.12266	Pancreas	NA			
NA	NA			No	No				
PANC 968	PANC 968 PLS 1	#N/A	Negative	0.10671	Pancreas	NA			
NA	NA			No	No				
PANC 969	PANC 969 PLS 1	#N/A	Negative	0.02900	Pancreas	NA			
NA	NA			No	No				
PANC 970	PANC 970 PLS 1	#N/A	Negative	0.02056	Pancreas	NA			
NA	NA			No	No				
PANC 971	PANC 971 PLS 1	#N/A	Positive	0.80115	Pancreas	NA			
NA	NA			No	No				
PANC 972	PANC 972 PLS 1	#N/A	Negative	0.10053	Pancreas	NA			
NA	NA			No	No				
PANCA 1010	PANCA 1010 PLS 1	Negative	Positive	0.65207	Pancreas	Adenocarcinoma			
IA	Moderately differentiated		No	No					
PANCA 1011	PANCA 1011 PLS 1	Positive	Negative	0.32672	Pancreas	Adenocarcinoma			
IIB	Moderately differentiated		No	No					
PANCA 1012	PANCA 1012 PLS 1	Negative	Negative	0.02891	Pancreas	Adenocarcinoma			
IIB	Moderately differentiated		No	No					
PANCA 1013	PANCA 1013 PLS 1	Positive	Negative	0.37652	Pancreas	Adenocarcinoma			
III	NA			No	No				
PANCA 1014	PANCA 1014 PLS 1	Positive	Positive	0.68843	Pancreas	Adenocarcinoma			
IIB	Moderately differentiated		No	No					
PANCA 1015	PANCA 1015 PLS 1	Positive	Negative	0.51841	Pancreas	Adenocarcinoma			
III	Moderately differentiated		No	No					
PANCA 1016	PANCA 1016 PLS 1	Negative	Negative	0.22932	Pancreas	Adenocarcinoma			
IA	Well differentiated		Yes	No					
PANCA 1018	PANCA 1018 PLS 1	Positive	Negative	0.19895	Pancreas	Adenocarcinoma			

Table59.txt

IIB poorly differentiated No No
PANCA 1019 PANCA 1019 PLS 1 #N/A Negative
0.20404 Pancreas Adenocarcinoma
IV Moderately differentiated No No
PANCA 1020 PANCA 1020 PLS 1 Positive Negative
0.03518 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1021 PANCA 1021 PLS 1 #N/A Negative
0.13392 Pancreas Adenocarcinoma
IV poorly differentiated No No
PANCA 1022 PANCA 1022 PLS 1 Positive Negative
0.12608 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1023 PANCA 1023 PLS 1 #N/A Negative
0.05882 Pancreas Adenocarcinoma
IV NA Yes No
PANCA 1024 PANCA 1024 PLS 1 Negative Negative
0.02691 Pancreas Adenocarcinoma
IIB poorly differentiated No No
PANCA 1025 PANCA 1025 PLS 1 Positive Negative
0.20311 Pancreas Adenocarcinoma
III NA No No
PANCA 1028 PANCA 1028 PLS 1 Negative Negative
0.08155 Pancreas Adenocarcinoma
III NA No No
PANCA 1029 PANCA 1029 PLS 1 #N/A Negative
0.20237 Pancreas Adenocarcinoma
IV NA No No
PANCA 1030 PANCA 1030 PLS 1 Positive Negative
0.06307 Pancreas Adenocarcinoma
IIA Moderately differentiated No No
PANCA 1031 PANCA 1031 PLS 1 Positive Negative
0.03384 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1032 PANCA 1032 PLS 1 #N/A Negative
0.01161 Pancreas Adenocarcinoma
IV Moderately differentiated No No
PANCA 1033 PANCA 1033 PLS 1 #N/A Negative
0.33589 Pancreas Adenocarcinoma
IV T4NxM1 No No
PANCA 1034 PANCA 1034 PLS 1 Negative Negative
0.03709 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1035 PANCA 1035 PLS 1 #N/A Negative
0.00905 Pancreas Adenocarcinoma
IV Moderately differentiated Yes No
PANCA 1036 PANCA 1036 PLS 1 Negative Negative
0.31290 Pancreas Adenocarcinoma

Table59.txt

```
   IIA      Moderately differentiated   No              No
PANCA 1037        PANCA 1037 PLS 1   Positive           Negative
0.39879         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   Yes             No
PANCA 1039        PANCA 1039 PLS 1   Positive           Negative
0.04116         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1040        PANCA 1040 PLS 1   Negative           Negative
0.14397         Pancreas      Adenocarcinoma
   IIA      Moderately differentiated   No              No
PANCA 1041        PANCA 1041 PLS 1   #N/A               Negative
0.34420         Pancreas      Adenocarcinoma
   TxN0M0   NA                          Yes             No
PANCA 1042        PANCA 1042 PLS 1   Negative           Negative
0.29881         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1043        PANCA 1043 PLS 1   Positive           Negative
0.00806         Pancreas      Adenocarcinoma
   IIA      Moderately differentiated   No              No
PANCA 1044        PANCA 1044 PLS 1   Positive           Negative
0.23198         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1045        PANCA 1045 PLS 1   #N/A               Negative
0.04929         Pancreas      Adenocarcinoma
   IV       NA                          Yes             No
PANCA 1047        PANCA 1047 PLS 1   Negative           Negative
0.45968         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANCA 1048        PANCA 1048 PLS 1   Positive           Positive
0.80085         Pancreas      Adenocarcinoma
   III      NA                          No              No
PANCA 1050        PANCA 1050 PLS 1   Positive           Negative
0.57359         Pancreas      Adenocarcinoma
   IIB      poorly differentiated       No              No
PANCA 1051        PANCA 1051 PLS 1   Positive           Negative
0.43598         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1052        PANCA 1052 PLS 1   Negative           Negative
0.29385         Pancreas      Adenocarcinoma
   IIA      Moderately differentiated   No              No
PANCA 1053        PANCA 1053 PLS 1   Positive           Positive
0.76938         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1054        PANCA 1054 PLS 1   Positive           Negative
0.27158         Pancreas      Adenocarcinoma
   IIB      Moderately differentiated   No              No
PANCA 1055        PANCA 1055 PLS 1   Negative           Negative
0.10356         Pancreas      Adenocarcinoma
```

Table59.txt

IIB Moderately differentiated No No
PANCA 1056 PANCA 1056 PLS 1 Positive Negative
0.06807 Pancreas Adenocarcinoma
IIA Moderately differentiated No No
PANCA 1057 PANCA 1057 PLS 1 Positive Negative
0.52209 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1058 PANCA 1058 PLS 1 Positive Negative
0.54510 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1059 PANCA 1059 PLS 1 Positive Negative
0.19093 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1060 PANCA 1060 PLS 1 #N/A Negative
0.22676 Pancreas NA
NA NA No No
PANCA 1061 PANCA 1061 PLS 1 Positive Negative
0.06208 Pancreas Adenocarcinoma
IIB Moderately differentiated No No
PANCA 1062 PANCA 1062 PLS 1 #N/A Negative
0.07054 Pancreas NA
NA NA No No
PANCA 1063 PANCA 1063 PLS 1 Positive Negative
0.07491 Pancreas Adenocarcinoma
IIB poorly differentiated No No
PANCA 1064 PANCA 1064 PLS 1 #N/A Negative
0.18707 Pancreas NA
NA NA No No
PANCA 1065 PANCA 1065 PLS 1 #N/A Negative
0.48735 Pancreas Adenocarcinoma
IV Moderately differentiated No No
PANCA 1067 PANCA 1067 PLS 1 #N/A Positive
0.64974 Pancreas NA
NA NA No No
INDI 001 INDI 001 PLS 1 Positive Negative
0.06116 Lung Non-small cell lung cancer
IIB G2 No No
INDI 002 INDI 002 PLS 1 Negative Negative
0.01584 Lung Non-small cell lung cancer
IIA G3 No No
INDI 003 INDI 003 PLS 1 Positive Negative
0.04041 Lung Non-small cell lung cancer
IIIA G3 No No
INDI 004 INDI 004 PLS 1 Positive Negative
0.24186 Lung Non-small cell lung cancer
IA G3 No No
INDI 005 INDI 005 PLS 1 Negative Negative
0.46863 Lung Non-small cell lung cancer

Table59.txt

IB	G3			No	No		
INDI 006		INDI 006 PLS 1	#N/A		Positive		
0.74920		Lung	carcinoid tumor				
IV	NA			No	No		
INDI 007		INDI 007 PLS 1	Positive		Negative		
0.01516		Lung	Non-small cell lung cancer				
IIA	G2			No	No		
INDI 008		INDI 008 PLS 1	#N/A		Negative		
0.39686		Lung	Non-small cell lung cancer				
IIIB	G2			No	No		
INDI 009		INDI 009 PLS 1	Positive		Positive		
1.00000		Lung	Non-small cell lung cancer				
IIA	G3			No	No		
INDI 010		INDI 010 PLS 1	Positive		Negative		
0.18695		Lung	Non-small cell lung cancer				
IIB	NA			No	No		
INDI 011		INDI 011 PLS 1	Negative		Negative		
0.11446		Lung	Non-small cell lung cancer				
IB	G3			No	No		
INDI 012		INDI 012 PLS 1	Positive		Negative		
0.23751		Lung	Non-small cell lung cancer				
IB	G2			No	No		
INDI 013		INDI 013 PLS 1	Negative		Negative		
0.09554		Lung	Non-small cell lung cancer				
IIIA	G3			No	No		
INDI 014		INDI 014 PLS 1	Positive		Negative		
0.51284		Lung	Non-small cell lung cancer				
IIA	G3			No	No		
INDI 015		INDI 015 PLS 1	Negative		Negative		
0.36316		Lung	Non-small cell lung cancer				
IB	G3			No	No		
INDI 016		INDI 016 PLS 1	Positive		Negative		
0.05984		Lung	Non-small cell lung cancer				
IIIA	G3			No	No		
INDI 017		INDI 017 PLS 1	Negative		Negative		
0.44475		Lung	Non-small cell lung cancer				
IB	G3			No	No		
INDI 018		INDI 018 PLS 1	Positive		Negative		
0.29419		Lung	Non-small cell lung cancer				
IIIB	G3			No	No		
INDI 019		INDI 019 PLS 1	#N/A		Negative		
0.48948		Lung	carcinoid tumor				
IIIA	G4			No	No		
INDI 020		INDI 020 PLS 1	#N/A		Negative		
0.50930		Lung	Non-small cell lung cancer				
IV	G4			No	No		
INDI 021		INDI 021 PLS 1	#N/A		Positive		
1.00000		Lung	Non-small cell lung cancer				

Table59.txt

IV	G3				No	No			
INDI 022		INDI 022	PLS 1		Positive	Positive			
0.70168		Lung			Non-small cell lung cancer				
IIIA	G4				No	No			
INDI 023		INDI 023	PLS 1		Positive	Negative			
0.54269		Lung			Non-small cell lung cancer				
IIB	G2				No	No			
INDI 024		INDI 024	PLS 1		Negative	Negative			
0.27833		Lung			Non-small cell lung cancer				
IIA	G3				No	No			
INDI 025		INDI 025	PLS 1		Positive	Negative			
0.11983		Lung			Non-small cell lung cancer				
IB	NA				No	No			
INDI 026		INDI 026	PLS 1		Negative	Negative			
0.01959		Lung			Non-small cell lung cancer				
IB	G3				No	No			
INDI 220		INDI 220	PLS 1		Positive	Negative			
0.04212		Lung			Non-small cell lung cancer				
IB	G2				No	No			
INDI 224		INDI 224	PLS 1		Positive	Negative			
0.39782		Lung			Non-small cell lung cancer				
IIIA	G3				No	No			
INDI 227		INDI 227	PLS 1		Negative	Negative			
0.04650		Lung			Non-small cell lung cancer				
IIA	G2				No	No			
INDI 231		INDI 231	PLS 1		Positive	Positive			
1.00000		Lung			Non-small cell lung cancer				
IIIA	G4				No	No			
INDI 235		INDI 235	PLS 1		#N/A	Negative			
0.05427		Lung			carcinoid tumor				
IA	G1				No	No			
INDI 239		INDI 239	PLS 1		Positive	Negative			
0.25736		Lung			Non-small cell lung cancer				
IIIA	G2				No	No			
INDI 242		INDI 242	PLS 1		#N/A	Negative			
0.23317		Lung			Non-small cell lung cancer				
IV	G3				No	No			
INDI 246		INDI 246	PLS 1		Negative	Negative			
0.16832		Lung			Non-small cell lung cancer				
IIB	G3				No	No			
INDI 247		INDI 247	PLS 1		Positive	Negative			
0.36973		Lung			Non-small cell lung cancer				
IA	G3				No	No			
INDI 252		INDI 252	PLS 1		Positive	Negative			
0.19486		Lung			Non-small cell lung cancer				
IIB	G2				No	No			
INDI 257		INDI 257	PLS 1		Positive	Negative			
0.01750		Lung			Non-small cell lung cancer				

Table59.txt

```
   IIIA     G3                          No              No
INDI 264          INDI 264 PLS 1     Positive            Negative
0.11937         Lung          Non-small cell lung cancer
   IIIA     G3                          No              No
INDI 266          INDI 266 PLS 1     Negative            Negative
0.25824         Lung          Non-small cell lung cancer
   IA       G2                          No              No
INDI 269          INDI 269 PLS 1     Negative            Negative
0.15052         Lung          Non-small cell lung cancer
   IIIA     G2                          No              No
INDI 273          INDI 273 PLS 1     Positive            Negative
0.05009         Lung          Non-small cell lung cancer
   IB       G3                          No              No
INDI 283          INDI 283 PLS 1     Negative            Negative
0.04523         Lung          Non-small cell lung cancer
   IB       G1                          No              No
INDI 285          INDI 285 PLS 1     Positive            Negative
0.23961         Lung          Non-small cell lung cancer
   IIA      G3                          No              No
INDI 288          INDI 288 PLS 1     Positive            Positive
1.00000         Lung          Non-small cell lung cancer
   IIIB     G3                          No              No
INDI 291          INDI 291 PLS 1     Negative            Negative
0.29163         Lung          Non-small cell lung cancer
   IB       G2                          No              No
INDI 292          INDI 292 PLS 1     Negative            Negative
0.04611         Lung          Non-small cell lung cancer
   IIIB     NA                          No              No
INDI 324          INDI 324 PLS 1     Positive            Negative
0.10742         Lung          Non-small cell lung cancer
   IA       G3                          No              No
INDI 326          INDI 326 PLS 1     Negative            Negative
0.02431         Lung          Non-small cell lung cancer
   IA       G3                          No              No
INDI 413          INDI 413 PLS 1     Positive            Negative
0.09525         Lung          Non-small cell lung cancer
   IB       G3                          No              No
INDI 414          INDI 414 PLS 1     Positive            Negative
0.02962         Lung          Non-small cell lung cancer
   IIA      G3                          No              No
INDI 415          INDI 415 PLS 1     Positive            Negative
0.03425         Lung          Non-small cell lung cancer
   IIA      NA                          No              No
INDI 417          INDI 417 PLS 1     Positive            Negative
0.38244         Lung          Non-small cell lung cancer
   IA       G3                          No              No
INDI 491          INDI 491 PLS 1     Negative            Negative
0.34481         Lung          Non-small cell lung cancer
```

Table59.txt

IA	G3			No	No		
INDI 492		INDI 492 PLS 1		Negative	Negative		
0.12868		Lung		Non-small cell lung cancer			
IB	G3			No	No		
INDI 494		INDI 494 PLS 1		Positive	Negative		
0.21055		Lung		adenocarcinoma			
IIIA	NA			No	No		
INDI 495		INDI 495 PLS 1		Negative	Negative		
0.02560		Lung		adenocarcinoma			
IB	NA			No	No		
INDI 496		INDI 496 PLS 1		#N/A	Negative		
0.09601		Lung		squamous cell carcinoma			
IIIA	NA			No	No		
INDI 497		INDI 497 PLS 1		Negative	Negative		
0.07540		Lung		neuroendocrine and small cell carcinoma			
IIA	NA			No	No		
INDI 499		INDI 499 PLS 1		Positive	Negative		
0.05591		Lung		adenocarcinoma			
IB	NA			No	No		
INDI 503		INDI 503 PLS 1		Positive	Negative		
0.14349		Lung		squamous cell carcinoma			
IB	NA			No	No		
INDI 505		INDI 505 PLS 1		Positive	Negative		
0.07542		Lung		Non-small cell lung cancer			
IIa	G3			No	No		
INDI 507		INDI 507 PLS 1		Positive	Negative		
0.30009		Lung		Non-small cell lung cancer			
IIa	G3			No	No		
INDI 513		INDI 513 PLS 1		Negative	Negative		
0.05097		Lung		Non-small cell lung cancer			
IA	G1			No	No		
INDI 519		INDI 519 PLS 1		Positive	Negative		
0.13375		Lung		Non-small cell lung cancer			
IA	G3			No	No		
INDI 077		INDI 077 PLS 1		Positive	Positive		
0.76771		Liver		Hepatocellular Carcinoma			
II	G1			No	No		
INDI 078		INDI 078 PLS 1		Positive	Negative		
0.17689		Liver		Hepatocellular Carcinoma			
II	G2			No	No		
INDI 079		INDI 079 PLS 1		Positive	Negative		
0.56941		Liver		Hepatocellular Carcinoma			
II	G3			No	No		
INDI 080		INDI 080 PLS 1		Positive	Negative		
0.08995		Liver		Hepatocellular Carcinoma			
I	G2			No	No		
INDI 081		INDI 081 PLS 1		Positive	Negative		
0.58169		Liver		Adenocarcinoma			

Table59.txt

IIB	G2				No		No		
INDI 129		INDI 129	PLS 1		Positive		Positive		
0.61023		Liver			Hepatocellular Carcinoma				
II	G2				No		No		
INDI 147		INDI 147	PLS 1		Positive		Negative		
0.59580		Stomach			Adenocarcinoma				
II	G2				No		No		
INDI 149		INDI 149	PLS 1		#N/A		Negative		
0.42203		Stomach			Gastro-Intestinal Stromal Tumor				
IB	G1				No		No		
INDI 151		INDI 151	PLS 1		Positive		Positive		
0.73594		Stomach			Adenocarcinoma				
II	G3				No		No		
INDI 153		INDI 153	PLS 1		Positive		Positive		
0.60372		Stomach			Adenocarcinoma				
II	G2				No		No		
INDI 166		INDI 166	PLS 1		#N/A		Positive		
1.00000		Liver			cholangiocarcinoma				
IV	G2				No		No		
INDI 167		INDI 167	PLS 1		Positive		Positive		
0.67473		Stomach			Adenocarcinoma				
II	G3				No		No		
INDI 168		INDI 168	PLS 1		Positive		Negative		
0.37736		Stomach			Adenocarcinoma				
II	G3				No		No		
INDI 171		INDI 171	PLS 1		Positive		Negative		
0.25130		Stomach			Adenocarcinoma				
IIIA	G3				No		No		
INDI 172		INDI 172	PLS 1		Positive		Positive		
0.65076		Stomach			Adenocarcinoma				
II	G3				No		No		
INDI 173		INDI 173	PLS 1		Positive		Negative		
0.28505		Stomach			Adenocarcinoma				
IB	G3				No		No		
INDI 176		INDI 176	PLS 1		Positive		Positive		
0.64723		Stomach			Adenocarcinoma				
II	G3				No		No		
INDI 177		INDI 177	PLS 1		Positive		Positive		
0.76004		Liver			Hepatocellular Carcinoma				
IIIA	G3				No		No		
INDI 182		INDI 182	PLS 1		Positive		Negative		
0.37238		Liver			Hepatocellular Carcinoma				
IIIA	G2				No		No		
INDI 190		INDI 190	PLS 1		Positive		Negative		
0.19046		Liver			Hepatocellular Carcinoma				
IIIA	G3				No		No		
INDI 205		INDI 205	PLS 1		Positive		Negative		
0.59657		Liver			Hepatocellular Carcinoma				

Table59.txt

IIIA	G1				No		No		
INDI 208		INDI 208 PLS 1			Positive		Positive		
1.00000		Liver			Hepatocellular Carcinoma				
II	G2				No		No		
INDI 214		INDI 214 PLS 1			Positive		Negative		
0.29499		Stomach			Adenocarcinoma				
IIA	G2				No		No		
INDI 215		INDI 215 PLS 1			Positive		Positive		
0.74408		Liver			Hepatocellular Carcinoma				
II	G2				No		No		
INDI 219		INDI 219 PLS 1			Positive		Positive		
0.79216		Liver			Hepatocellular Carcinoma				
IIIA	G2				No		No		
INDI 238		INDI 238 PLS 1			Positive		Negative		
0.11665		Liver			Hepatocellular Carcinoma				
II	G2				No		No		
INDI 249		INDI 249 PLS 1			#N/A		Positive		
0.80706		Liver			Hepatocellular Carcinoma				
NA	G1				No		No		
INDI 272		INDI 272 PLS 1			#N/A		Positive		
1.00000		Liver			cholangiocarcinoma				
IVB	NA				No		No		
INDI 295		INDI 295 PLS 1			Positive		Negative		
0.14679		Colorectal			Adenocarcinoma				
II	G1				No		No		
INDI 296		INDI 296 PLS 1			Negative		Negative		
0.30702		Colorectal			Adenocarcinoma				
IIB	G1				No		No		
INDI 298		INDI 298 PLS 1			Negative		Negative		
0.11442		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 299		INDI 299 PLS 1			Negative		Positive		
0.82892		Colorectal			Adenocarcinoma				
I	G3				No		No		
INDI 302		INDI 302 PLS 1			Negative		Negative		
0.09978		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 303		INDI 303 PLS 1			Positive		Negative		
0.10462		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 304		INDI 304 PLS 1			Positive		Positive		
0.81534		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 305		INDI 305 PLS 1			Positive		Positive		
1.00000		Colorectal			Adenocarcinoma				
IIB	G2				No		No		
INDI 306		INDI 306 PLS 1			Positive		Positive		
1.00000		Colorectal			Adenocarcinoma				

Table59.txt

IIIB	G3				No		No		
INDI 307		INDI 307	PLS 1		Positive		Negative		
0.49704		Colorectal			Adenocarcinoma				
IIIB	G3				No		No		
INDI 308		INDI 308	PLS 1		Positive		Positive		
0.62477		Liver			Hepatocellular Carcinoma				
II	G2				No		No		
INDI 309		INDI 309	PLS 1		Positive		Positive		
0.67011		Colorectal			Adenocarcinoma				
IIA	G3				No		No		
INDI 310		INDI 310	PLS 1		Positive		Positive		
0.80288		Colorectal			Adenocarcinoma				
IIA	G3				No		No		
INDI 311		INDI 311	PLS 1		Positive		Positive		
0.72655		Colorectal			Adenocarcinoma				
III	G3				No		No		
INDI 314		INDI 314	PLS 1		Negative		Positive		
0.76373		Colorectal			Adenocarcinoma				
I	G3				No		No		
INDI 341		INDI 341	PLS 1		Positive		Positive		
1.00000		Liver			cholangiocarcinoma				
II	G3				No		No		
INDI 367		INDI 367	PLS 1		Positive		Negative		
0.13900		Liver			Hepatocellular Carcinoma				
I	G2				No		No		
INDI 375		INDI 375	PLS 1		Positive		Negative		
0.13322		Liver			Hepatocellular Carcinoma				
I	G2				No		No		
INDI 387		INDI 387	PLS 1		Positive		Negative		
0.06868		Liver			Hepatocellular Carcinoma				
I	G2				No		No		
INDI 391		INDI 391	PLS 1		Positive		Positive		
1.00000		Liver			cholangiocarcinoma				
II	G2				No		No		
INDI 393		INDI 393	PLS 1		Positive		Positive		
1.00000		Liver			Hepatocellular Carcinoma				
II	G3				No		No		
INDI 401		INDI 401	PLS 1		#N/A		Positive		
0.87217		Liver			Hepatocellular Carcinoma				
NA	G2				No		No		
INDI 406		INDI 406	PLS 1		#N/A		Positive		
0.68404		Liver			Hepatocellular Carcinoma				
NA	NA				No		No		
INDI 418		INDI 418	PLS 1		Negative		Negative		
0.42015		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 419		INDI 419	PLS 1		Positive		Negative		
0.44222		Colorectal			Adenocarcinoma				

Table59.txt

I	G2				No	No			
INDI 420		INDI 420 PLS 1	#N/A		Positive				
0.84280		Colorectal	Adenocarcinoma						
IIB	G3				No	No			
INDI 421		INDI 421 PLS 1	Negative		Negative				
0.09820		Colorectal	Adenocarcinoma						
IIB	G2				No	No			
INDI 422		INDI 422 PLS 1	Positive		Negative				
0.47696		Colorectal	Adenocarcinoma						
IIB	G3				No	No			
INDI 423		INDI 423 PLS 1	Positive		Negative				
0.33761		Colorectal	Adenocarcinoma						
IIB	G2				No	No			
INDI 427		INDI 427 PLS 1	Positive		Negative				
0.42997		Colorectal	Adenocarcinoma						
IIB	G2				No	No			
INDI 428		INDI 428 PLS 1	Positive		Negative				
0.13021		Colorectal	Adenocarcinoma						
IIIB	G3				No	No			
INDI 429		INDI 429 PLS 1	Positive		Positive				
0.62380		Colorectal	Adenocarcinoma						
IIA	G2				No	No			
INDI 430		INDI 430 PLS 1	#N/A		Negative				
0.22898		Colorectal	Adenocarcinoma						
IVA	G3				No	No			
INDI 431		INDI 431 PLS 1	Negative		Positive				
0.66028		Colorectal	Adenocarcinoma						
IIA	G2				No	No			
INDI 432		INDI 432 PLS 1	#N/A		Negative				
0.33507		Colorectal	Adenocarcinoma						
IVA	G3				No	No			
INDI 433		INDI 433 PLS 1	Positive		Negative				
0.26338		Colorectal	Adenocarcinoma						
IIB	G2				No	No			
INDI 434		INDI 434 PLS 1	Negative		Negative				
0.07780		Colorectal	Adenocarcinoma						
IIB	G3				No	No			
INDI 435		INDI 435 PLS 1	#N/A		Negative				
0.16878		Colorectal	Adenocarcinoma						
IVA	G2				No	No			
INDI 436		INDI 436 PLS 1	Positive		Negative				
0.56528		Colorectal	Adenocarcinoma						
IIIB	G2				No	No			
INDI 437		INDI 437 PLS 1	Positive		Negative				
0.25716		Colorectal	Adenocarcinoma						
I	G2				No	No			
INDI 438		INDI 438 PLS 1	Negative		Negative				
0.47847		Colorectal	Adenocarcinoma						

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IIA	G3			No		No	
INDI 439		INDI 439 PLS 1		Positive		Negative	
0.34184		Colorectal		Adenocarcinoma			
IIIA	G2			No		No	
INDI 441		INDI 441 PLS 1		Positive		Negative	
0.59799		Esophagus		Squamous Cell Carcinoma			
II	G3			No		No	
INDI 444		INDI 444 PLS 1		Positive		Positive	
0.71790		Colorectal		Adenocarcinoma			
II	G2			No		No	
INDI 446		INDI 446 PLS 1		Positive		Negative	
0.54121		Esophagus		Squamous Cell Carcinoma			
II	G1			No		No	
INDI 450		INDI 450 PLS 1		Positive		Positive	
0.67904		Esophagus		Squamous Cell Carcinoma			
IIB	G2			No		No	
INDI 452		INDI 452 PLS 1		Positive		Negative	
0.51321		Colorectal		Adenocarcinoma			
II	G2			No		No	
INDI 456		INDI 456 PLS 1		Positive		Negative	
0.08004		Colorectal		Adenocarcinoma			
IIA	G2			No		No	
INDI 461		INDI 461 PLS 1		Negative		Negative	
0.31093		Colorectal		Adenocarcinoma			
III A	G3			No		No	
INDI 463		INDI 463 PLS 1		Positive		Positive	
0.86376		Colorectal		Adenocarcinoma			
II A	G2			No		No	
INDI 464		INDI 464 PLS 1		Positive		Positive	
0.72789		Liver		Hepato-Cholangiocarcinoma			
III A	G3			No		No	
INDI 466		INDI 466 PLS 1		Positive		Positive	
0.65579		Colorectal		Adenocarcinoma			
II A	G3			No		No	
INDI 467		INDI 467 PLS 1		Positive		Negative	
0.25970		Colorectal		Adenocarcinoma			
II A	G3			No		No	
INDI 468		INDI 468 PLS 1		Positive		Positive	
0.72139		Colorectal		Adenocarcinoma			
II A	G2			No		No	
INDI 470		INDI 470 PLS 1		Positive		Positive	
0.80305		Colorectal		Adenocarcinoma			
III A	G3			No		No	
INDI 472		INDI 472 PLS 1		Positive		Negative	
0.06503		Colorectal		Adenocarcinoma			
II A	G2			No		No	
INDI 475		INDI 475 PLS 1		Positive		Negative	
0.56761		Liver		Hepatocellular Carcinoma			

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III A	G1			No	No		
INDI 477		INDI 477 PLS 1		Positive	Negative		
0.02252		Colorectal		Adenocarcinoma			
III A	G3			No	No		
INDI 481		INDI 481 PLS 1		#N/A	Positive		
0.76232		Liver		cholangiocarcinoma			
IV	G2			No	No		
INDI 482		INDI 482 PLS 1		Positive	Positive		
0.82255		Liver		Hepatocellular Carcinoma			
II	G2			No	No		
INDI 483		INDI 483 PLS 1		Negative	Negative		
0.05369		Colorectal		Adenocarcinoma			
II A	G3			No	No		
INDI 486		INDI 486 PLS 1		#N/A	Negative		
0.07683		Liver		Hepatocellular Carcinoma			
NA	G2			No	No		
INDI 543		INDI 543 PLS 1		#N/A	Positive		
0.85097		Lung		carcinoid tumor			
IIA	G4			No	No		
INDI 545		INDI 545 PLS 1		Positive	Negative		
0.06469		Lung		Non-small cell lung cancer			
IA	G3			No	No		
INDI 546		INDI 546 PLS 1		Negative	Negative		
0.05724		Lung		Non-small cell lung cancer			
IIB	G1			No	No		
INDI 549		INDI 549 PLS 1		Positive	Negative		
0.01110		Lung		Non-small cell lung cancer			
IIIA	G3			No	No		
INDI 550		INDI 550 PLS 1		Negative	Negative		
0.07776		Lung		Non-small cell lung cancer			
IIIA	G1			No	No		
INDI 552		INDI 552 PLS 1		#N/A	Positive		
1.00000		Lung		carcinoid tumor			
IIA	G4			No	No		
INDI 557		INDI 557 PLS 1		#N/A	Negative		
0.08885		Liver		cholangiocarcinoma			
NA	NA			No	No		
INDI 558		INDI 558 PLS 1		Positive	Negative		
0.52402		Colorectal		Adenocarcinoma			
I	G3			No	No		
INDI 560		INDI 560 PLS 1		Negative	Negative		
0.36067		Colorectal		Adenocarcinoma			
I	G3			No	No		
INDI 562		INDI 562 PLS 1		Positive	Positive		
0.62978		Colorectal		Adenocarcinoma			
I	G2			No	No		
INDI 563		INDI 563 PLS 1		#N/A	Negative		
0.48101		Colorectal		Adenocarcinoma			

Table59.txt

I	G2			No	No		
INDI 564		INDI 564 PLS 1		Negative	Negative		
0.01655		Colorectal		Adenocarcinoma			
I	G2			No	No		
INDI 567		INDI 567 PLS 1		Positive	Positive		
0.70738		Colorectal		Adenocarcinoma			
II B	G2			No	No		
INDI 570		INDI 570 PLS 1		Positive	Negative		
0.12994		Colorectal		Adenocarcinoma			
II B	G3			No	No		
INDI 572		INDI 572 PLS 1		Negative	Negative		
0.23158		Colorectal		Adenocarcinoma			
II B	G2			No	No		
INDI 573		INDI 573 PLS 1		Negative	Negative		
0.18879		Colorectal		Adenocarcinoma			
I	G2			No	No		
INDI 574		INDI 574 PLS 1		Positive	Negative		
0.05342		Colorectal		Adenocarcinoma			
III B	G2			No	No		
INDI 576		INDI 576 PLS 1		#N/A	Negative		
0.20777		Colorectal		Adenocarcinoma			
I	G2			No	No		
INDI 580		INDI 580 PLS 1		#N/A	Positive		
1.00000		Colorectal		Adenocarcinoma			
IV	G2			No	No		
INDI 581		INDI 581 PLS 1		Positive	Positive		
0.75000		Colorectal		Adenocarcinoma			
II A	G3			No	No		
INDI 582		INDI 582 PLS 1		Positive	Negative		
0.48887		Colorectal		Adenocarcinoma			
II A	G1			No	No		
INDI 583		INDI 583 PLS 1		Positive	Negative		
0.59491		Colorectal		Adenocarcinoma			
II A	G3			No	No		
INDI 584		INDI 584 PLS 1		Positive	Negative		
0.23091		Colorectal		Adenocarcinoma			
II A	G3			No	No		
INDI 586		INDI 586 PLS 1		Positive	Negative		
0.18172		Liver		Hepatocellular Carcinoma			
III A	G3			No	No		
INDI 587		INDI 587 PLS 1		Positive	Negative		
0.38840		Colorectal		Adenocarcinoma			
II A	G3			No	No		
INDI 590		INDI 590 PLS 1		#N/A	Positive		
0.80943		Colorectal		Adenocarcinoma			
IV	G2			No	No		
INDI 591		INDI 591 PLS 1		Positive	Positive		
0.85504		Colorectal		Adenocarcinoma			

Table59.txt

II A	G3				No		No		
INDI 594		INDI 594	PLS 1		Positive		Negative		
0.48548		Colorectal		Adenocarcinoma					
III A	G3				No		No		
INDI 598		INDI 598	PLS 1		Positive		Negative		
0.11013		Colorectal		Adenocarcinoma					
II A	G2				No		No		
INDI 599		INDI 599	PLS 1		Positive		Positive		
0.82030		Colorectal		Adenocarcinoma					
II A	G3				No		No		
INDI 600		INDI 600	PLS 1		Negative		Negative		
0.59262		Colorectal		Adenocarcinoma					
II A	G2				No		No		
INDI 602		INDI 602	PLS 1		Positive		Negative		
0.11568		Colorectal		Adenocarcinoma					
II A	G3				No		No		
INDI 605		INDI 605	PLS 1		Positive		Negative		
0.15055		Colorectal		Adenocarcinoma					
II A	G2				No		No		
INDI 608		INDI 608	PLS 1		Positive		Negative		
0.46730		Colorectal		Adenocarcinoma					
II B	G2				No		No		
INDI 609		INDI 609	PLS 1		Positive		Negative		
0.38022		Colorectal		Adenocarcinoma					
II B	G3				No		No		
INDI 611		INDI 611	PLS 1		Positive		Negative		
0.09623		Colorectal		Adenocarcinoma					
II B	G2				No		No		
INDI 612		INDI 612	PLS 1		Positive		Negative		
0.02057		Colorectal		Adenocarcinoma					
II B	G2				No		No		
INDI 614		INDI 614	PLS 1		Positive		Negative		
0.34876		Colorectal		Adenocarcinoma					
II A	G3				No		No		
INDI 615		INDI 615	PLS 1		Positive		Positive		
0.67623		Colorectal		Adenocarcinoma					
II A	G3				No		No		
INDI 617		INDI 617	PLS 1		Positive		Negative		
0.13592		Colorectal		Adenocarcinoma					
IIIB	G3				No		No		
INDI 618		INDI 618	PLS 1		Positive		Positive		
0.73846		Colorectal		Adenocarcinoma					
IIIB	G3				No		No		
INDI 620		INDI 620	PLS 1		Positive		Negative		
0.56134		Colorectal		Adenocarcinoma					
IIA	G2				No		No		
INDI 621		INDI 621	PLS 1		Negative		Negative		
0.28048		Colorectal		Adenocarcinoma					

Table59.txt

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   IIA      G2                          No              No
INDI 622          INDI 622 PLS 1     Positive            Negative
0.51135         Liver          Hepatocellular Carcinoma
   IIIA     G3                          No              No
INDI 636          INDI 636 PLS 1     Positive            Positive
0.83816         Liver          Hepatocellular Carcinoma
   III A    1                           No              No
INDI 639          INDI 639 PLS 1     Positive            Negative
0.51417         Liver          Hepatocellular Carcinoma
   II       2                           No              No
INDI 645          INDI 645 PLS 1     Positive            Positive
1.00000         Liver          Hepatocellular Carcinoma
   III A    3                           No              No
INDI 652          INDI 652 PLS 1     #N/A                Positive
0.77313         Lung           NA
   NA       NA                          No              No
INDI 653          INDI 653 PLS 1     #N/A                Negative
0.00858         Lung           NA
   NA       NA                          No              No
INDI 661          INDI 661 PLS 1     Positive            Negative
0.44916         Liver          cholangiocarcinoma
   III A    G2                          No              No
INDI 669          INDI 669 PLS 1     Positive            Positive
0.65418         Liver          Hepatocellular Carcinoma
   III A    G2                          No              No
INDI 671          INDI 671 PLS 1     Positive            Negative
0.10384         Lung           Non-small cell lung cancer
   IB       G2                          No              No
INDI 674          INDI 674 PLS 1     Negative            Negative
0.06164         Lung           Non-small cell lung cancer
   IA       G2                          No              No
INDI 676          INDI 676 PLS 1     #N/A                Negative
0.07131         Lung           carcinoid tumor
   IA       G1                          No              No
INDI 681          INDI 681 PLS 1     Negative            Negative
0.40787         Lung           Non-small cell lung cancer
   IIA      G2                          No              No
INDI 684          INDI 684 PLS 1     Negative            Negative
0.19815         Liver          Hepatocellular Carcinoma
   III A    G2                          No              No
INDI 687          INDI 687 PLS 1     Positive            Negative
0.12941         Lung           Non-small cell lung cancer
   III A    G3                          No              No
INDI 690          INDI 690 PLS 1     Negative            Negative
0.06830         Lung           Non-small cell lung cancer
   III A    G3                          No              No
INDI 691          INDI 691 PLS 1     Negative            Negative
0.15008         Lung           Non-small cell lung cancer
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Table59.txt

IB	G3			No	No				
INDI 693		INDI 693 PLS 1		Positive	Positive				
1.00000		Lung		Non-small cell lung cancer					
III A	G3			No	No				
INDI 694		INDI 694 PLS 1		Negative	Negative				
0.21820		Lung		Non-small cell lung cancer					
IA	G3			No	No				
INDI 696		INDI 696 PLS 1		Positive	Negative				
0.05143		Lung		Non-small cell lung cancer					
IIA	G2			No	No				
INDI 700		INDI 700 PLS 1		Positive	Negative				
0.12829		Lung		Non-small cell lung cancer					
III A	G3			No	No				
INDI 738		INDI 738 PLS 1		#N/A	Positive				
0.88456		Liver		cholangiocarcinoma					
NA	NA			No	No				
INDI 760		INDI 760 PLS 1		Positive	Positive				
1.00000		Liver		Hepatocellular Carcinoma					
IIIA	G1			No	No				
INDI 771		INDI 771 PLS 1		Positive	Negative				
0.23794		Liver		Hepatocellular Carcinoma					
II	G1			No	No				
INDI 775		INDI 775 PLS 1		Positive	Negative				
0.08344		Liver		Hepatocellular Carcinoma					
II	G2			No	No				
INDI 778		INDI 778 PLS 1		Positive	Negative				
0.58408		Liver		Hepatocellular Carcinoma					
II	G1			No	No				
INDI 846		INDI 846 PLS 1		Positive	Negative				
0.59405		Colorectal		Adenocarcinoma					
IIA	G2			No	No				
INDI 847		INDI 847 PLS 1		Positive	Positive				
0.69001		Liver		Hepatocellular Carcinoma					
IIIA	G2			No	No				
INDI 848		INDI 848 PLS 1		Negative	Negative				
0.06801		Colorectal		Adenocarcinoma					
IIA	G3			No	No				
INDI 849		INDI 849 PLS 1		Negative	Negative				
0.25905		Colorectal		Adenocarcinoma					
IIA	G3			No	No				
INDI 854		INDI 854 PLS 1		Positive	Negative				
0.01876		Colorectal		Adenocarcinoma					
IIA	G3			No	No				
INDI 855		INDI 855 PLS 1		Positive	Negative				
0.24880		Colorectal		Adenocarcinoma					
IIA	G3			No	No				
INDI 861		INDI 861 PLS 1		Positive	Positive				
0.80128		Liver		Hepatocellular Carcinoma					

Table59.txt

II	G1				No		No		
INDI 864		INDI 864	PLS 1		Positive		Negative		
0.49847		Liver			Hepatocellular Carcinoma				
IIIA	G2				No		No		
INDI 868		INDI 868	PLS 1		Positive		Negative		
0.41002		Liver			Hepatocellular Carcinoma				
IIIA	G2				No		No		
INDI 894		INDI 894	PLS 1		#N/A		Negative		
0.01435		Liver			Hepatocellular Carcinoma				
NA	NA				No		No		
INDI 901		INDI 901	PLS 1		#N/A		Negative		
0.57471		Liver			Adenocarcinoma				
NA	G3				No		No		
INDI 075		INDI 075	PLS 1		Positive		Positive		
1.00000		Ovarian			Epithelial carcinoma				
IIIC	G3				No		No		
INDI 244		INDI 244	PLS 1		Positive		Negative		
0.05776		Colorectal			Adenocarcinoma				
IIIC	G2				No		No		
INDI 245		INDI 245	PLS 1		Positive		Negative		
0.11751		Colorectal			Adenocarcinoma				
IIIB	G3				No		No		
INDI 248		INDI 248	PLS 1		Negative		Negative		
0.07970		Colorectal			Adenocarcinoma				
IIA	G2				No		No		
INDI 250		INDI 250	PLS 1		Positive		Negative		
0.04010		Colorectal			Adenocarcinoma				
IIA	G2				No		No		
INDI 256		INDI 256	PLS 1		Positive		Positive		
0.84942		Colorectal			Adenocarcinoma				
IIIB	G2				No		No		
INDI 258		INDI 258	PLS 1		Negative		Negative		
0.05098		Colorectal			Adenocarcinoma				
I	G2				No		No		
INDI 263		INDI 263	PLS 1		#N/A		Positive		
1.00000		Colorectal			Adenocarcinoma				
IVB	G3				No		No		
INDI 271		INDI 271	PLS 1		Negative		Negative		
0.03453		Colorectal			Adenocarcinoma				
IIIA	G2				No		No		
INDI 278		INDI 278	PLS 1		Positive		Positive		
1.00000		Ovarian			Epithelial carcinoma				
IIIC	G3				No		No		
INDI 279		INDI 279	PLS 1		Positive		Positive		
0.70686		Colorectal			Adenocarcinoma				
IIA	G1				No		No		
INDI 281		INDI 281	PLS 1		Negative		Negative		
0.29251		Colorectal			Adenocarcinoma				

Table59.txt

I	G3			No	No				
INDI 293		INDI 293 PLS 1		Positive	Negative				
0.22167		Colorectal		Adenocarcinoma					
IIC	G2			No	No				
INDI 388		INDI 388 PLS 1		Positive	Negative				
0.04368		Pancreas		Adenocarcinoma					
IIB	G3			No	No				
INDI 510		INDI 510 PLS 1		#N/A	Positive				
1.00000		Ovarian		Epithelial carcinoma					
IV	G3			No	No				
INDI 537		INDI 537 PLS 1		Positive	Negative				
0.01028		Ovarian		Epithelial carcinoma					
IA	G1			No	No				
INDI 699		INDI 699 PLS 1		Positive	Negative				
0.25204		Pancreas		Adenocarcinoma					
IIB	G2			No	No				
INDI 702		INDI 702 PLS 1		Positive	Negative				
0.04478		Lung		Non-small cell lung cancer					
IIA	G3			No	No				
INDI 703		INDI 703 PLS 1		Negative	Negative				
0.28325		Lung		Non-small cell lung cancer					
IB	G2			No	No				
INDI 706		INDI 706 PLS 1		Positive	Negative				
0.15001		Lung		Non-small cell lung cancer					
IA	G2			No	No				
INDI 707		INDI 707 PLS 1		#N/A	Negative				
0.03910		Lung		Non-small cell lung cancer					
IV	G2			No	No				
INDI 730		INDI 730 PLS 1		#N/A	Negative				
0.24113		Pancreas		Adenocarcinoma					
IV	G2			No	No				
INDI 736		INDI 736 PLS 1		Positive	Negative				
0.04424		Lung		Non-small cell lung cancer					
III A	G2			No	No				
INDI 740		INDI 740 PLS 1		Positive	Negative				
0.03858		Pancreas		Adenocarcinoma					
IIB	G3			No	No				
INDI 741		INDI 741 PLS 1		Positive	Negative				
0.17184		Pancreas		Adenocarcinoma					
III	G2			No	No				
INDI 742		INDI 742 PLS 1		Positive	Negative				
0.09003		Breast		carcinoma					
IIA	G3			No	No				
INDI 888		INDI 888 PLS 1		Positive	Negative				
0.04768		Pancreas		Adenocarcinoma					
IIB	G2			No	No				
INDI 895		INDI 895 PLS 1		#N/A	Negative				
0.15836		Pancreas		Adenocarcinoma					

Table59.txt

IV	NA			No	No		
INDI 896		INDI 896	PLS 1	Positive	Negative		
0.00897		Lung		Non-small cell lung cancer			
IA	G3			No	No		
INDI 899		INDI 899	PLS 1	Negative	Negative		
0.07778		Breast		carcinoma			
IA	G2			No	No		
INDI 117		INDI 117	PLS 1	#N/A	Negative		
0.18877		Pancreas		Mixed cell adenocarcinoma			
NA	G1			No	No		
INDI 284		INDI 284	PLS 1	Positive	Negative		
0.03673		Colorectal		Adenocarcinoma			
IIA	G2			No	No		
INDI 331		INDI 331	PLS 1A	Positive	Positive		
1.00000		Lung		adenocarcinoma			
IIIA	G3			No	No		
INDI 333		INDI 333	PLS 1A	Negative	Negative		
0.35030		Lung		squamous cell carcinoma			
IIB	G3			No	No		
INDI 335		INDI 335	PLS 1A	Positive	Positive		
1.00000		Lung		adenocarcinoma			
IB	G3			No	No		
INDI 336		INDI 336	PLS 1A	Positive	Negative		
0.42516		Lung		squamous cell carcinoma			
IIIA	G3			No	No		
INDI 342		INDI 342	PLS 1A	Negative	Negative		
0.02737		Lung		adenocarcinoma			
IIIA	NA			No	No		
INDI 346		INDI 346	PLS 1A	Positive	Negative		
0.01202		Lung		adenocarcinoma			
IA	G3			No	No		
INDI 353		INDI 353	PLS 1A	Positive	Positive		
0.66145		Lung		large cell carcinoma			
IIA	G4			No	No		
INDI 355		INDI 355	PLS 1A	Negative	Negative		
0.10778		Lung		adenocarcinoma			
IB	G3			No	No		
INDI 357		INDI 357	PLS 1A	Negative	Negative		
0.36431		Lung		large cell carcinoma			
IB	G4			No	No		
INDI 358		INDI 358	PLS 1A	Negative	Negative		
0.00604		Lung		large cell carcinoma			
IIA	G4			No	No		
INDI 360		INDI 360	PLS 1A	Positive	Negative		
0.25116		Lung		carcinoma			
IIB	G4			No	No		
INDI 364		INDI 364	PLS 1A	Negative	Negative		
0.11730		Lung		adenocarcinoma with acinar type			

Table59.txt

IB	G3			No	No	
INDI 369	INDI 369 PLS 1A	Negative	Negative			
0.03843	Lung	squamous cell carcinoma				
IB	G3			No	No	
INDI 371	INDI 371 PLS 1A	Positive	Negative			
0.25174	Lung	adenocarcinoma				
IIIA	G3			No	No	
INDI 372	INDI 372 PLS 1A	Positive	Negative			
0.45764	Lung	adenocarcinoma				
IIA	G2			No	No	
INDI 373	INDI 373 PLS 1A	Negative	Negative			
0.13914	Lung	squamous cell carcinoma				
IB	G3			No	No	
INDI 381	INDI 381 PLS 1A	Negative	Negative			
0.39407	Lung	squamous cell carcinoma				
IIIA	G2			No	No	
INDI 383	INDI 383 PLS 1A	Positive	Negative			
0.01914	Lung	squamous cell carcinoma				
IIIB	G3			No	No	
INDI 389	INDI 389 PLS 1A	Positive	Negative			
0.01987	Lung	adenocarcinoma				
IIIA	G3			No	No	
INDI 392	INDI 392 PLS 1A	Negative	Negative			
0.02858	Lung	squamous cell carcinoma				
IB	NA			No	No	
INDI 394	INDI 394 PLS 1A	Positive	Negative			
0.22624	Lung	squamous cell carcinoma				
IIA	G3			No	No	
INDI 395	INDI 395 PLS 1A	Positive	Negative			
0.12706	Lung	squamous cell carcinoma				
IB	G3			No	No	
INDI 403	INDI 403 PLS 1A	Negative	Negative			
0.18055	Lung	squamous cell carcinoma				
IIIA	G3			No	No	
INDI 405	INDI 405 PLS 1A	Negative	Negative			
0.01316	Lung	adenocarcinoma				
IB	G3			No	No	
INDI 624	INDI 624 PLS 1	Positive	Negative			
0.58724	Colorectal	Adenocarcinoma				
II A	3			No	No	
INDI 635	INDI 635 PLS 1	Positive	Negative			
0.26081	Colorectal	Adenocarcinoma				
II A	2			No	No	
INDI 640	INDI 640 PLS 1	Positive	Negative			
0.15824	Colorectal	Adenocarcinoma				
II B	3			No	No	
INDI 643	INDI 643 PLS 1	Positive	Negative			
0.32234	Colorectal	Adenocarcinoma				

Table59.txt

II B	2			No	No		
INDI 644		INDI 644 PLS 1		Positive	Positive		
0.77053		Colorectal		Papillary Adenocarcinoma			
I A	2			No	No		
INDI 647		INDI 647 PLS 1		Positive	Positive		
0.86745		Colorectal		Mucin-producing adenocarcinoma			
IIIA	G3			No	No		
INDI 648		INDI 648 PLS 1		Positive	Positive		
1.00000		Colorectal		Mucinous adenocarcinoma			
IIIB	G3			No	No		
INDI 649		INDI 649 PLS 1		Positive	Negative		
0.22796		Colorectal		Signet ring cell carcinoma			
IIIB	G3			No	No		
INDI 650		INDI 650 PLS 1		Negative	Negative		
0.47213		Colorectal		Adenocarcinoma			
IIIB	G3			No	No		
INDI 651		INDI 651 PLS 1		Negative	Negative		
0.29573		Colorectal		Adenocarcinoma			
IIIA	G3			No	No		
INDI 654		INDI 654 PLS 1		Negative	Positive		
0.69897		Colorectal		Adenocarcinoma with Mucinous Differentiation			
II A	G2			No	No		
INDI 655		INDI 655 PLS 1		Negative	Positive		
0.75685		Colorectal		Mucinous Adenocarcinoma			
II A	G2			No	No		
INDI 657		INDI 657 PLS 1		Positive	Positive		
0.83144		Colorectal		Adenocarcinoma			
II	G2			No	No		
INDI 658		INDI 658 PLS 1		Positive	Negative		
0.05832		Colorectal		Papillary Adenocarcinoma			
I	G2			No	No		
INDI 660		INDI 660 PLS 1		Negative	Negative		
0.57653		Colorectal		Papillary Adenocarcinoma			
II A	G2			No	No		
INDI 708		INDI 708 PLS 1		Positive	Positive		
0.68083		Colorectal		adenocarcinoma			
III B	G2			No	No		
INDI 718		INDI 718 PLS 1		Negative	Negative		
0.03041		Colorectal		adenocarcinoma			
IIA	G2			No	No		
INDI 720		INDI 720 PLS 1		Negative	Negative		
0.31272		Colorectal		mucinous adenocarcinoma			
III B	G2			No	No		
INDI 721		INDI 721 PLS 1		Negative	Negative		
0.10347		Breast		ductal carcinoma			
IIA	G1			No	No		
INDI 722		INDI 722 PLS 1		Negative	Negative		
0.12820		Breast		ductal carcinoma			

Table59.txt

IA	G3			No	No		
INDI 723		INDI 723 PLS 1		Positive	Negative		
0.10057		Ovarian		ovarian carcinoma - serous papillary type			
III C	G3			No	No		
INDI 724		INDI 724 PLS 1		Negative	Negative		
0.15577		Colorectal		adenocarcinoma			
IIA	G2			No	No		
INDI 725		INDI 725 PLS 1		Positive	Negative		
0.05383		Colorectal		adenocarcinoma			
IIA	G2			No	No		
INDI 726		INDI 726 PLS 1		Negative	Negative		
0.38574		Colorectal		adenocarcinoma			
I	G2			No	No		
INDI 727		INDI 727 PLS 1		#N/A	Positive		
1.00000		Colorectal		adenocarcinoma			
IVA	G2			No	No		
INDI 729		INDI 729 PLS 1		Negative	Negative		
0.06858		Colorectal		adenocarcinoma			
IIA	G2			No	No		
INDI 731		INDI 731 PLS 1		Positive	Negative		
0.07494		Pancreas		ductal adenocarcinoma			
IIA	G3			No	No		
INDI 744		INDI 744 PLS 1		#N/A	Negative		
0.09915		Pancreas		ductal adenocarcinoma			
IV	G2			No	No		
INDI 745		INDI 745 PLS 1		Positive	Positive		
0.63332		Pancreas		ductal adenocarcinoma			
IIB	G2			No	No		
INDI 746		INDI 746 PLS 1		Positive	Positive		
0.74897		Colorectal		Adenocarcinoma			
IIIA	G2			No	No		
INDI 747		INDI 747 PLS 1		Positive	Negative		
0.32105		Colorectal		Adenocarcinoma			
IIIA	G2			No	No		
INDI 748		INDI 748 PLS 1		#N/A	Positive		
0.85370		Colorectal		Adenocarcinoma			
IV	G3			No	No		
INDI 749		INDI 749 PLS 1		Negative	Positive		
0.69086		Colorectal		Adenocarcinoma			
IIIC	G3			No	No		
INDI 750		INDI 750 PLS 1		Positive	Negative		
0.12541		Colorectal		Adenocarcinoma			
IIIB	G2			No	No		
INDI 751		INDI 751 PLS 1		Positive	Negative		
0.24666		Colorectal		Adenocarcinoma			
IIIB	G2			No	No		
INDI 752		INDI 752 PLS 1		Positive	Positive		
0.65027		Colorectal		Adenocarcinoma			

Table59.txt

IIIB	G2			No		No	
INDI 758		INDI 758 PLS 1		Positive		Negative	
0.05869		Colorectal		Mucinous adenocarcinoma			
IIA	G3			No		No	
INDI 761		INDI 761 PLS 1		Positive		Negative	
0.55463		Colorectal		Adenocarcinoma			
IIA	G2			No		No	
INDI 763		INDI 763 PLS 1		Negative		Negative	
0.05308		Colorectal		Adenocarcinoma			
I	G2			No		No	
INDI 764		INDI 764 PLS 1		Positive		Negative	
0.45218		Colorectal		Adenocarcinoma			
IIA	G2			No		No	
INDI 765		INDI 765 PLS 1		Positive		Positive	
0.80129		Colorectal		Papillary adenocarcinoma			
IB	G1			No		No	
INDI 767		INDI 767 PLS 1		Positive		Negative	
0.28914		Colorectal		Adenocarcinoma			
IIA	G2			No		No	
INDI 768		INDI 768 PLS 1		Positive		Negative	
0.36734		Colorectal		Adenocarcinoma			
IIB	G2			No		No	
INDI 769		INDI 769 PLS 1		Positive		Negative	
0.05323		Colorectal		Adenocarcinoma			
IIB	G2			No		No	
INDI 770		INDI 770 PLS 1		Positive		Negative	
0.05761		Colorectal		Adenocarcinoma			
IIA	G3			No		No	
INDI 772		INDI 772 PLS 1		Positive		Positive	
0.66417		Colorectal		Papillary adenocarcinoma			
IIA	G2			No		No	
INDI 773		INDI 773 PLS 1		Positive		Negative	
0.19720		Colorectal		Adenocarcinoma			
IIB	G3			No		No	
INDI 774		INDI 774 PLS 1		Positive		Negative	
0.08705		Colorectal		Adenocarcinoma			
I	G2			No		No	
INDI 777		INDI 777 PLS 1		Positive		Negative	
0.33606		Colorectal		Adenocarcinoma			
IIA	G2			No		No	
INDI 779		INDI 779 PLS 1		Positive		Negative	
0.11222		Colorectal		Adenocarcinoma			
IIB	G3			No		No	
INDI 780		INDI 780 PLS 1		Positive		Negative	
0.04804		Colorectal		Mucinous adenocarcinoma			
II	G3			No		No	
INDI 781		INDI 781 PLS 1		Positive		Negative	
0.08716		Colorectal		Adenocarcinoma			

Table59.txt

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   IIA      G2                          No              No
INDI 782          INDI 782 PLS 1     Positive            Positive
0.77913         Colorectal    adenocarcinoma
   III C    G3                          No              No
INDI 783          INDI 783 PLS 1     Negative            Negative
0.25374         Colorectal    adenocarcinoma
   III B    G2                          No              No
INDI 785          INDI 785 PLS 1     Negative            Negative
0.02830         Colorectal    adenocarcinoma
   I        G2                          No              No
INDI 787          INDI 787 PLS 1     Negative            Negative
0.05012         Breast        ductal carcinoma
   IIA      G2                          No              No
INDI 788          INDI 788 PLS 1     Positive            Negative
0.13139         Colorectal    signet-ring cells carcinoma
   IIA      G3                          No              No
INDI 789          INDI 789 PLS 1     Negative            Negative
0.03818         Breast        ductal carcinoma
   IIA      G3                          No              No
INDI 790          INDI 790 PLS 1     Positive            Negative
0.03241         Breast        lobular carcinoma
   IIB      G2                          No              No
INDI 791          INDI 791 PLS 1     Negative            Negative
0.05204         Breast        ductal carcinoma
   III A    G2                          No              No
INDI 793          INDI 793 PLS 1     Negative            Positive
0.60520         Breast        ductal carcinoma
   IIB      G2                          No              No
INDI 794          INDI 794 PLS 1     Negative            Negative
0.15645         Breast        ductal carcinoma
   IIB      G3                          No              No
INDI 795          INDI 795 PLS 1     Negative            Negative
0.06709         Breast        ductal carcinoma
   IIB      G2                          No              No
INDI 798          INDI 798 PLS 1     Positive            Positive
1.00000         Ovarian       ovarian carcinoma - endometrioid type
   IIC      G2                          No              No
INDI 802          INDI 802 PLS 1     Positive            Negative
0.23676         Pancreas      ductal adenocarcinoma
   IIA      G3                          No              No
INDI 804          INDI 804 PLS 1     #N/A                Positive
1.00000         Colorectal    adenocarcinoma
   IVA      G2                          No              No
INDI 805          INDI 805 PLS 1     Negative            Negative
0.30751         Colorectal    adenocarcinoma
   IIA      G2                          No              No
INDI 806          INDI 806 PLS 1     Positive            Negative
0.03921         Colorectal    adenocarcinoma
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Table59.txt

IIA	G2				No		No		
INDI 808		INDI 808	PLS 1		Negative		Negative		
0.30521		Colorectal		adenocarcinoma					
III A	G2				No		No		
INDI 809		INDI 809	PLS 1		Negative		Negative		
0.10214		Colorectal		adenocarcinoma					
III A	G2				No		No		
INDI 810		INDI 810	PLS 1		#N/A		Negative		
0.33433		Colorectal		signet-ring cells carcinoma					
IVA	G3				No		No		
INDI 811		INDI 811	PLS 1		#N/A		Negative		
0.05671		Colorectal		adenocarcinoma					
III B	G2				No		No		
INDI 812		INDI 812	PLS 1		Positive		Negative		
0.48664		Ovarian		ovarian carcinoma - endometrioid type					
IIA	G1				No		No		
INDI 815		INDI 815	PLS 1		Positive		Negative		
0.12364		Colorectal		mucinous adenocarcinoma					
IIA	G1				No		No		
INDI 816		INDI 816	PLS 1		Negative		Negative		
0.07835		Colorectal		adenocarcinoma					
IIA	G2				No		No		
INDI 818		INDI 818	PLS 1		Positive		Positive		
1.00000		Ovarian		adenocarcinoma					
III B	G3				No		No		
INDI 819		INDI 819	PLS 1		Positive		Positive		
1.00000		Breast		lobular carcinoma					
III C	G2				No		No		
INDI 820		INDI 820	PLS 0		#N/A		Positive		
1.00000		Colorectal		Adenocarcinoma					
NA	G2				No		No		
INDI 821		INDI 821	PLS 1		Positive		Positive		
1.00000		Colorectal		adenocarcinoma					
III A	G2				No		No		
INDI 823		INDI 823	PLS 1		Negative		Negative		
0.18139		Breast		ductal carcinoma					
IIA	G2				No		No		
INDI 825		INDI 825	PLS 1		Negative		Negative		
0.07579		Colorectal		adenocarcinoma					
III B	G2				No		No		
INDI 826		INDI 826	PLS 1		Positive		Negative		
0.02114		Colorectal		adenocarcinoma					
IIA	G2				No		No		
INDI 827		INDI 827	PLS 1		Positive		Negative		
0.28577		Colorectal		adenocarcinoma					
III B	G2				No		No		
INDI 828		INDI 828	PLS 1		Negative		Negative		
0.08298		Breast		mucinous carcinoma					

Table59.txt

IIA	G2			No	No		
INDI 829		INDI 829 PLS 1		Negative	Negative		
0.06898		Colorectal		adenocarcinoma			
III B	G2			No	No		
INDI 830		INDI 830 PLS 0		Negative	Negative		
0.43378		Breast		ductal carcinoma			
IIA	G3			No	No		
INDI 831		INDI 831 PLS 1		Negative	Negative		
0.19309		Breast		ductal carcinoma			
IA	G2			No	No		
INDI 832		INDI 832 PLS 1		Negative	Negative		
0.09737		Breast		lobular carcinoma			
IIA	G2			No	No		
INDI 833		INDI 833 PLS 1		Positive	Negative		
0.38065		Breast		ductal carcinoma			
IA	G2			No	No		
INDI 834		INDI 834 PLS 1		#N/A	Negative		
0.08383		Ovarian		ovarian carcinoma - serous papillary type			
IV	G2			No	No		
INDI 835		INDI 835 PLS 1		Positive	Negative		
0.11074		Colorectal		adenocarcinoma			
III B	G2			No	No		
INDI 837		INDI 837 PLS 1		Negative	Negative		
0.21813		Colorectal		adenocarcinoma			
IIA	G2			No	No		
INDI 838		INDI 838 PLS 1		Positive	Negative		
0.06208		Colorectal		adenocarcinoma			
III B	G2			No	No		
INDI 839		INDI 839 PLS 1		Negative	Negative		
0.49284		Breast		lobular carcinoma			
IIA	G1			No	No		
INDI 840		INDI 840 PLS 0		Negative	Negative		
0.12717		Breast		ductal carcinoma			
IIA	G3			No	No		
INDI 841		INDI 841 PLS 1		Positive	Negative		
0.07063		Colorectal		adenocarcinoma			
III C	G2			No	No		
INDI 842		INDI 842 PLS 1		Negative	Negative		
0.01684		Breast		ductal carcinoma			
IA	G1			No	No		
INDI 845		INDI 845 PLS 1		#N/A	Negative		
0.03543		Colorectal		adenocarcinoma			
IVA	G2			No	No		
INDI 862		INDI 862 PLS 1		Positive	Negative		
0.35042		Pancreas		Ductal carcinoma			
IIA	G1			No	No		
INDI 904		INDI 904 PLS 1		#N/A	Positive		
1.00000		Esophagus		Neuroendocrine carcinoma			

Table59.txt

IIA	G3			No	No		
INDI 905		INDI 905 PLS 1		Positive	Negative		
0.43947		Esophagus		Squamous cell carcinoma, keratinizing			
IIA	G2			No	No		
INDI 906		INDI 906 PLS 1		#N/A	Positive		
0.78997		Pancreas		Intraductal papillary carcinoma			
III	G1			No	No		
INDI 907		INDI 907 PLS 1		Negative	Positive		
0.73764		Esophagus		Squamous cell carcinoma			
IIA	G3			No	No		
INDI 908		INDI 908 PLS 1		Positive	Negative		
0.55494		Esophagus		Squamous cell carcinoma, keratinizing			
IIA	G2			No	No		
INDI 909		INDI 909 PLS 1		Positive	Negative		
0.51959		Esophagus		Squamous cell carcinoma			
IIB	G3			No	No		
INDI 910		INDI 910 PLS 1		#N/A	Negative		
0.51260		Esophagus		Squamous cell carcinoma, keratinizing			
III	G3			No	No		
INDI 911		INDI 911 PLS 1		Positive	Positive		
0.71346		Esophagus		Squamous cell carcinoma, keratinizing			
IIA	G2			No	No		
INDI 912		INDI 912 PLS 1		#N/A	Positive		
0.65364		Esophagus		Squamous cell carcinoma, keratinizing			
IIB	G1			No	No		
INDI 913		INDI 913 PLS 1		Negative	Positive		
0.60098		Esophagus		Squamous cell carcinoma, nonkeratinizing,			
III	G3			No	No		
INDI 914		INDI 914 PLS 1		#N/A	Positive		
0.84339		Esophagus		Squamous cell carcinoma, nonkeratinizing,			
III	G2			No	No		
PANC 482		PANC 482 PLS 1		#N/A	Negative		
0.04579		Pancreas		Adenocarcinoma			
IIB	3			No	No		
PANC 483		PANC 483 PLS 1		#N/A	Negative		
0.16394		Pancreas		Adenocarcinoma			
IIB	3			No	No		
PANC 484		PANC 484 PLS 1		#N/A	Positive		
1.00000		Pancreas		Adenocarcinoma			
I	2			No	No		
PANC 485		PANC 485 PLS 1		#N/A	Negative		
0.06603		Pancreas		Adenocarcinoma			
IB	3			No	No		
PANC 486		PANC 486 PLS 1		#N/A	Negative		
0.06133		Pancreas		Adenocarcinoma			
IIB	2			No	No		
PANC 487		PANC 487 PLS 1		#N/A	Negative		
0.03108		Pancreas		Adenocarcinoma			

Table59.txt

IB	2				No	No			
PANC 488		PANC 488 PLS 1		#N/A		Negative			
0.31238		Pancreas		Adenocarcinoma					
IV	NA				No	No			
PANC 490		PANC 490 PLS 1		#N/A		Negative			
0.58122		Pancreas		adenocarcinoma					
IIB	2				No	No			
PANC 491		PANC 491 PLS 1		#N/A		Negative			
0.12559		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 492		PANC 492 PLS 1		#N/A		Negative			
0.17738		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 493		PANC 493 PLS 1		#N/A		Negative			
0.37292		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 494		PANC 494 PLS 1		#N/A		Negative			
0.14724		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 495		PANC 495 PLS 1		#N/A		Negative			
0.36771		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 497		PANC 497 PLS 1		#N/A		Negative			
0.20214		Pancreas		Adenocarcinoma					
IV	NA				No	No			
PANC 499		PANC 499 PLS 1		#N/A		Negative			
0.27391		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 501		PANC 501 PLS 1		#N/A		Negative			
0.02381		Pancreas		Adenocarcinoma					
IV	3				No	No			
PANC 503		PANC 503 PLS 1		#N/A		Negative			
0.14145		Pancreas		Adenocarcinoma					
IV	3				No	No			
PANC 504		PANC 504 PLS 1		#N/A		Negative			
0.47862		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 506		PANC 506 PLS 1		#N/A		Negative			
0.18341		Pancreas		Adenocarcinoma					
IIB	2				No	No			
PANC 507		PANC 507 PLS 1		#N/A		Negative			
0.41212		Pancreas		Adenocarcinoma					
IA	2				No	No			
PANC 509		PANC 509 PLS 1		#N/A		Negative			
0.05462		Pancreas		Adenocarcinoma					
IIB	3				No	No			
PANC 510		PANC 510 PLS 1		#N/A		Negative			
0.10171		Pancreas		Adenocarcinoma					

Table59.txt

```
   IIB      2                          No              No
PANC 512          PANC 512 PLS 1     #N/A               Negative
0.11167         Pancreas      Adenocarcinoma
   IIA      2                          No              No
PANC 513          PANC 513 PLS 1     #N/A               Negative
0.02917         Pancreas      Adenocarcinoma
   IA       2                          No              No
PANC 520          PANC 520 PLS 1     #N/A               Negative
0.54079         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 522          PANC 522 PLS 1     #N/A               Negative
0.40145         Pancreas      NA
   NA       NA                         No              No
PANC 525          PANC 525 PLS 1     #N/A               Negative
0.39630         Pancreas      NA
   NA       NA                         No              No
PANC 526          PANC 526 PLS 1     #N/A               Negative
0.27699         Pancreas      NA
   NA       NA                         No              No
PANC 527          PANC 527 PLS 1     #N/A               Negative
0.37998         Pancreas      NA
   NA       NA                         No              No
PANC 528          PANC 528 PLS 1     #N/A               Negative
0.02459         Pancreas      NA
   NA       NA                         No              No
PANC 529          PANC 529 PLS 1     #N/A               Negative
0.31728         Pancreas      Adenocarcinoma
   IIA      Poor                       No              No
PANC 530          PANC 530 PLS 1     #N/A               Negative
0.04212         Pancreas      NA
   NA       NA                         No              No
PANC 531          PANC 531 PLS 1     #N/A               Negative
0.10066         Pancreas      Adenocarcinoma
   III      Poor-Moderate              No              No
PANC 532          PANC 532 PLS1      #N/A               Negative
0.05021         Pancreas      Adenocarcinoma
   IB       2                          No              No
PANC 533          PANC 533 PLS1      #N/A               Negative
0.14674         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 533          PANC 533 PLS 2     #N/A               Positive
0.81472         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 533          PANC 533 PLS3      #N/A               Positive
0.81191         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 534          PANC 534 PLS 2     #N/A               Positive
0.72890         Pancreas      Adenocarcinoma
```

Table59.txt

IIB 3 No No
PANC 534 PANC 534 PLS 3 #N/A Positive
0.81626 Pancreas Adenocarcinoma
IIB 3 No No
PANC 535 PANC 535 PLS 1 #N/A Negative
0.33774 Pancreas Adenocarcinoma
IIB 3 No No
PANC 536 PANC 536 PLS 1 #N/A Negative
0.46947 Pancreas Adenocarcinoma
IIB 2 No No
PANC 537 PANC 537 PLS 1 #N/A Negative
0.03365 Pancreas Adenocarcinoma
IB 2 No No
PANC 538 PANC 538 PLS 1 #N/A Negative
0.01463 Pancreas Adenocarcinoma
IIA 1 No No
PANC 538 PANC 538 PLS 2 #N/A Positive
0.62968 Pancreas Adenocarcinoma
IIA 1 No No
PANC 538 PANC 538 PLS 3 #N/A Positive
0.75175 Pancreas Adenocarcinoma
IIA 1 No No
PANC 539 PANC 539 PLS 1 #N/A Negative
0.08368 Pancreas Adenocarcinoma
IIA 2 No No
PANC 540 PANC 540 PLS 1 #N/A Negative
0.20661 Pancreas Adenocarcinoma
IIB 2 No No
PANC 541 PANC 541 PLS 1 #N/A Negative
0.46250 Pancreas Adenocarcinoma
IIB 3 No No
PANC 542 PANC 542 PLS 1 #N/A Negative
0.03345 Pancreas Adenocarcinoma
IIB 3 No No
PANC 543 PANC 543 PLS 1 #N/A Negative
0.04523 Pancreas Adenocarcinoma
IIA 2 No No
PANC 544 PANC 544 PLS 1 #N/A Negative
0.12529 Pancreas Adenocarcinoma
IB G2 No No
PANC 544 PANC 544 PLS 2 #N/A Positive
0.64721 Pancreas Adenocarcinoma
IB G2 No No
PANC 545 PANC 545 PLS 1 #N/A Positive
1.00000 Pancreas Adenocarcinoma
IIB G3 No No
PANC 545 PANC 545 PLS 2 #N/A Positive
0.68228 Pancreas Adenocarcinoma

Table59.txt

IIB G3 No No
PANC 546 PANC 546 PLS 1 #N/A Positive
0.67832 Pancreas Adenocarcinoma
IB G3 No No
PANC 546 PANC 546 PLS 2 #N/A Positive
0.70652 Pancreas Adenocarcinoma
IB G3 No No
PANC 547 PANC 547 PLS 1 #N/A Negative
0.08018 Pancreas Adenocarcinoma
IIB G2 No No
PANC 548 PANC 548 PLS 1 #N/A Negative
0.16868 Pancreas Adenocarcinoma
IIB G2 No No
PANC 548 PANC 548 PLS 2 #N/A Negative
0.25560 Pancreas Adenocarcinoma
IIB G2 No No
PANC 549 PANC 549 PLS 1 #N/A Negative
0.32246 Pancreas Adenocarcinoma
IB G2 No No
PANC 550 PANC 550 PLS 1 #N/A Negative
0.06238 Pancreas Adenocarcinoma
IIA G3 No No
PANC 551 PANC 551 PLS 1 #N/A Positive
0.68091 Pancreas Adenocarcinoma
IV G2 No No
PANC 552 PANC 552 PLS 1 #N/A Negative
0.08568 Pancreas Adenocarcinoma
IIB G3 No No
PANC 601 PANC 601 PLS 1 #N/A Negative
0.20559 Pancreas NA
NA NA No No
PANC 602 PANC 602 PLS 1 #N/A Negative
0.42349 Pancreas NA
NA NA No No
PANC 603 PANC 603 PLS 1 #N/A Negative
0.00547 Pancreas NA
NA NA No No
PANC 604 PANC 604 PLS 1 #N/A Negative
0.40913 Pancreas NA
NA NA No No
PANC 605 PANC 605 PLS 1 #N/A Negative
0.07601 Pancreas NA
NA NA No No
PANC 606 PANC 606 PLS 1 #N/A Positive
0.68402 Pancreas NA
NA NA No No
PANC 607 PANC 607 PLS 1 #N/A Negative
0.26822 Pancreas NA

Table59.txt

NA	NA				No	No			
PANC 608		PANC 608 PLS 1	#N/A		Negative				
0.37067		Pancreas	NA						
NA	NA				No	No			
PANC 609		PANC 609 PLS 1	#N/A		Negative				
0.58894		Pancreas	NA						
NA	NA				No	No			
PANC 610		PANC 610 PLS 1	#N/A		Negative				
0.24520		Pancreas	NA						
NA	NA				No	No			
PANC 611		PANC 611 PLS 1	#N/A		Negative				
0.12648		Pancreas	NA						
NA	NA				No	No			
PANC 612		PANC 612 PLS 1	#N/A		Positive				
0.72259		Pancreas	NA						
NA	NA				No	No			
PANC 613		PANC 613 PLS 1	#N/A		Negative				
0.19684		Pancreas	NA						
NA	NA				No	No			
PANC 614		PANC 614 PLS 1	#N/A		Negative				
0.06835		Pancreas	NA						
NA	NA				No	No			
PANC 615		PANC 615 PLS 1	#N/A		Negative				
0.02430		Pancreas	NA						
NA	NA				No	No			
PANC 616		PANC 616 PLS 1	#N/A		Negative				
0.12201		Pancreas	NA						
NA	NA				No	No			
PANC 617		PANC 617 PLS 1	#N/A		Negative				
0.55721		Pancreas	NA						
NA	NA				No	No			
PANC 618		PANC 618 PLS 1	#N/A		Positive				
0.80725		Pancreas	NA						
NA	NA				No	No			
PANC 619		PANC 619 PLS 1	#N/A		Negative				
0.05973		Pancreas	NA						
NA	NA				No	No			
PANC 620		PANC 620 PLS 1	#N/A		Positive				
0.63761		Pancreas	NA						
NA	NA				No	No			
PANC 621		PANC 621 PLS 1	#N/A		Negative				
0.54987		Pancreas	NA						
NA	NA				No	No			
PANC 622		PANC 622 PLS 1	#N/A		Negative				
0.16751		Pancreas	NA						
NA	NA				No	No			
PANC 623		PANC 623 PLS 1	#N/A		Negative				
0.19067		Pancreas	NA						

Table59.txt

```
   NA       NA                          No              No
PANC 624          PANC 624 PLS 1     #N/A               Negative
0.12397         Pancreas      NA
   NA       NA                          No              No
PANC 625          PANC 625 PLS 1     #N/A               Positive
0.72850         Pancreas      NA
   NA       NA                          No              No
PANC 626          PANC 626 PLS 1     #N/A               Negative
0.40571         Pancreas      NA
   NA       NA                          No              No
PANC 627          PANC 627 PLS 1     #N/A               Positive
0.70651         Pancreas      NA
   NA       NA                          No              No
PANC 628          PANC 628 PLS 1     #N/A               Negative
0.51240         Pancreas      NA
   NA       NA                          No              No
PANC 629          PANC 629 PLS 1     #N/A               Negative
0.58219         Pancreas      NA
   NA       NA                          No              No
PANC 630          PANC 630 PLS 1     #N/A               Positive
0.79198         Pancreas      NA
   NA       NA                          No              No
PANC 631          PANC 631 PLS 1     #N/A               Negative
0.41117         Pancreas      NA
   NA       NA                          No              No
PANC 632          PANC 632 PLS 1     #N/A               Negative
0.07187         Pancreas      NA
   NA       NA                          No              No
PANC 633          PANC 633 PLS 1     #N/A               Negative
0.42659         Pancreas      NA
   NA       NA                          No              No
PANC 634          PANC 634 PLS 1     #N/A               Positive
0.75290         Pancreas      NA
   NA       NA                          No              No
PANC 635          PANC 635 PLS 1     #N/A               Positive
0.70030         Pancreas      NA
   NA       NA                          No              No
PANC 636          PANC 636 PLS 1     #N/A               Negative
0.15801         Pancreas      NA
   NA       NA                          No              No
PANC 637          PANC 637 PLS 1     #N/A               Positive
0.67528         Pancreas      NA
   NA       NA                          No              No
PANC 638          PANC 638 PLS 1     #N/A               Negative
0.30434         Pancreas      NA
   NA       NA                          No              No
PANC 639          PANC 639 PLS 1     #N/A               Negative
0.10701         Pancreas      NA
```

Table59.txt

NA	NA				No	No			
PANC 640		PANC 640 PLS 1			#N/A		Negative		
0.24454		Pancreas		NA					
NA	NA				No	No			
PANC 641		PANC 641 PLS 1			#N/A		Negative		
0.03313		Pancreas		NA					
NA	NA				No	No			
PANC 642		PANC 642 PLS 1			#N/A		Negative		
0.04294		Pancreas		NA					
NA	NA				No	No			
PANC 643		PANC 643 PLS 1			#N/A		Negative		
0.04391		Pancreas		NA					
NA	NA				No	No			
PANC 644		PANC 644 PLS 1			#N/A		Negative		
0.05608		Pancreas		NA					
NA	NA				No	No			
PANC 645		PANC 645 PLS 1			#N/A		Negative		
0.18868		Pancreas		NA					
NA	NA				No	No			
PANC 646		PANC 646 PLS 1			#N/A		Negative		
0.05442		Pancreas		NA					
NA	NA				No	No			
PANC 647		PANC 647 PLS 1			#N/A		Negative		
0.28890		Pancreas		NA					
NA	NA				No	No			
PANC 648		PANC 648 PLS 1			#N/A		Negative		
0.01994		Pancreas		NA					
NA	NA				No	No			
PANC 649		PANC 649 PLS 1			#N/A		Negative		
0.09869		Pancreas		NA					
NA	NA				No	No			
PANC 650		PANC 650 PLS 1			#N/A		Negative		
0.09220		Pancreas		NA					
NA	NA				No	No			
PANC 651		PANC 651 PLS 1			#N/A		Positive		
0.84407		Pancreas		NA					
NA	NA				No	No			
PANC 652		PANC 652 PLS 1			#N/A		Negative		
0.18578		Pancreas		NA					
NA	NA				No	No			
PANC 653		PANC 653 PLS 1			#N/A		Negative		
0.13047		Pancreas		NA					
NA	NA				No	No			
PANC 654		PANC 654 PLS 1			#N/A		Negative		
0.03341		Pancreas		NA					
NA	NA				No	No			
PANC 655		PANC 655 PLS 1			#N/A		Negative		
0.01990		Pancreas		NA					

Table59.txt

| | | |

Table59.txt

IIB	Moderately differentiated	No	No			
PANC 672	PANC 672 PLS 1	Positive	Negative			
0.08516	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	Yes	Yes			
PANC 673	PANC 673 PLS 1	Negative	Negative			
0.30252	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	Yes	Yes			
PANC 674	PANC 674 PLS 1	Positive	Negative			
0.35040	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	Yes	Yes			
PANC 675	PANC 675 PLS 1	Positive	Negative			
0.16397	Pancreas	Adenocarcinoma				
IIB	poorly differentiated	Yes	Yes			
PANC 676	PANC 676 PLS 1	Positive	Negative			
0.02575	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	No	Yes			
PANC 677	PANC 677 PLS 1	Positive	Negative			
0.08552	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	No	No			
PANC 678	PANC 678 PLS 1	Negative	Negative			
0.22407	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	No	Yes			
PANC 679	PANC 679 PLS 1	Negative	Negative			
0.01684	Pancreas	Adenocarcinoma				
IIA	poorly differentiated	Yes	Yes			
PANC 680	PANC 680 PLS 1	Positive	Negative			
0.11527	Pancreas	Adenocarcinoma				
IIB	Moderately differentiated	Yes	Yes			
INDI 915	INDI 915 PLS 1	Negative	Negative			
0.23550	Breast	ductal carcinoma				
IIA	G2	No	No			
INDI 916	INDI 916 PLS 1	#N/A	Negative			
0.43986	Liver	hepatocellular carcinoma				
II	G2	No	No			
INDI 917	INDI 917 PLS 1	Positive	Positive			
1.00000	Liver	NA				
IIIA	G2	No	No			
INDI 918	INDI 918 PLS 1	#N/A	Negative			
0.03686	Stomach	NA				
IV	G3	No	No			
INDI 919	INDI 919 PLS 1	Negative	Negative			
0.09669	Breast	NA				
IIA	G2	No	No			
INDI 920	INDI 920 PLS 1	Positive	Positive			
0.71170	Ovarian	NA				
IIIC	NA	No	No			
INDI 921	INDI 921 PLS 1	Negative	Negative			
0.25608	Breast	ductal carcinoma				

Table59.txt

IIA G2 No No
INDI 922 INDI 922 PLS 1 Negative Negative
0.02740 Breast NA
IIB G3 No No
INDI 923 INDI 923 PLS 1 Negative Negative
0.32969 Esophagus NA
IB G2 No No
INDI 924 INDI 924 PLS 1 Negative Negative
0.07993 Breast NA
IIIA G2 No No
INDI 925 INDI 925 PLS 1 #N/A Positive
1.00000 Stomach adenocarcinoma, partially of signet ring cell-type -
diffIV G3 No No
INDI 926 INDI 926 PLS 1 Negative Negative
0.01600 Breast NA
IV G3 No No
INDI 927 INDI 927 PLS 1 Negative Negative
0.18567 Breast NA
IIA G2 No No
INDI 928 INDI 928 PLS 1 Positive Negative
0.26522 Stomach adenocarcinoma - intestinal type
IIB G2 No No
INDI 929 INDI 929 PLS 1 Negative Negative
0.06499 Stomach adenocarcinoma
IIB G3 No No
INDI 930 INDI 930 PLS 1 Negative Negative
0.10758 Stomach adenocarcinoma
IIB G3 No No
INDI 931 INDI 931 PLS 1 Positive Negative
0.00717 Ovarian NA
IIIB NA No No
INDI 932 INDI 932 PLS 1 Positive Positive
1.00000 Ovarian carcinoma - serous papillary type
III C G3 No No
INDI 933 INDI 933 PLS 1 Negative Negative
0.07277 Esophagus adenocarcinoma - intestinal type
III B G2 No No
INDI 934 INDI 934 PLS 1 #N/A Negative
0.02807 Ovarian carcinoma - serous type
IV G3 No No
INDI 935 INDI 935 PLS 1 Negative Negative
0.06934 Esophagus NA
IA G1 No No
INDI 936 INDI 936 PLS 1 Negative Negative
0.10921 Ovarian NA
IC G3 No No
INDI 937 INDI 937 PLS 1 Negative Negative
0.05491 Esophagus adenocarcinoma

Table59.txt

III C G2 No No
INDI 276 INDI 276 PLS 1 Positive Positive
1.00000 Liver combined hepatocellular carcinoma and
cholangiocarcinoma NA NA No No
PANC 694 PANC 694 PLS1 #N/A Negative
0.04552 Pancreas Adenocarcinoma
IIB 2 No No
PANC 695 PANC 695 PLS 1 #N/A Negative
0.07935 Pancreas Adenocarcinoma
IIB 3 No No
PANC 695 PANC 695 PLS 2 #N/A Positive
0.78338 Pancreas Adenocarcinoma
IIB 3 No No
PANC 695 PANC 695 PLS 3 #N/A Positive
0.81129 Pancreas Adenocarcinoma
IIB 3 No No
PANC 696 PANC 696 PLS 1 #N/A Positive
0.78966 Pancreas Adenocarcinoma
IIB 3 No No
PANC 697 PANC 697 PLS 1 #N/A Negative
0.26394 Pancreas Adenocarcinoma
IIB 3 No No
PANC 698 PANC 698 PLS 1 #N/A Positive
0.64961 Pancreas adenocarcinoma
III 2 No No
PANC 699 PANC 699 PLS 1 #N/A Negative
0.41305 Pancreas Adenocarcinoma
IIB 3 No No
PANC 700 PANC 700 PLS 1 #N/A Negative
0.36779 Pancreas Adenocarcinoma
IIB 4 No No
PANC 701 PANC 701 PLS 1 #N/A Negative
0.13569 Pancreas Adenocarcinoma
IA 2 No No
PANC 702 PANC 702 PLS 1 #N/A Negative
0.19659 Pancreas Adenocarcinoma
IIB 2 No No
PANC 702 PANC 702 PLS 2 #N/A Positive
0.72228 Pancreas Adenocarcinoma
IIB 2 No No
PANC 702 PANC 702 PLS 3 #N/A Negative
0.33052 Pancreas Adenocarcinoma
IIB 3 No No
PANC 703 PANC 703 PLS 1 #N/A Negative
0.11521 Pancreas Adenocarcinoma
IIB 2 No No
PANC 704 PANC 704 PLS 1 #N/A Negative
0.42378 Pancreas Adenocarcinoma

Table59.txt

IIB 3 No No
PANC 705 PANC 705 PLS 1 #N/A Negative
0.10581 Pancreas Adenocarcinoma
IIB 3 No No
PANC 706 PANC 706 PLS 1 #N/A Negative
0.13533 Pancreas Adenocarcinoma
IIA 2 No No
PANC 707 PANC 707 PLS 1 #N/A Negative
0.01455 Pancreas Adenocarcinoma
IIA 2 No No
PANC 707 PANC 707 PLS 3 #N/A Negative
0.06958 Pancreas Adenocarcinoma
IIA 2 No No
PANC 709 PANC 709 PLS 1 #N/A Negative
0.04017 Pancreas Adenocarcinoma
IB 3 No No
PANC 710 PANC 710 PLS 1 #N/A Negative
0.05958 Pancreas Adenocarcinoma
IIB 3 No No
PANC 711 PANC 711 PLS 1 #N/A Negative
0.12109 Pancreas Adenocarcinoma
IIB 2 No No
PANC 712 PANC 712 PLS 1 #N/A Negative
0.32084 Pancreas Adenocarcinoma
IIB 2 No No
PANC 713 PANC 713 PLS 1 #N/A Negative
0.32889 Pancreas Adenocarcinoma
IIB 2 No No
PANC 714 PANC 714 PLS 1 #N/A Negative
0.42528 Pancreas Adenocarcinoma
IIB 1 No No
PANC 714 PANC 714 PLS 2 #N/A Positive
0.79120 Pancreas Adenocarcinoma
IIB 1 No No
PANC 714 PANC 714 PLS 3 #N/A Positive
0.62615 Pancreas Adenocarcinoma
IIB 1 No No
PANC 716 PANC 716 PLS 1 #N/A Negative
0.03173 Pancreas Adenocarcinoma
IA 2 No No
PANC 717 PANC 717 PLS 1 #N/A Negative
0.57025 Pancreas Adenocarcinoma
IIB 2 No No
PANC 718 PANC 718 PLS 1 #N/A Negative
0.40277 Pancreas adenocarcinoma
IIB 3 No No
PANC 719 PANC 719 PLS 1 #N/A Positive
0.72417 Pancreas Adenocarcinoma

Table59.txt

```
   IIB      2                          No              No
PANC 720          PANC 720 PLS 1     #N/A                Positive
0.77023         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 721          PANC 721 PLS 1     #N/A                Negative
0.38429         Pancreas      Adenocarcinoma
   IB       2                          No              No
PANC 722          PANC 722 PLS 1     #N/A                Negative
0.30598         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 723          PANC 723 PLS 1     #N/A                Negative
0.09029         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 723          PANC 723 PLS 2     #N/A                Negative
0.47499         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 723          PANC 723 PLS 3     #N/A                Negative
0.50699         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 724          PANC 724 PLS 1     #N/A                Positive
0.77293         Pancreas      Adenocarcinoma
   IIB      3                          No              No
PANC 725          PANC 725 PLS 1     #N/A                Positive
1.00000         Pancreas      Adenocarcinoma
   IB       3                          No              No
PANC 726          PANC 726 PLS 1     #N/A                Negative
0.56650         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 726          PANC 726 PLS 2     #N/A                Positive
0.79776         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 726          PANC 726 PLS 3     #N/A                Positive
0.60840         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 727          PANC 727 PLS 1     #N/A                Negative
0.00272         Pancreas      Adenocarcinoma
   IV       NA                         No              No
PANC 728          PANC 728 PLS 1     #N/A                Negative
0.05654         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 729          PANC 729 PLS 1     #N/A                Negative
0.58171         Pancreas      Adenocarcinoma
   IIB      2                          No              No
PANC 730          PANC 730 PLS 1     #N/A                Negative
0.37371         Pancreas      Adenocarcinoma
   IIB      2                          No              No
```

Table59.txt

Mutant Allele Fraction	Mutation	Gene	Estimated Fraction	Age	Sex	Ethnicity
0.02	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.04	61	Male	Caucasian
0.005	TP53_0272_0283.chr17.7577120.C>A	TP53	0.009	63	Male	Caucasian
0.001	TP53_219_224.chr17.7578191.A>G	TP53	0.001	70	Female	Caucasian
0.001	TP53_262_267.chr17.7577141.C>A	TP53	0.002	66	Male	Caucasian
0	TP53_219_224.chr17.7578190.T>C	TP53	0.001	60	Male	Caucasian
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	69	Male	Caucasian
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	55	Female	Caucasian
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	68	Female	Caucasian
0.013	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.026	63	Female	Caucasian
0.009	TP53_262_267.chr17.7577141.C>T	TP53	0.019	73	Male	Caucasian
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.015	73	Male	Caucasian
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	63	Male	Caucasian
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	63	Male	Caucasian
0.001	TP53_151_163.chr17.7578466.G>T	TP53	0.001	69	Female	Caucasian
0.016	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.033	45	Male	Caucasian
0	GNAS_201.chr20.57484420.C>T	GNAS	0.001	51	Male	Black
0.001	TP53_098_109.chr17.7579389.G>A	TP53	0.002	82	Female	Caucasian
0	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	69	Male	Caucasian
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	62	Male	Caucasian
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.002	69	Male	Caucasian
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	70	Male	Caucasian
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.014	62	Female	Black

Table59.txt

0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	50
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	65
Female	Caucasian			
0.001	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA
NA	NA			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	50
Male	Black			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	50
Male	Black			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	65
Male	Caucasian			
0.214	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.427	NA
NA	NA			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA
NA	NA			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	NA
NA	NA			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	60
Male	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA
NA				
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	NA
NA				
0.001	TP53_0272_0283.chr17.7577111.G>A	TP53	0.002	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.003	NA
NA	NA			
0.001	TP53_151_163.chr17.7578461.C>T	TP53	0.002	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	NA
NA				
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.002	NA
NA	NA			
0.004	TP53_0196_0205.chr17.7578263.G>A	TP53	0.007	NA
NA	NA			
0.001	TP53_172A.chr17.7578389.G>A	TP53	0.001	NA
NA	NA			
0	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA
NA	NA			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577536.T>A	TP53	0.001	44
Male	Caucasian			
0.003	TP53_167_177.chr17.7578406.C>T	TP53	0.007	68
Male	Caucasian			

Table59.txt

0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.001	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	72
Female	Caucasian			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.002	62
Male	Caucasian			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.003	69
Male	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA
NA	NA			
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.005	63
Female	Hispanic			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	40
Female	Caucasian			
0.001	TP53_167_177.chr17.7578401.G>A	TP53	0.002	74
Male	Caucasian			
0.002	TP53_167_177.chr17.7578421.G>A	TP53	0.003	74
Male	Caucasian			
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.016	70
Male	Caucasian			
0.004	TP53_0272_0283.chr17.7577124.C>T	TP53	0.009	79
Male	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.008	48
Female	Caucasian			
0.008	TP53_0248_0261.chr17.7577536.T>A	TP53	0.016	69
Male	Caucasian			
0	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	NA
NA	NA			
0	TP53_262_267.chr17.7577153.C>A	TP53	0.001	86
Female	Caucasian			
0	TP53_132_142.chr17.7578527.A>C	TP53	0.001	63
Female	Caucasian			
0.002	TP53_172A.chr17.7578400.G>A	TP53	0.004	72
Male	Caucasian			
0.001	PTEN_91_98.chr10.89692791.A>G	PTEN	0.002	66
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	73
Female	Caucasian			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	68
Male	Caucasian			
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA
NA	NA			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	73
Male	Caucasian			
0.001	TP53_172A.chr17.7578396.G>T	TP53	0.003	54.3
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	76.7
Female	Caucasian			

Table59.txt

0.001	TP53_151_163.chr17.7578463.C>G	TP53	0.001	72.3
Male	Caucasian			
0.001	KRAS_144_147A.chr12.25378562.C>T	KRAS	0.001	85.3
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	78.6
Male	Caucasian			
0	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	59.6
Female	Caucasian			
0.046	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.092	77.5
Male	Caucasian			
0.001	PTEN_136.chr10.89692923.G>A	PTEN	0.001	47.6
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.002	82
Male	Caucasian			
0.001	TP53_113_125.chr17.7579350.A>C	TP53	0.001	69
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.001	66
Female	Caucasian			
0	KRAS_0057_0064.chr12.25380276.T>C	KRAS	0.001	75
Male	Caucasian			
0.047	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.094	48
Female	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	66
Male	Caucasian			
0.001	TP53_151_163.chr17.7578464.G>A	TP53	0.002	59
Female	Caucasian			
0.001	PIK3CA_0345.chr3.178921548.G>A	PIK3CA	0.002	79
Female	Caucasian			
0.002	GNAS_201.chr20.57484420.C>T	GNAS	0.004	63
Female	Caucasian			
0.005	TP53_188_195.chr17.7578265.A>G	TP53	0.009	58
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	66
Female	Caucasian			
0	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	67
Female	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	76
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	71
Female	Caucasian			
0.001	TP53_151_163.chr17.7578461.C>A	TP53	0.001	78
Male	Black			
0	TP53_0227_0236.chr17.7577580.T>C	TP53	0.001	69.4
Male	Caucasian			
0.001	TP53_172A.chr17.7578407.G>A	TP53	0.001	67.2
Female	Caucasian			
0.001	TP53_167_177.chr17.7578431.G>A	TP53	0.001	63.5
Male	Caucasian			

Table59.txt

0.003	TP53_0227_0236.chr17.7577571.A>T	TP53	0.006	52.9
Female	Caucasian			
0	TP53_151_163.chr17.7578475.G>A	TP53	0.001	60.5
Male	Caucasian			
0	TP53_208_218.chr17.7578204.A>T	TP53	0.001	56.5
Male	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	90.3
Female	Caucasian			
0.001	TP53_233_245.chr17.7577548.C>T	TP53	0.003	75.7
Female	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	68.8
Female	Caucasian			
0	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.001	74.3
Male	Caucasian			
0	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	76.9
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.003	67.6
Male	Caucasian			
0.001	GNAS_201.chr20.57484420.C>T	GNAS	0.001	69.2
Male	African American			
0.001	PTEN_136.chr10.89692923.G>A	PTEN	0.002	60.4
Female	NA			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	59.5
Female	Caucasian			
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.016	67.4
Male	Caucasian			
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	67.7
Male	Caucasian			
0	TP53_167_177.chr17.7578408.C>A	TP53	0.001	77.3
Female	Caucasian			
0	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	83.3
Female	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	NA
NA	NA			
0.022	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.044	70
Male	Caucasian			
0	TP53_167_177.chr17.7578410.T>C	TP53	0.001	78
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	56
Female	Caucasian			
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.002	51
Female	Caucasian			
0	TP53_172A.chr17.7578389.G>A	TP53	0.001	52
Male	Caucasian			
0.008	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.015	27
Male	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	67
Male	Caucasian			

Table59.txt

0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.003	64
Female	Caucasian			
0.001	TP53_219_224.chr17.7578191.A>G	TP53	0.001	65
Female	Caucasian			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	41
Male	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.003	53
Female	Caucasian			
0.002	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.003	NA
NA	NA			
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	51
Male	Caucasian			
0.001	TP53_126_131.chr17.7578538.T>C	TP53	0.001	51
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.001	63
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	63
Female	Caucasian			
0	TP53_233_245.chr17.7577550.C>T	TP53	0.001	63
Female	Caucasian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	85
Male	Other			
0	TP53_342.chr17.7574018.G>A	TP53	0.001	85
Male	Other			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	77
Male	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	77
Male	Caucasian			
0	TP53_132_142.chr17.7578530.A>C	TP53	0.001	77
Male	Caucasian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	69
Male	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	69
Male	Caucasian			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	69
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	78
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	78
Male	Caucasian			
0.001	TP53_151_163.chr17.7578464.G>A	TP53	0.002	78
Male	Caucasian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0	78
Female	Caucasian			
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.003	78
Female	Caucasian			
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	78
Female	Caucasian			

Table59.txt

0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	72
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	72
Male	Caucasian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	72
Male	Caucasian			
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.001	80
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.005	79
Male	Caucasian			
0.005	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.009	79
Male	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	79
Male	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA
NA	NA			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA
NA	NA			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.002	NA
NA	NA			
0	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.001	65
Male	Caucasian			
0	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA
NA	NA			
0.013	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.026	58
Male	Caucasian			
0.001	TP53_342.chr17.7574018.G>A	TP53	0.003	61
Female	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	66
Male	Caucasian			
0	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	54
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.002	85
Male	Caucasian			
0.002	TP53_0248_0261.chr17.7577538.C>T	TP53	0.003	72
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.003	82
Female	Caucasian			
0.003	TP53_233_245.chr17.7577559.G>T	TP53	0.007	71
Female	Caucasian			
0	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	81
Female	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	81
Female	Caucasian			
0	TP53_298_306.chr17.7577022.G>A	TP53	0.001	81
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	44
Male	Caucasian			

Table59.txt

0.002	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	67
Male	Caucasian			
0.002	TP53_0280_0289.chr17.7577094.G>A	TP53	0.003	67
Male	Caucasian			
0.002	TP53_0280_0289.chr17.7577094.G>A	TP53	0.003	67
Male	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	80
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	80
Female	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	80
Female	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	80
Female	Caucasian			
0.001	TP53_172A.chr17.7578407.G>A	TP53	0.001	48
Male	Caucasian			
0	TP53_262_267.chr17.7577139.G>A	TP53	0.001	61
Male	Caucasian			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	75
Male	Caucasian			
0.231	TP53_0248_0261.chr17.7577505.T>A	TP53	0.461	84
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.004	82
Male	Caucasian			
0	TP53_0196_0205.chr17.7578253.C>A	TP53	0.001	64
Female	Caucasian			
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.002	64
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	64
Female	Caucasian			
0.003	NRAS_4_14.chr1.115258747.C>T	NRAS	0.006	80
Male	Caucasian			
0	BRAF_594_602.chr7.140453145.A>T	BRAF	0.001	70
Male	Other			
0.001	TP53_0196_0205.chr17.7578235.T>C	TP53	0.002	79
Female	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	68
Male	Black			
0.002	TP53_172A.chr17.7578403.C>T	TP53	0.004	63
Male	Caucasian			
0	TP53_172A.chr17.7578407.G>A	TP53	0.001	56
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577517.A>C	TP53	0.003	71
Female	Caucasian			
0	CDKN2A_7_88.chr9.21971098.C>T	CDKN2A	0.001	81
Female	Caucasian			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	58
Female	Black			

Table59.txt

0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.004	49
Male	Caucasian			
0.006	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.011	66
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577093.C>T	TP53	0.004	83
Female	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.005	65
Male	Caucasian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	68
Female	Caucasian			
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.005	72
Male	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	74
Male	Caucasian			
0.001	TP53_233_245.chr17.7577568.C>T	TP53	0.002	56
Female	Caucasian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	70
Male	Caucasian			
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.001	65
Male	Caucasian			
0.001	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.002	65
Male	Caucasian			
0	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.001	65
Male	Caucasian			
0.001	TP53_0227_0236.chr17.7577571.A>T	TP53	0.001	59
Female	Caucasian			
0.001	PTEN_130.chr10.89692905.G>A	PTEN	0.001	59
Female	Caucasian			
0	PTEN_130.chr10.89692905.G>A	PTEN	0.001	59
Female	Caucasian			
0	TP53_122.chr17.7579313.G>A	TP53	0.001	70
Female	Caucasian			
0	TP53_0227_0236.chr17.7577604.C>A	TP53	0.001	70
Female	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	56
Male	Caucasian			
0.001	TP53_342.chr17.7574018.G>A	TP53	0.001	56
Male	Caucasian			
0.004	TP53_167_177.chr17.7578403.C>T	TP53	0.007	56
Female	Caucasian			
0.007	TP53_172A.chr17.7578403.C>T	TP53	0.014	56
Female	Caucasian			
0.029	TP53_233_245.chr17.7577559.G>A	TP53	0.057	48
Male	Caucasian			
0.034	TP53_233_245.chr17.7577559.G>A	TP53	0.068	48
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	53
Male	Caucasian			

Table59.txt

0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	53
Male	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	70
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	70
Female	Caucasian			
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.007	NA
NA	NA			
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.005	NA
NA	NA			
0	TP53_172A.chr17.7578407.G>A	TP53	0.001	58
Male	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.004	58
Male	Caucasian			
0.001	TP53_098_109.chr17.7579358.C>G	TP53	0.002	48
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	72
Male	Caucasian			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.001	72
Male	Caucasian			
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.002	70
Male	Caucasian			
0.001	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.003	70
Male	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	59
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005	59
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	59
Male	Caucasian			
0	TP53_172A.chr17.7578407.G>A	TP53	0.001	59
Male	Caucasian			
0.001	TP53_132_142.chr17.7578524.G>C	TP53	0.001	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577117.A>G	TP53	0.002	NA
NA	NA			
0.04	TP53_0280_0289.chr17.7577096.T>C	TP53	0.08	NA
NA	NA			
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.003	NA
NA	NA			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	NA
NA	NA			
0.006	TP53_342.chr17.7574021.C>A	TP53	0.013	NA
NA	NA			
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	NA
NA	NA			
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003	74
Female	Caucasian			

Table59.txt

0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	NA
NA	NA			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	NA
NA	NA			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA
NA	NA			
0.003	TP53_0280_0289.chr17.7577094.G>A	TP53	0.005	NA
NA	NA			
0	PTEN_91_98.chr10.89692803.C>T	PTEN	0.001	NA
NA	NA			
0.001	TP53_132_142.chr17.7578513.C>A	TP53	0.002	NA
NA	NA			
0.002	TP53_151_163.chr17.7578461.C>T	TP53	0.003	NA
NA	NA			
0.133	GNAS_201.chr20.57484421.G>A	GNAS	0.266	NA
NA	NA			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.003	NA
NA	NA			
0.012	GNAS_201.chr20.57484421.G>A	GNAS	0.025	NA
NA	NA			
0.001	TP53_172A.chr17.7578407.G>A	TP53	0.002	43
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	72
Female	Caucasian			
0.003	TP53_167_177.chr17.7578406.C>T	TP53	0.005	NA
NA	NA			
0.001	TP53_151_163.chr17.7578457.C>T	TP53	0.001	NA
NA	NA			
0.002	TP53_233_245.chr17.7577580.T>C	TP53	0.004	NA
NA	NA			
0.002	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	74
Male	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA
NA	NA			
0.002	TP53_0280_0289.chr17.7577070.G>A	TP53	0.004	NA
NA	NA			
0.005	TP53_113_125.chr17.7579313.G>A	TP53	0.01	60
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	62
Male	Caucasian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	78
Female	Caucasian			
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.003	50
Male	Caucasian			

Table59.txt

0.018	TP53_188_195.chr17.7578266.T>A	TP53	0.036	66
Female	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.008	66
Male	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.008	66
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	54
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.004	65
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577124.C>T	TP53	0.002	68
Female	Caucasian			
0.001	PTEN_91_98.chr10.89692802.C>G	PTEN	0.002	NA
NA	NA			
0.001	CTNNB1_0032_0039.chr3.41266104.G>A	CTNNB1	0.002	NA
NA	NA			
0.001	TP53_342.chr17.7574003.G>A	TP53	0.002	NA
NA	NA			
0.001	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.001	NA
NA	NA			
0.002	TP53_167_177.chr17.7578406.C>T	TP53	0.004	NA
NA	NA			
0.001	PTEN_91_98.chr10.89692802.C>G	PTEN	0.003	NA
NA	NA			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	NA
NA	NA			
0.007	TP53_167_177.chr17.7578406.C>T	TP53	0.013	NA
NA	NA			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.001	NA
NA	NA			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.003	NA
NA	NA			
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.001	NA
NA	NA			
0	TP53_167_177.chr17.7578407.G>A	TP53	0.001	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA
NA	NA			
0.002	TP53_208_218.chr17.7578208.T>C	TP53	0.004	NA
NA	NA			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA
NA	NA			
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.002	NA
NA	NA			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	NA
NA	NA			
0.004	GNAS_201.chr20.57484421.G>A	GNAS	0.007	NA
NA	NA			

Table59.txt

0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.003	NA
NA	NA			
0.003	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.005	NA
NA	NA			
0.004	TP53_219_224.chr17.7578190.T>C	TP53	0.008	NA
NA	NA			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	NA
NA	NA			
0.001	TP53_083_94.chr17.7579414.C>T	TP53	0.002	NA
NA	NA			
0.002	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	NA
NA	NA			
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.002	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	86
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	72
Male	Caucasian			
0.001	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.001	69
Female	African American			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	61
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	65
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.003	72
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	54
Male	NA			
0	TP53_098_109.chr17.7579378.G>C	TP53	0.001	53
Female	Caucasian			
0.002	FBXW7_505.chr4.153247288.C>T	FBXW7	0.003	62
Female	Caucasian			
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	56
Female	Caucasian			
0.005	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.01	65
Male	Caucasian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	70
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577103.C>T	TP53	0.002	56
Male	Caucasian			
0.002	TP53_0248_0261.chr17.7577539.G>A	TP53	0.004	58
Female	Caucasian			
0.012	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.025	79
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001	64
Male	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	81
Female	Caucasian			

Table59.txt

0.002	TP53_0272_0283.chr17.7577114.C>T	TP53	0.005	69
Male	Caucasian			
0.002	FBXW7_505.chr4.153247289.G>A	FBXW7	0.004	82
Female	Caucasian			
0.001	TP53_026.chr17.7579717.G>A	TP53	0.002	74
Male	Caucasian			
0.002	TP53_122.chr17.7579313.G>A	TP53	0.003	65
Male	Caucasian			
0.002	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.004	63
Female	Caucasian			
0.001	TP53_219_224.chr17.7578190.T>C	TP53	0.002	65
Male	Caucasian			
0.001	APC_1450_1458.chr5.112175639.C>T	APC	0.002	69
Female	Caucasian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	63
Female	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.001	68
Male	Caucasian			
0	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	63
Male	Caucasian			
0.003	TP53_167_177.chr17.7578407.G>A	TP53	0.006	52
Male	Caucasian			
0.002	TP53_208_218.chr17.7578212.G>A	TP53	0.004	75
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.002	63
Male	Caucasian			
0.004	TP53_0227_0236.chr17.7577580.T>C	TP53	0.007	56
Female	Caucasian			
0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.002	60
Female	Caucasian			
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	48
Male	Other			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	82
Female	Caucasian			
0	TP53_122.chr17.7579315.G>T	TP53	0.001	68
Female	Caucasian			
0	TP53_0272_0283.chr17.7577111.G>A	TP53	0.001	62
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	78
Male	Caucasian			
0.001	TP53_122.chr17.7579315.G>T	TP53	0.001	78
Female	Caucasian			
0.487	CDKN2A_051_057.chr9.21971188.G>A	CDKN2A	0.974	75
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.003	60
Male	Caucasian			
0.001	TP53_0227_0236.chr17.7577586.A>T	TP53	0.002	64
Male	Caucasian			

Table59.txt

0.001	TP53_233_245.chr17.7577570.C>T	TP53	0.002	71
Male	Caucasian			
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.002	68
Female	Caucasian			
0.001	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.003	55
Male	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA
NA	NA			
0.003	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.006	67
Male	Caucasian			
0.003	TP53_233_245.chr17.7577581.A>G	TP53	0.006	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577106.G>T	TP53	0.002	62
Male	Caucasian			
0.158	TP53_233_245.chr17.7577568.C>T	TP53	0.317	NA
NA	NA			
0.008	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.017	73
Male	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA
NA	NA			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	70
Female	Caucasian			
0.001	APC_1450_1458.chr5.112175639.C>T	APC	0.002	55
Female	Caucasian			
0.001	PTEN_130.chr10.89692907.A>G	PTEN	0.002	78
Male	Caucasian			
0.001	FBXW7_464_472A.chr4.153249384.C>T	FBXW7	0.002	75
Male	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.002	70
Male	Caucasian			
0.001	TP53_098_109.chr17.7579377.G>A	TP53	0.002	73
Male	Caucasian			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001	69
Female	Caucasian			
0.017	FBXW7_474_482.chr4.153247367.G>C	FBXW7	0.034	61
Male	Caucasian			
0.013	TP53_167_177.chr17.7578403.C>A	TP53	0.025	67
Male	Caucasian			
0.003	TP53_0272_0283.chr17.7577121.G>A	TP53	0.006	76
Male	Caucasian			
0.001	PTEN_136.chr10.89692925.G>A	PTEN	0.001	60
Male	Caucasian			
0.001	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.003	65
Male	Caucasian			
0.001	TP53_188_195.chr17.7578265.A>G	TP53	0.001	78
Male	Caucasian			
0.014	TP53_298_306.chr17.7577046.C>A	TP53	0.027	45
Male	Caucasian			

Table59.txt

0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.001	80
Female	Caucasian			
0.002	TP53_0248_0261.chr17.7577535.C>A	TP53	0.003	63
Female	Caucasian			
0.001	TP53_098_109.chr17.7579368.A>C	TP53	0.002	66
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>G	KRAS	0.001	62
Female	Caucasian			
0.006	TP53_151_163.chr17.7578457.C>A	TP53	0.011	55
Male	Caucasian			
0.002	TP53_151_163.chr17.7578469.C>A	TP53	0.004	73
Male	Caucasian			
0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.002	63
Male	Caucasian			
0.001	PIK3CA_1039_1050.chr3.178952082.C>T	PIK3CA	0.002	44
Female	Caucasian			
0.009	TP53_262_267.chr17.7577141.C>A	TP53	0.018	66
Male	Caucasian			
0.001	TP53_041_052.chr17.7579542.C>T	TP53	0.002	71
Female	unknown			
0.002	TP53_151_163.chr17.7578479.G>C	TP53	0.003	86
Female	Caucasian			
0.001	PIK3CA_1039_1050.chr3.178952068.A>T	PIK3CA	0.002	81
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577121.G>A	TP53	0.003	51
Female	Caucasian			
0.007	TP53_0248_0261.chr17.7577539.G>A	TP53	0.014	67
Male	Caucasian			
0.001	TP53_151_163.chr17.7578449.C>A	TP53	0.003	55
Male	Caucasian			
0.094	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.189	54
Female	Caucasian			
0.001	TP53_233_245.chr17.7577581.A>G	TP53	0.002	72
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>C	TP53	0.002	70
Male	Caucasian			
0.002	TP53_208_218.chr17.7578208.T>C	TP53	0.004	72
Male	Caucasian			
0.004	TP53_0272_0283.chr17.7577099.C>T	TP53	0.009	80
Male	Caucasian			
0.003	TP53_208_218.chr17.7578203.C>T	TP53	0.005	72
Female	Caucasian			
0	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	75
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	69
Male	Caucasian			
0.001	FBXW7_361_371.chr4.153251907.G>A	FBXW7	0.003	54
Female	Caucasian			

Table59.txt

0	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	69
Male	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	66
Male	Caucasian			
0.003	TP53_262_267.chr17.7577142.C>A	TP53	0.006	71
Female	Caucasian			
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	73
Female	Caucasian			
0.013	TP53_342.chr17.7574012.C>A	TP53	0.026	57
Female	Caucasian			
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.001	75
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	71
Male	Asian			
0.002	TP53_122.chr17.7579315.G>T	TP53	0.004	73
Female	Asian			
0.001	TP53_188_195.chr17.7578268.A>T	TP53	0.002	58
Female	Caucasian			
0.001	FBXW7_361_371.chr4.153251907.G>A	FBXW7	0.003	54
Male	Caucasian			
0	PIK3CA_0345.chr3.178921546.A>G	PIK3CA	0.001	65
Female	Caucasian			
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.002	71
Male	Asian			
0.014	GNAS_201.chr20.57484420.C>T	GNAS	0.028	63
Male	Asian			
0.004	TP53_342.chr17.7574026.C>A	TP53	0.007	68
Male	Asian			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	70
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	65
Male	Caucasian			
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.002	83
Male	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	60
Female	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398282.C>A	KRAS	0.006	75
Male	Caucasian			
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.004	68
Male	Caucasian			
0.001	PIK3CA_0345.chr3.178921548.G>A	PIK3CA	0.002	60
Female	Caucasian			
0.001	TP53_0227_0236.chr17.7577604.C>T	TP53	0.001	67
Male	Caucasian			
0.003	TP53_188_195.chr17.7578268.A>C	TP53	0.006	77
Male	Caucasian			
0.006	TP53_0272_0283.chr17.7577120.C>T	TP53	0.012	57
Male	Caucasian			

Table59.txt

0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	55
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	80
Male	Caucasian			
0.046	TP53_132_142.chr17.7578535.T>C	TP53	0.092	77
Male	Caucasian			
0	NRAS_4_14.chr1.115258744.C>A	NRAS	0.001	56
Male	Caucasian			
0.001	TP53_167_177.chr17.7578403.C>A	TP53	0.002	42
Male	Asian			
0.001	TP53_0272_0283.chr17.7577121.G>A	TP53	0.002	70
Male	Asian			
0.002	TP53_053.chr17.7579529.C>T	TP53	0.005	70
Male	Asian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0	63
Female	Asian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	62
Female	Asian			
0	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	59
Female	Asian			
0.005	TP53_219_224.chr17.7578190.T>C	TP53	0.009	59
Female	Asian			
0	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0	42
Female	Asian			
0	TP53_298_306.chr17.7577022.G>A	TP53	0.001	89
Male	Asian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	45
Male	Asian			
0	PTEN_136.chr10.89692941.G>A	PTEN	0.001	51
Male	Asian			
0	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	64
Male	Asian			
0.032	TP53_0248_0261.chr17.7577538.C>T	TP53	0.064	44
Female	Asian			
0	TP53_298_306.chr17.7577022.G>A	TP53	0.001	76
Male	Asian			
0	TP53_298_306.chr17.7577022.G>A	TP53	0.001	61
Male	Asian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	42
Female	Asian			
0.002	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.003	69
Male	Asian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	52
Male	Asian			
0	CTNNB1_0039_0046.chr3.41266137.C>T	CTNNB1	0.001	59
Male	Asian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	52
Male	Asian			

Table59.txt

0.002	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.004	77
Male	Asian			
0.004	TP53_0196_0205.chr17.7578263.G>A	TP53	0.009	65
Female	Asian			
0.005	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.01	54
Male	Caucasian			
0.01	TP53_0248_0261.chr17.7577534.C>A	TP53	0.019	67
Female	Caucasian			
0.004	FBXW7_505.chr4.153247289.G>A	FBXW7	0.008	68
Male	Caucasian			
0.087	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.174	77
Male	Caucasian			
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.004	59
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	43
Female	Caucasian			
0.001	BRAF_594_602.chr7.140453139.G>A	BRAF	0.001	42
Female	Caucasian			
0	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0	73
Male	Caucasian			
0.001	TP53_233_245.chr17.7577556.C>T	TP53	0.002	69
Male	Caucasian			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.001	66
Male	Caucasian			
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	53
Male	Caucasian			
0.123	APC_1450_1458.chr5.112175639.C>T	APC	0.246	55
Male	Caucasian			
0.462	TP53_172A.chr17.7578406.C>T	TP53	0.924	66
Male	Caucasian			
0	TP53_233_245.chr17.7577548.C>T	TP53	0	64
Male	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	39
Male	Asian			
0	TP53_172A.chr17.7578406.C>T	TP53	0	39
Male	Asian			
0.007	PIK3CA_0542_0551.chr3.178936092.A>C	PIK3CA	0.014	78
Male	Asian			
0	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	52
Female	Asian			
0	TP53_122.chr17.7579312.C>T	TP53	0.001	46
Female	Caucasian			
0.001	CDKN2A_7_88.chr9.21971111.G>A	CDKN2A	0.003	74
Female	Caucasian			
0.003	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.006	72
Male	Caucasian			
0.003	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.007	51
Male	Caucasian			

Table59.txt

0.005	TP53_188_195.chr17.7578265.A>G	TP53	0.01	62
Male	Caucasian			
0.002	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.005	46
Female	Caucasian			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001	66
Male	unknown			
0.044	CTNNB1_0032_0039.chr3.41266097.G>T	CTNNB1	0.087	71
Male	Caucasian			
0.001	TP53_323.chr17.7576853.C>A	TP53	0.001	65
Male	Caucasian			
0.006	TP53_113_125.chr17.7579329.T>C	TP53	0.013	63
Female	Caucasian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	56
Male	Caucasian			
0.125	TP53_151_163.chr17.7578449.C>T	TP53	0.249	62
Male	Caucasian			
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	67
Female	Caucasian			
0	TP53_172A.chr17.7578403.C>T	TP53	0.001	79
Female	Caucasian			
0	TP53_0248_0261.chr17.7577539.G>A	TP53	0.001	65
Male	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	73
Female	Caucasian			
0	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	65
Male	Caucasian			
0	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	65
Female	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	34
Female	Caucasian			
0.037	TP53_0272_0283.chr17.7577117.A>C	TP53	0.075	57
Male	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.001	73
Female	Caucasian			
0	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	62
Female	Caucasian			
0.001	TP53_208_218.chr17.7578208.T>C	TP53	0.002	73
Female	Caucasian			
0.007	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.014	73
Female	Caucasian			
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	59
Female	Caucasian			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	74
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577105.G>C	TP53	0.002	59
Male	Caucasian			
0.01	TP53_0196_0205.chr17.7578263.G>A	TP53	0.02	72
Male	Asian			

Table59.txt

0.001	TP53_233_245.chr17.7577578.T>C	TP53	0.003	61
Male	Asian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	64
Male	Asian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.003	52
Male	Asian			
0.478	TP53_026.chr17.7579705.C>T	TP53	0.955	60
Male	Asian			
0.002	TP53_233_245.chr17.7577581.A>T	TP53	0.004	72
Male	Asian			
0	TP53_0248_0261.chr17.7577498.C>A	TP53	0.001	59
Female	Asian			
0.003	TP53_167_177.chr17.7578416.C>A	TP53	0.007	49
Male	Asian			
0.023	TP53_0272_0283.chr17.7577121.G>A	TP53	0.047	33
Female	Asian			
0.004	TP53_126_131.chr17.7578536.T>A	TP53	0.008	67
Male	Asian			
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	60
Female	Asian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	82
Female	Asian			
0	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	62
Female	Asian			
0.003	TP53_098_109.chr17.7579389.G>A	TP53	0.006	60
Female	Asian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	51
Female	Asian			
0.001	PTEN_91_98.chr10.89692791.A>G	PTEN	0.001	62
Male	Asian			
0	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001	30
Male	Asian			
0.002	TP53_233_245.chr17.7577578.T>C	TP53	0.004	65
Female	Caucasian			
0.002	TP53_262_267.chr17.7577144.A>G	TP53	0.004	74
Female	Caucasian			
0.001	TP53_298_306.chr17.7577022.G>A	TP53	0.001	54
Female	Caucasian			
0	TP53_151_163.chr17.7578458.G>A	TP53	0.001	58
Female	Caucasian			
0.03	TP53_098_109.chr17.7579373.C>G	TP53	0.06	68
Male	Caucasian			
0.001	FBXW7_505.chr4.153247289.G>A	FBXW7	0.001	71
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	76
Female	Caucasian			
0.005	TP53_0196_0205.chr17.7578263.G>A	TP53	0.009	74
Female	Caucasian			

Table59.txt

0	TP53_151_163.chr17.7578464.G>A	TP53	0.001	52
Male	Caucasian			
0.06	TP53_233_245.chr17.7577568.C>A	TP53	0.121	70
Female	Caucasian			
0.032	TP53_0227_0236.chr17.7577574.T>C	TP53	0.064	69
Male	Asian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	57
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.002	72
Male	Caucasian			
0	TP53_113_125.chr17.7579337.C>T	TP53	0.001	78
Female	Caucasian			
0.001	TP53_0196_0205.chr17.7578263.G>A	TP53	0.001	59
Female	Caucasian			
0.001	PTEN_130.chr10.89692893.C>A	PTEN	0.002	66
Male	Caucasian			
0.026	TP53_172A.chr17.7578406.C>T	TP53	0.053	64
Male	Caucasian			
0.001	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.002	46
Male	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.002	59
Male	Caucasian			
0.001	TP53_167_177.chr17.7578406.C>T	TP53	0.002	51
Female	Caucasian			
0.002	TP53_233_245.chr17.7577548.C>T	TP53	0.003	60
Female	Caucasian			
0.024	TP53_151_163.chr17.7578479.G>A	TP53	0.048	61
Male	Caucasian			
0.291	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.583	72
Female	Asian			
0.034	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.068	79
Female	Asian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	72
Male	Asian			
0	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	67
Female	Asian			
0.001	FBXW7_474_482.chr4.153247384.C>A	FBXW7	0.001	80
Male	Asian			
0.003	TP53_233_245.chr17.7577578.T>C	TP53	0.005	59
Female	Asian			
0.001	TP53_0272_0283.chr17.7577090.C>T	TP53	0.001	64
Male	Asian			
0.003	TP53_0272_0283.chr17.7577117.A>T	TP53	0.007	63
Male	Asian			
0.001	TP53_233_245.chr17.7577556.C>T	TP53	0.002	81
Male	Asian			
0	TP53_151_163.chr17.7578461.C>T	TP53	0.001	56
Female	Asian			

Table59.txt

0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	84
Male	Asian			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002	50
Female	Asian			
0.016	GNAS_201.chr20.57484421.G>A	GNAS	0.033	85
Male	Asian			
0.004	TP53_0196_0205.chr17.7578239.C>A	TP53	0.007	47
Female	Asian			
0	TP53_298_306.chr17.7577022.G>A	TP53	0.001	58
Female	Asian			
0	TP53_167_177.chr17.7578407.G>A	TP53	0.001	51
Female	Asian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	60
Male	Asian			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	59
Male	Asian			
0	TP53_233_245.chr17.7577581.A>G	TP53	0.001	55
Female	Asian			
0.001	NRAS_4_14.chr1.115258747.C>T	NRAS	0.002	64
Female	Asian			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	67
Male	Asian			
0.001	TP53_0272_0283.chr17.7577093.C>T	TP53	0.002	22
Male	Asian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	54
Male	Asian			
0.001	PTEN_91_98.chr10.89692794.A>G	PTEN	0.002	55
Male	Asian			
0.002	TP53_172A.chr17.7578406.C>T	TP53	0.003	58
Male	Asian			
0.002	TP53_262_267.chr17.7577144.A>G	TP53	0.005	65
Male	Asian			
0.045	CTNNB1_0039_0046.chr3.41266124.A>G	CTNNB1	0.091	63
Male	Asian			
0.002	TP53_151_163.chr17.7578457.C>A	TP53	0.004	53
Male	Asian			
0.079	TP53_0248_0261.chr17.7577534.C>A	TP53	0.157	54
Male	Asian			
0	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA
NA	NA			
0.002	TP53_126_131.chr17.7578553.T>C	TP53	0.004	NA
NA	NA			
0.001	TP53_0280_0289.chr17.7577097.C>A	TP53	0.001	58
Female	Asian			
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	61
Male	Caucasian			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002	61
Female	Caucasian			

Table59.txt

0.001	PIK3CA_0542_0551.chr3.178936092.A>C	PIK3CA	0.001	70
Male	Caucasian			
0.001	BRAF_594_602.chr7.140453134.T>C	BRAF	0.002	75
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577106.G>T	TP53	0.001	73
Male	Caucasian			
0	TP53_208_218.chr17.7578211.C>T	TP53	0.001	66
Male	Caucasian			
0.052	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.104	56
Male	Caucasian			
0	TP53_151_163.chr17.7578454.G>A	TP53	0.001	80
Male	Caucasian			
0	KRAS_0057_0064.chr12.25380275.T>G	KRAS	0.001	74
Female	Caucasian			
0.223	TP53_188_195.chr17.7578272.G>A	TP53	0.446	70
Male	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	55
Female	Caucasian			
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.008	76
Male	Caucasian			
0.002	TP53_0280_0289.chr17.7577082.C>A	TP53	0.004	67
Male	Caucasian			
0.001	CDKN2A_7_88.chr9.21971120.G>A	CDKN2A	0.003	56
Male	Caucasian			
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	65
Male	Asian			
0	TP53_0196_0205.chr17.7578263.G>A	TP53	0.001	60
Male	Asian			
0.001	TP53_167_177.chr17.7578404.A>T	TP53	0.002	76
Male	Asian			
0.001	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.002	57
Male	Asian			
0.001	TP53_208_218.chr17.7578204.A>C	TP53	0.002	44
Male	Asian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	51
Female	Asian			
0.002	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.004	47
Male	Asian			
0.001	TP53_208_218.chr17.7578204.A>T	TP53	0.002	80
Male	Asian			
0.002	TP53_233_245.chr17.7577580.T>C	TP53	0.005	59
Male	Asian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	71
Male	Asian			
0	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	69
Male	Asian			
0	TP53_0280_0289.chr17.7577097.C>A	TP53	0.001	28
Male	Asian			

Table59.txt

0.001	KRAS_144_147A.chr12.25378561.G>A	KRAS	0.001	58
Male	Asian			
0.001	CTNNB1_0032_0039.chr3.41266107.T>G	CTNNB1	0.001	70
Male	Caucasian			
0.011	TP53_0272_0283.chr17.7577099.C>T	TP53	0.023	62
Female	Caucasian			
0.085	TP53_219_224.chr17.7578190.T>C	TP53	0.169	58
Female	Asian			
0.007	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.013	85
Male	Caucasian			
0.012	KRAS_0057_0064.chr12.25380277.G>T	KRAS	0.024	87
Female	Caucasian			
0.002	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.004	55
Male	Caucasian			
0.003	TP53_0280_0289.chr17.7577082.C>T	TP53	0.006	81
Male	Caucasian			
0.04	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.08	73
Female	Caucasian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	64
Female	Caucasian			
0.513	TP53_0280_0289.chr17.7577097.C>T	TP53	0.513	70
Male	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	93
Male	Caucasian			
0.118	TP53_0272_0283.chr17.7577120.C>T	TP53	0.235	57
Female	Caucasian			
0	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	87
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	78
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	81
Female	Asian			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	77
Male	Caucasian			
0.241	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.483	40
Female	Caucasian			
0.001	TP53_188_195.chr17.7578280.G>A	TP53	0.002	52
Female	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.008	74
Female	Caucasian			
0.004	TP53_0272_0283.chr17.7577124.C>A	TP53	0.008	74
Male	Caucasian			
0.001	PTEN_136.chr10.89692941.G>A	PTEN	0.001	79
Male	Caucasian			
0.001	TP53_262_267.chr17.7577138.C>T	TP53	0.002	65
Female	Caucasian			
0.002	TP53_262_267.chr17.7577139.G>A	TP53	0.003	59
Female	Caucasian			

Table59.txt

0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	74
Female	Caucasian			
0.003	TP53_0272_0283.chr17.7577106.G>T	TP53	0.007	66
Male	Caucasian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	86
Female	Caucasian			
0	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	67
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715986.C>T	PPP2R1A	0.001	72
Female	Caucasian			
0	TP53_167_177.chr17.7578406.C>T	TP53	0.001	70
Male	Caucasian			
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.013	92
Male	Caucasian			
0.022	TP53_342.chr17.7574017.C>A	TP53	0.044	65
Male	Caucasian			
0.002	PIK3CA_1039_1050.chr3.178952077.T>G	PIK3CA	0.003	75
Female	Caucasian			
0.001	TP53_219_224.chr17.7578191.A>G	TP53	0.002	51
Female	Asian			
0.011	APC_1450_1458.chr5.112175639.C>T	APC	0.023	75
Female	Caucasian			
0.109	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.218	55
Female	Caucasian			
0.02	TP53_0248_0261.chr17.7577539.G>A	TP53	0.039	72
Male	Caucasian			
0.001	TP53_026.chr17.7579705.C>T	TP53	0.002	55
Female	Caucasian			
0	PTEN_145_153.chr10.89692961.C>T	PTEN	0.001	71
Male	Caucasian			
0.002	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.005	82
Male	Caucasian			
0.003	TP53_172A.chr17.7578403.C>A	TP53	0.007	57
Male	Caucasian			
0.002	TP53_132_142.chr17.7578534.C>A	TP53	0.005	66
Female	Caucasian			
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.005	73
Male	Caucasian			
0.006	FBXW7_474_482.chr4.153247367.G>A	FBXW7	0.012	73
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.002	64
Female	Caucasian			
0.006	TP53_342.chr17.7574021.C>A	TP53	0.012	59
Female	Caucasian			
0.002	TP53_233_245.chr17.7577565.T>C	TP53	0.005	72
Female	Caucasian			
0.013	TP53_126_131.chr17.7578553.T>C	TP53	0.026	81
Male	Caucasian			

Table59.txt

0.077	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.155	63
Male	Caucasian			
0	TP53_0272_0283.chr17.7577096.T>C	TP53	0.001	67
Female	Caucasian			
0.001	TP53_233_245.chr17.7577548.C>T	TP53	0.002	72
Male	Caucasian			
0.02	PIK3CA_1039_1050.chr3.178952085.A>T	PIK3CA	0.041	54
Male	Caucasian			
0.001	TP53_0196_0205.chr17.7578235.T>C	TP53	0.003	54
Male	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.005	57
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	57
Male	Caucasian			
0.001	PIK3CA_0542_0551.chr3.178936082.G>A	PIK3CA	0.002	77
Male	unknown			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.002	79
Female	Caucasian			
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	63
Male	Caucasian			
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	64
Male	Caucasian			
0.004	TP53_172A.chr17.7578403.C>T	TP53	0.008	55
Female	Asian			
0.005	PIK3CA_80_89.chr3.178916876.G>A	PIK3CA	0.009	50
Male	Asian			
0.007	TP53_132_142.chr17.7578508.C>T	TP53	0.013	65
Male	Asian			
0.003	TP53_233_245.chr17.7577548.C>T	TP53	0.006	67
Female	Asian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	67
Male	Asian			
0.047	TP53_0248_0261.chr17.7577538.C>A	TP53	0.094	61
Male	Asian			
0.292	TP53_0248_0261.chr17.7577508.T>C	TP53	0.584	63
Male	Asian			
0.006	TP53_208_218.chr17.7578208.T>C	TP53	0.013	51
Male	Asian			
0.002	TP53_0227_0236.chr17.7577575.A>G	TP53	0.004	34
Male	Asian			
0.004	TP53_0248_0261.chr17.7577538.C>A	TP53	0.007	74
Male	Asian			
0.005	PTEN_136.chr10.89692923.G>A	PTEN	0.01	69
Male	Asian			
0.001	TP53_298_306.chr17.7577022.G>A	TP53	0.002	46
Female	Asian			
0.02	TP53_151_163.chr17.7578457.C>T	TP53	0.04	49
Female	Asian			

Table59.txt

0.002	TP53_113_125.chr17.7579313.G>A	TP53	0.003	37
Female	Asian			
0.03	GNAS_201.chr20.57484421.G>A	GNAS	0.06	79
Female	Asian			
0.003	BRAF_594_602.chr7.140453145.A>C	BRAF	0.007	58
Male	Caucasian			
0	TP53_151_163.chr17.7578458.G>A	TP53	0.001	61
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.002	52
Male	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	56
Female	Caucasian			
0.001	TP53_167_177.chr17.7578407.G>A	TP53	0.001	75
Female	Caucasian			
0.007	TP53_208_218.chr17.7578205.C>A	TP53	0.014	74
Female	Caucasian			
0	TP53_122.chr17.7579313.G>A	TP53	0.001	67
Male	Caucasian			
0.001	PIK3CA_0542_0551.chr3.178936095.A>C	PIK3CA	0.002	61
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	60
Male	Caucasian			
0	TP53_122.chr17.7579313.G>A	TP53	0.001	67
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003	63
Male	Caucasian			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.001	65
Male	Caucasian			
0	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	75
Male	Caucasian			
0	TP53_208_218.chr17.7578211.C>T	TP53	0.001	65
Male	Asian			
0	TP53_188_195.chr17.7578275.G>A	TP53	0.001	51
Male	Asian			
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.002	24
Female	Asian			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	47
Female	Asian			
0	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	50
Female	Asian			
0.002	KRAS_0057_0064.chr12.25380289.C>T	KRAS	0.003	49
Male	Asian			
0.084	PIK3CA_0345.chr3.178921553.T>A	PIK3CA	0.169	44
Male	Asian			
0.007	TP53_172A.chr17.7578406.C>T	TP53	0.013	58
Male	Asian			
0	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	82
Female	Asian			

Table59.txt

0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	63
Female	Asian			
0.001	PIK3CA_1039_1050.chr3.178952082.C>T	PIK3CA	0.002	59
Female	Asian			
0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	61
Male	Asian			
0	TP53_0272_0283.chr17.7577090.C>T	TP53	0.001	68
Male	Asian			
0.004	APC_1450_1458.chr5.112175639.C>T	APC	0.008	62
Male	Asian			
0	TP53_167_177.chr17.7578406.C>T	TP53	0.001	49
Male	Asian			
0.002	TP53_151_163.chr17.7578442.T>C	TP53	0.005	46
Male	Asian			
0.002	PIK3CA_0542_0551.chr3.178936091.G>A	PIK3CA	0.004	61
Female	Asian			
0.001	CDKN2A_051_057.chr9.21971186.G>A	CDKN2A	0.001	52
Female	Asian			
0.001	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.002	77
Male	Asian			
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.003	67
Female	Asian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0	67
Female	Asian			
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	61
Female	Asian			
0.003	TP53_0272_0283.chr17.7577121.G>A	TP53	0.005	52
Female	Asian			
0.006	BRAF_594_602.chr7.140453154.T>C	BRAF	0.012	57
Male	Asian			
0.029	BRAF_594_602.chr7.140453136.A>T	BRAF	0.058	92
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.004	55
Male	Caucasian			
0	TP53_151_163.chr17.7578458.G>A	TP53	0.001	77
Male	Caucasian			
0.001	TP53_151_163.chr17.7578461.C>T	TP53	0.001	89
Female	Caucasian			
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.002	77
Female	Caucasian			
0.001	PTEN_91_98.chr10.89692790.G>T	PTEN	0.002	70
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.003	53
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.001	52
Female	Caucasian			
0	TP53_0272_0283.chr17.7577124.C>T	TP53	0.001	83
Female	Caucasian			

Table59.txt

0.001	PTEN_91_98.chr10.89692794.A>G	PTEN	0.002	43
Female	Caucasian			
0.001	TP53_233_245.chr17.7577568.C>T	TP53	0.002	68
Female	Caucasian			
0.073	TP53_151_163.chr17.7578442.T>C	TP53	0.147	75
Female	Caucasian			
0.001	PTEN_91_98.chr10.89692802.C>T	PTEN	0.003	60
Female	Caucasian			
0.303	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.606	69
Male	Caucasian			
0.001	NRAS_0055_0062.chr1.115256528.T>G	NRAS	0.002	61
Female	Caucasian			
0.001	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	65
Female	Caucasian			
0.001	TP53_342.chr17.7574018.G>A	TP53	0.001	73
Male	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	67
Male	Caucasian			
0.001	GNAS_201.chr20.57484420.C>A	GNAS	0.002	68
Male	Caucasian			
0	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	81
Male	Caucasian			
0.035	KRAS_012_+13_-4.chr12.25398285.C>A	KRAS	0.07	56
Female	Caucasian			
0.002	BRAF_594_602.chr7.140453136.A>T	BRAF	0.004	77
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.002	58
Female	Caucasian			
0	TP53_122.chr17.7579313.G>A	TP53	0.001	73
Female	Caucasian			
0.061	AKT1_0016_0017.chr14.105246551.C>T	AKT1	0.122	63
Female	Caucasian			
0.246	TP53_172A.chr17.7578382.G>C	TP53	0.492	62
Male	Caucasian			
0.006	TP53_0272_0283.chr17.7577124.C>T	TP53	0.011	67
Female	Caucasian			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	73
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715986.C>T	PPP2R1A	0.001	68
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	60
Male	Caucasian			
0.004	TP53_172A.chr17.7578406.C>T	TP53	0.007	74
Female	Caucasian			
0.001	TP53_098_109.chr17.7579378.G>C	TP53	0.001	78
Female	Caucasian			
0	APC_1450_1458.chr5.112175639.C>T	APC	0.001	47
Male	Caucasian			

Table59.txt

0.001	FBXW7_505.chr4.153247289.G>A	FBXW7	0.001	61
Female	Caucasian			
0	TP53_0280_0289.chr17.7577093.C>T	TP53	0.001	79
Female	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.002	84
Female	Caucasian			
0.001	TP53_167_177.chr17.7578410.T>A	TP53	0.002	78
Female	Caucasian			
0.002	TP53_151_163.chr17.7578479.G>A	TP53	0.005	73
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	66
Male	Caucasian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	67
Female	Caucasian			
0.001	APC_1304_1310.chr5.112175207.G>T	APC	0.002	62
Female	Caucasian			
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	74
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	71
Female	Caucasian			
0.01	TP53_0248_0261.chr17.7577539.G>A	TP53	0.02	84
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	52
Female	Caucasian			
0.007	KRAS_012_+13_-4.chr12.25398281.C>T	KRAS	0.014	72
Female	Caucasian			
0.001	TP53_0227_0236.chr17.7577580.T>C	TP53	0.002	67
Male	Asian			
0.003	TP53_132_142.chr17.7578508.C>T	TP53	0.006	62
Male	Asian			
0.006	TP53_132_142.chr17.7578535.T>C	TP53	0.013	67
Male	Asian			
0.003	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.005	66
Female	Asian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	63
Male	Asian			
0	TP53_0272_0283.chr17.7577094.G>A	TP53	0.001	46
Male	Asian			
0.001	TP53_151_163.chr17.7578475.G>A	TP53	0.001	60
Female	Asian			
0.001	TP53_188_195.chr17.7578271.T>A	TP53	0.002	53
Male	Asian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	49
Male	Asian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	65
Male	Asian			
0	TP53_172A.chr17.7578407.G>A	TP53	0.001	77
Female	Asian			

Table59.txt

0.022	TP53_233_245.chr17.7577547.C>T	TP53	0.044	59
Male	Asian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	67
Male	Caucasian			
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.007	83
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577108.C>A	TP53	0.002	85
Male	Caucasian			
0.001	TP53_208_218.chr17.7578212.G>A	TP53	0.002	78
Female	Caucasian			
0.001	TP53_098_109.chr17.7579389.G>A	TP53	0.002	54
Female	Caucasian			
0.001	TP53_151_163.chr17.7578458.G>A	TP53	0.002	57
Male	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.001	41
Female	Caucasian			
0.001	TP53_233_245.chr17.7577556.C>A	TP53	0.001	69
Female	Asian			
0.001	TP53_0248_0261.chr17.7577539.G>A	TP53	0.002	86
Female	Caucasian			
0	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.001	48
Male	Caucasian			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	81
Male	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.009	51
Male	Other			
0.001	TP53_208_218.chr17.7578211.C>T	TP53	0.002	66
Male	Caucasian			
0.003	TP53_167_177.chr17.7578413.C>G	TP53	0.006	63
Female	Caucasian			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	67
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.003	78
Male	Caucasian			
0.001	TP53_172A.chr17.7578407.G>C	TP53	0.002	76
Female	Caucasian			
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	52
Male	Caucasian			
0.001	CDKN2A_7_88.chr9.21971098.C>T	CDKN2A	0.002	54
Female	Caucasian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	56
Female	Caucasian			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.003	53
Female	Other			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	72
Male	Caucasian			
0.001	TP53_132_142.chr17.7578526.C>T	TP53	0.002	51
Male	Caucasian			

Table59.txt

0.001	TP53_219_224.chr17.7578190.T>C	TP53	0.002	83
Male	Other			
0	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	67
Male	Other			
0.001	TP53_233_245.chr17.7577551.C>T	TP53	0.002	NA
NA	NA			
0	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.001	NA
NA	NA			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.002	NA
NA	NA			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.001	NA
NA	NA			
0.001	TP53_167_177.chr17.7578413.C>T	TP53	0.002	NA
NA	NA			
0	TP53_233_245.chr17.7577548.C>T	TP53	0.001	65
Male	Caucasian			
0.001	TP53_172A.chr17.7578400.G>C	TP53	0.003	NA
NA	NA			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	58
Male	Caucasian			
0	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	77
Female	Caucasian			
0.001	TP53_026.chr17.7579705.C>T	TP53	0.002	76
Female	Caucasian			
0	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	76
Female	Caucasian			
0	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	76
Female	Caucasian			
0.003	TP53_233_245.chr17.7577551.C>T	TP53	0.006	77
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	77
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	78
Male	Caucasian			
0.02	TP53_233_245.chr17.7577551.C>A	TP53	0.04	65
Male	Caucasian			
0.004	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.007	75
Female	Caucasian			
0.001	TP53_262_267.chr17.7577138.C>T	TP53	0.002	70
Male	Caucasian			
0	TP53_132_142.chr17.7578518.C>T	TP53	0.001	70
Male	Caucasian			
0	TP53_0248_0261.chr17.7577535.C>G	TP53	0.001	70
Male	Caucasian			
0.001	TP53_0280_0289.chr17.7577070.G>A	TP53	0.002	79
Male	Caucasian			
0.004	TP53_233_245.chr17.7577581.A>T	TP53	0.008	64
Male	Caucasian			

Table59.txt

0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	70
Female	Caucasian			
0.001	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.003	59
Female	Caucasian			
0.008	TP53_167_177.chr17.7578413.C>A	TP53	0.017	71
Female	Caucasian			
0.002	TP53_113_125.chr17.7579313.G>A	TP53	0.003	59
Female	Caucasian			
0	PTEN_136.chr10.89692923.G>A	PTEN	0.001	59
Female	Caucasian			
0.002	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.004	74
Female	Caucasian			
0.001	TP53_0227_0236.chr17.7577574.T>C	TP53	0.002	74
Female	Caucasian			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	58
Male	Caucasian			
0	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	58
Male	Caucasian			
0.001	TP53_233_245.chr17.7577580.T>C	TP53	0.001	57
Female	Caucasian			
0.001	GNAS_201.chr20.57484420.C>T	GNAS	0.001	57
Female	Caucasian			
0	FBXW7_464_472A.chr4.153249385.G>A	FBXW7	0.001	57
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	69
Male	Caucasian			
0	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	80
Male	Caucasian			
0.018	TP53_172A.chr17.7578393.A>C	TP53	0.035	84
Male	Caucasian			
0.004	KRAS_0057_0064.chr12.25380275.T>A	KRAS	0.007	73
Female	Caucasian			
0.002	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.003	NA
NA	NA			
0	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA
NA	NA			
0.001	TP53_172A.chr17.7578389.G>A	TP53	0.002	NA
NA	NA			
0.001	PTEN_91_98.chr10.89692802.C>T	PTEN	0.002	NA
NA	NA			
0.002	TP53_098_109.chr17.7579377.G>A	TP53	0.004	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.002	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA
NA	NA			
0.001	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.003	NA
NA	NA			

Table59.txt

0.001	CDKN2A_7_88.chr9.21971120.G>A	CDKN2A	0.002	NA
NA	NA			
0.001	TP53_132_142.chr17.7578518.C>T	TP53	0.001	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA
NA	NA			
0	CDKN2A_7_88.chr9.21971132.C>T	CDKN2A	0.001	NA
NA	NA			
0.001	TP53_083_94.chr17.7579442.G>A	TP53	0.001	NA
NA	NA			
0.001	TP53_172A.chr17.7578394.T>A	TP53	0.001	NA
NA	NA			
0.002	TP53_262_267.chr17.7577138.C>T	TP53	0.005	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.003	NA
NA	NA			
0.001	TP53_233_245.chr17.7577556.C>G	TP53	0.002	NA
NA	NA			
0	TP53_122.chr17.7579315.G>T	TP53	0.001	NA
NA	NA			
0	TP53_208_218.chr17.7578205.C>A	TP53	0.001	NA
NA	NA			
0.001	TP53_262_267.chr17.7577139.G>A	TP53	0.003	NA
NA	NA			
0	TP53_262_267.chr17.7577138.C>T	TP53	0.001	NA
NA	NA			
0.001	HRAS_007_018.chr11.534289.C>T	HRAS	0.001	NA
NA	NA			
0	TP53_219_224.chr17.7578191.A>G	TP53	0.001	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.002	NA
NA	NA			
0.004	TP53_233_245.chr17.7577568.C>T	TP53	0.008	NA
NA	NA			
0.005	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.009	NA
NA	NA			
0	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	NA
NA	NA			
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.003	NA
NA	NA			
0.001	FBXW7_474_482.chr4.153247373.C>T	FBXW7	0.001	NA
NA	NA			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	NA
NA	NA			
0.001	BRAF_594_602.chr7.140453155.C>T	BRAF	0.002	NA
NA	NA			
0.001	FBXW7_474_482.chr4.153247366.C>T	FBXW7	0.002	NA
NA	NA			

Table59.txt

0.001	TP53_208_218.chr17.7578205.C>A	TP53	0.003	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.002	NA
NA	NA			
0.004	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.007	NA
NA	NA			
0.001	TP53_0248_0261.chr17.7577538.C>T	TP53	0.002	NA
NA	NA			
0	TP53_172A.chr17.7578406.C>T	TP53	0.001	NA
NA	NA			
0.025	PIK3CA_0542_0551.chr3.178936092.A>G	PIK3CA	0.051	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	NA
NA	NA			
0.031	TP53_219_224.chr17.7578190.T>C	TP53	0.063	NA
NA	NA			
0.003	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.006	NA
NA	NA			
0.001	PIK3CA_0542_0551.chr3.178936091.G>C	PIK3CA	0.002	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA
NA	NA			
0.001	PTEN_136.chr10.89692925.G>A	PTEN	0.001	NA
NA	NA			
0.001	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.003	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	NA
NA	NA			
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.001	NA
NA	NA			
0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA
NA	NA			
0.001	FBXW7_505.chr4.153247288.C>T	FBXW7	0.001	NA
NA	NA			
0.001	TP53_233_245.chr17.7577557.A>C	TP53	0.001	NA
NA	NA			
0.001	CTNNB1_0039_0046.chr3.41266136.T>C	CTNNB1	0.001	NA
NA	NA			
0.003	TP53_233_245.chr17.7577547.C>A	TP53	0.006	NA
NA	NA			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	NA
NA	NA			
0.001	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	NA
NA	NA			
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.005	NA
NA	NA			
0.001	TP53_0280_0289.chr17.7577094.G>A	TP53	0.002	NA
NA	NA			

Table59.txt

0.001	TP53_0280_0289.chr17.7577090.C>T	TP53	0.001	NA	NA
0.001	TP53_132_142.chr17.7578526.C>T	TP53	0.002	NA	NA
0.002	TP53_219_224.chr17.7578190.T>C	TP53	0.004	NA	NA
0.002	TP53_0248_0261.chr17.7577538.C>A	TP53	0.003	NA	NA
0	TP53_0248_0261.chr17.7577538.C>T	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	NA	NA
0.001	TP53_233_245.chr17.7577557.A>G	TP53	0.001	NA	NA
0.001	TP53_122.chr17.7579313.G>A	TP53	0.001	NA	NA
0.001	KRAS_012_+13_-4.chr12.25398285.C>G	KRAS	0.001	NA	NA
0.003	KRAS_012_+13_-4.chr12.25398285.C>T	KRAS	0.007	NA	NA
0	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	NA	NA
0	PPP2R1A_176_187.chr19.52715979.C>T	PPP2R1A	0.001	NA	NA
0.001	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	82	Male Caucasian
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	44	Female Caucasian
0	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	64	Male Caucasian
0	TP53_0280_0289.chr17.7577094.G>A	TP53	0.001	69	Male Caucasian
0.002	TP53_151_163.chr17.7578457.C>T	TP53	0.004	61	Female Caucasian
0	TP53_033_040.chr17.7579575.G>A	TP53	0.001	56	Male Caucasian
0.022	TP53_098_109.chr17.7579362.A>C	TP53	0.043	77	Female Caucasian
0.001	TP53_0272_0283.chr17.7577120.C>A	TP53	0.001	65	Female Caucasian
0.006	TP53_233_245.chr17.7577568.C>T	TP53	0.012	73	Male Caucasian
0	PPP2R1A_176_187.chr19.52715983.G>A	PPP2R1A	0.001	48	Male African American
0.001	TP53_233_245.chr17.7577575.A>T	TP53	0.001	53	Male Caucasian
0	CDKN2A_7_88.chr9.21971108.C>T	CDKN2A	0.001	57	Female Caucasian

Table59.txt

0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	71
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	82
Female	Caucasian			
0.002	GNAS_201.chr20.57484421.G>A	GNAS	0.004	66
Male	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005	77
Male	Caucasian			
0.006	TP53_151_163.chr17.7578475.G>A	TP53	0.013	67
Female	Caucasian			
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005	59
Female	Caucasian			
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.006	67
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	49
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.002	72
Male	Caucasian			
0.003	GNAS_201.chr20.57484421.G>A	GNAS	0.006	73
Female	Caucasian			
0.181	TP53_0196_0205.chr17.7578263.G>A	TP53	0.362	85
Male	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	51
Female	Caucasian			
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.008	59
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	75
Male	Caucasian			
0.005	TP53_0272_0283.chr17.7577120.C>T	TP53	0.01	75
Male	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	75
Male	Caucasian			
0.003	TP53_0272_0283.chr17.7577120.C>T	TP53	0.005	50
Female	Caucasian			
0.004	TP53_0272_0283.chr17.7577120.C>T	TP53	0.007	71
Female	Caucasian			
0.002	TP53_0272_0283.chr17.7577120.C>T	TP53	0.004	67
Male	Caucasian			
0.004	TP53_298_306.chr17.7577022.G>A	TP53	0.009	68
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	75
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	72
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	60
Male	Caucasian			
0.061	TP53_151_163.chr17.7578461.C>A	TP53	0.122	63
Male	Caucasian			

Table59.txt

0.002	TP53_172A.chr17.7578406.C>T	TP53	0.004	60
Male	Caucasian			
0	TP53_0272_0283.chr17.7577120.C>T	TP53	0.001	74
Male	Caucasian			
0.001	TP53_126_131.chr17.7578541.A>C	TP53	0.002	74
Male	Caucasian			
0	TP53_126_131.chr17.7578541.A>C	TP53	0.001	74
Male	Caucasian			
0.001	TP53_172A.chr17.7578406.C>T	TP53	0.001	79
Male	Caucasian			
0.003	TP53_113_125.chr17.7579315.G>T	TP53	0.006	63
Male	Caucasian			
0	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	75
Female	Caucasian			
0.001	TP53_172A.chr17.7578393.A>C	TP53	0.001	63
Male	Caucasian			
0	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.001	68
Female	Caucasian			
0	GNAS_201.chr20.57484420.C>T	GNAS	0.001	64
Female	Caucasian			
0.001	TP53_113_125.chr17.7579313.G>A	TP53	0.002	85
Female	Caucasian			
0	TP53_0272_0283.chr17.7577093.C>T	TP53	0.001	85
Female	Caucasian			
0	TP53_219_224.chr17.7578190.T>C	TP53	0.001	62
Female	Caucasian			
0	KRAS_012_+13_-4.chr12.25398279.C>T	KRAS	0.001	68
Female	Caucasian			
0	TP53_0272_0283.chr17.7577121.G>A	TP53	0.001	65
Female	Caucasian			
0.01	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.021	68
Male	Caucasian			
0.001	PIK3CA_1039_1050.chr3.178952085.A>T	PIK3CA	0.003	54
Female	Caucasian			
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.002	54
Female	Caucasian			
0.001	TP53_233_245.chr17.7577547.C>T	TP53	0.003	54
Female	Caucasian			
0.003	TP53_151_163.chr17.7578475.G>A	TP53	0.006	81
Male	Caucasian			
0.001	TP53_342.chr17.7574021.C>A	TP53	0.002	78
Male	Caucasian			
0.001	TP53_167_177.chr17.7578403.C>A	TP53	0.002	72
Male	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	76
Female	Caucasian			
0.001	TP53_0272_0283.chr17.7577120.C>T	TP53	0.003	72
Male	Caucasian			

Table59.txt

0.001	TP53_0227_0236.chr17.7577580.T>C	TP53	0.001	65
Male	Caucasian			
0.001	TP53_0248_0261.chr17.7577534.C>A	TP53	0.001	65
Male	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.001	65
Male	Caucasian			
0.001	CDKN2A_7_88.chr9.21971099.G>A	CDKN2A	0.002	62
Male	Caucasian			
0.001	TP53_151_163.chr17.7578457.C>T	TP53	0.002	76
Female	Caucasian			
0	TP53_172A.chr17.7578407.G>C	TP53	0.001	55
Female	Caucasian			
0.001	KRAS_012_+13_-4.chr12.25398284.C>A	KRAS	0.002	68
Female	Black			
0	TP53_342.chr17.7574003.G>A	TP53	0.001	57
Male	Caucasian			
0.001	TP53_0272_0283.chr17.7577094.G>A	TP53	0.002	81
Male	Caucasian			
0.001	TP53_113_125.chr17.7579350.A>C	TP53	0.002	91
Female	Black			
0.002	TP53_219_224.chr17.7578191.A>G	TP53	0.003	80
Male	Caucasian			
0.002	TP53_219_224.chr17.7578191.A>G	TP53	0.004	80
Male	Caucasian			
0.003	TP53_219_224.chr17.7578191.A>G	TP53	0.006	80
Male	Caucasian			
0.007	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.014	84
Female	Caucasian			
0.005	TP53_298_306.chr17.7577022.G>A	TP53	0.009	76
Male	Caucasian			
0.001	GNAS_201.chr20.57484421.G>A	GNAS	0.002	72
Male	Caucasian			
0	GNAS_201.chr20.57484421.G>A	GNAS	0.001	72
Male	Caucasian			
0	PPP2R1A_176_187.chr19.52715982.C>T	PPP2R1A	0.001	72
Male	Caucasian			
0	TP53_233_245.chr17.7577548.C>T	TP53	0.001	62
Male	Caucasian			
0.001	KRAS_144_147A.chr12.25378561.G>A	KRAS	0.001	65
Female	Caucasian			
0	TP53_113_125.chr17.7579313.G>A	TP53	0.001	73
Male	Caucasian			
0.006	KRAS_012_+13_-4.chr12.25398284.C>T	KRAS	0.011	58
Female	Caucasian			

CLAIMS

1. A method of evaluating a subject for the presence of a plurality of cancers, comprising:

(a) evaluating a first biological sample obtained from the subject for the presence of one or more driver gene mutations in cell-free tumor DNA derived from a gene selected from the group consisting of NRAS, KRAS, PIK3CA, HRAS, CDKN2A, TP53, AKT1, CTNNB1, APC, EGFR, GNAS, PPP2R1A, BRAF, FBXW7, PTEN, FGFR2, and combinations thereof,

(b) evaluating in a second biological sample isolated from the subject the absence of one or more driver gene mutations in DNA derived from a gene selected from the group consisting of: NRAS, KRAS, PIK3CA, HRAS, CDKN2A, TP53, AKT1, CTNNB1, APC, EGFR, GNAS, PPP2R1A, BRAF, FBXW7, PTEN, FGFR2, and combinations thereof, wherein the second biological sample is isolated from white blood cells of the subject;

(c) detecting a level of one or more protein biomarkers in a third biological sample isolated from the subject, wherein the one or more protein biomarkers are selected from the group consisting of: carbohydrate antigen 19-9 (CA19-9), carcinoembryonic antigen (CEA), hepatocyte growth factor (HGF), osteopontin (OPN), CA125, AFP, prolactin, TIMP-1, follistatin, G-CSF, CA15-3, and combinations thereof;

(d) comparing the detected levels of the one or more protein biomarkers to one or more reference levels of the protein biomarkers; and

(e) identifying the presence of at least one of the plurality of cancers in the subject when:

(i) at least one driver gene mutation is detected as present in cell-free tumor DNA in the first biological sample and is detected as absent in DNA the second sample; or the detected level of at least one of the one or more protein biomarkers is higher than its reference level, or

(ii) at least one driver gene mutation is detected as present in cell-free tumor DNA in the first biological sample and is detected as absent in DNA in the second sample and the detected level of at least one of the one or more protein biomarkers is higher than its reference level.

2. The method of claim 1, wherein:

(i) the subject has not yet been determined to have cancer;

(ii) the subject has not yet been determined to harbor a cancer cell, or

(iii) the subject does not exhibit, or has not exhibited, a symptom associated with cancer.

3. The method of claim 1, wherein the first biological sample and the second biological sample are from the same initial sample, the first biological sample and the third biological sample are from the sample initial sample, the second biological sample and the third biological sample are from the same initial sample, or the first biological sample and the second biological sample and the third biological sample are from the same initial sample.

4. The method of claim 1, wherein the one or more protein biomarkers include CA19-9.

5. The method of claim 4, wherein the reference level of the CA19-9 protein biomarker is 92 U/mL.

6. The method of claim 1, wherein the one or more protein biomarkers include CEA.

7. The method of claim 6, wherein the reference level of the CEA protein biomarker is 7.5 ng/mL.

8. The method of claim 1, wherein the one or more protein biomarkers include CA125.

9. The method of claim 8, wherein the reference level of the CA125 protein biomarker is 577 U/mL.

10. The method of claim 1, wherein the one or more protein biomarkers include CA15-3.

11. The method of claim 10, wherein the reference level of the CA15-3 protein biomarker is 98 U/mL.

12. The method of claim 1, wherein the presence of one or more driver gene mutations in cell-free tumor DNA in the first biological sample, the absence of one or more driver gene mutations in DNA in the second biological sample, or both are detected by amplifying DNA to form families of amplicons in which each member of a family is derived from a single template molecule in the DNA, wherein each member of a family comprises a common oligonucleotide barcode, and wherein each family comprises a distinct oligonucleotide barcode.

13. The method of claim 12, wherein the distinct oligonucleotide barcode is introduced into the template molecule by a step of amplifying with a population of primers which collectively contain a plurality of distinct oligonucleotide barcodes.

14. The method of claim 12, wherein the distinct oligonucleotide barcode is endogenous to the template molecule, and an adapter comprising a DNA synthesis priming site is ligated to an end of the template molecule adjacent to the distinct oligonucleotide barcode.